EvolDir

January 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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Conferences

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 Susanne Pfeifer <spfeife1@asu.edu>

Berlin EvoDevo Feb26-28

The note: A reminder, the registration deadline for our conference/workshop on Patterning and Timing in Development and Evolution is coming soon (Dec 20th).

The link: https://mbi.nus.edu.sg/events/joint-nus-hu-workshop-on-patterning-and-timing-in-development-and-evolution/ The cost: Free

The location: Berlin

The when: 26-28 February

The blurb: Embryonic development represents a balancing act between robustness and evolvability. For individual organisms, developmental processes must be robust to environmental fluctuations and the influence of segregating mutations. But at the same time, development must be able to evolve if populations are to adapt. Understanding this interplay requires the integration of genetic and evolutionary approaches, a physical understanding of how the embryo develops, and modern methods for assessing developmental phenotypes (from developmental rate to embryonic shape to developmental gene expression profiles).

Recently, there has been increasing interest in the importance of temporal regulation during development. How such temporal regulation emerged and how it is controlled at a molecular level are still poorly understood. We aim to bring together a broad range of research interests - from evolution to timing to cell biology - to build potential collaborations to tackle this intriguing problem.

David Garfield, PhD

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David Garfield <david.garfield@hu-berlin.de>

Cambridge SpeciationGenomics Mar19

We are pleased to announce a one-day meeting to address the challenges in the field of speciation genomics. The meeting will be held on Monday 19th March 2018 at St Johns College Cambridge and is organised by Simon Martin, Mark Ravinet and Chris Jiggins.

The format will include short talks by early career researchers working with data and theory and opportunity for discussion led by more senior researchers.

Confirmed speakers so far include Anja Westram, Camille Roux, Joana Meier, Reto Burri, Dorothea Lindke and Simon Aeschbacher. Ole Seehausen, Konrad Lohse, and Roger Butlin are confirmed attendees and will help lead discussion groups.

There is a registration page now open http://onlinesales.admin.cam.ac.uk/conferences-and-events/department-of-zoology/speciation-genomics-meeting/speciation-genomics-meeting The registration fee includes dinner in the evening and all tea and coffee etc. Note that accommodation is not included 'V we recommend that you look for B&B options at the university accommodation site < https://www.accommodation.cam.ac.uk/ >. Note that this meeting coincides with our annual EGGS meeting < http://evolutionarygenetics.heliconius.org/2017/eggs-2018-on-march-20-cambridge/ > to be held the following day on the 20th March 'V we encourage you to attend both meetings. https://evolutionarygeneticsandgenomics.wordpress.com Background: Thanks to new methods and advances in sequencing technology, generating genomic data for speciation research has never been so affordable, accessible or straightforward. Huge datasets of tens of thousands (and often many more) loci make it possible to estimate demographic history, identify signatures of divergent selection and quantify gene flow with considerable accuracy. This genomic perspective has changed our understanding of how the speciation process unfolds. Hybridisation and introgression need not be detrimental but instead may promote divergence through the formation of new species, the introduction of novel genetic variation and the introgression of adaptive alleles. Peaks and troughs of relative differentiation measures (i.e. FST) that emerged from early genome scan studies have been interpreted as putative ' Â¥speciation islands' Â. The rationale is simple; strong divergent selection on barrier loci reduces effective migration at these targets and the loci closely linked to them. However, researchers using population genomic patterns to identify the processes and genes involved in speciation are beginning to recognize that factors such evolutionary history, recombination and mutation rate variation and gene density confound this interpretation of the genomic landscape.

There is now an opportunity to move beyond debate about the validity of identifying ' Â¥speciation islands' Â. This meeting aims to bring together those working on the empirical and theoretical challenges that face speciation genomics. The meeting will begin with a series of short seminars from researchers using novel approaches to account for factors that confound our understanding of the genomic landscape and will build towards in-depth discussion in the later part of the day.

Professor of Evolutionary Biology (2014) Department of Zoology University of Cambridge Tel: (+44)(0)1223 769021 Mob: (+44)(0) 7549-524-481 http://www.heliconius.org/ http://heliconius.zoo.cam.ac.uk/ @mel_rosina

Fellow of St John's College, Cambridge, UK. CB2 1TP

The Ecology and Evolution of Heliconius Butterflies Available through all good bookshops, or direct from Oxford University Press

Chris Jiggins <c.jiggins@zoo.cam.ac.uk>

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>

Izmir Turkey EcolEvolution Jul18-20

Dear Colleagues,

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

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

Stay tuned for more information.

Hope to see you in Ãzmir

Efe Sezgin, PhD.

On behalf of the EEBST'18 Organizing Committee

Efe Sezgin <efeszgn0@gmail.com>

Madison Wisconsin PopEvolQuantGenetics May13-16

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

REGISTRATION AND ABSTRACT SUBMISSION NOW OPEN.

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

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

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

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

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

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

Dmitri Petrov - Co-Chair Stanford University

Matthew Hahn Indiana University

Hopi Hoekstra Harvard University

Lauren M. McIntyre University of Florida

Matt Rockman New York University

Sarah Bay <SBay@genetics-gsa.org>

Marseilles Evolution Sep25-28

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

contact Marie-Hélène Rome

marie-helene-rome@univ-amu.fr best regards Pierre

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

Montpellier ESEB Aug18-22 Phylogeography

Dear EvolDir community,

We wanted to call your attention to a symposium that we are organising - “Comparative and mechanistic phylogeography in the big data era” (S29) - for the 2018 Joint Congress on Evolutionary Biology to be held in Montpellier, France (18-22 August 2018).

We strongly encourage you to consider submitting an abstract to this symposium if you think your research aligns with our vision of the symposium content (described bellow).

Abstracts are due January 15 and the list of contributed talks and posters selected is going to be communicated by February 28.

Note that unlike many conferences, there will be a limited number of talks and posters presented. Because the conference will be capped in size, confirmed presenters will have the opportunity to register early in advance of open registration.

We hope to see you there!

Roberta Damasceno, Katharine Marske, Andrea Paz, Cynthia Riginos (organizers)

“Comparative and mechanistic phylogeography in the big data era” Multi-taxon, multi-region investigations of spatial genetic diversity and differentiation enable testing of long-standing hypotheses regarding influences of environment, topography, and specific biological traits on intraspecific diversity. These “big data” approaches can yield new insights into the connections between ecology, evolution and biogeography. Whereas data necessary for large-scale comparative analyses already exist, and many groups are synthesizing this published 'legacy' data to explore continental to global-scale patterns of genetic diversity, many practical challenges for assembling and analyzing these datasets remain. A concurrent challenge in phylogeography is to statistically assess potential causative mechanisms and move beyond correlational analyses. Thus, as a multidisciplinary field, phylogeography should seek robust approaches to integrate different and large datasets and characterize large-scale patterns. This symposium will feature theoretical, analytical, and computational advances to approach such issues by showcasing: ideas for handling big and integrated data; methods for quantifying multi-taxon, intraspecific patterns; and the development of process-focused modeling tools. A reinvigorated comparative and mechanistic phylogeography can be integral to predicting future shifts in distribution ranges, spatial patterns of functional diversity, community composition, ecological interactions, and ecosystem services.

Dra. Roberta Damasceno Pós-doc do Laboratório de Herpetologia Universidade de São Paulo rpdama@gmail.com

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Roberta Damasceno <rpdama@gmail.com>

Montpellier ESEB Aug19-22 PredictingEvolution

Working on evolutionary prediction? Please submit an abstract to ESEB Symposium 20 at http://evolutionmontpellier2018.org/call-abstracts. We are seeking a wide variety of talks from diverse speakers, from basic science (e.g., repeatable patterns in evolution experiments) to applied issues (e.g., evolution in response to climate change, drugs, etc).

Summary:

In his best-selling book Wonderful Life Stephen Jay Gould famously argued that the process of evolution is not predictable because it is highly contingent on chance events. The field of evolutionary biology has progressed enormously since then and most scientists now agree that evolution can be predictable. Like weather forecasting, however, our ability to make evolutionary predictions depends on the scale and timeframe of interest. And as with weather forecasting, this predictive ability is rapidly advancing due to expanding databases and increasingly sophisticated models. Our symposium will bring together researchers with diverse skills and interests working at the cutting edge of this exciting area. Research on evolutionary prediction spans a range of topics, from basic science (e.g., repeatable patterns in evolution experiments) to applied issues (e.g., evolution in response to climate change or antibiotics). The timing for this symposium is perfect given the growing focus on evolutionary applications, from evolution in response to medical interventions to adaption to novel environments.

Invited speaker: Michael Lässig "Predicting Evolution"

Organizers: Troy Day & Sally Otto

Troy Day <day@queensu.ca>

Montpellier ESEB PathogenEvolution CallAbstracts

We would like to invite submissions for an ESEB symposium (symposium S13) on the evolution and management of pathogens during chronic infection. We welcome scientists of all career stages, and from diverse backgrounds. We encourage submissions from scientists working on pathogens from a wide variety of study systems, such as humans, other animals, and plants.

The abstract deadline in January 15, 2018. For more information, please see http://evolutionmontpellier2018.org/call-abstracts . Symposium abstract: The evolution of bacterial pathogens is an ever increasing problem for healthcare and agriculture. During chronic infection, a bacterial pathogen colonizes a single host for many years and is often recalcitrant to treatment with conventional antibiotic therapy. For example, long-term colonization of the lung by Mycobacterium or by Pseudomonas presents a myriad of challenges to which the pathogen must adapt or face extinction. The drivers of long term infection remain poorly understood but a growing body of evidence points, unsurprisingly, to evolutionary processes playing a critical role and this, consequently, raises the possibility of new treatment and management strategies informed by evolutionary thought. For example, evolving resistance to one antibiotic can make pathogens more susceptible to other antibiotics, antagonists, or parasites, when resistance mutations show pleiotropic effects. Trade-offs between pathogen life-history traits might be leveraged to control disease if traits selected by one treatment render a pathogen easier to eradicate with another. This symposium will highlight recent developments in the evolution of bacterial pathogens during chronic infection, focusing on how evolutionary principles could be applied in disease management across host-pathogens systems. We welcome people from various research fields, including the microbiome, systems biology, experimental evolution and mathematical modelling, who share common interests in infectious disease biology and the evolutionary theory of adaptation.

Invited speaker: David Guttman, University of Toronto.

We look forward to seeing you in Montpellier!

Ville-Petri Friman, Alexandre Jousset, Rees Kassen, Alex Wong, Wei Zhong

Alex Wong

Associate Professor Department of Biology Carleton University carleton.ca/eme

Alex Wong <AlexWong@cunet.carleton.ca>

Montpellier Evol2018 Aug18-22 CallAbstracts

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

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 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

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Montpellier Evol2018 Aug18-22 Mutation

Dear Colleagues:

We are happy to announce a Mutation Symposium at the Joint Congress on Evolutionary Biology: Evolution 2018, a joint meeting of ESEB, ASN, SSE and SSB in Montpellier, France (Aug 18-22, 2018).

The meeting format follows ESEB conferences, all presentations are submitted to a particular symposium.

We invite abstracts for the symposium "Fitness effects of mutations" (S54). Please note that abstracts are due Jan 15, 2018. http://evolutionmontpellier2018.org/-call-abstracts The invited speaker to our symposium is Ruth G. Shaw (U. Minnesota), her talk is entitled "Fitness effects of mutations: setting the stage for evolutionary change". http://evolutionmontpellier2018.org/-symposia Symposium Abstract.

Mutation is "the ultimate source of new variation" on which other evolutionary mechanisms may act. The nature and properties of mutation influence disease phenotypes, estimates of molecular clocks, prediction of population trajectories, and the degree to which populations can respond to natural or artificial selection. Emerging data suggest that mutation rates are not static, rather vary by species, population, across areas of a chromosome, as well as temporally. In addition, in some systems somatic mutation may contribute to ecologically important genetic variation. Furthermore, there are also new data on the distribution of mutational effects on phenotypes, enhancing our ability to predict mutational effects on fitness. New technologies allow us to detect mutation at unprecedented speed and combined with experimental approaches (e.g. mutation accumulation studies, mutagenesis studies) to assess fitness across ecologically relevant environments, we are at an exciting time in mutation study where established labs and early career scientists are actively engaged. In this symposium we aim to bring together scholars tackling these questions from molecular, field, computational, theoretical and experimental approaches.

Organizers: Charles Fenster (U. South Dakota);

Courtney Murren (College of Charleston

charles.fenster@sdstate.edu; murrenc@cofc.edu

"Murren, Courtney J" <MurrenC@cofc.edu>

Montpellier Evol2018 Aug19-22 Diversification

We invite the submission of abstracts to our symposium: Experimental and theoretical studies of the origins and consequences of diversification

at the Evolution 2018 conference August 19-22, 2018 in Montpellier, France. Abstracts are due January 15, 2018 and can be submitted to the conference website: http://eseb2018.europa-inviteo.com/callfor/ Symposium summary: The process of diversification from a single ancestral genotype into two or more types which can stably coexist underlies the development of the complex ecological systems which now exist nearly everywhere on Earth. Yet diversification is not inevitable, nor does it occur to the same degree in all conditions. Factors such as spatial structure or temporal heterogeneity can influence whether organisms diversify, evolve to be generalists, or evolve plasticity. Furthermore, the same environment can select for diversification in some organisms, but not others. We invite contributions which address the causes of diversification and also those which consider the ecological and evolutionary consequences of diversification. How does the diversification of organisms affect their environment? Does coexistence of newly diversified types influence the subsequent evolution of those types? This symposium will focus on the origin and early divergence of ecologically distinct clades from a recent common ancestor and will highlight theoretical advances as well as experimental studies of diversification whether in the laboratory or in the field.

Invited speaker: Michael Travisano, University of Minnesota Organizers: Vaughn Cooper and Caroline Turner, University of Pittsburgh

Caroline Turner <cbt12@pitt.edu>

Montpellier Evol2018 Aug19-22 Epigenetics

Dear Colleagues,

We welcome abstract submissions to our symposium "Epigenetics and Adaptation" (symposium #48) for the 2018 Joint SSE+ESEB Congress in Montpellier, France

Abstracts may be submitted at: http://evolutionmontpellier2018.org/call-abstracts The deadline for abstract submission is January 15th 2018

*** symposium #48: Epigenetics and Adaptation ***

It has become clear that epigenetic mechanisms are often involved in organismal responses to the environment, and at the same time, that part of the epigenetic code is transgenerationally stable. However, the extent to which these two phenomena are linked and contribute to the adaptive capacity of natural populations remains unclear. So far, most knowledge about the determinants of epigenetic variation comes from studies of a few model species. However, high-resolution analysis methods are increasingly being adopted to investigate epigenetic variation also in non-model species and in natural environments. This rapidly broadens our knowledge of the patterns, causes and consequences of epigenetic variation in natural systems. In this session, we will provide an update of this research field, including studies on both plants and animals in the goal to better understand the stability of inherited epigenetic marks, the type of sequences affected in the genome, the effects of epige netic variants on phenotypic variation, and the epigenetic mechanisms underlying phenotypic plasticity and adaptation.

Invited speaker: Christoph Grunau, University of Perpignan

Organizers: Oliver Bossdorf, Martin Laporte, Jérémy Le Luyer, Koen Verhoeven

"K.Verhoeven@nioo.knaw.nl"
<K.Verhoeven@nioo.knaw.nl>

Montpellier Evol2018 Aug19-22 EvolApplications

Dear all,

We are pleased to announce our symposium - Celebrating 10 years of Evolutionary Applications and a look to the future (symposium 66) - as part of the Evolution 2018 Joint Congress in Montpellier, France, 19th-22nd August next year.

SYNOPSIS. Until a decade ago, concepts from evolutionary biology were rarely applied to fields of applied relevance, such as medicine, food production and environmental health. This is despite some notable contributions highlighting the importance of human-driven evolutionary change and their consequences. In 2008, however, two important publications appeared that voiced the importance of evolution to practical issues and with this paced the way to establish a new journal. The new journal was named 'Evolutionary Applications' and it became the first and only peer reviewed (open access) journal providing a top tier outlet for research studies pertaining to applied evolution. Since then, an ever expanding number of studies have been published in this journal, and elsewhere, and have contributed to firmly establish the field of applied evolution as a relevant discipline that can no longer be ignored in human affairs. This symposium will celebrate and showcase the past 10 years of Evolutionary Applications by conveying some of the most active researchers in this field. We will present a broad array of both empirical and theoretical research across wide range of taxonomic groups to address pressing issues pertaining to human health, food security, global change, ecosystem functioning and the conservation of biodiversity.

Our Invited speaker is Frédéric Thomas who will talk about: “Evolutionary cancerology: Where are we and where should we go?”

We invite you to submit an abstract following the online instructions on the Congress website. The Symposium will be sponsored by Wiley and we anticipate that we will be able to cover registration fees for some of the participants. Deadline for submission is 15th January 2018.

Sincerely, Louis Bernatchez, Britt Koskella (organisers)

Louis Bernatchez <Louis.Bernatchez@bio.ulaval.ca>

Montpellier Evol2018 Aug19-22 EvolutionaryImmunology

Dear all,

We are pleased to announce 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.

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.

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.

Our invited speaker, Scott Edwards, will talk about “Beyond candidate genes in ecological immunology: some examples from birds.”

The deadline for abstract submission is January 15, 2018. For further information please see http://-evolutionmontpellier2018.org/symposia Sincerely,

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

Jamie Winternitz Emmy Noether Group for Evolutionary Immunogenomics Department of Evolutionary Ecology Max Planck Institute for Evolutionary Biology August-Thienemann-Str. 2, 24306 Ploen, Germany Email: jcwinternitz@gmail.com Web: http://www.jcwinternitz.com Jamie Winternitz <jcwinternitz@gmail.com>

Montpellier Evol2018 Aug19-22 EvolutionaryInference

Dear colleagues,

We are pleased to invite abstract submissions to our symposium on “From theory to genome-wide data: inferring selection, demography, gene flow and admixture” (S42) at the joint Evolution 2018 conference in Montpellier, France. Our invited speaker is Dr. Mattias Jakobsson from Uppsala University.

Abstracts may be submitted at http://-evolutionmontpellier2018.org/call-abstracts - the deadline is January 15th 2018.

Symposium summary: Population genomics has shown great use in understanding and reconstructing evolutionary processes and histories of populations. The increasing availability of genome-wide datasets allows investigation of numerous aspects of this evolutionary history including comparison of theoretical expectations to empirical datasets. Understanding the relative importance of natural selection and adaptation in the context of random genetic drift, population structure, mutation, and genetic linkage remains a central challenge in evolutionary studies. In this context, adapting and advancing classical population genetics tools to the study of genomic data has become crucial to infer increasingly complex demographic processes such as population size changes over time, and complex gene flow and admixture patterns. Furthermore, identifying signatures of adaptive and deleterious processes at the genomic level requires new theoretical developments, to assess for example whether selection occurs on standing genomic variation, and how often structural as opposed to single-nucleotide variants contribute to adaptive evolution. Bridging the gaps between theory, experimental evidence, and applications to real datasets requires the use of sophisticated and highly intensive computational methods such as Approximate Bayesian Computation (ABC) or Monte Carlo Markov Chains (MCMC). We aim at presenting theoretical advances, new methodological developments, and applications to data in all kinds of organisms.

Kimberly Gilbert, Nathaniel Sharp, Paul Verdu, and Frédéric Austerlitz

kimberly.gilbert@iee.unibe.ch

Montpellier Evol2018 Aug19-22 EvolutionaryManagement

Dear all,

you have seen several recent emails on the next evolution congress in Montpellier in 2018. We would like to draw your attention on the symposium 76: “Evolutionary management of wild populations” where we would like to exchange on evolution, conservation and management, whatever the species and ecosystems. You can see the abstract below.

Here is the call, deadline January 15th: http://-evolutionmontpellier2018.org/call-abstracts Abstract:

Through the direct and indirect effects of human activities, global change is a major threat for biodiversity and for the associated ecosystem services. This is also an important evolutionary challenge for many species with several potential responses: acclimation, genetic adaptation, range shift, local or global extinction. Adequate management of biodiversity should take into account the main evolutionary factors acting on these responses such as connectivity, drift, local selection. The study of these processes is now strengthened by the integration of analytical and genomic approaches (e.g. for biodiversity surveys or for adaptation studies). This symposium will discuss why and how evolution can and should be integrated into management and conservation practice. It will be opened to different species and ecosystems (both terrestrial and marine), with a focus on wild populations, exploited or not. The interaction with socio-economic processes will also be discussed, with the goal or making common and idiosyncratic patterns emerge across biomes. Empirical and theoretical communications are welcome.

Invited speaker: Sean Hoban “Conservation genetics and consequences for management”

Didier Aurelle and Bruno Fady

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Montpellier Evol2018 Aug19-22 EvolutionResistance

Dear colleagues,

We are pleased to invite abstract submission for our symposium on “The evolution of resistance” (S12) at the Evolution 2018 conference in Montpellier, France. The invited speaker is Dr. Claudia Bank from the Gulbenkian Institute.

Please submit your abstract at http://-evolutionmontpellier2018.org/call-abstracts - the deadline is January 15th 2018.

Summary: The rapid evolution of resistance to xenobiotics among viruses, microbes, plants, and insects is a compelling example of rapid evolution in action and a major challenge of the XXIst century. Resistance to antivirals, antibiotics, herbicides, fungicides, and insecticides each have distinct ecologies, however, each provide a unique opportunity for the study of adaptation in real time. Resistance research occurs at both the applied and basic levels: applied work leads to crucial policies designed to limit the emergence and spread of resistance, whereas basic research provides a conceptual understanding of the nature of adaptation. This symposium aims at bringing together researchers from different backgrounds working on the evolution of resistance from an ecological and evolutionary perspective. Progress in sequencing technology, high-throughput experimental methods, and mathematical and statistical modelling allow for sophisticated approaches to tackle key questions su ch as: Is the convergent evolution of resistance due to parallel molecular changes? Which species- and population-level characteristics determine the rate of adaptation? What are the costs of and extent of epistasis for resistance mutations? How does resistance evolve under complex spatiotemporal patterns of selection? We welcome submissions of experimental, observational, and theoretical work on the broad topic of resistance evolution, and are particularly interested in those that bridge several of these approaches.

Best wishes,

François Blanquart & Julia Kreiner

"francois.blanquart@college-de-france.fr"

Montpellier Evol2018 Aug19-22 FormFunction

Dear colleagues,

The 2nd Joint Congress on Evolutionary Biology will be held in Montpellier (France) in August 19-22, 2018 http://evolutionmontpellier2018.org .Abstracts are welcome for the symposium S25 - MACROEVOLUTIONARY DYNAMICS OF FORM-FUNCTION RELATIONSHIPS organized by Christine Böhmer, Alexandra Houssaye, Brandon Kilbourne, Martha Muñoz, Josef Uyeda. End of call for contributed talks/posters: January 15, 2018.

It's our great pleasure that Stephanie Pierce from Harvard University accepted our invitation to give a talk as invited speaker in our symposium!

By focusing on the relationships between form, function, fossils and phylogeny, this symposium aims to bring together experts in three fields: in vivo organismal function, reconstruction of function in fossil taxa, and phylogenetic comparative methods and trait evolution. http://evolutionmontpellier2018.org/symposia ABSTRACT Macroevolutionary studies applied to comparative and paleontological datasets have revealed much about the dynamics of adaptation across deep time. While such studies commonly examine the evolution of morphology, an important intermediary connecting adaptive landscapes to phenotypic traits is organismal performance. Performance generally more closely relates to organismal fitness and may exhibit very different dynamics than the morphological traits underlying them. Thus, understanding the biomechanics and performance of biological systems can provide key insights into the connections between macroevolutionary models and adaptive landscapes and give greater insights into the functional and ecological implications of major evolutionary transitions. Recent advances in the collection and availability of performance data from comparative and paleontological datasets combined with novel macroevolutionary and biomechanical models are allowing researchers to identify predictable patterns of evolution in response to phylogenetically replicated ecological shifts. By focusing on the relationships between form, function, fossils and phylogeny, this symposium will bring together experts in functional morphology and biomechanical modeling with developers and practitioners of phylogenetic comparative methods–with the goal of cultivating a deeper relationship between macroevolutionary models and biomechanical data and theory.

Your contribution is highly appreciated! In order to submit your abstract, please use the following link that will lead you to the offical conference website: http://evolutionmontpellier2018.org/call-abstracts Christine Böhmer (on behalf of the organizers)

tini.boehmer@gmail.com

Montpellier Evol2018 Aug19-22 GenomicDivergence

Dear all,

We are pleased to announce our symposium - Towards an integrated understanding of genomic and phenotypic divergence - which will be taking place at the Evolution 2018 Joint Congress in Montpellier, France, 19th-22nd August next year.

"Identifying the molecular basis of adaptation and reproductive isolation has relied heavily on investigating genomic landscapes of differentiation. Although this has undoubtedly increased our understanding of both adaptation and speciation, it has also become clear that genomic landscapes are a complex product of a diverse array of processes. The extent to which evolutionary processes related to adaptation and speciation (including natural and sexual selection), as opposed to unrelated processes (including, for example, background selection, genetic drift, and gene flow), contribute to the evolution of landscapes of differentiation remains unclear. We would also like to know how genome structure, gene density, mutation and recombination rate variation may have modulated these processes.

Similarly, we still know little about the effect of the genetic architecture of the phenotypes involved, or the role of phenotypically plastic traits (including learning) on genomic landscapes. From another viewpoint, how is phenotypic differentiation affected by these same factors? How are loci underlying ecological traits, mating cues and preferences arranged in the genome? And how does this, and their ecological, developmental and genetic interactions, influence the evolution of reproductive isolation?

Ultimately we would like to understand the divergence of genomes in the context of the evolution of phenotypes on which selection acts, and vice versa. This symposium will consider both theoretical and empirical research aiming to better understand genomic and phenotypic divergence in the context of speciation and adaptation."

Our main speaker is Stuart Baird, who will talk on "Maintaining perspective in the study of speciation". We invite researchers who are interested in addressing questions of speciation and adaptation using a combination of phenotypic, ecological and genomic data to participate.

To submit an abstract, see here. Please note the deadline for submission is 15th January 2018.

Reto Burri, Violaine Llaurens, David Marques, Richard Merill, Marina RafajiloviÃ & Mark Ravinet

Mark Ravinet <mark.ravinet@ibv.uio.no>

Montpellier Evol2018 Aug19-22 GlobalChange

Dear Colleagues,

We welcome abstract submissions to our symposium on: "Rapid Evolutionary Responses to Global Change"

For the 2018 Joint SSE+ESEB Congress in Montpellier, France

Abstracts may be submitted at: http://-evolutionmontpellier2018.org/call-abstracts ***The deadline is January 15th 2018***

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 Carol Eunmi Lee <carollee@wisc.edu>

Montpellier Evol2018 Aug19-22 HostParasiteCoevolution

We would like to highlight our symposium entitled

'New Horizons in Host-Parasite Co-Genomics and Co-Evolution',

to be held during the *Joint Evolution Meeting in Montpellier* (France) in August 2018 and featuring our invited speaker Charissa de Bekker. Abstract submission is now open (deadline is January 15)!

This Meeting is the largest of its kind in the field of Evolutionary Biology. It is a joint conference of the

European Society for Evolutionary Biology, the American Society of Naturalists, the Society for the Study of Evolution, and the Society of Systematic Biologists. In this setting, our symposium will provide a prime spot to showcase your most exciting research on host-parasite coevolution.

Symposium description: Host-parasite co-evolution represents one of the most dynamic processes in evolution. Much of the research on the signatures of coevolutionary dynamics to date has typically focused on only a single interactant, or are limited to the study of extant populations, and these omissions impede the understanding of the reciprocal nature of the co-evolutionary process. Our symposium will be presented in the explicit context of looking at how the members of a coevolutionary process interact at the molecular, cellular and physiological levels, thereby generating a range of signatures of the co-evolutionary process both in historical and recently derived samples. The aim of this symposia is to create bridges among a range of disciplines in biology, combining talks featuring complementary expertise in empirical (genomics, proteomics, bioinformatics, ancient DNA, and environmental DNA) and a computational/theory focused methodologies in order to synthesize what we know on how the genome of two species interact and co-evolve through time. The 2018 Joint Congress would be an excellent time to present these exciting new avenues for understanding the many facets of co-evolution.

Invited speaker: Charissa de Bekker (University of Central Florida, USA) will give a talk entitled "Genomics as a way to elucidate the interactions between behavior manipulating fungi and their ant hosts" The de Bekker lab studies the co-evolution between a fungal parasite manipulating the behavior of Carpenter ants as a model system to study how a microbe can manipulate the behavioral output of an animal's brain. http://biology.cos.ucf.edu/debekkerlab/ Please see here for a list of all symposia and abstract info: http://-evolutionmontpellier2018.org/symposia _Organizers:_ Nadia Aubin-Horth, Sebastien Calvignac-Spencer, Dieter Ebert, Peter Fields, Tobias Lenz

"lenz@evolbio.mpg.de" <lenz@evolbio.mpg.de>

Montpellier Evol2018 Aug19-22 Hybridization

We are pleased to invite abstract submission to our exciting symposium that focuses on the consequences of hybridization for the 2018 Joint Congress on Evolutionary Biology. Please see description and details below, and consider submitting an abstract. The deadline for abstract submission is January 15th 2018. Link to abstract submission: http://evolutionmontpellier2018.org/call-abstracts Title: Consequences of hybridization: from swamping to speciation

Organizers: Meredith L. Cenzer, Aaron Comeault, Joana Meier and Anna Runemark

Invited speaker: Molly Schumer

Abstract: Hybridization, although it occurs across the tree of life, has historically been treated as the result of rare mistakes that have little effect on important evolutionary processes. Recent advances in sequencing technologies have greatly facilitated the detection of hybridization and we now recognize interspecific hybridization as a common phenomenon that can either generate or swamp diversity at the level of the genotype, phenotype, and species. The goal of this symposium is to forge connections between, and integrate, studies addressing the diverse consequences of hybridization, from divergence despite of gene flow to hybridization facilitating adaptation or speciation. We are targeting speakers applying approaches that range from ecological and behavioral studies of the proximate effects of hybridization to genomic or theoretical studies exploring the consequences of historical and contemporary hybridization on genomic differentiation and diversification.?

Anna Runemark <anna.runemark@ibv.uio.no>

Montpellier Evol2018 Aug19-22 MorphoConvergences

Dear colleagues,

We are pleased to invite abstract submissions to our symposium "From development to function: what does drive morphological convergences?" (S23) at the 2^nd Joint Congress on Evolutionary Biology in Montpellier, France (August 2018).

Our invited speaker is Karen Sears from UCLA, Los Angeles, USA.

Abstracts may be submitted at http://-evolutionmontpellier2018.org/call-abstracts The deadline is January 15th, 2018.

Symposium summary:

Convergent traits are very informative on the nature of processes driving, channeling or constraining evolution. Recurrent questions are whether convergent evolution is driven by adaptive or neutral processes and following internal (e.g. developmental gene networks, ontogeny) or external constraints (e.g. competition, environmental changes). Here, we want to focus on convergent evolution of morphological traits. This focus is necessary because the above-mentioned questions are made especially challenging by very complex relationships between genes, development and morphology on one hand, and morphology and function on the other hand.

The symposium will be dedicated to the origins of morphological convergences in animals and plants. The aim is to highlight how developmental mechanisms on the one hand, and functional characteristics on the other hand, may explain the multiple occurrences of traits both in the fossil record and in extant species, in well-controlled phylogenetic contexts. It will be an opportunity for different communities of evolutionary biologists (e.g. geneticists, developmental biologists, paleobiologists, anatomists) to share their views on convergent evolution.

Helder GOMES RODRIGUES and Sophie PANTALACCI

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Helder Gomes Rodrigues <helder.gomes-rodrigues@umontpellier.fr>

Montpellier Evol2018 Aug19-22 MultilevelSelection

Dear EvolDir Community,

We are pleased to invite abstract submission to our symposium "Multi-level Selection and the Origins of Life" (S11) at the Evolution 2018 conference in Montpellier (France). We are excited to explore the overlap between origins of life theories and classical organismal evolutionary biology, with an emphasis on how selection can operate at the chemical, individual, and population levels to foster abiogenesis.

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

Our invited speaker is Dr. Wim Hordijk, an expert on autocatalytic set theory.

Our symposium abstract:

How living systems evolve from non-living matter is one of the greatest unsolved scientific problems. New paleontological data suggests that life might have arisen very soon after Earth became habitable and new models suggest that chemical systems with some life-like properties might emerge more easily than previously suspected. As a result, evolutionary biologists are becoming more involved in origin of life science, a field that has been dominated historically by chemists, geologists, and theoretical physicists. A role for evolutionary biology is highly relevant given that the capacity for adaptive evolution is often viewed as the primary defining feature of life. Furthermore, multi-level selection theory is proving relevant insofar as the emergence of collectively autocatalytic chemical systems (of which life is an example) is analogous to the emergence of higher-level individuals (e.g., multicellular organisms) as new targets of selection. The symposium will cover both theoretical work and the role of evolutionary theory in guiding empirical research.

We look forward to seeing you in Montpellier!

David Baum (dbaum@wisc.edu), Michael Travisano (travisan@umn.edu), and Niles Lehman (niles@pdx.edu)

"niles@pdx.edu" <niles@pdx.edu>

Montpellier Evol2018 Aug19-22 ParallelEvolution

Dear colleagues,

We invite abstract submission to our symposium at the joint Evolution 2018 meeting in Montpellier, France.

Our symposium is titled: $B!H(BThe molecular basis of convergent evolution: shared and unique features$B!I(B (S22).

Our invited speaker is Dr. Graham Coop, from the University of California at Davis. His talk is titled: $B!H(BPopulation Genomics of Convergence$B!I(B.

Abstracts can be submitted at http://-evolutionmontpellier2018.org/call-abstracts. Abstract deadline is January 15, 2018.

Symposium Summary:

Examples of convergent evolution, where independent populations repeatedly evolve similar phenotypes in similar environments, are heralded in evolutionary biology as strong evidence for natural selection and adaptation. Recent methodological advances for detecting convergent evolution in genomic data make it increasingly possible to investigate how taxa evolve under similar selection pressures. In some instances, populations evolve different phenotypic solutions to the same challenge. In other instances, the same phenotypes may evolve by similar or different genetic means. Thus, there is a continuum of varying degrees of convergence (or, parallelism) at the molecular or phenotypic level. Even in lineages famous for convergence, unique features of evolution within populations often outnumber shared features among populations. To explain why convergent evolution occurs inconsistently, we need to answer lingering questions such as: Are similar or different genetic architectures are tapped to achieve convergence? Are individual traits that are frequently gained and lost during evolution more likely to have a simple genetic basis? Does repeated loss of traits require different genetic pathways and generate different genomic signatures than repeated gain of traits? Do pleiotropy and other genetic constraints bias evolution towards convergence? To what extent are selective pressures really repeated among ostensibly similar environments? This symposium invites empirical and methodological abstracts that investigate the genetic and ecological underpinnings of convergent and unique evolution at multiple biological levels, with an emphasis on genetic architecture.

Darrin Hulsey, Susanne McGaugh, Marie Semon, Yoel Stuart

yestuart@utexas.edu

Yoel E Stuart <yestuart@utexas.edu>

Montpellier Evol2018 Aug19-22 PhenotypicPlasticity

Dear EvolDir Community,

We are pleased to invite abstract submission to our symposium " Role of phenotypic plasticity in evolution: Where are we now? (S46) at the Evolution 2018 conference in Montpellier (France). We are excited to hear about research exploring the relationship between the plastic responses observed within a generation and the evolutionary changes observed across generations. We are particularly interested in capturing a diversity of perspectives from theoretical to empirical studies, molecular to whole organism, and laboratory to the field environments.

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

Our invited speaker is: Dr. Carl D. Schlichting, who has played an instrumental role in cultivating an increased appreciation for the role of plasticity in evolution.

Our symposium abstract: Over the past decades there has been a resurgence of interest in evaluating the role of phenotypic plasticity in micro- and macroevolution. This growing body of work has provided new insights on the complex relationship between the environment as both a cue that predictably alters the distribution of molecular, physiological, morphological, and behavioral phenotypes via plasticity, and as a source of selection acting on this variation. For example, the development of new theory has explored how plasticity, demography, and evolution interact when environments change. Molecular methods have provided new insights into how patterns of gene expression are altered by the environment, the expression. Lastly, field and common garden studies are challenging long-held assumptions on how the costs, benefits, and limits of plasticity influence evolutionary change. These and other recent developments, make the timing of this symposium fitting to assess $B!H(Bwhere we are$B!I(B. We will welcome speakers across a broad range of sub-disciplines who are asking the type of questions that are changing our views on the interplay between plasticity and evolution.

We look forward to seeing you in Montpellier!

Cameron Ghalambor (cameron1@colostate.edu), Patricia Gibert (patricia.gibert@univ-lyon1.fr)

Ghalambor,Cameron Professor Department of Biology Colorado State University Fort Collins, CO 80523 cameron1@colostate.edu

"Ghalambor,Cameron" <Cameron.Ghalambor@colostate.edu>

Montpellier Evol2018 Aug19-22 Phylogenetics

We would like to call your attention to SYMPOSIUM S30: Novel Approaches in Phylogenetic Comparative Methods for Modelling Trait Evolution, that will be held in the context of the Evolution 2018 conference next August in Montpellier. More details: http://evolutionmontpellier2018.org/symposia Deadline for abstract submissions is January 15, and notification on the acceptance of abstracts will be provided before registration to the conference opens.

Funding is available for supporting the participation of students and early-career researchers, to contribute to travel and/or dependent care expenses: http://evolutionmontpellier2018.org/travel-grants We hope to see you in Montpellier,

The symposium organizers Cécile Ané, Julien Clavel, Michael Collyer, Alejandro Gonzalez-Voyer, Antigoni Kaliontzopoulou, Susana Magallón

– Antigoni Kaliontzopoulou

Assistant Researcher CIBIO/InBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos University of Porto Campus Agrário de Vairão, 4485-661 Vairão PORTUGAL

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Montpellier Evol2018 Aug19-22 PollinationFlowerEvolution

Dear colleagues,

We invite abstract submission to our symposium at the joint Evolution 2018 meeting in Montpellier, France.

Our symposium is titled: Floral evolution: breeding systems, pollinators, and beyond (S70). 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. Abstract deadline is January 15, 2018. Talks and posters of this symposium will be invited to submit for publication in a special issue of the International Journal of Plant Sciences. We encourage you to present your new exciting results on pollination/floral evolution and 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 and University of Wisconsin-Madison, USA. Diane Byers, Illinois State University. Eric Imbert, University of Montpellier, France. Yuval Sapir, Tel Aviv University, Israel. Jürg Schönenberger and Yannick Staedler, University of Vienna, Austria.

Yuval Sapir, PhD The Botanical Garden School of Plant Sciences and Food Security Tel-Aviv University, Tel Aviv, 69978 Israel Tl: +972(0)3-6407354 (lab); +972(0)54-7203140 (mobile)http://botanic.tau.ac.il/- http://labsapir.wix.com/labsapir Plant Ecology Conference, Tel Aviv 29-30 Jan 2018

https://labsapir.wixsite.com/plant-ecology-2018 yuval sapir <sapiryuval@gmail.com>

Montpellier Evol2018 Aug19-22 Polyploidy

Dear colleagues,

We are happy to invite abstract submission to our symposium on "*Ecological and evolutionary genomics of polyploidy"* (S55) 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 _Symposium abstract: _ Whole genome duplication (i.e. polyploidy) appears as a central process generating biodiversity and adaptation. The last decade has seen tremendous progress in deciphering large, complex plant and animal genomes, providing an unprecedented opportunity to perform comparative analyses and to decipher the impact of polyploid genome dynamics on phenotypic evolution. Understanding the genetic and genomic consequences of genome duplication on physiology, development, species evolution and ecology represents critical challenges of the post-genomic era. This symposium aims at promoting knowledge exchanges and discussion on the developments made in the recent years to expand the perspective of our understanding to various evolutionary time scales (i.e. neo-polyploids, stabilized polyploids that share paleoduplication events) and to both natural systems of ecological interests and domesticated systems of economic importance, thus filling an important gap in the knowledge of genomic determinants of phenotypic novelties that allow species expansion, adaptation and domestication.

Invited speaker: Dr.Jonathan F Wendel (Iowa State University, Ames USA).

Organizers: Malika AINOUCHE (University of Rennes, France) & Olivier PANAUD (University of Perpignan, France).

– Malika AINOUCHE UMR CNRS 6553 Ecologie Biodiversité Evolution Université de Rennes 1 Bât 14A, Campus de Beaulieu 35 042 Rennes Cedex (France) Tel. (+33) (0)2 23 23 51 11

Malika Ainouche <malika.ainouche@univ-rennes1.fr>

Montpellier Evol2018 Aug19-22 RepeatsGenomeEvol

Dear colleagues,

We are accepting abstracts for a symposium on "The role of repetitive genetic elements in genome evolution and adaptation and speciation" at the Joint Congress on Evolutionary Biology (18-22 August 2018) in Montpellier, France.

The abstract deadline is 15 January. Symposium details are below:

Invited speaker: Cédric Feschotte "Mobile DNA as catalyst of convergent evolution"

Summary: Repetitive DNA is ubiquitous in eukaryotes. Work over several decades has revealed a staggering diversity of repetitive elements, including microsatellites, transposable elements (TEs), and large blocks of tandemly repeated sequences (satellite DNA). These repeats are associated with essential chromosomal features, such as centromeres and telomeres, and mediate recombination, transcriptional regulation, and structural rearrangements. TE evolution is especially dynamic: TEs are usually silenced through epigenetic mechanisms; however occasional bursts of transposition occur, with major genomic consequences. Comparative analyses show that lineage-specific cycles of activity and extinction alter the TE content of genomes, and affect their diversity and age. TE activity can give birth to new genes and result in the reshaping of regulatory networks. This turnover of repeats, both satellite DNA and TEs, may contribute to genomic and phenotypic diversity, and even lead to reproductive isolation between species. New advances in genome sequencing, including long read technologies, have circumvented the inherent difficulties in sequencing repeats, and yielded new insights into the landscape of repeats across genomes, their structural features, and functional roles. The focus of this symposium is on the timely topic of repeat evolution and its impact on biological diversity, adaptation, and speciation.

Organizers: Frédéric Brunet, Amanda Larracuente, Matthias Weissensteiner

Submit your abstract by 1/15 and choose symposium S28. http://evolutionmontpellier2018.org/call-abstracts We hope to see you there!

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Montpellier Evol2018 Aug19-22 SexChromosomes

Dear colleagues,

We are pleased to announce our symposium S52 "New directions in sex chromosome evolution" at the joint congress on Evolutionary Biology in Montpellier, France (19th-22nd August 2018), with invited speaker Beatriz Vicoso from IST Austria. Deadline for abstract submission is January 15th.

Symposium abstract: "Over a century of research on sex chromosomes and sex determination evolution has given us some of the most iconic models in evolutionary biology. While many major discoveries in this field have relied on the study of a few model organisms, the recent explosion of new genomic technologies has enabled the expansion of the field to a plethora of new non-model organisms, revealing that they do not all fit predictions from canonical models. This increase in the taxonomic breadth of data will undoubtedly produce results requiring new theory for consolidation. However when generating new theoretical models we must account for the ecology of the systems studied, an area that has received little attention in the past. With this new-found accessibility to data from non-model species, and with all the new approaches at our disposal, now is the perfect time to bring together researchers in the field to share ideas and approaches for the future. The aim of this symposium is therefore to marry research on both model and non-model organisms, using genomic techniques, manipulative experiments or developmental approaches and to highlight studies at the interface between ecology and evolution."

See you in Montpellier.

Jessica Abbott, Bengt Hansson, Daniel Jeffries, Paul Saunders.

– Dr. Paul A. Saunders Department of Ecology and Evolution University of Lausanne CH-1015 Lausanne Switzerland

Office: +41 21 692 5615 Mobile: +33 6 32 80 78 31

Paul Alan Saunders <paulalan.saunders@unil.ch>

Montpellier Evol2018 Aug19-22 SocialEvol

Dear colleagues,

We are pleased to invite abstract submission to our symposium "Social evolution and kin selection confronting nature with theory" (S7) at the Evolution 2018 conference in Montpellier (France). Abstract submission is open until January, 15th 2018 at: http://evolutionmontpellier2018.org/call-abstracts

Invited speaker : Susan Dudley

Symposium abstract:

Social organization represents one of the major transitions in the evolution of life. Although social complexity has evolved in different lineages, most research has focused on societies of sentient animals, but prokaryotes, protists, fungi and plants often occur in structured populations in which closely related neighbours interact. The impact of such social interactions on trait evolution has been studied independently using either quantitative genetic (e.g. in plant and animal breeding) or kin selection approaches (e.g. in evolutionary biology). The former considers indirect genetic effects (IGEs), where the phenotype of an individual depends on the genes of its social partners, whereas the latter considers the balance between individual fitness costs and benefits.

This symposium aims to showcase a diversity of taxa and contexts in which social interactions may play a key role in evolution. It particularly aims to connect empirical research with recent theoretical advances, seeking unity between quantitative genetic and kin selection approaches. We hope to foster discussion between theoreticians and empiricists, and to prompt theoreticians to identify new avenues of synthesis.

We look forward to seeing you in Montpellier!

Florence Débarre, John Pannell, Nicolas Rode, Rubén Torices Blanco

Nicolas Rode <nicolas.o.rode@gmail.com>

Montpellier Evol2018 Aug19-22 TheoryOfFitnessLandscapes

Dear Colleagues,

We are pleased to invite abstract submissions for our symposium on "The theory of fitness landscapes: where is this path taking us?" at the Evolution 2018 conference in Montpellier, France. This symposium aims to gather a diverse group of scientists from different career stages that is interested in discussing theoretical fitness landscapes and in identifying future steps to be taken in this research area.

The deadline for abstract submission is January 15, 2018. Abstracts can be submitted using the following link: http://evolutionmontpellier2018.org/call-abstracts Symposium summary: Fitness landscapes have developed from a mere illustration of the constraints and complexity of evolution into a theoretical concept that is ubiquitously studied across the natural sciences and across multiple levels of biological organization. Recent technological advances allow for the generation of experimental fitness landscapes, potentially transforming this previously theoretical field into a statistical tool for quantifying evolutionary processes and therefore calling for an assessment of the current theory. This symposium aims at connecting theoretical work in fitness landscapes from different fields, ranging from the molecular to the interspecific level. Such an integration will be essential for the successful evaluation and application of fitness landscape theory to experimental data in the future. Through this symposium we intend to (1) highlight the overlap between existing theoretical concepts across levels of biological observation and how we can connect them, (2) illustrate recent developments in fitness landscape theory in the different fields, and (3) determine future research directions to capture fitness landscape properties and categorize experimental fitness landscapes.

Invited speaker: Richard Goldstein Organizers: Ines Fragata, Alexandre Blanckaert, Claudia Bank

Ines Fragata, PhD Evolutionary Dynamics Group Instituto Gulbenkian de Ciencia Oeiras, Portugal

Inês Fragata <irfragata@gmail.com>

Montpellier Evol2018 Aug19-22 TreeComparison

We are organizing a symposium for the 2018 Joint Congress on Evolutionary Biology that focuses on comparison of phylogenetic trees. Please see description and details below, and consider submitting an abstract. The deadline for abstract submission is in one month (15 January 2018).

Title: Comparing phylogenetic trees: why and how?

Organizers: Jeremy Brown, Sylvain Charlat, Damien de Vienne, Robert Thomson

Invited speaker: Céline Scornavacca

Comparing phylogenetic trees provides means to depict the evolutionary history of relationships among different biological entities. While similar processes are at play at different organizational levels, from genes to host-symbiont associations, different methods have been developed in different contexts. Some explicitly incorporate evolutionary processes such as gene loss, duplication and horizontal transfer, while others agnostically describe the variation in trees. Combining these approaches can provide deep insight into a wide variety of biological questions, including the drivers of gene tree variation, the prediction of protein-protein interactions, and co-evolutionary histories of interacting organisms and communities. This symposium will not only focus on methods for describing and comparing phylogenetic trees but will also allow discussing the many questions that these methods can be used to address. The goal of this discussion is to identify unifying themes in the questions, concepts, methodological needs and solutions used to understand and leverage phylogenetic variation.

Link for abstract submission: http://-evolutionmontpellier2018.org/call-abstracts Robert C. Thomson Associate Professor Department of Biology

University of Hawaii Honolulu, HI 96822

808.956.6476 http://thomsonlab.org/ "thomsonr@hawaii.edu" <thomsonr@hawaii.edu>

Montpellier Evol Aug19-22 EvolutionOnTheEdge

Dear Colleagues -

We are pleased to invite members of the evolution community to submit abstracts for talks to our symposium focusing on the interaction of demography, ecology and evolution on range margins at the 2018 joint Evolution meetings in Montpellier, France. Please see description and details below, and submit an abstract via the following link:

http://evolutionmontpellier2018.org/call-abstracts The deadline for abstract submission is January 15, 2018.

We hope to attract a diverse group of exciting speakers, and welcome submissions from scientists at all career stages!

Title: Evolution on the edge: eco-evolutionary dynamics, range expansion, and local adaptation.

Symposium summary: It has become increasingly clear that evolutionary processes and population dynamics are intertwined, and that they often occur on similar time-scales. For instance, range expansions, contractions or shifts can impose severe constraints on the evolution and adaptive potential of edge populations, and recent theoretical, experimental and empirical research has shown that evolution can severely affect the outcome of seemingly purely demographic processes such as range expansions or range shifts. Understanding these conflicting forces is critical both to predicting how populations will respond to changing environmental conditions, and to predicting the fate of invasive species as they spread. It is however still unclear which demographic processes facilitate or hinder adaptive evolution, or what are the exact factors determining the limits of species ranges. Mating and reproductive systems, dispersal distances and priority effects, and explicitly spatial processes such as clonal spread and gene flow, are all expected to play important roles in determining how space and selection shape adaptation at the edge of species ranges. This symposium will bring together empirical and theoretical scientists investigating the interactions between demography, ecology and evolution on range margins.

Invited speakers: Michael Whitlock, University of British Columbia Kimberly Gilbert, University of Bern

Organizers: Maria E. Orive, Stephan Peischl, Eric Petit, and Laurent Excoffier

Maria E. Orive morive@ku.edu

"morive@ku.edu" <morive@ku.edu>

Montpellier Evolution2018 Aug19-22 Phylogenomics

Dear colleagues,

We are pleased to invite abstract submission for our symposium on "New approaches to phylogenomics" (S31) at the joint Evolution 2018 and ESEB conference 19th-22nd August 2018 in Montpellier, France. Please submit your abstracts at http://evolutionmontpellier2018.org/call-abstracts by the deadline on the 15th January 2018. The invited speakers are Andrew Roger (Dalhousie University, Canada) and Tanja Stadler (ETH Zurich, Switzerland).

Abstract: Genomes maintain a chronicle of their own history, from short scale evolution (e.g. cancer and within-host viral evolution) to the last common ancestor of all extant life. For some organisms, such as most microbial lineages, it is practically the sole source of evolutionary information available. For others, the interdependence between genome evolutionary patterns and life history traits (phenotype, ecology, epigenetic;) documented using other techniques remains largely obscure. Recent methodological developments in comparative genomics allow for gene tree / species tree reconciliation and the identification of horizontal gene transfer, for estimating the age, polymorphism and gene repertoire of ancestral populations, for tracing back the history of migrations, population splits and admixtures, and for reconstructing mutational and selective pressures. Understanding the link of these patterns to life history traits, population dynamics and evolutionary success remains a major question and methodological challenge. This symposium is dedicated to new methodological developments in integrating genomic data with other sources of information, from fossils, to phenotypic, epidemiological, epigenetic and geographical data. Looking forward seeing you in Montpellier!

Organisers: Vincent Daubin, Nicola De Maio, Laura Eme, Carolin Kosiol

Carolin Kosiol <ck202@st-andrews.ac.uk>

Montpellier Evolution2018 Outreach Aug19-22

Are you interested in Evolution communication and outreach?

Do you have an evolution outreach/communication project you would like to share with evolutionary biologists?

Would you like share your experiences, results and resources on evolution communication?

Join us at Evolution 2018 joint meeting in Montpellier. Submit your communication to the S75 Symposium (Public communication? Don't shout... SCREAM (Science Communication Research Empowers AMazing) outreach. Submit your abstract here < https://urldefense.proofpoint.com/v2/url?u=3Dhttp-3A__eseb2018.europa-2Dinviteo.com_callfor_&d=DwMFaQ&c=imBPVzF25OnBgGmVOlcsiEgHoG1i6YHLR0Sj_gZ4adc&r=YrGA5qcbzTtWGsGwQJMaGA&m=34tOOGv5cn-n-RFhPtkc8Svd3yn-tpGnoz9S_3nh8i0&s=YPR9R6LqOWIiiH2baEfKFsJn8xYJM-Qv2nVvhsIPEXA&e= > until 15th January.

xanasapinto@gmail.com

Montpellier France Evol2018 Aug19-22 EvolutionaryEpidemiology

Dear EvolDir community,

We would like to inform you about our upcoming symposium, "Evolutionary Epidemiology Across Multiple Scales" (S17) at the 2018 Joint Congress on Evolutionary Biology in Montpellier, with Jamie Lloyd-Smith as the keynote speaker. We are keen to have as much diversity as possible among our speakers, so we would be grateful if you could help spread the news about our symposium among your colleagues, from any career stage, that you think would be interested. Our aim is to cover a wide range of topics at the interface between epidemiology and disease evolution.

The deadline for abstract submission is January 15th of 2018. For further information please see http://evolutionmontpellier2018.org/symposia Best wishes,

Chris Illingworth, Ryosuke Iritani, Katrina Lythgoe, Jayna Raghwani, Senay Yitbarek

"jayna.raghwani@zoo.ox.ac.uk"
<jayna.raghwani@zoo.ox.ac.uk>

Shenzhen Evolution Apr18-20

here is the link: http://asianevo.org/programme/program_schedule.html Aibin Zhan, PhD Professor and Vice Director Key laboratory of Environmental Biotechnology Research Center for Eco-Environmental Sciences Chinese Academy of Sciences

Professor College of Resources and Environment University of Chinese Academy of Sciences

Associate Editor Diversity and Distributions (http://onlinelibrary.wiley.com/journal/10.1111/(ISSN)1472-4642) Biological Invasions (http://www.springer.com/life+sciences/ecology/journal/10530) Aquatic Invasions (http://www.aquaticinvasions.net/) Aquatic Ecosystem Health & Management (http://www.tandfonline.com/toc/uaem20/current)

Editor World Register of Introduced Marine Species (WRIMS) (http://www.marinespecies.org/introduced/)

18 Shuangqing Road, Haidian District, Beijing 100085, China E-mail: zhanaibin@hotmail.com (preferred); azhan@rcees.ac.cn Tel & Fax: (+86)10-6284-9882 (office) https://sites.google.com/site/zhanaibin/ ÃÂ½ÂºÂÂ±ó
<azhan@rcees.ac.cn>

Shenzhen Evolution Apr18-20 HumanGenomics

First AsianEvo Conference in Shenzhen, China, April 18-20, 2017.

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

The Human Genomic History of Southeast Asia

Invited speakers:

Mark Stoneking, Max Planck Institute for Evolutionary Anthropology, Germany Murray Cox, Massey University, New Zealand Maude Phipps, Monash University, Malaysia Wibhu Kutanan, Khoen Kaen University, Thailand Nguyen Thuy Dong, Institute for Genome Research, Vietnam

Southeast Asia is a pivotal region for understanding the dispersals and history of modern humans, and yet has been relatively neglected in terms of genomic studies. Standing at the crossroads of East Asia and Oceania, Southeast Asia witnessed one of the earliest dispersals of modern humans from Africa that passed through Sunda and reached Sahul at least 50,000 years ago. Other major expansions, associated with the spread of various language families 'V in particular, the Austronesian expansion, which spread Austronesian languages from Taiwan through the Philippines, Indonesia, Near and Remote Oceania, and even Madagascar 'V occurred within the past 5,000 years or so. However, major questions remain concerning the origins, pathways, and overall impact of these and other possible dispersals. Moreover, different groups of archaic humans lived in the area and thus may have interacted with modern humans, including Homo erectus (surviving in Indonesia until at least 100,000 years ago) and H. floriensis (surviving in Flores until at least 50,000 years ago). In addition, modern populations in Southeast Asia and Oceania harbor the highest amount of Denisovan-related ancestry, even though fossils attributed to Denisovans are so far only known from Denisova Cave, in the Altai region of southern Siberia. The aim of this symposium is to bring together researchers using cutting-edge genomic data and analytical methods to investigate various aspects of the prehistory of Southeast Asia.

Deadline for abstracts is December 15th

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

Mark Stoneking (stoneking@eva.mpg.de)

Murray Cox (M.P.Cox@massey.ac.nz)

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Prof. Dr. Mark Stoneking Dept. of Evolutionary Genetics Max Planck Institute for Evolutionary Anthropology Deutscher Platz 6 D04103 Leipzig Germany Phone: +49-341-3550-502 Secretary: +49-341-3550-504 FAX: +49-341-3550-555

Now available: Introduction to Molecular Anthropology (Wiley 2017)

Mark Stoneking <stonekg@eva.mpg.de>

Shenzhen Evolution Apr18-29 Dispersal

We are pleased to announce the call for abstracts for a symposium on

Evolution of dispersal: from mathematical modeling to field studies

Invited speakers:

Yasuo Ihara, University of Tokyo, Japan

Shoji Naoe, Forestry and Forest Products Research Institute, Japan

Xiang-Yi Li, University of Zurich, Switzerland

Dispersal is a crucial and ubiquitous phenomenon that spreads through the entire tree of life. The evolution of dispersal directly affects the balance between local adaptation and gene flow, and thus has great influence on the spatial and temporal distributions of species. How and why species disperse are not only questions out of pure academic curiosity'Xthey also hold the keys to the solutions of many pressing problems in the world, such as the loss of biodiversity and natural resources due to climate change, the introduction of invasive species, and the spread of infectious diseases. Empowered with the latest progress in both empirical and theoretical methods (e.g. tracking the origin of seeds with the ratio of stable oxygen isotopes, as well as high efficiency individual-based computer simulations), we are now granted the opportunity to look deep into the proximate and ultimate drivers of dispersal, unraveling its past and making predictions of the future, handling the complexity that has never been achieved before.

Among our invited speakers, Yasuo Ihara will present mathematical models of the earliest cross-oceanic migrations by Paleolithic humans (e.g. from Indonesia to Australia and from Taiwan to Japanese archipelago). Xiang-Yi Li will present individual-based simulations that disentangle the effect of kin competition on sex-biased dispersal commonly observed in natural populations. Shoji Naoe will present empirical works on seed dispersal by frugivorous mammals and birds in respond to climate change, as well as its impact on forest recruitment in a changing world.

Deadline for abstracts is 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 Conference homepage: http://www.asianevo.org/index.html Symposium organizer

Xiang-Yi Li (xiangyi.li@ieu.uzh.ch)

–

Dr. Xiang-Yi Li Department of Evolutionary Biology and Environmental Studies University of Zurich Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Xiangyi Li <xiangyi.li@ieu.uzh.ch>

Shenzhen FitnessLandscapes Apr18-20

1st AsianEvo Conference in Shenzhen, China, April 18-20, 2017.

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

Fitness landscapes, experimental evolution, and evolutionary forecasting

Invited speakers:

Kavita Jain, Jawaharlal Nehru Centre for Advanced Scientific Research, Bangalore, India

Arjan de Visser, Wageningen University, Netherlands

Ryan Calsbeek, Dartmouth College, US

The inference of past evolutionary processes from genotype and phenotype data has been one of the cornerstones of modern evolutionary biology in the last decades. The success of these methods has suggested that it could be possible to forecast future evolutionary patterns. Developments in this direction are crucial for many applications, including anti-microbial resistance and evolution of cancer. This endeavour requires a solid and rigorous ground where theoretical predictions on the dynamics and repeatability of evolution could be effectively developed and tested. The key framework for these studies - the concept of the “fitness landscape” - was proposed by Sewall Wright in 1932. This theoretical concept has been debated for the last century, but it has become a very active research field only in the last decade, with the advent of genomics and next-generation sequencing and the recent developments in experimental evolution and genome editing. It is now possible to test the fitness effects of specific sets of mutations in controlled environment, to infer features of the fitness landscape, as well as observing evolutionary trajectories of specific mutants. These approaches can be combined with population genetics to forecast the short-term evolution of natural and experimental populations. The aim of this symposium will be a synthesis of the current approaches to fitness landscapes from four complementary points of view - the theory of fitness landscapes, population genetics, and evolution on fitness landscapes (with Kavita Jain), eco-evolutionary interactions and dynamics (with Ryan Calsbeek), and empirical results from experimental evolution (with Arjan de Visser) - as well as a place to discuss the goals and the potential developments in the field. This is a timely symposium to explore several exciting topics, including quantification and visualisation of fitness landscapes, eco-evolutionary dynamics, cross-organismal landscape comparisons, and evolutionary prediction/forecasting.

Deadline for abstracts is December 15th

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

Prof. Ping Ao, Shanghai University, China

Dr. Bjørn Ãstman, UC Los Angeles, US

BJORN OSTMAN <ostman@ucla.edu>

StAndrews MASAMB Mar19-20

Mathematical and Statistical Aspects of Molecular Biology

28th annual MASAMB workshop

University of St Andrews

19/20 March 2018

Call for Abstracts

Abstracts for Talks and Posters are invited for the 28th annual MASAMB workshop which will come the first time to the continent and will be held at the University of St Andrews, Scotland from the 19^th to the 20^th March 2018.

Bioinformatics and statistical genetics, twin themes of the long-running series of annual MASAMB meetings, have gained huge impetus from large-scale genome sequencing projects and development of high-throughput biological assay systems, including gene-expression microarrays, proteomic, metabolomic and single-cell genomics technologies. These immense data resources, and the underlying complexities of molecular and cell biology, provide exciting research opportunities for numerate scientists.

With typically around 80-120 participants from mathematics, statistics, computer science, bioinformatics, biology and related fields, the MASAMB meetings provide an intimate setting for exchanging ideas in methodological and applied research. Research students and scientists newly entering the field of genomic research are particularly welcome and encouraged to submit abstracts. Details of previous meetings are available at the MASAMB archive.

For more information, submission of abstracts and registration please go to:

https://synergy.st-andrews.ac.uk/masamb/ Likely topics for sessions this year:

Next Generation Sequencing

Population Genetics

Phylogeny and Comparative Genomics

Personalised Medicine

Systems Biology

Important dates:

Registration opens: 15th December 2017

Abstract submission: 1st February 2018

Registration closes: 12th February 2018

Conference: 19th-20th March 2018

Carolin Kosiol Centre for Biological Diversity University of St Andrews ck202@st-andrews.ac.uk https://synergy.st-andrews.ac.uk/genomemoleculardating/ Carolin Kosiol <ck202@st-andrews.ac.uk>

Toronto AGA WildQuantGen Mar23-25

DEADLINE DEC 31 for FREE STUDENT REGISTRATION

The AGA is offering multiple free registration slots to graduation students who submit an abstract for the American Genetic Association Symposium, “Evolutionary Quantitative Genetics in the Wild”.

For all others, early registration by Dec 31st is $150 and includes receptions, meals, and complimentary membership in the American Genetic Association with subscription to Journal of Heredity.

AGA symposia are small, friendly gatherings, and provide wonderful opportunities for students and researchers to engage with one another and share their science. This spring’s meeting will take place March 23-25, 2018, at the University of Toronto, Canada. It will focus 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 is open! For all details, visit http://www.theaga.org . Best wishes,

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

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Speakers:

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

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

Jeff Conner, Mich State ˜ “Mechanisms of rapid adaptation”

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

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

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

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

Adam Jones, U. Idaho ˜ “Epistasis in the wild”

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

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

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

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

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

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

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

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

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

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

Anjanette Baker <theaga@theaga.org>

Toronto AGA WildQuantGen Mar23-25 StdReg

Several spots remain for FREE STUDENT REGISTRATION

The AGA is offering multiple free registration slots to graduation students who submit an abstract for the American Genetic Association Symposium, "Evolutionary Quantitative Genetics in the Wild".

For all others, early registration includes receptions, meals, and complimentary membership in the American Genetic Association with subscription to Journal of Heredity.

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

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

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

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

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

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

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

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

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

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

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

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

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"

abroniko@iastate.edu

Toronto ConservationBiol Jul21-26

On behalf of the Society for Conservation Biology North America and the Toronto Organizing Committee, I am excited to announce and extend an invitation to the 4th biannual North American Congress for Conservation Biology (NACCB), taking place July 21st ’V 26th, 2018 at the Westin Harbour Castle Convention Center in Toronto, Ontario, Canada.

This event brings together conservation professionals and students working across a wide variety of disciplines and institutions for discussion, innovation, and opportunities in science. The goal of NACCB is to provide a forum for presenting and discussing new research, developments, and strategies that will inform policy changes and conservation practices to address today’Âs conservation challenges. Most importantly, these conferences connect our regional community of conservation professionals and serve as the major networking outlet for anyone interested in conservation in North America. NACCB attendees are scientists, students, managers, decision-makers, writers, educators, and other conservation professionals from throughout the world. Many come to present, learn, discuss and enjoy the incredible networking opportunities of this event.

The 2018 congress theme is Conservation Science, Policy, and Practice: Connecting the Urban to the Wild. There are various ways to participate in the 2018 congress, and we invite faculty, staff, researchers, and students in your department to attend and participate in the congress.

Upcoming opportunities -

NACCB’Âs Call for Abstracts: Open December 8th 2017 An invitation to submit abstracts for contributed talks, speed talks, and posters

NACCB’Âs Call for Sponsors, Exhibitors, Advertisements: ongoing Please see our conference prospectus for details

Student Competitions/Opportunities: Students may submit an extended abstract for consideration in the Student Presentation Awards, and also apply for a travel grant provided by SCB North America. Details will be announced at a later date.

The content of NACCB is interdisciplinary in scope, and we welcome proposals and abstracts of many types, including and not limited to topics in indigenous-led conservation, education, policy, management, and diversity in conservation leadership. Please share this announcement with your colleagues and students.

We hope you will join us!

Sincerely,

Christopher Blackford

Society for Conservation Biology Toronto Chapter

Website: http://scbtoronto.com/ Email: scbtoronto@gmail.com

Biology Undergraduate <biology@mcmaster.ca>

UCambridge EvolutionaryGenetics Mar20

Dear Colleague,

The annual Evolutionary Genetics and Genomics Symposium (EGGS) will take place on Tuesday 20th March 2018 at the University of Cambridge. The aim of this meeting is 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. Please register at

https://goo.gl/wuW5iq Abstract submission is now open and the deadline is 22/01/2018. 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.

“ar885@cam.ac.uk” <ar885@cam.ac.uk>

UMichigan EarlyCareerScientists Mar9-11

CALL FOR NOMINATIONS 14th ANNUAL EARLY CAREER SCIENTISTS SYMPOSIUM

Ecology and Evolution of Color

The Department of Ecology and Evolutionary Biology at the University of Michigan invites nominations of outstanding scientists early in their careers to participate in an exciting international symposium about the ecology and evolution of color. The symposium events will take place from 9-11th of March 2018, in Ann Arbor, Michigan.

Eight early career scientists, alongside two keynote speakers, will be selected to present their work and to participate in discussions. We welcome nominations of early career scientists who are studying topics related to the ecology and evolution color. This symposium will highlight the work of up-and-coming scientists whose research foci span a breadth of subfields and levels of organization, including but not limited to: function of color, visual ecology, micro- and macroevolutionary mechanisms mediating pigmentation diversity, pollination biology, and mechanisms of color production. We champion diversity and encourage the nomination of members of groups underrepresented in science.

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

The nomination consists of a brief letter of recommendation addressing the nominee's scientific promise and ability to give a compelling talk, the nominee's curriculum vitae, and a brief abstract of the proposed presentation ($<$ 200 words, written by the nominee). Nominations may be sent electronically (in one pdf file, please) to eeb-ecss-nomination@umich.edu using the nominee's name as the subject line (last name first). Information about Early Career Scientist Symposia held in past years can be found at http://sites.lsa.umich.edu/ecss/ . Topic description: Coloration is fundamental to the ecology and evolution of organisms and has a valuable research legacy across plants and animals. Recent innovations in both technology and investigative approaches have propelled coloration to an exciting emerging frontier in integrative biology. We seek to invite scientists studying color from diverse perspectives across spatial and temporal scales, potentially including (but not limited to): genetics of color production and pigmentation, development and plasticity of color phenotypes, visual ecology, color polymorphism, flower ecology and evolution, plant-pollinator interactions, aposematism and crypsis, visual mimicry, signalling theory and behavioral ecology, symbiosis and its role in coloration, sexual selection, trait evolution, speciation, and diversification. We envision 1-2 synthetic keynotes that explore the current state of coloration research and suggest exciting future research directions. The causes and consequences of color diversity provide a compelling and interdisciplinary topic spanning diverse research interests across our department.

Review of nominations will begin on Jan 7, 2018.

Selected participants will be contacted in mid January and will have all expenses covered (registration, travel, and accommodation). An official announcement of the slate of speakers will be issued soon thereafter.

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

The 2018 Early Career Scientists Symposium scientific committee includes:

Leslie Decker Jon Massey Talia Moore Alison Davis Rabosky Carol Solomon Liz Tibbetts Oscar Vargas Lisa Walsh

Oscar Mauricio Vargas Hernandez <oscarvargash@gmail.com>

Ventura California Speciation Mar10-15 2019

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

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

Invited presentations and discussion sessions at both the GRC and GRS will cover a broad array of timely topics in speciation research.

Registration for both conferences will open during the summer, 2018.

Please send questions to Rebecca.Safran@colorado.edu

Sincerely

Rebecca Safran, Katie Peichel, Martin Gorlovsky, Sheela Turbek

Dr. Rebecca Jo Safran

Associate Professor Department of Ecology & Evolutionary Biology N317 Ramaley Hall University of Colorado

Boulder Colorado 80309 USA

email: rebecca.safran@colorado.edu

phone: 303.735.1495

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

Rebecca J Safran <rebecca.safran@colorado.edu>

Warsaw PolishSocietyForHumanAndEvolutionStudies Sep24-26

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

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

We are pleased to announce our distinguished plenary speakers for the 2018 conference: Russell Gray, Max Planck, Jena (evolutionary linguistics), Johannes Krause, Max Planck, Jena (archaeogenetics), Jan Havlicek, Charles University, Prague (social perception) and Grazyna Jasienska, Jagiellonian University, Cracow (reproductive ecology).

The PTNCE 2018 conference website is already available to you at www.ptnce2018.pl. On the website you will find further information about the speakers and the conference. Gradually we will be publishing more information about registration dates and fees (which should be close to the 2017 fees, ie. very affordable), as well as associated events and travel tips. Therefore, we encourage you to keep checking the website updates as well as to look out for the upcoming circulars.

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

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

Kind regards,

Martyna Molak, PhD Polish Academy of Sciences Head of the 2018 PTNCE Warsaw conference organising committee

&

Prof. BogusÂ³aw PawÂ³owski University of WrocÂ³aw President of the Polish Society for Human and Evolution Studies

martyna.molak@gmail.com

WashingtonDC SexRatioVariation May22-25

Dear colleagues,

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

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

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

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

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

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

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

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

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

Christine Ewers <ewers.christine@gmail.com>

Yosemite 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 7th 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 information will be announced soon!

Where: SNRS has a set of cabins in Wawona and all within a short walk of the conference room. < http://snri.ucmerced.edu/symbiosis >

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>

GradStudentPositions

AcademiaSinica Taiwan AntEvolution

One or two PhD positions are available to study fire ant social biology or nematode sex ratios in the laboratory of John Wang at the Biodiversity Research Center, Academia Sinica (Taipei, Taiwan) beginning in the Fall of 2018.

Our lab uses the invasive pest species, the red imported fire ant, to study social biology and sex determination and their evolution. We are also investigating the evolution and genetics of skewed sex ratios in Caenorhabditis nematode. We use multiple techniques to address these questions including behavioral observations, bioinformatics, genomics, genetics, genome manipulation, and molecular biology.

Funding - The PhD fellowship includes a monthly stipend of NT$34,000 (~1,133 USD) for up to 3 years through the TIGP (Taiwan International Graduate Program), a joint graduate program between Academia Sinica and National Taiwan Normal University.

Eligibility - The position is open to all applicants that meet TIGP admission criteria, but preference will be given to students with a master degree or prior experience in insect behavior, bioinformatics, molecular biology, population genetics, or genetics. Criteria and material used to evaluate the applicant's qualifications for the admission: (http://tigp-bp.biodiv.tw/)

Interested students should prepare (1) a CV, (2) a list of prior experience, (3) three references (contact info & emails), and (4) a one-page statement of research interests in one PDF file, and email the file to John Wang (johnwang@gate.sinica.edu.tw) with the subject line “TIGP application”.

Additionally, a formal online application for admission must be submitted to TIGP-Biodiversity (http://db1x.sinica.edu.tw/tigp/index.php). Deadline for early admissions is January 15th. For bioinformatically inclined students, application can be made through TIGP-Bioinformatics (http://tigpbp.iis.sinica.edu.tw/tigpbio/).

Academia Sinica is located in Taipei, Taiwan. Taipei is a vibrant, global city, rich in cultural and near to both oceans and mountains for both research and pleasure.

If you have any questions please feel free to contact me, John.

John's faculty website: (http://biodiv.sinica.edu.tw/en/index.php?pi=3D157)

Biodiversity Research Center, Academia Sinica (http://biodiv.sinica.edu.tw/en/)

John Wang Taipei, Taiwan

johnwang@gate.sinica.edu.tw

AuburnU 3 EvolutionaryEcol

Title: 2 Funded PhD positions in Evolutionary Ecology at Auburn

2 Funded PhD positions beginning Fall 2018

The Wolak Research Group at Auburn University is looking for PhD students that are motivated to develop projects addressing key outstanding questions in evolutionary ecology. The group studies the link between evolutionary change and ecological processes acting upon variability among individuals in survival and reproduction and hence population growth, persistence, and structure. We measure natural and sexual selection, the quantitative genetic basis to trait variation, and population demography to quantitatively predict ecological and evolutionary dynamics. We also develop statistical methods and software. Two potential projects include:

Evolutionary Quantitative Genetics: The student will develop and test theory for the evolution of sexual size dimorphism using a combination of simulation, artificial selection, experimental evolution, and/or large scale mating designs with laboratory populations of seed beetles (*Callosobruchus maculatus*). There will be opportunities to collaborate with a postdoctoral research associate developing testable theory on a complementary project.

Evolutionary Ecology in Natural Populations: This student will conduct field work, analyses, and/or simulations to extend the conceptual framework and state of empirical knowlege for the interplay between mating system, population dynamics, and phenotypic selection. We will use a population of diamondback terrapins (*Malaclemys terrapin*) to characterize mating and reproductive biology, measure key demographic parameters, and identify the form and magnitude of selection acting in this population.

I encourage all interested students to contact me, by sending a CV and *brief* description of research interests to matthew.wolak@auburn.edu. PhD students are expected to develop their own research questions within the broader contexts outlined above. Students will also be expected to aggressively pursue fellowship and research funding opportunities and publish their research in high quality journals.

Deadline for admission to the program with guaranteed support (10 semesters of Graduate Teaching Assistantships, GTAs) is **February 1st**. Please **contact me immediately** to discuss the opportunity for an **on-campus visit**. Summer Graduate Research Assistantships with Dr. Wolak will be available for top applicants, otherwise students have the opportunity to compete for a number of summer GTAs.— More information is available on the webpages of the Dept. of Biological Sciences (http://www.auburn.edu/-cosam/departments/biology/index.htm) and DBS Graduate Studies Program (http://www.auburn.edu/cosam/-departments/biology/grad/index.htm)

Auburn graduate students enjoy a thriving community, recognized as one of the "best small towns in America," with moderate climate and easy access to major cities, major international airports, or to beach and mountain recreational facilities. Situated along the rapidly developing I-85 corridor between Atlanta, GA and Montgomery, AL, the combined Auburn-Opelika-Columbus statistical area has a population of over 500,000.

"' Matthew Wolak Assistant Professor Dept. of Biological Sciences Auburn University Auburn, AL email: matthew.wolak@auburn.edu "'

Matthew Wolak <mew0099@auburn.edu>

AustinPeayStateU PlantPopGenetics

MS Position, Comparative Plant Population Genetics

Graduate Research Assistantship, Austin Peay State University (Clarskville, TN, U.S.A.)

Annual stipend of $15,750 and a tuition waiver for two years

Start Date: summer 2018 (preferably June)

Contact Person: Carol Baskauf (baskaufc@apsu.edu)

Highly motivated students wishing to earn an MS in Biology and interested in plant population genetics research are invited to apply for a Graduate Research Assistantship in Dr. Carol Baskauf's lab at Austin Peay State University (APSU) in Clarksville, TN. The assistantship includes a tuition waiver and stipend for two years ($15,750 annually), and the successful candidate will begin lab/field work in the summer of 2018 before beginning graduate classes in the fall.

Generally, research in the Baskauf lab includes plant population genetics, ecology, and ecophysiology, with a particular interest in rare plant species and comparative studies. Specifically, this NSF funded Graduate Research Assistantship will involve genetic analysis of several rare and widespread congeners as part of a larger collaborative research project examining correlations between genetic diversity and phenotypic plasticity as well as potential adaptive and/or acclimatory responses to future environmental change by rare and widespread species.

An undergraduate degree in a biology-related field is required. Competitive applicants will have excellent written and oral communication skills and the ability to work independently and carefully, with attention to detail. They should also be able to work collaboratively and to supervise undergraduates carrying out related research. In addition to an unofficial copy of college transcripts, prospective students should send Dr. Carol Baskauf (baskaufc@apsu.edu) a single pdf file consisting of a brief letter of interest and background, a CV or resume (including GPA, GRE scores, and, if applicable, TOEFL scores), and the names and contact information for 3 academic or profession references. Review of applicants will begin Jan. 2 and continue until a suitable candidate is found. For full consideration, submit all materials prior to Feb. 1, 2018.

The successful applicant will enroll in the Masters program prior to APSU's March 15, 2018 application deadline in order to be eligible to complete coursework and a thesis leading to an M.S. degree in Biology. Information about the graduate program is at the Biology Department's web page (http://www.apsu.edu/grad-studies/-graduateprograms/biology.php). General questions can be directed to Graduate Admissions (1-800-859-4723, gradadmissions@apsu.edu). APSU is an equal opportunity employer, and underrepresented and minority groups are encouraged to apply.

"Baskauf, Carol" <BaskaufC@apsu.edu>

BielefeldU FunctionalGenomics

2 PhD positions in Evolutionary Ecology and Functional Genomics

Two PhD positions in behavioural/evolutionary ecology and functional genomics are available at the Faculty of Biology at Bielefeld University; one in the Department of Animal Behaviour with Dr. Peter Korsten (see www.uni-bielefeld.de/biologie/-animalbehaviour) and one in the Evolutionary Biology group with Dr. Tim Schmoll (see www.uni-bielefeld.de/-(en)/biologie/Evolutionsbiologie/). The positions run from early 2018 for 36 months and are funded by the German Research Foundation (DFG) within the recently approved collaborative research centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

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

The collaborative research centre: The positions will be embedded within a larger collaborative research centre (SFB) comprising 18 principle investigators, 8 postdocs and 16 PhD students based at Bielefeld University, the University of Münster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programmes. Full details of the SFB can be found at www.uni-bielefeld.de/-biologie/crc212 . Main responsibilities

Research tasks (90%): - Designing and conducting laboratory experiments in which zebra finch males are exposed to different levels of sperm competition - Maintaining a zebra finch stock population and breeding of experimental birds - Collecting and processing of behavioural recordings (sub-project A) - Collecting and processing of hormone samples (sub-project A) - Setting up a computer-assisted sperm analysis (CASA) system (sub-project B) - Phenotyping sperm samples using CASA and other methods (sub-project B) - Processing of tissue samples for transcriptomic analyses - Bioinformatic processing of high-throughput sequencing data to quantify gene expression (sub-project B) - Statistical analyses of complex experimental data - Collaborating with other research groups in the collaborative research centre - Writing scientific publications for international peer-reviewed journals

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

Applicants' profiles

We are seeking two bright, highly motivated and creative students with - a university degree in a relevant discipline with specializations in one or more of the following fields: evolutionary ecology, behavioural ecology, animal behaviour, behavioural physiology, bioinformatics, endocrinology, neuro-ethology, transcriptomics, and/or veterinary science, - a keen interest in using genetic and/or endocrinological methods to answer behavioural and life history questions, - experience with carrying out animal experiments, preferably in birds, - experience with bioinformatic processing of high-throughput sequencing data (sub-project B), - experience with statistical analyses of complex data sets (preferably using R), - ability to work both independently and as part of a team, and - excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage: - publications in peer-reviewed international journals,

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BielefeldU NicheSpecialization

— PhD or Postdoc position in Meta-analysis of Individual Niche Specialization

A PhD position in meta-analysis of individual niche specialization that can be upgraded to a Post-doc position is available at the Faculty of Biology at Bielefeld University. The position is funded by the German Research Foundation (DFG) for a duration of 40 to 45 months within the recently granted collaborative research center (SFB/TRR 212) entitled: A Novel Synthesis of Individualization across Behavior, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

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 master's degree, and for the Post-doc position 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 scientific writing will be advantageous

Remuneration

Salary will be paid according to Remuneration level E13 (65% for PhD candidates, 100% for Post-docs) of the Wage Agreement for Public Service in the Federal States (TV-L).

Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programs. Employees have the opportunity to use a variety of health, counselling, and prevention programs. Bielefeld University places great importance on a work-family balance for all its employees.

Application procedure

The deadline for application is January 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 SFB has currently advertised at PhD position at Jena University with Holger Schielzeth (holger.schielzeth@uni-jena.de) and you may want to indicate whether you are interested in either of these positions.

Bielefeld is a city of 325,000 inhabitants with all expected amenities and easy access to the Teutoburger Wald for hiking and other outdoor

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CharlesU CzechRep PollinationEcol

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 trait matching, and spatio-temporal overlap of interacting organisms. The

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CityUNewYork EvolutionLysis

Doctoral student opportunities are available for highly motivated and independent PhD students in the Dennehy Lab < https://dennehylab.org/ > at Queens College CUNY < http://www.qc.cuny.edu/Pages/home.aspx > to work on an NIH-funded project < https://projectreporter.nih.gov/project_info_description.cfm?aid=9367413&icde=37245771 > on the control of cellular event timing

The project involves the manipulation of phage gene expression to understand how control strategies that buffer randomness in gene expression affecting lysis time and macromolecular assembly evolve. We are recruiting researchers with diverse backgrounds, but experience with phages/microbiology is desirable.

Students admitted to the CUNY Biology doctoral program < https://www.gc.cuny.edu/Page-Elements/Academics-Research-Centers-Initiatives/Doctoral-Programs/Biology > receive an admissions package that guarantees a $30,000 annual stipend, health insurance, and tuition remission for five years and no teaching responsibilities in the first year.

Apply by January 1st 2018 at https://www.gc.cuny.edu/Prospective-Current-Students/Prospective-Students/Admissions .

Email john.dennehy@qc.cuny.edu for more information.

John J. Dennehy, PhD Associate Professor of Biology Deputy Executive Officer, Biology PhD Program Director of Undergraduate Research Queens College and The Graduate Center of CUNY john.dennehy@qc.cuny.edu Office SB D322 (718) 997-3411 Lab SB D343 (718) 997-3419 dennehylab.org ougr.qc.cuny.edu https://twitter.com/DrJDennehy John Dennehy <john.dennehy@qc.cuny.edu>

ClarksonU ExperimentalEvolution

PhD position in Evolutionary Biology: Using use microbial experimental evolution to explore drivers of parallel evolution and adaptation in heterogeneous environments.

The Bailey Lab at Clarkson University, Potsdam NY is looking to fill a PhD position in the Bioscience and Biotechnology (B&B) PhD Program starting summer or fall 2018. The successful candidate would use microbial experimental evolution to explore processes driving parallel evolution, and/ or local adaptation and dispersal evolution in heterogeneous environments. Some practical experience in microbiology is desired but training will be provided. Along with experimental evolution, the Bailey lab also uses a range of quantitative approaches including statistical modelling of genome data and computer simulations, and so these other approaches can also be incorporated into the PhD project depending on student interest and prior experience.

For more information on research in the Bailey lab, see susanfbailey.wixsite.com/home. For more information on the Clarkson University B&B program, see www.clarkson.edu/graduate/bioscience-and-biotechnology . The successful candidate will have a BSc or MSc degree in biology or a related field, preferably one that included a research component (e.g., a dissertation or a thesis). The position will be funded by a Graduate Teaching Assistantship, which involves about 20 hours of TA work each week during the fall and spring semesters. Qualifications for this assistantship include good interpersonal skills and good to excellent command of the English language.

Interested students can contact Dr. Susan Bailey (sbailey@clarkson.edu) for more details, or apply directly at www.clarkson.edu/graduate/bioscience-and-biotechnology. Please indicate in your application that you are responding to this ad and are specifically interested to work with Dr. Bailey.

Submitted application materials must include an official transcript, statement of purpose, three letters of recommendation, and score results of the GRE aptitude test (may be waived for some applicants). International students for whom English is not a first language must also submit a TOEFL score unless their BSc or MSc degree was in English language.

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Dr. Susan Bailey Assistant Professor Department of Biology Clarkson University Potsdam, NY sbailey@clarkson.edu susanfbailey.wixsite.com/home

"sbailey@clarkson.edu" <sbailey@clarkson.edu>

ColoradoStateU BeeEvolution

I am recruiting highly motivated and independent graduate students with strong quantitative skills to join my lab. The position/s will begin with fieldwork in the summer of 2018, before progressing to graduate classes at CSU in the fall. Research projects are broadly structured to understand phytochemical bases of honeybee health and related aspects. Knowledge of beekeeping is not required but is a plus. Successful candidates are expected be comfortable working with honey bees, performing regular hive maintenance, conducting behavioral and chemical assays in the lab, interacting with stake holders and extension personnel. Teaching and research assistantships are available. Please see the lab website for the different ongoing projects (https://pollinationbiologylab.wordpress.com/). Interested candidates are encouraged to send a preliminary application (CV, unofficial transcripts, GRE scores, contact information for three references) to Arathi Seshadri, Department of Soil and Crop Sciences, Colorado State University, at arathi@colostate.edu. Candidates should apply to the graduate program at the Department of Soil and Crop Sciences, College of Agriculture, (http://-soilcrop.agsci.colostate.edu/) before March 1 2018. Candidates can also apply through the Graduate Degree Program in Ecology (http://www.ecology.colostate.edu/-prospective.aspx) by Jan 1 2018.

"Arathi.Seshadri@colostate.edu"
<Arathi.Seshadri@colostate.edu>

Copenhagen 3 Evogenomics

Three Positions in Evogenomics: Danish Natural History Museum

eDNA

PhD fellow in shotgun sequencing for comparative diet analysis of capercaillies

Ancient Protein PhD fellow in Ancient Proteins: Proteios PhD 1 The role of organic mineral interactions in the survival of ancient proteins PhD fellow in Ancient Proteins: Proteios PhD2 Mapping protein decay

Niels Bohr Professor University of Copenhagen Natural History Museum of Denmark m: +4593 565659 a: Solvgade 83, Opg. S 1307 Kobenhavn K, Denmark w: www.palaeome.org e: matthew@palaeome.org Professor of Archaeology University of York BioArCh, Archaeology

p: +44 1904 328806 (when in York Jan - March) m: +447955 888101 a: BioArCh, Environment 83, Wentworth Way, Heslington York YO10 5NG UK

w: http://www.york.ac.uk/archaeology | BioArCh | MSc in Bioarchaeology | BioArchaeology on G+ e:matthew.collins@york.ac.uk York Office Hours: Jan - March: Friday 10:00 - 14:00 Book Appointment Disclaimer: http://www.york.ac.uk/docs/disclaimer/-email.htm Matthew Collins <matthew@palaeome.org>

DurhamU EcologyEvolutionGenetics

Please note there is an updated application due date of January 12, 2018, for project 2 on Reconstructing the evolutionary history of ecological dynamics and extinction risk in seabirds (see below). If interested in applying, please contact Dr. Andreanna Welch well in advance of this date for information about how to submit an application.

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

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

AVAILABLE PROJECTS:

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

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

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

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

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

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

Primary supervisor: Dr. Andreanna Welch (Durham University) Collaborators: Dr Helen James (Smithsonian Institution), Dr Terry Chesser (US Geological Survey), Dr Vincent Bretanolle (Equipe AGRIPOP, CEBC-CNRS) Eligibility: Open to all students Full Application Deadline: 12 January 2018, but contact Dr Welch by early January to express interest

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

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DurhamU EvolutionaryAnthropology

PhD opportunities in evolutionary anthropology/ecology, Durham University, UK The Department of Anthropology at Durham University is currently advertising three PhD studentships through the

IAPETUS Doctoral Training Partnership. Applications are encouraged from UK/EU candidates; successful candidates for these fully funded studentships would start in October 2018.

The three projects broadly address the theme of how global environmental change and human-animal interactions affect vertebrate populations. Please see the links provided below for further details on each individual project.

Citizen Scientist Engagement in Mammal Monitoring through MammalWeb (lead supervisor Prof Russell Hill): http://www.iapetus.ac.uk/wp-content/uploads/2017/11/IAP-17-67-Hill-Durham.pdf Most UK mammals are poorly monitored despite their ecological, economic and cultural significance, and the high public profile of many species. Camera traps offer a solution, but require citizen scientists to help implement a successful programme of mammal monitoring. What motivates citizen scientists to volunteer their time and effort for the conservation of mammal populations? Building upon the volunteer driven monitoring system MammalWeb (http://www.mammalweb.org), this project will examine volunteer motivations and develop strategies for enhancing volunteer engagement and retention to produce robust mammal monitoring data.

Integrated Modelling of Environmental Adaptation for a Model Species, the Chacma Baboon (lead supervisor Prof Ann MacLarnon): http://www.iapetus.ac.uk/wp-content/uploads/2017/11/IAP-17-66-MacLarnon-Durham.pdf How do animals integrate behavioural and physiological adaptations to their environment? Using behavioural observation, ecological data and non-invasive hormone analyses, the student will investigate the environmental adaptations of the chacma baboon, a large-bodied, highly socially and ecologically flexible mammal living in the Soutpansberg Mountains, South Africa, a challenging environment. The project explores how chacma baboons optimise resource usage, how they cope with major environmental stressors and which environmental features most test their resilience.

Understanding Reintroduction Biases and their Consequences in Vertebrates (lead supervisor Dr Sally Street): http://www.iapetus.ac.uk/wp-content/uploads/2017/11/IAP-17-57-Street-Durham-1.pdf Why are efforts to reintroduce threatened species biased towards some mammal and bird species over others, and how do these biases affect the outcomes of reintroduction programmes? The project will investigate these questions using a combination of phylogenetic comparative analyses to identify predictors of reintroduction bias and success, and human experimental studies to identify perceptions of non-human species that underpin these patterns.

IAPETUS is a multidisciplinary Doctoral Training Partnership (DTP) for the environmental sciences funded and accredited by the Natural Environment Research Council (NERC). IAPETUS DTP studentships offer PhD students world-class research and training opportunities, designed to train the next generation of leaders in the science of the natural environment. Successful candidates will benefit from supervision by diverse and experienced teams, with specialised research skills in the relevant project methodologies.

Applications are due before 5pm on 19th January 2018, although applicants are encouraged to discuss things with the lead supervisor well before this date. Please see http://www.iapetus.ac.uk/aboutstudentships/ for full information on the application process.

Candidates should contact the named supervisors on each project in advance before applying. Informal enquiries are welcome and can be made to Prof Russell Hill (r.a.hill@durham.ac.uk), Prof Ann MacLarnon (ann.m.maclarnon@durham.ac.uk) or Dr Sally Street (sally.e.street@durham.ac.uk).

We embrace excellence in all its forms and invite all qualified candidates to apply. We particularly welcome applications from women, candidates with disabilities, black and minority ethnic candidates and other groups who are under-represented in the University.

"sally.e.street@durham.ac.uk"
<sally.e.street@durham.ac.uk>

DurhamU FishClimateAdaptation

Competitive PhD project available in the Department of Biosciences, Durham, UK

Title: Predicting risk and planning mitigation against regional impact from climate change on populations of Arctic char (Salvelinus alpines)

Description:

Arctic char have a circumpolar distribution in high boreal, alpine and arctic habitats in the Northern Hemisphere. Many southern populations are stationary in freshwater habitats, but some especially in the north are anadromous (moving between marine and freshwater habitats). In many high latitude environments Arctic char is the only fish species found in freshwater lakes. There the lake may freeze almost to the bottom, and yet the fish survive through the winter. Some data suggest seasonality to feeding in these environments. The habitat is distinctive and they are well adapted to it, but with climate change all Arctic habitats are undergoing a period of transition and at risk. In the case of Arctic char, polar populations may need to become more like those living further south. The objective of this study is to better understand what those requirements and transitions will need to be, and to better understand how the impact on polar populations and the human communities that depend on them can be mitigated. Arctic char are an important resource and component of local cultural traditions for a range of Arctic communities. For example, Tagish fishermen used moose antlers to drill through ice to access char, and various Inuit people use nets set below ice and jigs for capture. Several cultures in the high Arctic travel to set up char fishing camps in September through November and stay for a month, fishing for char. While seal meat is the staple today for many of these communities, char remains an important resource, especially in the summer months.

In this study the student will integrate data from fatty acid analyses with ecological and genetic analyses. The key objective will be to compare high Arctic populations from Svalbard with lower latitude populations in the UK to better understand the adaptive differences and potential for adaptation or acclimation to a changing climate in the Arctic environment. Arctic char are polymorphic within and among lakes, forming different ecotype morphs suited to foraging in different habitats. This includes anadromous vs stationary life histories, and various morphologies ranging from the small 'Âdwarf'Â form to a very much larger cannibalistic form. An annotated genome has recently been developed, and in the context of ecological differences, this will allow for the assessment of key differences among southern and Arctic populations by comparison of candidate genes, potentially important as adaptation markers. Data on feeding ecology, habitat usage, morphotypic variation and life history strategies will help determine the evolutionary response to environmental change and facilitate the interpretation of genetic results. A 3-month secondment will be undertaken in an Arctic research institution in Norway (Akvaplan-niva AS, TromsÂ©Â, Norway) where there is extensive research on the biology and management of char. Impact will be investigated in the context of the cultural and economic consequences for indigenous peoples of the Arctic.

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Scholarship available on a home fees (UK or EU) basis. For more information about the DTC please see https://durhamarctic.wordpress.com/ To apply please in the first instance send you c.v., transcripts and cover letter explaining why you'Âd be well suited to this project to a.r.hoelzel@dur.ac.uk. Two letters of reference should be sent to the same address. Full funding in most instances will be for UK or EU students. For any questions please contact Prof. Rus Hoelzel (a.r.hoelzel@dur.ac.uk).

DurhamARCTIC < https://durhamarctic.wordpress.com/ > This is the temporary, provisional website of the Durham Arctic Research Centre for Training and Interdisciplinary Collaboration

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

GeorgiaSouthernU PlantEvolution

M.S. Position, Plant Evolution and Systematics, Georgia Southern University

The Schenk lab at Georgia Southern University invites applicants for a Masters Degree in plant systematics and evolution, starting Fall semester, 2018. Our lab group is interested in how botanical diversity has been shaped by the interactions among morphological, ecological, and species diversification. We apply statistical phylogenetic approaches that quantify and incorporate molecular, morphological, and ecological variation to plant systems in order to understand the evolutionary processes of how and why species diversify.

An ideal candidate will have interest in using plant systems to better understand the evolutionary processes of diversification by applying statistical phylogenetic approaches. Competitive students that meet all requirements will be supported with either a teaching or research assistantship.

Interested students should contact Dr. John Schenk (jschenk@georgiasouthern.edu) prior to submitting an application (the earlier the better).

For more information, visit the Schenk lab website (https://sites.google.com/a/georgiasouthern.edu/schenk) and the Department of Biology's website (http://cosm.georgiasouthern.edu/biology). More information about the Biology graduate program can be found at the departmental web page (http://cosm.georgiasouthern.edu/biology/graduate-program-2/).

Additional questions about the GSU graduate program can be directed to the Graduate Student Program Director: Dr. Checo Colon-Gaud (jccolon-gaud@georgiasouthern.edu). For full consideration, the application deadline is March 1st, 2018.

John J. Schenk, Ph.D. Assistant Professor of Plant Biology Georgia Southern University Herbarium (GAS), Curator Department of Biology 4324 Old Register Road Georgia Southern University Statesboro, GA 30460-8042 Office: 2260 Biology Building Office phone: (912) 478-0848 Lab website: http://sites.google.com/a/georgiasouthern.edu/schenk Herbarium website: http://sites.google.com/a/georgiasouthern.edu/gasherbarium jschenk <jschenk@georgiasouthern.edu>

IGB Berlin FishEvolution

Graduate student

“Transcriptomics in fish” (from now on for a 3-year period)

This position will focus on transcriptomics (taking advantage of whole genome information, available for two sturgeon species) in order to elucidate the genetic basis of variability in disease resistance and growth during early development as well as contribute to research on sex determination in /A. oxyrinchus /and /H. huso/.

The candidate will have the opportunity for collaboration and short research stays in the facilities of the other project partners (INRA Rennes, University of Würzburg, DDNI Tulcea).

Applicants should have a master’s degree or equivalent in bioinformatics or a relevant life science (molecular biology, evolutionary biology); excellent communication skills in English are required. Experience with bioinformatics tools and pipelines (namely RNAseq and transcriptome analysis, NGS) is highly preferred.

Salary will be given according to TVöD (50%). In keeping with the IGB’s policy regarding gender equity, female applicants are particularly encouraged. Among candidates of equal aptitude and qualifications, a person with disabilities will be given preference.

Review of applications meeting the required standards will start immediately and continue until a candidate is appointed. Please send your application and further inquiries to Dr. Sven Würtz (wuertz@igb-berlin.de), Dr. Heiner Kuhl (kuhl@igb-berlin.de), Dr. Matthias Stöck (matthias.stoeck@igb-berlin.de).

Leibniz-Institute of Freshwater Ecology and Inland Fisheries - IGB (Forschungsverbund Berlin) Müggelseedamm 301, D-12587 Berlin, Germany

The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (www.igb-berlin.de) is the largest research institute for freshwater research in Germany. It is member of the Leibniz Association and the Forschungsverbund Berlin e.V. IGB has close links to all three universities in the German capital and currently hosts about 50 doctoral students from approximately 15 different nations. Since 1996, the IGB has been committed to research on sturgeon aquaculture, remediation and restoration, including several national and international projects and programs. Within the EU ERA-Net COFASP project STURGEoNOMICS (France, Romania, Germany), the Research Group Applied Fish Physiology and Aquaculture is led by Dr. Sven Würtz; this project is coordinated by Dr. Matthias Stöck. Applications are accepted from now until this position is filled.

Matthias Stoeck <matthias.stoeck@igb-berlin.de>

ImperialC London AvianInfidelity

Linking infidelity with behaviour in social networks

Infidelity is common among many taxa with prevailing social monogamy, but we still do not know what shapes variation in, and drives the evolution of, extra-pair behaviour. Males are expected to reap fitness benefits from siring extra-pair offspring, because extra-pair fathers do not expend resources on costly parental care. This is, however, not the case for females who raise the resulting extra-pair young, posing the question of why females take part in extra-pair matings. The indirect benefits hypothesis explains female infidelity, where females benefit indirectly from better, or more compatible genes for their offspring. However, this hypothesis is not well supported empirically, evidenced by two contradictory meta-analyses on the topic, and ongoing discussion in the field. Specifically, only one long-term study that quantified lifetime reproductive success supports the indirect fitness benefits hypothesis. Contradicting this result, extra-pair males have not been found to be superior, or more compatible, than a female’s within-pair male. Females were found to incur no indirect benefits, and even fitness costs by mating outside of their pair bond, suggesting that that this hypothesis does not satisfactorily explain why females cheat. Recently suggested novel, testable hypotheses provide a fresh perspective. These hypotheses explain female infidelity with intra- and intersexual antagonistic pleiotropy, and remain largely untested. This project aims to empirically test these hypotheses by using the powerful combination of long-term data from a wild population, state-of-the-art social network analysis and manipulative experiments on captive birds. This project will reap the benefits from long-term data in the wild, where precise fitness data and a genetic pedigree allow fitness costs and benefits to be measured, and quantitative genetic analyses. Given the long-standing conundrum of female extra-pair behaviour, this project has the potential forward this field significantly.

Students should be interested in extensive quantitative data analysis, and be able to handle, and preferably ring, birds. A BTO ringing license is beneficial.

Please send your CV and a short letter of motivation, and e-mail addresses of two academic referees, to Julia.schroeder@imperial.ac.uk before 30 December 2017.

The NERC Centre for Doctoral Training in Quantitative and Modelling Skills in Ecology and Evolution will train a cohort of PhD students to solve real-world ecological and evolutionary problems by connecting theory, data, and practice. We have assembled a world-leading set of research organisations who develop new ecological and evolutionary theory, new statistical and computational methods, and translate research findings into real-world impacts. Our aim is to bring students together from multiple disciplines to tackle big problems facing the natural world.

Are you from a biological background and wish to develop high-level quantitative skills? Or are you from a non-biological discipline such as maths or physics and wish to tackle ecological and evolutionary problems? The CDT will bring together students from multiple backgrounds and supervisors from multiple departments to deliver innovative PhD training, research opportunities and experiences working with a wide range of stakeholders.

http://www.imperial.ac.uk/qmee-cdt/ Applicants should meet the UK NERC eligibility criteria:

https://www.imperial.ac.uk/grantham/education/-science-and-solutions-for-a-changing-planet-dtp/-studentship-opportunities/ –

** check out our excellent Master course in Ecology, Evolution & Conservation

http://www.imperial.ac.uk/life-sciences/postgraduate/-masters-courses/masters-in-ecology-evolution–conservation-msc-and-mres/ Dr Julia Schroeder

Lecturer

Director MSc Ecology, Evolution and Conservation

Post-graduate tutor

Imperial College London, Silwood Park Campus Buckhurst Road, SL5 7PY Ascot, Berks, UK

+44 (0) 20 7594 9086

https://sites.google.com/site/evolbehavecol/home-1 Julia_Schroeder <julia.schroeder@gmail.com>

ImperialC London MosquitoEvolution

PhD studentship in the evolution of resistance, reproductive behaviour and population biology of Aedes mosquitoes in the Maldives (funding by NERC SSCP)

Lauren Cator, Richard Gill and Austin Burt, Imperial College London, Silwood Park campus, UK

Deadline: 8^th January 2018. Competitively funded position.

Summary:

Recognised as the most prominent vector for the transmission of disease, mosquitoes have been labelled as the deadliest animal in the world. Insecticidal spraying has remained a dominant Aedes mosquito control method to suppress adult populations, but the use of insecticides on mosquitoes also comes with its limitations and concerns, as persistent exposure can evolve resistance leading to ineffective control and inadvertent effects to the environment. The development and use of GM mosquitoes could provide a solution to reducing insecticidal applications, and both methods used in complementation (i.e. pesticide knock down followed by GM release) is considered an effective method. Small island ecosystems, in particular, would benefit from this as reducing insecticide usage is likely to have significant implications given the relatively enclosed and fragile nature of these ecosystems.

Success of applying such methods, however, requires knowledge of the mechanism(s) and evolution of Aedes resistance to insecticides, and the population demography, structure and breeding behaviours for GM to be effective. This PhD will address these aspects by gaining a handle on relatively isolated populations of Aedes across multiple Maldivian islands. The project will compare islands with different pesticide usage histories, and by studying such enclosed populations will further look at spatial genetic structure between islands and population dynamics over time, as well as plasticity in breeding/nesting behaviours.

This student will primarily focus on the mosquito A.

albopictus that has shown recent geographical spread (but also A. aegypti). The project will involve some or all of the following: field work sampling/monitoring populations, experimental manipulations of the environment, lab assays to test pesticide resistance, use of NGS to investigate genetic standing variation and population structure, investigating molecular basis of resistance, and elucidate timing and locations of breeding and possibly mating behaviours.

This is a CASE studentship supported by a leading resort company responsible for sustainable tourism and contributing to conservation issues. The student will be expected to work with the resort, intended to liaise with the pioneer company Oxitec Ltd who uses world class science to develop innovative solutions to controlling pest (mosquito) populations, and meet with organisations such as WHO and governmental departments such as Maldives Ministry of Fisheries and Agriculture.

For more information please see: https://drive.google.com/file/d/1b0pyt8T7vo6lsbHLzrzUuyHfhLOXxOlY/view
To apply: applicants should apply directly Lauren Cator with a CV & Cover letter (l.cator@imperial.ac.uk)

For applicant restrictions please go to: http://www.imperial.ac.uk/grantham/education/science-and-solutions-for- a-changing-planet-dtp/studentship-opportunities/

“Gill, Richard J” <r.gill@imperial.ac.uk>

IowaStateU EyeEvolution

PhD position in the evolution of visual systems: the origin of eyes and how proteins gain and lose functions and interactions

The Serb lab at Iowa State University is looking for motivated graduate students interested in the evolution of sensory systems and their influence on biological diversity. We focus on two broad topics: (a) evolutionary origin of eyes and the proteins underlying vision, and (b) the evolution of visually-mediated behaviors and shell shape in different habitat types among diverse bivalved mollusk species. We use a variety of approaches including comparative genomics, fieldwork, protein expression experiments, and phylogenetics. https://www.eeob.iastate.edu/people/jeanne-serb Access to recent publications from the Serb lab can be found here: https://www.researchgate.net/profile/Jeanne_Serb/contributions . Interested students should email Dr. Jeanne Serb (serb@iastate.edu) for more information. Students can apply through the Ecology and Evolutionary Biology (EEB) graduate program (https://eeb.iastate.edu/). Applications for full consideration for graduate college fellowships and the deadline for general consideration is 1 January 2018. ****I will be attending the SICB meeting in San Francisco (3-7 January), and would be happy to meet any interested student.****

EEB is an interdepartmental program of 50 faculty embedded in a highly integrative and collaborative campus (https://eeb.iastate.edu/dir/faculty/). Iowa State University is located in Ames, Iowa, a community of nearly 60,000, recently ranked as one of the most livable small cities in the nation. The University enrolls more than 33,000 students and is committed to achieving inclusive excellence through a diverse workforce. Iowa State University values diversity and is an AA/EEO employer with an ADVANCE program. The Serb lab is committed to a diverse workplace, and prospective students of all races, genders, and sexual orientations are encouraged to apply.

’X Jeanne M. Serb, PhD Associate Professor

Director, Ecology and Evolutionary Biology (EEB) Graduate Program

Dept Ecology, Evolution & Organismal Biology Iowa State University 2200 Osborn Dr. Room 251 Bessey Hall Ames, IA 50011

Office: 245 Bessey Hall Phone: 515-294-7479 Email: serb@iastate.edu

http://www.eeob.iastate.edu/people/jeanne-serb “Serb, Jeanne M [EEOBA]” <serb@iastate.edu>

IST Austria EvolutionaryBiol

The Institute of Science and Technology Austria (IST Austria) is looking for highly qualified candidates to apply for our ISTScholar PhD program. We offer fully-funded PhD positions in the natural and mathematical sciences in a world-class research environment on the outskirts of Vienna.

Our PhD program is characterized by innovative training with a special focus on interdisciplinarity, close mentoring by outstanding faculty within small research groups, and access to first-rate facilities. Students spend the first year completing coursework and rotations before choosing a thesis group and passing the qualifying exam. Our PhD graduates have gone on to top positions in academia and industry all over the world.

Students with a bachelor'Âs or master'Âs degree in a relevant field are encouraged to apply. We offer internationally competitive salaries co-funded by an EU Marie SkÂ©Â©odowska-Curie grant, full health benefits, and subsidized on-campus housing in the first year.

For more information about the ISTScholar PhD program and application process, as well as faculty profiles, please visit our website at http://phd.ist.ac.at The deadline for PhD applications is January 8th 2018 for a start date in September 2018.

Yours sincerely,

Graduate School Office Institute of Science and Technology Austria gradschool@ist.ac.at

Nick BARTON <nick.barton@ist.ac.at>

Jena Germany EvolEcol

PhD position in Meta-analysis of Individual Niche Specialization

A PhD position in meta-analysis of individual niche specialization is available at the Institute of Ecology and Evolution at Friedrich Schiller University Jena, Germany. The position is funded by the German Research Foundation (DFG) within the recently granted collaborative research center (SFB/TRR 212) entitled: A Novel Synthesis of Individualization across Behavior, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

The project: 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 positions 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 Master's degree in a relevant field, like evolutionary or behavioral ecology or statistics, - solid knowledge in basic statistics, including experience with statistical software such as R, - 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 scientific writing will be advantageous.

Remuneration The position is available from 01/02/2018 or as soon as possible thereafter and will be fixed-term till end of 2021 (almost 4 years). Salary will be paid according to Remuneration level 13 (65%) of the Wage Agreement for Public Service in the Federal States (TV-L). Severely handicapped people are given preference for equal qualifications, aptitude and professional qualifications.

Application procedure The deadline for application is 14th January 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 Holger Schielzeth (see email below) and/or visit the website of the Population Ecology Group Jena (www.popecol.uni-jena.de). Please note that a twin project within the SFB is currently advertised with Prof. Dr. Klaus Reinhold— at Bielefeld University (http://www.uni-bielefeld.de/biologie/-Evolutionsbiologie) and you may want to indicated if you are interested in either of these positions.

Prof. Dr. Holger Schielzeth, Friedrich Schiller University Jena, Institute of Ecology und Evolution, Population Ecology Group, Dornburger

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Jena Germany EvolEcolBehavior

PhD position in Evolutionary Ecology of Predictability in Behavior

A PhD position in evolutionary ecology of predictability in behavior is available at the Institute of Ecology and Evolution at Friedrich Schiller University Jena, Germany. The position is funded by the German Research Foundation (DFG) within the recently granted collaborative research center (SFB/TRR 212) entitled: A Novel Synthesis of Individualization across Behavior, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

The project: The project will use escape behavior in grasshoppers as the model system for studying the causes and consequences of (un)predictability and flexibility in behavior. While individuals are known to vary in average behavior ('animal personalities'), variation in predictability/flexibility has been largely neglected, partly because of the methodological challenges in estimating variability. The project thus aims to explore a new dimension of individual specialization in animal behavior. The evolutionary ecology of predictability will be approached from multiple angles, making use of field work, laboratory breeding, quantitative genetic analysis and experimentation. We will use newly developed statistical tools for estimating individual predictability.

The collaborative research center: The positions 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 - Management of a laboratory population and setup of mating experiments, - implementation of standardized behavioral trials with grasshoppers, - analysis of behavioral data using advanced statistical methods, - implementation of a computer simulation for studying the fitness consequences of predictability, - 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 Master's degree in a relevant field, like evolutionary or behavioral ecology, - solid knowledge in basic statistics, including experience with statistical software such as R, - interest in experimental laboratory and field work, - excellent oral and written communication skills in English, - programming experience and documented experience with scientific writing will be advantageous.

Remuneration The position is available from 01/02/2018 or as soon as possible thereafter and will be fixed-term till end of 2021 (almost 4 years). Salary will be paid according to Remuneration level 13 (65%) of the Wage Agreement for Public Service in the Federal States (TV-L). Severely handicapped people are given preference for equal qualifications, aptitude and professional qualifications.

Application procedure The deadline for application is 14th January 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 Holger Schielzeth (see email below) and/or visit the website of the Population Ecology Group Jena (www.popecol.uni-jena.de).

Prof. Dr. Holger Schielzeth, Friedrich Schiller University Jena, Institute of Ecology und Evolution, Population Ecology Group, Dornburger Str. 159, 07743 Jena, Germany, E-Mail: holger.schielzeth@uni-jena.de

"holger.schielzeth@uni-jena.de" <holger.schielzeth@uni-jena.de>

LeidenU ExperimentalEvolution

GraduatePosition:LeidenU.ExperimentalEvolution PhD position in Evolutionary Biology, Institute of Biology, Leiden University, The Netherlands A 4-year PhD position in Microbial Evolution is available at the Institute of Biology < https://www.universiteitleiden.nl/en/-science/biology > (Leiden) in The Netherlands starting in Spring 2018.

This NWO funded project, run jointly by Daniel Rozen and Dennis Claessen, will study the origin of complex cells using a multidisciplinary approach that combines experimental evolution, synthetic biology and mathematical modelling (with Hyun Youk, TU Delft). We will exploit a powerful experimental system using bacterial cells that proliferate without their cell wall, called L-forms, which can be fused to form polyploid cells containing chromosomes with complementary, essential functions. These fusions will give rise to synthetic mutualisms in a single cell with a division of labour, and which will allow us to elucidate the dynamics, stability and genetic underpinnings of transitions in complexity. Successful completion of the designated work will lead to a PhD.

Requirements The candidate will be part of an interdisciplinary research team with collaborators active in membrane chemistry and mathematical modelling. We aim to appoint a highly creative and motivated candidate to actively participate and function in our collaborative group, which provides an inspiring research environment with an excellent group of supervisors and academic staff.

* The candidate should have an MSc or equivalent experience in evolutionary biology, microbiology, synthetic biology, or related study with excellent final marks.

* The candidate should have experience in molecular biology.

* Experience with bioinformatics, programming and statistics is highly desirable.

* The candidate is expected to think creatively and to work independently and as part of a collaborative group.

* The candidate should have a strong and demonstrated command of spoken and written English.

* Further information

The PhD candidate will work at the Institute of Biology Leiden (IBL). The IBL is an internationally oriented institute for research and education in biology. We are part of the Faculty of Science at Leiden University. Our institute performs top-quality fundamental and strategic research that provides solutions for societal challenges, and generates industrial opportunities. The IBL represents the core of modern biological research in Leiden, and interacts closely with neighbouring institutes, including the Institute of Environmental Sciences (CML), the Leiden Institute of Chemistry (LIC), the Leiden Advanced Centre for Drug Research (LACDR), and the Leiden University Medical Centre (LUMC).

For more information, please contact Dr. Daniel Rozen, tel. +31 71 527 7990 e-mail d.e.rozen@biology.leidenuniv.nl, or Dr. Dennis Claessen, tel. +31 71 527 5052, email d.claessen@biology.leidenuniv.nl

How to apply â euro Â Written applications, including a motivation letter, a CV and the names of 2 references should be sent by email to d.e.rozen@biology.leidenuniv.nl and d.claessen@biology.leidenuniv.nl. Review of applications will begin on January 31st, 2018 and continue until the position is filled.

"Rozen, D.E." <d.e.rozen@biology.leidenuniv.nl>

LMU Munich Master Geobiology Paleobiology

Applications invited for the Master's program "Geobiology and Paleobiology" (MGAP) at the Ludwig-Maximilians-Universität (LMU) Munich (Germany) for international students until 31Jan 2018

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

The MGAP program is based on interdisciplinary, research-oriented courses in geo- and biosciences that address patterns and processes of evolutionary and environmental geobiology and paleobiology. The module-based curriculum provides an integrative approach facilitated by experts in different areas of expertise. Students will learn and acquire routines with a wide range of scientific methods such as modern techniques in molecular biology, fieldwork, collection management, comparative morphology, phylogeny, bioinformatics, statistics and (paleo-) biodiversity assessments. Students will learn independent scientific work in individual and intensively supervised research projects at early stages of the curriculum.

MGAP in brief

- International Master's program in Geobiology and Paleobiology (Master of Science, M.Sc.) at the LMU Munich

- 2 years, 4 semesters, start in October (winter semester)

- All courses taught in English

- Course total: 120 credit points (ECTS)

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

For the winter semester 2018-2019 (courses start mid-October) the application period for international applicants (from outside of the EU) ends on Jan 31, 2016. Applicants from the EU and Germany can submit their documents from mid Feb 2018 until May 31, 2018.

Applications have to be submitted via our online submission portal:

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

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

"oliver.voigt@lmu.de" <oliver.voigt@lmu.de>

MasseyU Auckland NZ MicrobialEvolution

Three PhD Positions in the lab of Olin Silander at Massey University, Auckland, NZ

We have three PhD scholarships available for students with interests in evolution, microbial behaviour, and/or microbial genomics. The positions are part of a new Marsden-funded project (Title: The Stuff Memories Are Made Of: How Bacteria Remember and Learn from Environmental Signals). The research will require a broad range of techniques: microfluidics, long read (nanopore) sequencing, high-throughput flow cytometry, and quantitative phenotypic analyses.

We are seeking students with wet lab experience (e.g. microbial genetics, molecular methods, microscopy) and/or computational experience (e.g. python, R). The strengths and interests of the student will determine the precise direction and methods for each project.

The lab is in the Institute of Natural and Mathematical Sciences at Massey University, Auckland. We study evolutionary processes in bacteria, primarily Escherichia coli, using genomic and quantitative phenotypic data (at both the population and single-cell level).

The Institute of Natural and Mathematical Sciences has a young and dynamic faculty with a broad range of research interests, from statistics to ecology to evolution. Massey University is located on the North Shore of Auckland, New Zealand, a city which is regularly ranked among the most liveable cities in the world.

Each three-year scholarship includes an annual tax-exempt stipend of $27,500 NZD and covers all university fees.

To apply, please send a cover letter and CV (including the names of two references) as a single pdf to Dr. Olin Silander (olinsilander@gmail.com). Application deadline is Jan. 15, 2018. Start date upon mutual agreement.

olinsilander@gmail.com

MasseyU PolyploidyEvolution

A Ph.D. position (starting in 2018) is available in the Tate lab (http://www.massey.ac.nz/~jtate/index.htm) to investigate the evolution of cytonuclear coordination in Tragopogon (Asteraceae) allopolyploids. Depending on the interests of the student, the project can involve different aspects of the larger project to include genomic, transcriptomic, proteomic, computational, or physiological work. This position will be funded by a Massey University Doctoral Scholarship (http://www.massey.ac.nz/massey/admission/scholarships-bursaries-awards /other-scholarships/search-results/search-results_home.cfm?page=award_d isplay&scholarship_id91) for which the successful applicant will need to have an outstanding academic record. An MSc in Plant Biology, Genetics, or a similar field is required. This project is in collaboration with Murray Cox at Massey University, Dan Sloan at Colorado State University, and the Soltis lab at the University of Florida.

To apply, please send a letter of interest, CV, academic transcript (unofficial is ok) and the names and contact details for three references to j.tate@massey.ac.nz with 'PhD scholarship' in the subject line. International applicants are welcomed. For full consideration, materials must be received by January 15^th 2018. Starting date is flexible but must be no later than 1 November 2018. Please feel free to email me with any questions about the scholarship or the project.

This position offers an opportunity to experience New Zealand's unique natural and cultural environment. Located in Palmerston North, a university town with a large international community which offers a range of social and cultural amenities, the city is located close to mountains, rivers and the sea, and presents regular opportunities for hiking, skiing, surfing, and adventure sports.

Jennifer A. Tate, Ph.D.

j.tate@massey.ac.nz

Senior Lecturer in Plant Systematics and Evolution

Curator, Dame Ella Campbell Herbarium (MPN) Plant Science major leader Massey University Institute of Fundamental Sciences Private Bag 11222 Palmerston North New Zealand

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

FAX: 64-6-350-5682

"Tate, Jennifer" <J.Tate@massey.ac.nz>

NHM Denmark DNABarcoding

PhD fellow in shotgun sequencing for comparative diet analysis of capercaillies

The EvoGenomics Group at the Natural History Museum of Denmark, Faculty of Science, University of Copenhagen is offering a fully funded PhD scholarship fellowship under the Plant.ID Horizon2020 European Training Network (http://www.plantid.uio.no/), starting April 2018 or as soon as possible thereafter.

The project explores applied use of the emerging genome skimming DNA reference databases, such as the Norwegian NorBol, the Alpine PhylpAlps and the Danish DNAmark reference databases. Specifically, the project explores species-level identification of plants in animal diets through a comparative shotgun sequencing diet study on capercailles (wood grouse) in the Alps and Norway.

Supervisor: Kristine Bohmann, Natural History Museum of Denmark, University of Copenhagen. Co-supervisors: Tom Gilbert (Copenhagen), Sanne Boessenkool (University of Oslo), and Eric Coissac (University of Grenoble, PhyloAlps project). Collaborators: Torbjørn Ekrem and Inger Greve Alsos (NorBOL).

Application deadline: 15 January 2018.

More details about the PhD fellowship, contact information, etc: http://jobportal.ku.dk/phd/?show=146109 kbohmann@snm.ku.dk

NIOO Wageningen BirdBehaviourEpigenetics

The department of Animal Ecology at NIOO-KNAW, NIN-KNAW and Hubrecht Institute offer a position for a

PhD-student position on the topic:

Ecological epigenetics and the brain: the evolutionary consequences of epigenomic modifications in a songbird

Project description:

This unique inter-disciplinary collaboration between three of the larger institutes of the KNAW aims to elucidate the function of epigenetic regulation in the great tit brain to be able to study its role for the evolution of behaviour. Epigenetic mechanisms, such as DNA methylation and histone modification, are key epigenetic mechanisms that can alter gene expression, thereby affecting behavioural variation, both short- and long-term. While we know that epigenetic mechanisms act on different time scales and may be expressed in different tissues or brain regions, an essential gap in our knowledge is: how do epigenomic alterations contribute to fitness variation and what is their role in the evolution of behavioural traits? To be able to answer this question, we will obtain detailed information on the epigenetic processes underlying behavioural traits in a species where we can measure the fitness consequences in a natural environment, the great tit (Parus major). However, our knowledge of epigenetic mechanisms underlying behavioural traits in wild vertebrates are limited to few studies on DNA methylation, thus severely hampering the field of ecological behavioural epigenetics. Furthermore, some of the more relevant epigenetic signatures that explain how tissues behave intrinsically as well as in response to the environment do not necessarily involve DNA methylation but are rather governed by histone modifications. Our main objective is to translate the knowledge from the seminal work done in model organisms and to convert this to an ecological model species to be able to study the ecological and evolutionary consequences of epigenomic alterations.

This PhD project will have three main aspects:

i) Measure DNA methylation and histone acetylation in specific brain regions in hand reared captive great tits and relate this to variation in a range of behavioural traits.

ii) Validate the link between epigenetic marks and behaviour in the mouse and the rat.

iii) Link variation in epigenetic marks to fitness measures in a natural population of great tits.

Requirements: We are looking for a highly motivated, inventive, communicative biologist with a background in behavioural (epi)genetics or behavioural neuroscience. Experience with NGS technologies and/or bioinformatics are important advantages. A high standard of spoken and written English is required, as are good quantitative and analytical capabilities. This is a collaborative project, excellent interpersonal and communication skills and required. - you should have an MSc or equivalent in Biology or a related discipline, preferably with a strong background in Ecological Genetics or Neurobiology. - you are expected to have an excellent academic record (list of examination marks from your university study) and be curious, creative and ambitious - you should be able to write scientific articles and reports (to be proven by your graduation thesis or another comparable report) and be fluent in English both in writing and speech.

Appointment: This is a temporary appointment, initially for 1 year and upon satisfaction to be prolonged for a maximum of 4 years total, hosted at the NIOO-KNAW, Department of Animal Ecology (1.0 fte). Starting date is 1 March 2018.

Salary: Salary depends on training and work experience. The gross salary starts at Â 2.222,- per month in the 1st year, and will gradually increase to a maximum of Â 2.840,- per month in the 4th year, scale P, 38 hours per week, Collective Agreement for Dutch Universities (CAO NU), plus 8% holiday pay and a year-end bonus. We offer an extensive package of fringe benefits.

Information: Additional information is available upon request from Dr. K. van Oers, k.vanoers@nioo.knaw.nl or +31 317-473456. Information on NIOO-KNAW can be found here http://www.knaw.nl How to apply: You may apply for this position before 8 January 2018 by means of sending an email to vacature@nioo.knaw.nl. Applications for the position should include a Curriculum vitae a motivation letter and names and (email) address of two academic references and Vacancy number (PhD-AnE-017011)

Interviews will take place early February 2018

“Oers, Kees van” <K.vanOers@nioo.knaw.nl>

NIOO Wageningen VirusEvolution

The Department of Microbial Ecology offers a PhD position on the topic:

Dynamics of adaptation in multipartite plant viruses

Project description

Multipartite viruses have two or more genome segments, packaged individually into virus particles. This virus-particle organization should have major drawbacks for infection efficiency, but surprisingly multipartite viruses are nevertheless common among plant viruses. The frequency of these different segments can vary, but appears to converge on a host-species-dependent equilibrium. As part of the NWO VIDI project of Dr. Mark P. Zwart on the evolution of multipartite viruses, we want to use experimental evolution to study how resistant this equilibrium is to perturbations. We also want to know what role variation in genome segment frequencies plays in adaptation to new environments, and how it affects the expression of virus and host genes. This project will be a close collaboration with Wageningen University, in particular with Prof. Dr.ir. René van der Vlugt and Prof. Dr. Monique van Oers (Laboratory of Virology) and Prof. Dr. Arjan de Visser (Laboratory of Genetics).

Requirements:

1. MSc degree in virology, microbiology, evolutionary biology or a closely related field 2. The ideal candidate will have demonstrable experience with both (plant) viruses and evolution 3. Highly motivated candidate with creative, critical and conceptual thinking skills 4. Experience with molecular methods 5. Good communication skills in English (written and spoken) and the ability to work in a team are essential

Interviews with selected candidates are scheduled for Thursday, 1 February 2018.

Appointment: This is a temporary appointment, initially for 1 year and upon satisfaction to be prolonged for a maximum of 4 years (1fte) or 5 years (0.8fte).

Starting date: March/April 2018

Salary: The gross salary starts at euro 2.174, - per month in the 1st year, and will gradually increase to a maximum of euro 2.779, - per month in the 4th year, scale P, Collective Agreement for Dutch Universities (CAO Nederlandse Universiteiten), excluding 8% holiday pay and a year-end bonus.

Location: The Netherlands Institute of Ecology, NIOO-KNAW in Wageningen, The Netherlands. For more information see: https://nioo.knaw.nl/en. < https://nioo.knaw.nl/en >

Information: Additional information is available upon request from Dr. Mark Zwart. Email: m.zwart@nioo.knaw.nl Tel:+31 (0317)-473431.

Applications: Please send your application, including full curriculum vitae and names of three referees and vacancy number, to vacature@nioo.knaw.nl The closing date for applications is 14 January, 2018. The vacancy number is ME-017707.

"M.Zwart@nioo.knaw.nl" <M.Zwart@nioo.knaw.nl>

NIOZ Netherlands EvolutionMarineCommunities

Dear colleagues, I am pleased to announce that a PhD position on "Community dynamics at deep-sea hydrothermal vents under different disturbance regimes" was opened at the NIOZ (Royal Netherlands Institute for Sea Research). A detailed description of the position and application instructions can be found here

https://www.workingatnioz.com/our-jobs/phd-student-"community-dynamic s-at-deep-sea-hydrothermal-vents-under-different-disturbance-regimes" .html

Interested applicants can contact me under sabine.gollner@nioz.nl for additional information.

Thank you for circulating this announcement,

Kind regards,

Sabine Gollner

Dr. Sabine Gollner

NIOZ Royal Netherlands Institute for Sea Research

Department of Ocean Systems (OCS)

Landsdiep 4 1797 SZ 't Horntje (Texel)

The Netherlands

phone: +31 222 369 426

E-mail: sabine.gollner@nioz.nl

PhD Student "Community Dynamics at Deep-sea Hydrothermal Vents Under Different Disturbance Regimes"

The department of Ocean Systems (OCS, department head prof. dr. Gert-Jan Reichart) is looking for a highly motivated PhD candidate that would like to contribute to the understanding of community dynamics at deep-sea hydrothermal vents under different disturbance regimes. 2017-11-20 14:43:15

LOCATION: ROYAL NIOZ-TEXEL (NL)

VACANCY ID: 2017-092

CLOSING DATE: January 14th, 2018

THE RESEARCH

The deep sea is changing. Future stressors, in the form of mineral mining, are expected at deep-sea hydrothermal vents, since the global need for minerals is rising. Vents host unique communities that live under extreme conditions of hot and toxic vent fluid emissions and face natural disturbance events such as volcanic eruptions. Currently, our knowledge of community dynamics at and next to vents is scarce and limits our ability to predict resilience to natural and mining-related disturbances.

Recent research has shown that vent communities in the Northern East Pacific Rise undergo quick succession after the frequent volcanic eruptions. In contrast, observations in the Western Pacific Lau back-arc basin have shown that geological setting and composition of vent megafauna communities are more stable. To understand the resilience of vent communities in different geological settings, we need to study diversity, succession, and connectivity.

THE PROJECT

In this multidisciplinary research project, you will assess temporal community dynamics of meio- and macrofauna at Lau Basin vents and will compare them to the dynamics at the East Pacific Rise. You will perform genetic analyses of selected species from Lau Basin and East Pacific Rise vents to unravel connectivity and population genetics in these distinct geological settings. This fundamental knowledge will help to elaborate environmental management plans in the context of mineral mining.

THE CANDIDATE

You are a highly motivated young researcher with an MSc degree in marine sciences, ecology, zoology, or environmental sciences. You are open-minded and want to work across disciplines - ranging from classical taxonomical work and ecological analyses to genetic applications and population genetics analyses.

Do you already have experience with genetic methods? Do you have a keen interest in hydrothermal vent fauna, including sorting and identification of animals? Want to join research cruises at high seas? Join our research team and help us fathom community dynamics at deep-sea hydrothermal vents.

Since you will work in an international and interdisciplinary research environment it is essential that your oral and written English skills are good.

CONDITIONS

We are offering a 4-year full-time position with a pension scheme, a yearly 8% vacation allowance, a year-end bonus and flexible employment conditions. Working conditions are based on the Collective Labour Agreement for Research Institutes (WVOI). Cost of relocation and help with housing is provided by the Royal NIOZ.

MORE INFORMATION

For additional information about this vacancy, please contact Dr. Sabine Gollner.

For additional information about the procedure, please contact Jolanda Evers (senior HR advisor).

Learn more about the department of Ocean Systems here.

Please note: interviews will be held on the 23^rd and 24^th of January, 2018.

Sabine Gollner <Sabine.Gollner@nioz.nl>

NorthDakotaStateU EvolutionaryBiol

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 <ned.dochtermann@gmail.com>

RoyalHolloway ULondon EvolutionGenomicArchitecture

The following PhD studentship is available at Royal Holloway, University of London: The Evolution of genomic architecture

It is a 4 year funded PhD that will be part of the London NERC Doctoral Training Programme (see london-nerc-dtp.org/). The studentship is fully funded for 4 years for UK/EU applicants (residence conditions apply). Tuition Fees: pounds 4,195.00 p.a. Stipend: pounds 16,553.00 p.a. with London Weighting. Closing date 8/1/18.

For further details how to apply see https://www.royalholloway.ac.uk/biologicalsciences/study-here/research- degrees/phdstudentships2017.aspx

We are looking for candidates with an interest in this fundamental biological question, and preferably some modelling experience. This includes biologists with an interest and some experience in modelling as well as mathematicians/computer scientists/physiscists etc with an interest in evolutionary biology

For further information contact vincent.jansen@rhul.ac.uk

The Evolution of genomic architecture

Supervised by profs Vincent Jansen (Royal Holloway) and Nick Lane (UCL)

How did life on Earth form? Why are our cells the way they are? These are still open questions. Mitochondria transitioned from free-living bacteria to obligate symbionts of eukaryotic cells. In this process they gave up a good part of their genome (either lost or transferred to the nucleus of their host cell) and their reproductive independence (which is now controlled by the nucleus). Little is known regarding this fundamental transition (explained in detail in Nick Lane's book "The vital question"). What are the selective pressures on genes in the mitochondria and the nucleus? Is there an advantage to being in the mitochondria, where you will be passed on to all daughters, or is it better to be in the nucleus, where you could be passed on to sons and daughters? We are interested in which scenarios favour the transfer of genes from bacteria engulfed by a cell to the nucleus, and the transfer of reproductive control to the host nucleus. We do this through studying models of the evolutionary dynamics of mitochondrial genes, trying to quantify private interest and the common good of genes, building on recent modelling advances (as in Ubeda and Jansen 2017). In this work we will take a gene eye-view on the evolution of mitochondria we will be able to determine when the gene copies in the nuclear genome would outcompete the ones in the mitochondrial genome. In a further stage it might be possible to test model predictions using model organism such as Chlamydomonas and Yeast. Candidates interested in applying for this project will need an interest to work on questions relating to the fundamental principles in the evolution of life. We would be very happy to consider candidates with a background in quantitative sciences, such as mathematics, physics, or computer science.

References

N. Lane. The Vital Question. Profile Books 2015

F. Ãbeda & V. A. A. Jansen (2017) The evolution of sex-specific virulence in infectious diseases. Nature Communications 7, Article number: 13849 (2016) doi:10.1038/ncomms13849

van Baalen, M. and Jansen, V.A.A. (2001) Dangerous liaisons: the ecology of private interest and common good. Oikos 95: 211-224.

Hadjivasiliou, Z., Seymour, R. M., Lane, N. and Pomiankowski, A. (2013) Dynamics of mitochondrial inheritance in the evolution of binary mating types and two sexes. Proceedings of the Royal Society B 280: 1-8.

Vincent Jansen

"Jansen, Vincent" <Vincent.Jansen@rhul.ac.uk>

SouthDakotaStateU EvolutionaryGenomics

Master's Student Opportunity at the CBFenster Lab, SDSU

Project: Predict mutational effects using comparative genomic approaches

Research Area: Evolutionary Genomics of mutation at Arabidopsis thaliana

Location: South Dakota State University, Department of Biology and Microbiology/Department of Mathematics and Statistics, Brookings, SD

Mutations, the ultimate source of all genetic variation, provide the substrate that fuels evolution. However, most mutational input to genetic variation is subsequently eliminated by selection or drift in natural populations. Why some mutations are eliminated and others preserved or fixed in natural populations and whether there is a correlation between the preservation of a given mutation and the magnitude of the mutation effect are key questions in biology.

Equipped with the most comprehensive mutation profile of a plant species, Arabidopsis thaliana, the CBFenster lab (charlesbfenster.wordpress.com) in collaboration with Xijin Ge's lab (http://ge-lab.org/), both at South Dakota State University, provides a great opportunity for graduate students to study spontaneous mutations using computational tools. The collaboration reflects a joint mentoring opportunity from biological and mathematical/statistical perspectives and will include mentoring by Dr. Mao-Lun Weng, a postdoc on the project (https://maolunweng.wordpress.com/). Sequence data reflect a joint collaboration among the Fenster (SDSU), Rutter (CoC), Weigel (Max Planck) and Wright (U of Toronto) labs, funded by NSF.

The prospective student will investigate the effect of mutation at protein-coding genes from protein structure and gene network perspectives. Given an observed spontaneous mutation in mutation accumulation study, the student will: (1)Use protein structure prediction algorithms to simulate the protein structure from the mutated sequence and test whether the mutation has strong effects on protein structure stability. (2)Using a gene expression network investigate whether the mutation has a potentially large effect on network connectivity.

We hypothesize deleterious mutations will detrimentally change protein structure or be associated with proteins having high network connectivity. We can validate these hypotheses by comparing the mutated protein-coding genes in A. thaliana to other related species. If the mutated position in the protein-coding gene also shows sequence variation among related species, it suggests that this mutation did not have strong effects, i.e. less deleterious. Furthermore, we can compare overlap of these mutations in the mutation accumulation study and in natural populations. If mutations are deleterious, as predicted by protein structure stability, they are less likely to be present in natural populations.

This is a bioinformatics oriented project. The prospective student will obtain skills of computational approaches to study protein structure and gene network, and learn phylogenetic and population genetic theories on mutations.

Students can begin as early as January 2018, but more likely summer or fall 2018.

Funding will include teaching assistantship support and NSF funded summer salary.

Please email all mentors if you are interested in the project: charles.fenster@sdstate.edu; xijin.ge@sdstate.edu; maolun.weng@sdstate.edu

Mao-Lun Weng PostDoc Associate Department of Biology and Microbiology South Dakota State University Brookings, SD 57007 USA maolunweng.wordpress.com

“Weng, Mao-Lun” <MaoLun.Weng@sdstate.edu>

StAndrews EvolBiol

Dear EvolDir

The University of St Andrews, Scotland, in association with the Chinese Scholarship Council, is offering up to 30 fully funded 4-year PhD studentships for Chinese nationals. The deadline for applications is Fri 19 Jan 2018.

Full details of the programme are available at https://www.st-andrews.ac.uk/study/international/csc/ Applicants are strongly advised to make contact with prospective supervisors before applying. A full list of Principal Investigators at the School of Biology is available at http://biology.st-andrews.ac.uk/people/ Please do pass along this information to anyone who may be interested.

Best wishes Andy Gardner

– Dr Andy Gardner Reader in Biology University of St Andrews Dyers Brae St Andrews KY16 9TH United Kingdom

Email. andy.gardner@st-andrews.ac.uk Web. http://synergy.st-andrews.ac.uk/gardner/ Tel. +44 (0) 1334 463 385 Fax. +44 (0) 1334 463 366

“andy.gardner@st-andrews.ac.uk” <andy.gardner@st-andrews.ac.uk>

StirlingU WildMandrillsSexDifferences

Quantifying Sexual Partitioning in Diet and Habitat Use in Wild Mandrills in a Dynamic Rainforest Savannah Landscape (Ref IAP-17-126)

Project Description

As natural habitats are confronted with substantial environmental change, we urgently need more information on the resilience of at-risk populations in the face of disturbance. Historically, our efforts to predict responses to environmental stress has been hampered because of challenges in studying both how wild animals exploit space and what they eat. For example, although habitat and dietary choices differ substantially across species, inferring how these factors affect resilience to change is quite difficult because different taxa vary in many characters in addition to habitat and diet. Intraspecific sexual differences in functional traits also have dramatic effects on how individuals acquire and use environmental resources. Species with strong dimorphism are therefore ideal for studying how functional traits affect resilience to disturbance. The extreme sexual dimorphism of Mandrills (Mandrillus sphinx) presents an opportunity to study plasticity in diet and habitat use within the same species, a sharp contrast that isolates spatial and dietary differences from other variables including differences due to phylogenetic background.

Mandrills are the most sexually dimorphic primates: males possess remarkable ornaments that are important for sexual signalling, weigh three times as much as females and take much longer to reach sexual maturity. Both ornamental traits and size have strong links with resource availability, and may at least partly explain observations of sexual differences in space use within Lopé National Park in Gabon. Whatever the proximate cause of differences in space use, females exploit a wider range of habitats, and travel within very large groups, while mature males range less and spend much of the year outside of the group.

Work at Lopé has shown that forest structure and composition changes over relatively small temporal and spatial scales, and that fruit resources have recently declined and become less predictable; such changes mirror global forecasts of increasing uncertainty surrounding environmental change. Consequently, the sexual difference in mandrill space use (and its implications for how males and females exploit ephemeral and widely spaced food resources) may be a useful model for the prospects of at-risk populations. In addition, this work will shed light on condition-dependent sexual selection in heterogeneous environments.

Methodology This PhD studentship contributes to a broader, integrative, effort to study the natural history and resilience of Mandrills in the face of environmental change. It has three main aims: 1. To quantify sexual difference in habitat use, and relate this space use to the nutritional resources contained therein. Here we will exploit the existence of a number of radiocollared animals in the Lopé NP mandrill horde. The candidate will combine historical measures of animal movement with continued tracking of animals of both sexes using radio telemetry. 2. To quantify temporal variation in food resource availability, and relate this variation to diet and space use as well as sexual trait expression. Here we will take advantage of modern analytic tools and continued monitoring of the fruiting phenology of food producing trees in Lopé NP. The candidate will map resource availability alongside habitat use, monitor changes in sexual trait expression over time using camera trap networks, and collect dung and tissue samples to assess the effects of local environmental resources on both diet and habitat use for both sexes. We will analyse these samples using isotope ecology at the state-of-the-art Life Sciences Mass Spectrometry Facility at SUERC in East Kilbride. 3. To calibrate Stable Isotope Analysis estimates of diet use through careful measures of a captive mandrills. The candidate will measure tissue turnover rates (e.g., by examining growth rates of different hairs on different individuals), and use diet manipulations to calculate the diet-tissue discrimination factor for the different isotope ratios.

For more information and background reading, see: https://goo.gl/y4BHXd Funding Notes This competition-funded studentship is part of the NERC Doctoral Training Partnership IAPETUS (http://www.iapetus.ac.uk/). It will cover tuition fees and a stipend for UK students only (but see NERC funding rules for exceptions regarding EU citizens).

To apply, contact Luc Bussiere (luc.bussiere@stir.ac.uk) ASAP to indicate your interest and obtain further instructions. The formal application to the University of Stirling Graduate School (including a current CV, personal statement, two references, and full transcripts) is due no later

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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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StockholmNHM Mammoth Genomics

PhD student position on evolutionary genomics of the woolly mammoth

Swedish Museum of Natural History & Stockholm University

PROJECT DESCRIPTION The purpose of this PhD project is to use the woolly mammoth as a model system to investigate evolutionary changes in real time. At a genetic level, micro-evolution is the result of an interaction between natural selection and genetic drift, where the latter increases in importance the smaller a population becomes. To examine this interaction, we will generate up to 100 woolly mammoth genomes dated to the last 25,000 years of the species' Â existence. This time period encompasses several dramatic changes in climate at the end of the Pleistocene (15-11 kya) as well as the subsequent isolation of mammoths on Wrangel Island, where a very small population survived for 6,000 years until the species became extinct. The genomic data will be used to examine the impact of climate change as well as island isolation on adaptive evolution and demography in the woolly mammoth. Moreover, we will investigate the timing, rate and extent of genome erosion in the Wrangel Island population leading up to the species extinction. For this project, good knowledge in population genetics, bioinformatics as well as experience of laborative DNA analysis are important qualifications. The PhD project will be supervised by Professor Love Dal Â Ân at the Department of Bioinformatics and Genetics, Swedish Museum of Natural History. For more information about the research group, please visit www.palaeogenetics.com/adna ENVIRONMENT The PhD student will be employed by Stockholm University (Department of Zoology), but will be based at the Department of Bioinformatics and Genetics at the Swedish Museum of Natural History (SMNH). The museum is located in Stockholm, which by many is regarded as one of the most beautiful capitals in the world and is home to a vibrant scientific community with several leading research institutes as well as the National Genomics Infrastructure at the Science for Life Laboratory. The SMNH has a strong mission in natural history research, and its research division has more than 170 employees. The department of Bioinformatics and Genetics hosts three research groups, focused on ancient DNA and population genetics (PI: Prof. Love Dal Â Ân), avian systematics and biogeography (PI: Dr. Martin Irestedt), and phylogenomics (PI: Prof. Fredrik Ronquist).

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

TERMS OF EMPLOYMENT The four year PhD program includes three years of research and one year of course work. The salary follows the agreement for PhD positions at Stockholm University.

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

HOW TO APPLY Applications should be done using Stockholm University's online application system. Please follow the link below to obtain further information about how to write your application and how to access the online application system: http://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjobC37&rmlang=UK Closing date: 15 January 2018 Reference number: SU FV-3830-17

Love Dal Â Ân Professor of Evolutionary Genetics Department of Bioinformatics and Genetics Swedish Museum of Natural History Box 50007 SE-104 05 Stockholm, Sweden Email: love.dalen@nrm.se Webpage: www.palaeogenetics.com/ld Love.Dalen@nrm.se

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StockholmU BrainEvolution

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 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: http://www.zoologi.su.se/en/about/staff/-person.php?suuid=akotr Alexander Kotrschal <alexander.kotrschal@zoologi.su.se>

StockholmU ColourEvolution

PhD position in Ethology

at the Department of Zoology, Stockholm University, Sweden

Deadline for application: January 15, 2018.

A PhD position focused on colour evolution is available in John Fitzpatrick's research group in the Department of Zoology at Stockholm University. The aim of this project is to understand how natural and sexual selection influence the evolution of animal colouration. To achieve this aim, the project will use on both comparative and experimental approaches. To examine how natural selection influences animal colouration, the project will examine the evolution of distinct markings (spots and eyespots) in rays, a group of cartilaginous fish with extreme diversity in body patterns and colouration, and examine how marine and avian predators response to distinctive markings presented by rays. To examine how sexual selection influences sexual colouration, the project will use a comparative approach to quantify how variation in animal mating behaviours influences sexual dichromatism across a range of taxonomic groups. Finally, the project will experimentally examine how females evaluate male sexual ornaments using small tropical freshwater fish in the lab.

The work will be desk (for comparative studies) and lab (for experiments) oriented, taking advantage of the brand new tropical freshwater and marine fish labs in the Department of Zoology, with room for over 6,000 aquaria and several experimental rooms. The Department of Zoology is already home to extensive expertise in studying anti-predator colouration and signaling and state-of- the-art facilities to assess behaviour and sexually selected traits (e.g. unique 2D and 3D behavioural tracking software, computer-assisted sperm analysis software (similar to what is used in human fertility clinics), high-speed cameras, spectrophotometers for colour analyses). The successful candidate will join a rapidly growing sexual selection group in the Department and will be provided with excellent opportunities for personal and professional development towards a successful academic career.

Qualification requirements

We are looking in particular for candidates with a strong interest in evolutionary biology, with excellent analytical ability and experience quantifying animal colouration and in the analyses of behaviour and other traits of interest. Experience in working with phylogenetic comparative methods and aquatic animals in the lab is especially meriting. In particular, a background in research with rays, particularly from a comparative perspective, is especially desired for this project. Applicants who have in principle acquired the corresponding competence in Sweden or in another country are also qualified. Therefore, overseas applications are encouraged.

For more information on the position (Ref. nr. SU FV-4166-17) and to apply follow this link:

https://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjob=4439&rmlang=UK Contact Questions? Please contact Dr John Fitzpatrick, john.fitzpatrick@zoology.su.se

For more information about research in the Fitzpatrick lab see: http://www.zoologi.su.se/en/about/staff/-person.php?suuid=jfrit john.fitzpatrick@zoologi.su.se

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SU NHM Stockholm ArcticBiodiversity

PhD Student Position in Arctic and Alpine Biodiversity

Stockholm University and the Swedish Museum of Natural History

Closing date: 2 February 2018 Reference number: SU FV-4051-17

PROJECT DESCRIPTION This position will be associated with the Formas-funded project "Has altitude variation in species communities along the Fennoscandian mountains been shaped by neutral or competition based processes?". This project includes collaborators from the Swedish Museum of Natural History, Stockholm University and University of Oviedo. It is closely associated with Arctic Islands, a global research program evaluating the impacts of a climate driven fragmentation on Arctic ecosystems and biodiversity.

Arctic and alpine environments have a harsh climate and harbour simple ecosystems that are characterised by a low primary productivity. Productivity gradients in both latitude and altitude cause further declines in species richness and ecological complexity. Arctic and alpine species communities are particularly susceptible to ecological perturbations caused by global warming, such as north- and upward expansions of boreal and subalpine species. The Fennoscandian mountains contain sub-Arctic and alpine environments that provide important ecosystems services for diverse stakeholder groups. Although north- and upward expansions of some species is already ongoing, we have scant information of the likely effects of such range shifts for resident species communities. This project will apply concepts from community assembly theory to empirical data to illuminate the mechanisms by which we can expect climate change to influence biodiversity in the Fennoscandian mountains. Empirical data will be collected directly in the field as well as derived from modern genomic techniques.

We envision the project to work across broad taxonomic scales. The project will include quantifications of community composition of vascular plants, arthropods and vertebrates within altitude gradients along the Fennoscandian mountains using established protocols. These quantifications will require extended periods of field sampling along the Swedish mountains in summer. There will also be a significant laboratory component, were modern genetic barcoding techniques will be utilized to quantify community composition of collected samples, in particular for arthropods.

For this project, important qualifications are prior experience of biodiversity sampling in demanding conditions, a good ability to work in small groups in isolated environments, as well as prior experience either with genetic barcoding techniques or with field identification of Arctic/Alpine vascular flora. We are seeking an individual that is highly self motivated and has a strong capacity to work independently. Fluency in Swedish or Norwegian is an asset, but not a requirement.

QUALIFICATIONS In order to meet the general entry requirements, the applicant must have completed a second-cycle degree, completed courses equivalent to at least 240 higher education credits, of which 60 credits must be in the second cycle, or have otherwise acquired equivalent knowledge in Sweden or elsewhere.

In order to meet the specific entry requirements, the general syllabus for doctoral studies in the field of Systematics and Evolution stipulates that applicants must have completed a research degree (e.g. Master'Âs), or have passed at least 120 hp (2 years) of biological studies, including an approved independent project of at least 30 hp at advanced level (examensarbete) within systematics and evolution, ecology, population genetics, bioinformatics or a similar subject. Applicants who have in principle acquired the corresponding competence in

Sweden, or abroad, are also qualified. Only a person who will be or has already been admitted to a third-cycle program may be appointed to a doctoral studentship. The primary assessment criteria in appointing a doctoral student should be the capacity to benefit from the training.

The qualification requirements must be met by the deadline for applications.

CONTACT For more information, please contact Fredrik Dalerum, telephone: +34 664 170 144, fredrik.dalerum@zoologi.su.se. Further information about the position can be obtained from Love Dalen, telephone: +46 8 5195 4281, love.dalen@nrm.se.

HOW TO APPLY Applications should be done using Stockholm University's online application system. Please follow the link below to obtain further information about how to write your application and how to access the online application system: http://www.su.se/english/about/working-at-su/phd?rmpage=job&rmjob=4509&rmlang=UK Love Dalén <Love.Dalen@nrm.se>

TexasAMU ViralEvolution

The Labonté viral ecology lab at Texas A&M University at Galveston is looking for two motivated students to pursue graduate studies (one MSc and one PhD) in the department of Marine Biology through the Marine Biology Interdisciplinary Program (MARB-IDP). Students will work on research projects related to virus evolution, virus-host interactions, and characterization the role of viruses in marine (surface and subseafloor) environments.

Interested students should contact Dr. Jessica Labonté (labontej@tamug.edu <mailto:labontej@tamug.edu>) with their curriculum vitae and a cover letter presenting themselves and their interests in viral ecology research prior to submitting an application. The deadline to apply for the MARB-IDP program is February 15, 2018. Applications from women, military veterans, individuals with disabilities, and members of other traditionally underrepresented groups are encouraged.

Jessica Labonté | Assistant Professor Department of Marine Biology | Texas A&M University at Galveston http://www.tamug.edu P.O. Box 1675, OCSB Room 267 | Galveston, TX 77554

Ph: 409.740.4921 | labontej@tamug.edu

Catherine Risley <c.risley@tamu.edu>

TexasAM VeterinaryMed ComparativeEvolGenomics

PhD Student Position Open at Texas A&M College of Veterinary Medicine

Dear All,

There is a PhD student position available in Comparative Evolutionary Genomics at Texas A&M University College of Veterinary Medicine. We have multiple projects involving the analysis of whole genome and other data in the lab of Dr. Leif Andersson. This student will be primarily involved in population genomics of the Atlantic herring (Clupea harengus). Schools of Atlantic herring can contain billions of individuals, and this is one of the most numerous vertebrates on Earth. In previous work we have shown that Atlantic herring is an excellent model to explore the genetic basis of ecological adaptation and the action of natural selection in natural populations (see eLife: PMID: 27138043 and PMID: 28665273; PNAS: PMID: 28389569). In this project, we will study the genetic organization of major histocompatibility genes, to which extent MHC genes contribute to ecological adaptation. The MHC class I and class II genes are among the most polymorphic genes in vertebrate genomes, a polymorphism maintained by balancing selection. This project will study the evolution of MHC polymorphism in a species with an enormous census population size and in which genetic drift has a negligible effect on allele frequencies.

Strong candidates will have a background in evolutionary biology and genetics and be prepared to examine large datasets using bioinformatic and computational biology techniques involving short-read sequences, RNAseq and methylomic data. The starting date is flexible (any time during spring and summer of 2018). Review of applications will start immediately and the positions will remain open until a suitable candidate has been found.

Interested candidates are encouraged to submit a letter of explaining their background and career plans, accompanied by a C.V. and a description of relevant undergraduate experience and coursework to Dr. Brian W. Davis (bdavis@cvm.tamu.edu) at Texas A&M University. Dr. Davis will also be attending the International Plant & Animal Genome XXVI conference January 13-

17, 2018 in San Diego, CA if individuals would like to discuss graduate student opportunities in the lab.

Best regards,

Dr. Leif Andersson

Professor, Animal Genomics

Texas A&M University, College Station, Texas, USA

Professor, Functional Genomics

Uppsala University, Sweden

"Davis, Brian" <BDavis@cvm.tamu.edu>

TrentU Canada BlackBearGenomics

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

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

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

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

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

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

Christopher Kyle <christopherkyle@trentu.ca>

UAkron SexChromEvolution

Funding for a PhD student to study the evolution of sex chromosomes in crustaceans. We seek a student interested in bioinformatics to study sex chromosome evolution in androdioecious branchiopod crustaceans. We have whole genome sequence data, including sequencing of the sex chromosome, that need to be analyzed to test hypotheses of the evolution of sex chromosomes in these shrimp. We seek a student with good problem solving ability and programing experience in C++. Minimally the candidate should at least have some programming experience and be willing to learn C++. Funding is for 5 years (teaching assistantship) and includes both a stipend and tuition remission. Interested parties should contact Dr. Stephen C. Weeks (scw@uakron.edu or 330-972-6954). Visit http://blogs.uakron.edu/weeks/ for more information about these crustaceans.

Applications should be submitted by Jan. 15th, 2018 for full consideration and can be uploaded at http://www.uakron.edu/ib/academics/ib-admission-requirements.dot .Interested students should contact Dr. Weeks to receive information on application procedures before applying online.

"Weeks,Stephen C" <scw@uakron.edu>

UAlabama BeeGenomics

The Lozier Lab (lozierlab.ua.edu) at The University of Alabama, Dept. of Biological Sciences, is recruiting a highly motivated graduate students to start in the Fall 2018 semester. Students would work on projects related to ongoing NSF-funded studies of bumble bee population genomics to uncover signatures of adaptative and demographic processes within and among species. Students would specifically be working to generate and analyze population-level whole genome resequencing data across multiple species and broad environmental gradients at a large geographic scale, and could also be involved in sequencing and assembly of reference genomes from new bumble bee species using long-read sequencing technologies.

Students would have the opportunity to collaborate with project collaborators across institutions, and to integrate phenotypic data, including physiology and morphology, into genomic analyses.

Students with an interest in population genetics/genomics should contact Jeff Lozier (jlozier@ua.edu), with a brief statement of interest, a resume/CV, and an informal academic history (e.g., GPAs, GREs, and relevant coursework list, etc.).

The University of Alabama is the flagship campus of the University System of Alabama, with an enrollment of over 35,000 students.The University is committed to achieving excellence as one of the country's primary centers of research and education. It is located in the vibrant college town of Tuscaloosa, AL, which boasts many cultural and athletic activities. The campus also benefits from the close proximity to the Birmingham metropolitan community.

The University of Alabama is an Affirmative Action/Equal Opportunity Employer. Women and minorities are encouraged to apply.

Jeff Lozier Associate Professor Biological Sciences The University of Alabama Office 205-348-2754 jlozier@ua.edu | lozierlab.ua.edu

jlozier@ua.edu

UBarcelona EvoDevo

Need urgent candidates for PREDOC FPU-fellowship call (ASAP, now open) to work on #HeartEvoDevo #GeneLoss #Oikopleura

Cañestro's lab, Department of Genetics, University of Barcelona

https://goo.gl/0ZaDm0 oikocris@gmail.com

UBath ExperimentalEvolution

Fully funded 4-year PhD position in experimental evolution at the University of Bath (UK).

Application deadline: 11/01/2018

Apply here: https://www.findaphd.com/search/ProjectDetails.aspx?PJID=84040 The Role of Environmental Change in Gene Regulatory Network Evolution

Supervisors: Dr Tiffany Taylor < http://www.bath.ac.uk/bio-sci/contacts/academics/tiffany-taylor/ >; Prof Laurence Hurst < http://www.bath.ac.uk/bio-sci/contacts/academics/laurence_hurst/ >

How does novelty arise in evolution? Does environmental change drive genome complexity, and if so how? These are central questions in evolutionary biology, and they are the questions that drive research in our lab.

Using a combination of molecular genetic manipulations/analyses and experimental evolution, within the context of gene regulatory networks (GRNs) you will explore whether more complex GRNs promote survival and create opportunities for innovation in changeable environments. This project will conduct experiments with a genetically modified common soil bacterium that has had the 'master switch' of the flagellar network deleted. Firstly, it will address the role that gene duplication plays in the evolution of complex gene networks. It will do this by observing the divergence between duplicated genes from a different network that is capable of 'mending' flagellar function (1). Secondly, it will test the hypothesis that more complex networks provide a fitness benefit in less predictable environments (2). It will do this by using genetically manipulated bacteria with stepwise increases in network complexity and evolve them in static and changing environments. Lastly, it will look across a range of bacteria of the same species, which inhabit different environments, to link life-histories with network architecture (3).

Location: This project will be conducted under the direct supervision of Dr Tiffany Taylor with co-supervision from Prof Laurence Hurst, and based at the Department of Biology and Biochemistry at the University of Bath (UK) in the new Milner Centre for Evolution (http://www.bath.ac.uk/groups/milner-centre-for-evolution/). The Milner Centre is a new research centre focused on doing ground breaking research that addresses major questions in evolutionary biology. The Milner Genomics Centre provides on-site facilities and expertise for genome sequencing and analysis for evolution research, and the world-class researchers at the centre creates a vibrant research culture that ensures support and training for the next generation of evolutionary biologist.

Requirements: This is a fully-funded PhD studentship. We are looking for a biology graduate who has a strong interest in genetics and evolution. Some practical experience in microbiology and molecular techniques is highly desired but training will be provided. The successful candidate will be enthusiastic, highly motivated, independent, have experience in microbiology, molecular biology or evolutionary biology (or a combination), and have a relevant degree. The applicant must meet the standard University of Bath English language requirements.

Planned start date: 1 October 2018.

For informal enquiries, please contact Tiffany Taylor <T.B.Taylor@bath.ac.uk>

Funding notes: Funding is available for up to 4 years for an excellent UK/EU student. The studentship will include Home/EU tuition fees and a stipend of 14,553 (2017/18 rate). Applicants who are classed as Overseas for fee-paying purposes are not eligible to receive the funding.

Tiffany Taylor <T.B.Taylor@bath.ac.uk>

UBern SpeciationGenomics

PhD position:

Genomics of speciation of rodents and their microbes

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

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

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

The position is funded by the Swiss National Science Foundation for a maximum of four years. The anticipated starting date is Spring 2018. Please send your application as a single (!) pdf file to Prof. Gerald Heckel: gerald.heckel@iee.unibe.ch. To be considered, the pdf must include a letter describing your past research experience and particular skills and motivation for this position (max. 2 pages), the abstract of your Master thesis, a CV, and contact details of 2-3 referees. Review of applications will begin Januar 8 2018 and will continue until the positions are filled.

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

UBielefeld BehaviouralEvolution

PhD position in Behavioural Ecology

A PhD position in behavioural ecology is available at the Faculty of Biology at Bielefeld University, in the Department of Animal Behaviour (with Prof. Oliver Krueger, see http://www.uni-bielefeld.de/biologie/ animalbehaviour). The position runs from early 2018 to 2021 and is funded by the German Research Foundation (DFG) within the recently approved collaborative research centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

The aim of the PhD project (sub-project C03 of the collaborative research centre) is to conduct a field study on a common buzzard (Buteo buteo) population and to test for consequences of niche choice and niche construction in this species. Making full use of a thirty-year data set and enlarging it, the PhD student will look at the fitness consequences of nest site choice and nest construction with regard to chick growth rate, blood parasite load (Leucocytozoon) and chick survival. It is planned to also conduct field experiments where the amount of nest decoration with green plant material will be manipulated to test for anti-parasitic effects of this material. The ensuing fitness consequences for buzzard chicks will be monitored using lifelong wing-tags and survival and recruitment data will be collected. So far, over 2500 individual buzzards have already been fitted with lifelong wing tags and the resulting data set will be used.

The collaborative research centre: The position will be embedded within a larger collaborative research centre (SFB) comprising 18 principle investigators, 9 postdocs and 16 PhD students based at Bielefeld University, the University of Muenster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programmes. Full details of the SFB can be found at www.uni-bielefeld.de/-biologie/crc212 . Main responsibilities

- Research tasks (90%):

- Conducting field work on a buzzard population from late March to early July each year

- Participation in chick-ringing and the measurement of phenotypic traits from middle of May to early July

- Statistical analyses of complex and long-term data sets

- Collaboration with other research groups in the research centre

- Writing scientific publications

- Organizational tasks in the research group and research centre (10%)

Applicant's profile

We seek a bright and highly motivated student with

- a university degree in a relevant discipline with specialization in behavioural ecology, ornithology, population ecology,

- experience with field work, preferably in birds of prey

- experience with statistical software, preferably R

- interest in both behavioural and life history questions,

- ability to work both independently and as part of a team, and

- excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage:

- papers in peer-reviewed international journals,
- experience in tree-climbing with rope techniques
- experience with large-scale research projects.

Remuneration

Salary will be paid according to Remuneration level 13 (65%) of the Wage Agreement for Public Service in the Federal States (TV-L).

Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling, and prevention programmes. Bielefeld University places great importance on a work-family balance for all its

employees.

Application procedure

To apply, please provide: (i) a letter of motivation including a statement of your research interests and skills and experience relevant to the position; (ii) a CV including publication list; (iii) names and contact details of two referees willing to write confidential letters of recommendation. All materials should be emailed as a single PDF file to: oliver.krueger@uni-bielefeld.de. The application deadline is January 7th 2018 and interviews will take place shortly thereafter. After the decision, the position should start as soon as possible. For further information on the project and the department, please contact Oliver Kruger oliver.krueger@uni-bielefeld.de with any informal inquiries.

Bielefeld is a city of 325,000 inhabitants with all expected amenities and easy access to the Teutoburger Wald for hiking and other outdoor

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UCalifornia Merced InsectMicrobeSymbioses

Insect-Microbe Symbioses and Evolution Graduate Student Opportunity at University of California at Merced

The Bennett Laboratory in the Life and Environmental Sciences Unit at the University of California, Merced is seeking an exceptional Ph.D. student. The student will participate in on-going and emerging areas of research related to insect-microbial symbioses and evolution. The student can develop an original research project or push forward projects that are already established in the group. Preference will be given to an applicant with B.Sc. or M.Sc. in microbiology, entomology, evolution, or genetics.

Areas of active research in the Bennett lab include, but are not limited to: 1) Comparative genomics and molecular evolution of bacterial symbioses in sap-feeding insects. 2) Insect-microbe cellular and metabolic maintenance and integration. 3) The role of insect microbiomes in shaping endemic Hawaiian insect evolution.

Student support will include full tuition waiver, stipend, and Teaching Assistantship. To indicate your interest, please send 1) a cover letter with a brief description of past experience and reasons for interest in the position, 2) a curriculum vitae, and 3) contact information of three references to Gordon Bennett at gbennett2@ucm.edu. More information about this position and research in the Bennett lab is currently available at Bennett Lab Website (https://www.ctahr.hawaii.edu/BennettG/)

Official applications (http://graduatedivision.ucmerced.edu/prospective-students/how-apply) for graduate education in the Quantitative and Environmental Systems Groups at UC Merced (http://les.ucmerced.edu/) should be submitted to the Graduate Division before the deadline of January 15, 2018. Applicants are also encouraged to apply for university-wide fellowship programs (http://graduatedivision.ucmerced.edu/financial-support) for which they are eligible, most of which are due on or before January 15, 2018.

The University of California, Merced is centrally located with easy access to the Sierra Nevada Mountains, Yosemite National Park, the San Francisco Bay

Area, and the California coastline. The Bennett lab also maintains active research projects in the Hawaiian Archipelago, offering exceptional opportunities for natural ecosystems.

U.C. Merced is an affirmative action/equal opportunity employer with a strong institutional commitment to the achievement of diversity among its faculty, staff and students.

Links:

1. LES = http://les.ucmerced.edu/ 2. Official applications http://graduatedivision.ucmerced.edu/-prospective-students/how-apply 3. University-wide fellowship programs http://-graduatedivision.ucmerced.edu/financial-support
4. Current Bennett Lab Website = https:/-/www.ctahr.hawaii.edu/BennettG/ gbennett2@ucmerced.edu

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UCambridge NeuroEvoDevo

PHD: NEURO-EVO-DEVO We invite applications for a funded PhD position in the Department of Zoology in Central Cambridge on Downing Street with Dr Stephen Montgomery's research group.

Developmental basis of mushroom body expansion in Heliconius butterflies

Project summary: Mushroom bodies (MBs) are the most enigmatic structures in the insect brain. They have 'higher order' functions, integrating sensory information and storing memories of past experience. MBs share a conserved ground plan, but their size and structure varies extensively across species. MB volume in Heliconius butterflies are among the highest across insects, 3-4 times larger than typical for Lepidoptera, including their most closely related genera in the wider tribe of Heliconiini. This provides a novel system for investigating the developmental mechanisms that control neural proliferation and brain component size. However, nothing is known about the developmental changes that have produced such a dramatic expansion.

What the student will be doing: The project will involve core laboratory, microscopy and neuroanatomical techniques, insect rearing and experimental manipulation. You will construct the first time course of Heliconius brain development, from late larvae through pupation to adulthood. Using immunocytochemistry and confocal imaging you will determine key properties of MB growth trajectories, providing a template for developing hypotheses of when and how MB development in Heliconius diverged from related genera.

By adopting an evo-devo approach you will then conduct a series of comparative studies across Heliconiini to assess how increases in neuron number are produced, considering four potential mechanisms: i) an increase in the number of neural progenitor cells, ii) accelerated cell-cycle rates during neurogenesis, iii) an extension in the overall duration of neurogenesis including the possibility of adult neurogenesis, iv) reduced or delayed patterns of apoptosis among neural progenitor cells.

Finally, once key periods of developmental divergence have been identified between Heliconius and related genera, you will perform a second series of analyses to identify divergent patterns of gene regulation and expression as part of a project that aims to identify the genetic basis of MB expansion.

Some field/insectary work in Panama may be necessary/desirable. The studentship is funded by the European Research Council for 3.5 years. A student stipend of pounds 14,553 per annum, and tuition fees will be offered to a successful candidate.

FUNDING: The studentship is funded by the European Research Council for 3.5 years. A student stipend of pounds 14,553 per annum, and tuition fees will be offered to a successful candidate.

FURTHER INFORMATION: https://-www.zoo.cam.ac.uk/study/postgraduate/phd-and-mphil-studentships /developmental-basis-of-mushroom-body-expansion-in-heliconius-butterfli es APPLICATION DETAILS: Formal applications are welcome until 27th April.

Shortlisted candidates will be interviewed in early May and a decision will be made soon after. Informal enquiries to shm37@cam.ac.uk are welcome. For more details see: https://www.zoo.cam.ac.uk/-study/postgraduate RESEARCH GROUP: http://-www.shmontgomery.co.uk Dr. Stephen Montgomery NERC Independent Research Fellow Dept. of Zoology, University of Cambridge Downing St. Cambridge, CB2 3EJ Tel: 01223336678 Email: shm37@cam.ac.uk Twitter: @eohomo Departmental webpage Personal webpage

Stephen Montgomery <shm37@cam.ac.uk>

UDenver EvolutionAnimalBehavior

Graduate Positions in Behavioral Ecology in the Tinghitella Lab at the University of Denver.

The Tinghitella lab at the University of Denver (https://tinghitellalab.weebly.com) is recruiting motivated new graduate students to begin in the fall of 2018. Work in the lab centers on the roles of ecology and behavior in (rapid) evolutionary change. We mix field and laboratory work to understand the forces that shape diversity in animal communication and mating systems. Recently we've been thinking a lot about how human impacts alter the mating environment and the evolutionary implications of those perturbations. Graduate students will be supported through teaching assistantships (2 years MS and 5 years PhD). I am specifically recruiting students interested in working on Pacific field crickets. Graduate students will be expected to develop their own projects within the scope of the lab, but topics are open. Recent work in the field cricket system has addressed rapid evolution of sexual signals, plasticity in mate choice, and effects of anthropogenic noise on acoustically communicating invertebrates.

Please contact Robin Tinghitella, robin.tinghitella@du.edu, for more information. Additional information about our graduate program and DU's vibrant group of Organismal Biologists can be found at https://www.du.edu/nsm/departments/biologicalsciences/degreeprograms/phd.html and https://sites.google.com/site/duecoevo/home. The deadline for applications to the graduate program in Biological Sciences is January 1, 2018.

Robin Tinghitella <Robin.Tinghitella@du.edu>

UGlasgow CancerEvolution

4-year PhD studentship: Algorithmic analysis of clonal evolution and therapeutic resistance in pancreatic cancers

Web: https://www.gla.ac.uk/research/ourresearchenvironment/prs/kelvinsmith/shortlistedscholarshipprojectsfor201819/seyuanpancreaticcancer/#d.en.562042 Keywords: machine learning, statistical modelling, cancer genomics, metabolomics, pancreatic cancer

Project Summary Pancreatic cancer is the 4th leading cause of death in western societies, and predicted to be the second within a decade. Genomic sequencing of ~520 pancreatic cancer cases, by the Glasgow pancreatic cancer team, has provided the foundation to understand tumour biology and identify improved therapeutic options for pancreatic cancer, in which there has been minimal improvement in outcomes for 40 years.

These data suggest that many patients develop resistance with therapy either by selecting for resistant clones within the tumour, or through the rapid acquisition of secondary mutations. Understanding cancer evolution and the resulting subclonal architecture of cells within a tumour is thus essential to developing the next generation of therapeutics. This proposal aims to develop machine learning algorithms that reveal patterns of cancer evolution at multiple 'Vomics levels (genomics, transcriptomics, and metabolomics) and link these with therapy to identify mechanisms of resistance and inform combinatorial therapeutic strategies.

The project will be based on a solid foundation of algorithmic and experimental advances in genomics [1], transcriptomics [2] and metabolomics [3] by the team members. The candidate will have the opportunity to develop highly sophisticated probabilistic models and test them on large scale patient data, including data from ongoing clinical trials as part of the Precision-Panc project.

Reference: [1]. Yuan, K., et al. (2015) BitPhylogeny: a probabilistic framework for reconstructing intra-tumor phylogenies. Genome Biology, 16(1), p. 36. [2]. Bailey, P. et al. (2016) Genomic analyses identify molecular subtypes of pancreatic cancer. Nature, 531(7592), pp. 47-52. [3]. van Der Hooft et al (2016) Topic modeling for untargeted substructure exploration in metabolomics. Proceedings of the National Academy of Sciences of the United States of America, 113(48), pp. 13738-13743.

Project Team The successful candidate will be jointly supervised by Drs Ke Yuan and Simon Rogers at the School of Computing Science, Prof. Andrew Biankin, Drs Peter Bailey and David Chang at the Institute of Cancer Sciences.

The candidate will be primarily based in the Inference, Data, and Algorithms (IDA) section at the School of Computing Science where he or she will be benefit from interactions with experts in machine learning and statistical inference. In addition, the School is an integral part of the Scottish Informatics and Computer Science

Alliance (SICSA), which organise events in its Data Science section.

The candidate will also be a member of the Translational Research Centre at Institute of Cancer Sciences. This will enable the candidate to interact with leading biologists and clinicians from the greater cancer research community in Glasgow. In addition, the candidate will have the opportunity to collaborate in large international (International Cancer Genome Consortium), UK (Precision-Panc) and Scottish consortiums (Scottish Genome Partnership).

Person Specification This studentship is open to candidates of any nationality 'V UK, EU or International. Applicants should demonstrate the following: - Academic qualifications: Undergraduate Degree - 2:1/1; Master'Âs Degree (Desired) - Pass /Merit /Distinction - Experience: We welcome candidates from computational backgrounds (i.e. machine learning, statistics, and related fields) who are interest in developing methods for biomedical problems. Candidates with experimental backgrounds (i.e. molecular biology, systems biology and related fields) who want to move into computational biology are encouraged to apply as well. Previous experience with analysing sequencing data is a plus. - Skills: Good programing skills in Python or R.

Application Process In the first instance, prospective applicants should contact Dr Ke Yuan, ke.yuan@glasgow.ac.uk to discuss your eligibility. Applicants may submit applications up until the application deadline of 12 noon, Friday 12 January 2018. The following documentation will be required from applicants if they are invited to submit a full application: - LKAS Interdisciplinary Scholarships Application Form - 2 references in support of your application. (The references relevant to the application for admission to Glasgow for PhD study may be submitted to this process 'V they do not need to be tailored to this process.)

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UGothenburg 2 PlantSystematics

Within the Gothenburg Global Biodiversity Centre < https://ggbc.gu.se/ >, (GGBC) University of Gothenburg, Sweden, two PhD positions are open for application November 1st, 2017 until January 15th, 2018. The positions are part of the EU International Training Network programme PlantID < http://www.plantid.uio.no/ >, which announces 15 PhD student positions < http://www.plantid.uio.no/jobs/ > simultaneously. We seek highly motivated students to tackle taxonomic problems in the flowering plant genus *Silene* ranging from polyploidy, species delimitations, and it relations to conservation. The positions start in April 1st, 2018, and are fully funded including salary and social security benefits for four years. To be eligible to apply, you must not have been a resident in Sweden more than 12 months the last three years. See the below links for more details:

- Species, a taxonomic category distinct from the lineage concept? A case study on species delimitation in Silene sect. Dipterospermae in Southern Africa < http://www.plantid.uio.no/jobs/phd-fellowship-14.html >

- Polyploid phylogenetics under the multi-species coalescent < http://www.plantid.uio.no/jobs/phd-fellowship-01.html >

Supervisors:

Bengt Oxelman < https://www.gu.se/omuniversitetet/personal/?userId=xoxebe >

Christine Bacon < https://bioenv.gu.se/personal?userId=xbacoc >

– 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>

UGreifswald BiologicalAdaptation

University of Greifswald, Zoological Institute and Museum

PhD position in Animal Ecology

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/ . Job offers - Fakultät - Ernst-Moritz-Arndt-Universität ... < https://biologie.uni-greifswald.de/-forschung/dfg-graduiertenkollegs/research-training-group-2010/job-offers/ > biologie.uni-greifswald.de The Research Training Group "Biological responses to novel and changing environments - RESPONSE" (RTG 2010), funded by the Deutsche Forschungsgemeinschaft (DFG ...

Starting date: April 1st 2018.

Duration: 3 years.

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

Thesis topics: Genetic and environmental effects on the morphology, physiology and behaviour of a European butterfly.

Background: In holometabolous insects, adult characteristics are largely determined during their early stages of life (eggs, larvae). Accordingly, we recently found that Pieris napi butterflies exposed to a high temperature as pre-adults showed smaller wings, higher wing loading, and a change in the ratio between their forewing and hindwing when adults. Interestingly, these effects varied with the latitudinal origin of butterflies. This suggests that early thermal conditions may determine the ability of adult butterflies to disperse, and that these effects vary between populations. However, such changes in flight ability are likely to generate trade-offs with other energy-demanding functions (e.g. physiology, thermal tolerance), which may ultimately limit the dispersal potential of butterflies.

Goals of the project: Here, we will investigate plastic and genetic variation in the morphology (wing characteristics, pigmentation, body mass, thorax musculature), physiology (oxidative status, immune response, lipid composition, cuticle desiccation resistance, pigmentation) and behaviour (flight characteristics) of the butterfly Pieris napi exposed to different thermal regimes as pre-adults. We will use replicated populations of P. napi across a latitudinal gradient across Europe (i.e.from warm to cold environments) to establish the interrelations between these parameters and to examine their heritability under variable environmental conditions. Specifically, we will test the following hypotheses: (1) morphological, physiological and behavioural characteristics are inter-related; (2) the effects of early thermal conditions on the morphology, the physiology and the behaviour of butterflies vary with the latitudinal origin of butterflies, (3) flight ability determined by early thermal conditions is negatively related to the thermal tolerance of adults, (4) heritability of the investigated traits is not significantly affected by thermal conditions (parent-offspring regressions will be used to estimate heritability). Most of the project will be conducted in captivity but will also involve some fieldwork. This project will be conducted in collaboration with research partners at the Universities of Greifswald, Koblenz-Landau, Ljubliana and Amsterdam.

Required skills:

§Strong background in behavioural and evolutionary ecology

§Interest, knowledge and previous experience with biochemical analyses

§Knowledge in experimental design, data handling and statistical analyses

§Interest in entomology and lepidopterology

§Expertise in field methods (preferentially with insects and butterflies)

§Interest in flight biomechanics

§Good command of English; basic knowledge in German would be an advantage

§Organizational skills, willingness and ability to work in a team

To apply, please visit our website: https://www.uni-greifswald.de/universitaet/-information/stellenausschreibungen/oeffentliche-stellenausschreibungen/wissenschaftliches-personal/-graduiertenkolleg-rtg-2010-17wi23/ Graduiertenkolleg RTG 2010 17/Wi23 - Universität Greifswald < https://www.uni-greifswald.de/universitaet/-information/stellenausschreibungen/oeffentliche-stellenausschreibungen/wissenschaftliches-personal/-graduiertenkolleg-rtg-2010-17wi23/ >

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UHamburg SystematicsGastropods

Universität Hamburg, Center of Natural History, invites applications for a Research Associate for the project

"Exploring genomic methods for delimiting species in radiations of terrestrial snails"

in accordance with Section 28 subsection 3 of the Hamburg Higher Education Act (Hamburgisches Hochschulgesetz, HmbHG). The position commences earliest on 1.2.2018.

It is remunerated at the salary level TV-L 13 and calls for 65 % of standard work hours per week*.

The fixed-term nature of this contract is based upon Section 2 of the Academic Fixed-Term Labor Contract Act (Wissenschaftszeitvertragsgesetz, WissZeitVG). The term is fixed for a period of 3 years.

The metropolis Hamburg is one of the most popular cities in Europe and harbors one of the largest universities in Germany. The University aims to increase the number of women in research and teaching and explicitly encourages qualified women to apply. Equally qualified female applicants will receive preference in accordance with the Hamburg Equality Act (Hamburgisches Gleichstellungsgesetz, HmbGleiG).

Responsibilities: Duties include academic services in the project named above. Research associates can also pursue independent research and further academic qualifications.

Specific Duties: The doctoral student will study the evolutionary history of land snail radiations and evaluate and optimize different genomic approaches for delimiting closely related species, both with regard to laboratory and analytical methods, within the framework of the DFG SPP 1991 Taxon-OMICS (see http://taxon-omics.de/). Field work and the conservation of material also pertains to the duties.

Requirements: A university degree in a relevant field. The candidate should be experienced with molecular biological methods and preferentially also with "next generation sequencing" techniques and data analyses or a programming language (Perl, Python, R, etc.). The project requires analytical thinking and good English skills (German language skills are not absolutely necessary, the working language is English).

Severely disabled applicants will receive preference over equally qualified non-disabled applicants.

For further information, please contact Prof. Bernhard Hausdorf.

Applications should include a cover letter detailing your research interests and experience, curriculum vitae, and copies of degree certificates. The application deadline is December 22, 2017. Please send applications as a single pdf file to: Prof. Bernhard Hausdorf, hausdorf@zoologie.uni-hamburg.de.

– Prof. Dr. Bernhard Hausdorf Abteilungsleiter Malakologie Centrum für Naturkunde (CeNak) - Center of Natural History Universität Hamburg - Zoologisches Museum Martin-Luther-King-Platz 3 20146 Hamburg - Germany P +49 40 42 838 2284 Email: hausdorf@zoologie.uni-hamburg.de https://www.cenak.uni-hamburg.de/en/forschung/zoologie/malakologie/publikationen.html "hausdorf@zoologie.uni-hamburg.de"

UIllinois FishEvolution

The Fuller lab at the University of Illinois at Urbana-Champaign is looking for motivated graduate students interested in the evolution of fishes. The Fuller lab focuses on two broad topics: (a) speciation in fish as a function of local adaptation, chromosomal rearrangements, and community structure and (b) the evolution of color patterns, color vision, and sexual selection in different habitat types. We use a variety of approaches (fieldwork, lab experiments, sequencing, quantitative genetics) in three main study systems: Lucania killifish, darters, and largemouth bass. We are increasingly moving into genomics. Find out more about what we do at our website (http://beckyfullerlab.weebly.com/). Students can apply through either the Program in Ecology, Evolution and Conservation(http://sib.illinois.edu/peec/) or the Department of Animal Biology grad program (http://www.life.illinois.edu/animalbiology/graduate_program.htm). Applications are due by December 15, 2017 for full consideration for graduate college fellowships and the deadline for general consideration is January 1, 2018.

The University of Illinois at Urbana-Champaign also offers state-of-the-art research facilities in imaging, genomics, and engineering. Urbana-Champaign is a pleasant, affordable, university town with good music and restaurants. It has its own airport and is close to three major U.S. cities (Chicago, Indianapolis, St. Louis).

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

Email Becky Fuller (fuller@life.illinois.edu) for more information.

fuller@life.illinois.edu

UIowa EvolutionaryBiology

A number of graduate student (Ph.D. or MS) positions—are—available at the Department of Biology, University of Iowa to study a variety of topics related to the Biology of Stress Responses. Topics and Laboratories are detailed below.

The Department of Biology provides the opportunity for highly multidisciplinary training, with faculty with expertise in neurobiology, cellular and developmental biology, bioinformatics, genetics, genomics and evolution, and research that covers all eukaryotic model organisms. The University of Iowa is located in Iowa City, a vibrant mid-sized city that perennially ranks in the top 10 as a "Best Place to Live" http://www.iowacityareadevelopment.com/live/-rankings.aspx). It is the first UNESCO City of Literature in the U.S. and hosts a wide variety of cultural, artistic, and sporting events year-round.

—– Topic: Evolution of Gene Regulatory Networks Controlling Stress Responses in Commensal Yeast

Graduate student (Ph.D. or MS) positions—are—available in—the laboratory of Dr. Bin Z. He (https://-www.binhe-lab.org/). The Gene Regulatory Evolution (GRE) lab is led by the newest member of the Biology Department, Dr. Bin He, who recently finished his postdoc at Harvard University and Princeton University. The GRE lab investigates the genetic basis for the evolution of gene regulatory networks and how that impacts the biology of the organism. In particular, we focus on the networks controlling stress responses, which are evolutionarily dynamic because species encounter new environments constantly. Our previous work has revealed an intriguing phenomenon of network expansion in a commensal yeast, C. glabrata, whose close relatedness to the model species S. cerevisiae and yet distinct ecology of commensalism make it an ideal system to understand the evolution of stress responses. We are currently working to extend our previous work in a single starvation response to a broad array of starvation and stress responses. The goal is to obtain a comprehensive map for multiple stress responses in this species to understand the genetic mechanisms for adaptation. Potential graduate students seeking to join the lab will work closely with Bin to unravel the mystery of network evolution, using cutting edge functional genomics, biochemistry and bioinformatics tools. A high degree of motivation and commitment and integrity in science are expected. The GRE lab is affiliated with the Department of Biology (iBio; https://biology.uiowa.edu/ibio) graduate program. —

Most Relevant Publications: - He, B.Z., Zhou, X., and O'Shea, E.K. (2017). Evolution of reduced co- activator dependence led to target expansion of a starvation response pathway. eLife 6, e25157. For more information, check https://www.binhe- lab.org or https://binhe.org To apply please contact Bin Z. He (bin-he@uiowa.edu) and send a cover letter with a brief summary of research experience and interests, CV, and the contact information for 3 referees.

—– Josep M. Comeron (josep-comeron@uiowa.edu), Veena Prahlad (veena-prahlad@uiowa.edu) and Bin He (bin-he@uiowa.edu)

"Comeron, Josep M" <josep-comeron@uiowa.edu>

ULaval SticklebackEvolutionaryGenomics

Ph.D. position: Evolutionary genomics in Stickleback

The joint Bernatchez's https://www.bio.ulaval.ca/-louisbernatchez/presentation.htm and Aubin-Horth's http://wikiaubinhorth.ibis.ulaval.ca/Aubin-Horth:Lab_Members Labs at Université Laval (Québec City, Canada) https://www.ulaval.ca/en/research.html are currently searching for a Ph.D. candidate to be involved in our new research project:

Two sexes, one genome: source and consequences of sexually antagonistic selection in Stickleback.

The basic overarching goal of this project is to gain fundamental knowledge about the impact of intra-locus sexual selection in animal populations in their natural environment. Using the Threespine Stickleback in its natural environment as a study system, we will test the general hypothesis that differentially expressed genes between the two sexes are more subject to the effect of sexually antagonistic selection than other genomic regions, resulting in maintenance of superior genetic diversity.

The specific objectives of the project are: 1: To quantify the magnitude of the effect of sexually antagonistic intra- locus selection by comparing allele frequencies between males and females at three stages of life using whole genome resequencing; 2: Quantify the differential gene expression between sexes at different life stages by means of genome-wide RNAseq; 3: To test the hypothesis that the relationship between the magnitude of differential gene expression and the intensity of sexually antagonistic selection follows a bimodal "Twin Peaks" pattern; 4: To test the hypothesis that allelic variation of genes under sexually antagonistic selection affects reproductive success in both sexes and link fitness to the functions of these genes.

Required Qualifications: We are primarily searching for a prospective candidate combining a solid background in evolutionary biology, experience in field and molecular work, demonstrated bioinformatics skills and being familiar with scripting and programming. The ideal candidate should also be familiar with analyses of population data sets derived from whole genome resequencing and transcriptomic profiling.

We are looking for a candidate to join our team in early May for the beginning of the first field season. Salary established according to local University standards will be provided during the whole course of the Ph.D.

Université Laval is located in beautiful and historic Québec City http://www.quebecregion.com/en/ surrounded by stunning nature perfect for any outdoor experience: http://parcmarin.qc.ca/ https://www.sepaq.com/pq/jac/ https://www.sepaq.com/pq/grj/

Université Laval also offers the lowest tuition fees (2500$/year) in North America.

While the University is francophone, PhD defense and thesis can be done in English.

To apply, please send the following documents in a consolidated single PDF file: a cover letter describing your research interests and qualifications, a complete CV, and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca Nadia.Aubin-Horth@bio.ulaval.ca

Do not hesitate to contact us directly for any further details or questions.

Louis Bernatchez Canadian Research in Genomics and Conservation of Aquatic Resources Institut de Biologie Intégrative et des Systèmes, Pavillon Charles-Eugene Marchand Université Laval Québec, QC G1V 0A6 Canada Phone: 1 418 656-3402

Louis Bernatchez <Louis.Bernatchez@bio.ulaval.ca>

ULaval StickleBackGenomics

Ph.D. position: Evolutionary genomics in Stickleback

The joint Bernatchez's https://www.bio.ulaval.ca/louisbernatchez/presentation.htm and Aubin-Horth's http://wikiaubinhorth.ibis.ulaval.ca/Aubin-Horth:Lab_Members Labs at Université Laval (Québec City, Canada) https://www.ulaval.ca/en/research.html are currently searching for a Ph.D. candidate to be involved in our new research project:

Two sexes, one genome: source and consequences of sexually antagonistic selection in Stickleback.

The basic overarching goal of this project is to gain fundamental knowledge about the impact of intra-locus sexual selection in animal populations in their natural environment. Using the Threespine Stickleback in its natural environment as a study system, we will test the general hypothesis that differentially expressed genes between the two sexes are more subject to the effect of sexually antagonistic selection than other genomic regions, resulting in maintenance of superior genetic diversity.

The specific objectives of the project are: 1: To quantify the magnitude of the effect of sexually antagonistic intra- locus selection by comparing allele frequencies between males and females at three stages of life using whole genome resequencing; 2: Quantify the differential gene expression between sexes at different life stages by means of genome-wide RNAseq; 3: To test the hypothesis that the relationship between the magnitude of differential gene expression and the intensity of sexually antagonistic selection follows a bimodal "Twin Peaks" pattern; 4: To test the hypothesis that allelic variation of genes under sexually antagonistic selection affects reproductive success in both sexes and link fitness to the functions of these genes.

Required Qualifications: We are primarily searching for a prospective candidate combining a solid background in evolutionary biology, experience in field and molecular work, demonstrated bioinformatics skills and being familiar with scripting and programming. The ideal candidate should also be familiar with analyses of population data sets derived from whole genome resequencing and transcriptomic profiling.

We are looking for a candidate to join our team in early May for the beginning of the first field season. Salary established according to local University standards will be provided during the whole course of the Ph.D.

Université Laval is located in beautiful and historic Québec City http://www.quebecregion.com/en/- surrounded by stunning nature perfect for any outdoor experience: http://parcmarin.qc.ca/- https://www.sepaq.com/pq/jac/ https://-www.sepaq.com/pq/grj/ Université Laval also offers the lowest tuition fees (2500$/year) in North America.

While the University is francophone, PhD defense and thesis can be done in English.

To apply, please send the following documents in a consolidated single PDF file: a cover letter describing your research interests and qualifications, a complete CV, and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca Nadia.Aubin-Horth@bio.ulaval.ca

Do not hesitate to contact us directly for any further details or questions.

Louis Bernatchez Canadian Research in Genomics and Conservation of Aquatic Resources Institut de Biologie Intégrative et des Systèmes, Pavillon Charles-Eugene Marchand Université Laval Québec, QC G1V 0A6 Canada Phone: 1 418 656-3402

Louis Bernatchez <Louis.Bernatchez@bio.ulaval.ca>

ULeicester CancerEvolution

A competitive 4-year PhD studentship is available to study the mutation and evolution of somatic copy number changes in mesothelioma, the cancer caused by asbestos exposure, in collaboration with Prof Frank Dudbridge and Prof Dean Fennell.

UK/EU/EEA nationals only are eligible.

Details of the project are here https://www2.le.ac.uk/-departments/genetics/postgraduate/documents/cls-ggb-studentship-2018/Hollox_Genetics_PhD_2018.pdf Apply here https://www2.le.ac.uk/research-degrees/-phd/genetics Any other questions, please email me at ejh33@leicester.ac.uk

Dr Ed Hollox, Department of Genetics and Genome Biology, University of Leicester, UK

"ejh33@leicester.ac.uk" <ejh33@leicester.ac.uk>

ULeicester GibbonCopyNumberVariation

A competitive 4-year PhD studentship is available through the MIBTP (Midlands Innovative Biosciences Training partnership) doctoral programme to study the copy number variation of the gibbon genus with me, Dr Ed Hollox, and Dr Richard Badge, in collaboration with Twycross Zoo, Leicestershire.

UK/EU/EEA nationals only are eligible.

Details of the project are here https://www2.le.ac.uk/-research-degrees/doctoral-training-partnerships/-bbsrc/HolloxPhDproject.pdf Details of the MIBTP programme are here https://www2.le.ac.uk/research-degrees/doctoral-training-partnerships/bbsrc Any other questions, please email me at ejh33@leicester.ac.uk

Dr Ed Hollox, Department of Genetics and Genome Biology, University of Leicester, UK

"Hollox, Ed (Dr.)" <ejh33@leicester.ac.uk>

UMainz AntEvolution

PhD position (3 years) - Genetic components to division of labor in ant societies - JGU Mainz

Application deadline: January 20^th, 2018

Behavioral division of labor in ant societies stems from workers differing in their likelihood and efficiency to perform specific tasks (e.g., foraging for food or nursing the brood). However, many factors and mechanisms regulating such differences remain to be identified and understood. The Libbrecht group at the Johannes Gutenberg University of Mainz (Germany) is offering a 3-year PhD position (German Research Foundation, fully funded, 65% TVL E13) to study the genetic effects on worker behavior in the Argentine ant (Linepithema humile). The research will include ant collection in the field, controlled crosses in the lab, behavioral experiments, ant dissections, molecular biology techniques and RNA sequencing analyses. The student will get hands-on training in experimental design, statistics and bioinformatics.

We are looking for a highly motivated student with a Master degree (or equivalent) in biology, good English skills, and a keen interest in animal behavior and evolutionary biology. Previous experience with social insects, behavioral experiments, statistics and bioinformatics is advantageous, but not required.

The successful applicant will join an international, interactive, dynamic and English-speaking scientific environment in a brand new building with access to state-of-the-art, newly equipped laboratories and climate-controlled rooms. The Johannes Gutenberg University of Mainz hosts many excellent scientific institutions, and Mainz is a historic city located on the Rhine River with a large student population and a rich social and cultural life.

Applications should include a 1-page cover letter 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 the names and email addresses of two potential referees. Please send all documents as a single PDF file before January 20^th 2018 to Dr. Romain Libbrecht (romain.libbrecht@uni-mainz.de). The ideal starting date for the position is April 1^st 2018, but is negotiable.

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

Dr. Romain Libbrecht Assistant Professor / Junior Group Leader Institute of Organismic and Molecular Evolution Johannes Gutenberg University Mainz, Germany +49 6131 3927852 http://www.bio.uni-mainz.de/-zoo/evobio/608_ENG_HTML.php Romain Libbrecht <romain.libbrecht@gmail.com>

UMuenster DrosophilaEvolution

The Institute for Evolution and Biodiversity at the University of MÂÂ^{1}nster, Germany, is seeking to fill the post of a

*PhD Position *

(salary level TV-L E13, 65%)

to study social niche-mediated reproductive phenotypes

This fixed-term post will start on *1 February 2018* (or soon thereafter) and is available for 36 months. Currently, the regular working time for full employment is 39 hours and 50 minutes per week. The position is 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 (NC^3), as granted by the German Research Foundation (DFG).

This project involves studying the fruit fly /Drosophila melanogaster/ to determine how social interaction during development affects the evolutionary outcome of sexual trait expression, as the developmental social environment can provide an individual with cues about what to anticipate regarding the reproductive environment they will face during adulthood. Within this project, the successful candidate will study the effects of the social niche on male and female reproductive phenotypes combining behavioural, evolutionary and molecular techniques. In an experimental evolution study, the candidate will assess the long-term evolutionary consequences of manipulations of the social environment Additionally, short-term assays will provide information about if developmental plasticity in morphological and behavioural traits has consequences for fitness. This project will combine behavioural and fitness assays with molecular work and an experimental evolution approach to gain more insight into the evolutionary consequences of niche conformance.

Applicants should be highly motivated students of any nationality, and they should have the equivalent of a master'Âs degree in behavioural ecology or evolutionary ecology. A background in any of the following areas will be useful: previous experience with practical /Drosophila/ or other insect work, good molecular skills, and (of particular relevance) previous experience with 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.

The University of MÂÂ^{1}nster is a large vibrant university hosting a number of excellent scientific institutions (http://www.uni-muenster.de/en/). The Institute for Evolution and Biodiversity provides a stimulating research environment with a number of scientific groups researching diverse topics centred on different aspects of evolution. Additionally, students can benefit from the structured PhD program offered by the MÂÂ^{1}nster Graduate School of Evolution (http://www.uni-muenster.de/Evolution/mgse/). As a part of the Collaborative Research Centre SFB/TRR 212, the project will involve intensive collaboration with consortium partners at the Universities of MÂÂ^{1}nster and Bielefeld. The town of MÂÂ^{1}nster itself has many students and presents a dynamic environment with many cultural and social events throughout the year (http://www.muenster.de/en/).

The Universityof MÂÂ^{1}nster 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. Please send your application in one single PDF file by *14 January 2018* to Dr Claudia Fricke (Claudia.Fricke@uni-muenster.de <mailto:Claudia.Fricke@uni-muenster.de>). Applications should include 1) a cover letter with a statement of research interests and motivation (max. 1 page), 2) CV including details about research experience (please include the abstract of your master'Âs thesis) and 3) contact details of at least two referees.

– Claudia Fricke Junior Research Leader

University of Muenster Institute for Evolution and Biodiversity HÂÂ^{1}fferstr. 1 48 149 Muenster, Germany

Tel. ++49(0)251-83 21042 e-mail: Claudia.Fricke@uni-muenster.de http://ieb.uni-muenster.de/evolseco Claudia Fricke <Claudia.Fricke@uni-muenster.de>

UMuenster EvolutionaryCapacitance

PhD position: Evolutionary capacitance in the red flour beetle

We invite applications for a PhD position to study the role of evolutionary capacitance in the red flour beetle Tribolium castaneum. The position is available for three years at the Institute for Evolution and Biodiversity at the University of MÂÂ^{1}nster in Germany. It is 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 this 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 MÂÂ^{1}nster 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 MÂÂ^{1}nster and Bielefeld. The town of MÂÂ^{1}nster 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 a highly motivated student of any nationality and those with the equivalent of a Master'Âs degree in 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 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

Phone (secretary): + 49 251 83 21638 / 21027 Phone (direct): + 49 251 83 24661 Fax: + 49 251 83 24668 Room: 109 joachim.kurtz@uni-muenster.de http://www.uni-muenster.de/Evolution/animalevolecol/kurtz.shtml DFG Research Training Group GRK 2220 EvoPAD https://www.uni-muenster.de/EvoPAD/ DFG SFB-TRR 212 NC3 http://www.uni-bielefeld.de/biologie/crc212/index.html

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UMunich BorreliaPathogenAdaptation

PhD position at the University of Munich (LMU, Germany) as part of a project funded by the German Research Foundation (DFG).

*Duration: *3 years, Starting Date: Spring 2018

Topic: HOST AND VECTOR ADAPTATION IN THE TICK-BORNE HUMAN PATHOGENS BORRELIA

*Supervisor: *Dr. Noémie Becker (http://evol.bio.lmu.de/research/becker/index.html)

*Project summary**:*To be able to survive, parasitic vector-borne bacteria have developed a range of sophisticated means to adapt to their hosts and vectors. Here we plan to use population genomics methods to identify genetic factors involved in host and vector adaptation in two bacteria species responsible for Lyme disease: /Borrelia garinii/and /B. bavariensis/. Both species are present in Europe and Asia and both are human pathogens. They differ by the type of animal used as reservoir-host and /B. bavariensis/is composed of at least two separated populations using different tick vector species.In ourstudy we will reconstruct the evolutionaryhistory of these two species using strains from Eastern Asia, Western Europe and Russia. We will then study the evolution of genes that are candidates for playing a role in host and/or vector adaptation and test whether these genes are under selective pressure. Next, we will identify novel genes under selection that might be responsible for host or vector adaptation in the two species under study. Finally, we will look for functional validation of the role played by those genes in infection and survival in the host or the vector.

Our study will be ofepidemiological importance as it will help to predict the spread of the different /Borrelia/species andwill also ultimately contribute to the understanding of why certain /Borrelia/species are human pathogenic and how the genetic mechanisms involved in human immune system evasion evolved.

Necessary skills(or to be acquired within the first months of PhD):

- theoretical knowledge in population genetics

- some experience in omics: sequencing, assembly, mapping of NGS data

- basic microbiology lab skills

- basic R and statistics

- basic Ubuntu/Linux

Skills that will be acquired during the PhD:

- knowledge of the Lyme Borrelisosis system

- Borrelia lab work and sequencing

- Field work (Germany and Japan)

- Population genetic methods (phylogeny, recombination, selection)

- Protein-structure prediction

- Protein-binding assays

- Borrelia genetic manipulation

The successful applicant will join the group of Dr. Becker within the Division of Evolutionary Biology and will also be eligible to apply to jointhe Graduate School Life Science Munich (http://www.lsm.bio.lmu.de/) that proposes networking and specific training for PhD students.

How to apply:

Please send CV, motivation letter and contact of 2 referees as a single pdf file before *DECEMBER 18, 2017*to Noémie Becker (nbecker@bio.lmu.de).

– Dr. Noémie Becker Division of Evolutionary Biology Ludwig-Maximilian University Grosshaderner Str. 2 D-82152 Planegg-Martinsried, Germany Phone: +49 (0)89 2180 74106 Email: nbecker@bio.lmu.de Office: B.01.005

Noémie Becker <nbecker@biologie.uni-muenchen.de>

UOtago NZ 3 EvolutionaryBiol

Three PhD projects.

PhD Project Opportunity

Parasitic Puppeteers - How do They Pull the Strings? We are currently seeking a PhD student with interests in genetics, evolution, parasitology and neuroscience to investigate the molecular mechanisms through which parasitic worms alter the behaviour of their insect hosts.

Project Description Parasites can have profound effects on the animal hosts they invade, manipulating host biology with exquisite precision to enhance host-to-host transmission. One of the most extraordinary of these host manipulations is the water-seeking behaviour that some nematodes and hairworms induce in their hosts so that the worms might exit the host and reproduce. The process is the stuff of science fiction; the worm hijacks the host'Âs central nervous system forcing it to seek water. Once water is found the adult worm, often many times the size of the host, emerges, sacrificing the host. This amazing alteration in behaviour is induced by parasitic worms spanning two phyla (Nematoda and Nematomorpha) and is observed in a variety of arthropod hosts, notably crickets, weta, earwigs, and sandhoppers, leading us to hypothesise that a common and conserved mechanism is being utilised by the parasites to induce this behaviour in their hosts. Here we propose to couple field and laboratory studies of two phylogenetically distinct hosts and their parasites, with powerful genomic and bioinformatic comparisons to elucidate the trigger and genetic cascade through which these parasitic puppeteers elicit this highly conserved, yet astonishing behavioural response.

The project emerges from a Marsden Grant headed by Professor Neil Gemmell (Anatomy) in collaboration with Professor Robert Poulin (Zoology) and will be based in the Gemmell laboratory at the University of Otago.

The Ideal Candidate The ideal candidate will possess experience in molecular genetics/genomics, evolutionary biology and bioinformatics. Knowledge of NGS approaches and analyses us desirable, while past work in comparative genomics and an interest in parasitology and neurobiology may be helpful. They candidate will be motivated and organized, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research project. They will be collegial and able to work alongside a wide variety of people. In addition they will have a strong commitment to academic and research excellence. Minimum qualifications: B.Sc. (Hons) and/or M.Sc. in Genetics, Genomics, Molecular Biology or equivalent with an A-average or better.

Scholarship Funding: A scholarship NZ$25,000 p.a. plus fees will be available to the successful applicant.

Eligibility: Applications are invited from all nationalities. However, candidates for whom English is not a first language must satisfy the English language requirements to be eligible for study at the University of Otago. Our entrance requirements for international students are detailed here: http://www.otago.ac.nz/future-students/-international/index.html . How to Apply: Interested applicants are encouraged to make informal enquiries to Professor Neil Gemmell. Please send a cover letter explaining your interest in and suitability for the role together with a curriculum vitae, a copy of your academic transcript, a sample of your written scientific work, proof of English language competency (if necessary), and the names of three referees to:

Professor Neil J. Gemmell e-mail: neil.gemmell@otago.ac.nz

Further information Gemmell lab < http://gemmell-lab.otago.ac.nz/ >

Applications close on the 15/1/18. It would be desirable if the successful applicant were able to start by early 2018.

PhD Project Opportunity

Population Genomics of The New Zealand Lamprey We are currently seeking a PhD student with interests in genetics, evolution, and ecology to work on the population genomics of the New Zealand lamprey.

Project Description The New Zealand lamprey is an enigmatic, but culturally important species, found in the streams of rivers of both North and South Island. In this project we will undertake the first comprehensive analysis of the New Zealand lamprey population genetics using the latest population genomic approaches. We will use these data to explore issues spanning taxonomy, population genetic structure, population viability and health. These data are vital to the ongoing management of this species as its distribution and numbers both appear to be in steady decline, likely due to increased use on water resources, competition and potentially pollution. A further threat is a disease, known as lamprey reddening syndrome, that is observed now at high frequencies in some populations. There may be prospects to use genomic approaches to determine the underpinning causes of this emerging

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UOxford 2PhD EvolutionHumanBehaviour

* Project: The effect of network structure and dynamics on social behaviour in humans*

* Deadline for expressions of interest: 15 December 2017*

Applications are invited for two fully-funded Oxford-Calleva Graduate Scholarships, supported by the University of Oxford and the Calleva Research Centre at Magdalen College, Oxford. The successful applicants will be part of an interdisciplinary team working on a 4-year project funded by the Calleva Research Centre at Magdalen College, to begin in October 2018.

The project will bring together two research groups based at the University of Oxford, working on a range of topics relating to human social behaviour, including cultural evolution, the evolution of cooperation, and the social psychology of inter-group contact. The project's Principal Investigator, Laura Fortunato, is Associate Professor of Evolutionary Anthropology, a Fellow of Magdalen College, and an External Professor at the Santa Fe Institute. The Co-Principal Investigator, Miles Hewstone, is Professor of Social Psychology, a Fellow of New College, and Director of the Oxford Centre for the Study of Inter-Group Conflict.

The project aims to investigate the network structure and dynamics of intra- and inter-group interactions in humans, with a focus on cooperation and competition. The scholarships provide scope to pursue research in a variety of topics linked to cooperation, inter-group relations, cultural transmission (in both adults and children), and social networks (both real-world and online), including opportunities to conduct fieldwork in Italy.

The two fully-funded doctoral scholarships will begin in October 2018. One scholarship (DPhil Anthropology) will be based at the Institute of Cognitive and Evolutionary Anthropology, the other (DPhil Experimental Psychology) will be based in the Department of Experimental Psychology.

Applications are due on 2017-01-19 for the DPhil Anthropology and on 2018-01-08 for the DPhil Experimental Psychology. Potential applicants who meet the eligibility criteria are invited to submit an informal expression of interest well ahead of the official closing dates, and ideally before 2017-12-15, via email to Laura Fortunato. Further information about the awards, the project, and the application procedure is available at:

www.santafe.edu/ ~ fortunato/wp-content/uploads/2017/12/2017-12-02_Calleva-DPhil-advert.pdf – *Laura Fortunato* || Associate Professor of Evolutionary Anthropology | University of Oxford || External Professor | Santa Fe Institute ||

"fortunato@santafe.edu" <fortunato@santafe.edu>

UppsalaU WolfPopulationGenomics

PhD student in population genomics of wolves We are looking for a highly motivated PhD student to join Hans Ellegren'Âs lab group of about 10 PhD students, post-docs and bioinformaticians working with evolutionary and population genomic approaches to speciation, adaptation, molecular evolution and conservation genomics (http://www.ieg.uu.se/evolutionary-biology/ellegren/). The announced position is on an exciting project dealing population genomics and molecular evolutionary analyses of wolves.

The Scandinavian wolf population is a striking example of the impact of isolation on genetic diversity and survival. Wolves were once extinct in Scandinavia, but in the early 1980s two individuals re-entered the peninsula and successfully reproduced. Cut off from the larger Finnish-Russian metapopulation by the Reindeer husbandry area to the North, the population remained very small (less than 10 individuals) for a decade. However, in 1991 a single male immigrant entered the population and reproduced, resulting in genetic rescue through an increase in both genetic diversity and population size (VilÂÂ et al 2003 Proc R Soc Lond B 270:91-97). To this day the population remains characterised by prolonged periods of isolation with rare immigration events. Inbreeding is extensive.

We are sequencing the genomes of hundreds of wolves from both Scandinavia and the Finnish-Russian metapopulation. This dataset provides an ideal opportunity to study the consequences of population isolation and genetic rescue, as well as providing critical conservation information for the long-term viability of the population. It also provides unique possibilities to study the distribution of fitness effects in an inbred population and the accumulation of deleterious mutations in gene sequences. We have recently demonstrated how inbreeding translates into extensive arrays of runs of homozygosity in individual wolves, with some having entire chromosome that are identical-by-descent (Kardos et al 2017 Genomic consequences of intensive inbreeding in an isolated wolf population. Nature Ecology and Evolution doi: 10.1038/s41559-017-0375-4).

There are several possible lines to pursue depending on interest and background of the successful candidate/s. These include assessment of how genomic diversity varies over time and in relation to inbreeding, identification of candidate genomic regions for inbreeding depression, assessment of gene flow between populations, and molecular evolutionary analyses of large-scale sequence data.

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 can be directed to Hans Ellegren (hans.ellegren@ebc.uu.se).

Applications will only be accepted when submitted through the Uppsala University web portal no later than Jan 7 2018, using this link: http://uu.se/en/about-uu/join-us/details/?positionId=182339 Hans Ellegren <hans.ellegren@ebc.uu.se>

USheffield 2PhD EvolutionaryGenomics

We are seeking two highly motivated and enthusiastic PhD students to study sex chromosomes in birds and reptiles.

Deadline for applying: 9th January 2018

Evolution and implications of sex determination diversity

Lead supervisor: Dr Alison Wright, University of Sheffield

Co-supervisors: Prof Jon Slate (University of Sheffield), Prof Steve Paterson (University of Liverpool)

Sex chromosomes have evolved independently, multiple times across animals and closely related species often exhibit different sexual systems and modes of sex determination. Understanding the causes and consequences of this diversity is a major challenge in evolutionary biology, with important implications for sexual selection, sexual dimorphism and adaptation. The project will tackle these questions using cutting-edge bioinformatic techniques and next-generation sequence data across reptile species. Reptiles are an ideal group to study sex chromosome evolution as they exhibit an exceptional diversity in sex determination systems, where different types of sex chromosomes have evolved independently multiple times, making it possible to identify convergent evolutionary patterns.

The approach taken can be tailored to the particular interests of the student, and could include studies of sex chromosome degeneration and sexualisation, gene expression evolution and sexual conflict. Applicants should have strong analytical skills and an enthusiasm for evolutionary genomics.

Interested applicants are encouraged to contact Alison Wright before applying (a.e.wright@sheffield.ac.uk <alison.e.wright@ucl.ac.uk>) for more details on the project, funding and facilities. For details on current research in the Wright lab, see www.alisonewright.co.uk *Evolutionary genomics of zebra finch **supergenes*

Lead supervisor: Prof Jon Slate, University of Sheffield

Co-supervisors: Dr Alison Wright (University of Sheffield), Prof Steve Paterson (University of Liverpool)

Inversion polymorphisms ('supergenes') are increasingly recognised as an important source of genetic variation, responsible for some dramatic phenotypes (e.g. social system in fire ants, male morphs in ruffs, mimicry in butterflies etc.). We have recently shown that a supergene on the Z chromosome (a sex chromosome) explains nearly all of the heritable variation in sperm morphology in zebra finches (Kim et al. 2017; see also https://goo.gl/cCUQHu). However, the origin and evolution of the supergene are unknown.

This project will harness next-generation sequencing technology to understand the Z chromosome supergene, and the evolutionary importance of inversion polymorphisms more generally. The student will use long reads generated by 10X Genomics technology to:

1) Determine the origin of the Z chromosome inversion polymorphism; 2) Understand the molecular evolution of the genes within it; 3) Compare the Z inversion and at least three autosomal inversion polymorphisms to understand how, and wherein the genome, inversion polymorphisms arise.

The project will suit a candidate that is excited by analysing genomic datasets to address evolutionary questions.

Training

These PhD projects will provide an excellent opportunity to learn state-of-the-art genomic skills to study sex chromosomes and test clear theoretical predictions. The successful candidate will be trained in cutting-edge bioinformatics and genomic techniques. The applicant will benefit from the diverse range of expertise offered by the co-supervisors and researchers within the Animal and Plant Sciences Department at the University of Sheffield.

Funding Notes

For details on how to apply, including eligibility, see:

https://acce.shef.ac.uk/phd-opportunities/sheffield/ – 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 >

Alison E Wright <a.e.wright@sheffield.ac.uk>

USheffield ButterflyColourEvolution

NERC funded PhD opportunity on evolution and development of structural colour in Heliconius butterflies.

We are seeking an enthusiastic student with interests in evolution and developmental biology to work on a project investigating the developmental mechanisms controlling iridescent structural colouration in Heliconius butterflies.

Funding is through the NERC ACCE DTP and as such is only open to UK and EU applicants.

Closing date for applications is 9th Jan 2018.

Further info and to apply: http://nadeau-lab.group.shef.ac.uk/nerc-funded-phd-opportunity/ – Dr Nicola Nadeau Dept. of Animal and Plant Sciences Alfred Denny Building, University of Sheffield Western Bank, Sheffield S10 2TN, UK N.Nadeau@sheffield.ac.uk Tel: +44 (0)114 222 4717 http://nadeau-lab.group.shef.ac.uk/ "n.nadeau@sheffield.ac.uk" <n.nadeau@sheffield.ac.uk>

USouthernMississippi MarineInvertFitness

M.S. and Ph.D. STUDENT POSITIONS Marine Invertebrate Behavior, Ecophysiology, and Fisheries Division of Coastal Sciences, The University of Southern Mississippi Ocean Springs, MS

We seek highly motivated students to fill two graduate student positions in the laboratory of Dr. Zachary Darnell at The University of Southern Mississippi's Gulf Coast Research Laboratory in Ocean Springs, MS. Both positions will begin in August 2018. Students selected for these positions will pursue graduate degrees in the Division of Coastal Sciences and will be supported on research assistantships (details below). Both the M.S. and Ph.D. assistantship will include substantial flexibility in research topic, within the general realms of marine invertebrate behavior, ecophysiology, and fisheries.

Our current research focuses on environmental constaints on behavior, performance, and fitness of marine and estuarine invertebrates, and the strategies used by organisms to overcome these constraints. More specifically, this encompasses (1) plastic and adaptive behavioral and physiological responses to environmental change and environmental stress, (2) environmental effects on life histories, distributions, and population dynamics, and (3) anthropogenic impacts on organism-environment interactions. This research also has a strong applied focus, using ecophysiological approaches to address fisheries management and conservation questions. For more information on current research areas, visit http://sites.usm.edu/zdarnell/ . Details on each assistantship are below:

M.S. ASSISTANTSHIP: The M.S. assistantship includes a stipend of $22,800 per year, increasing to $23,400 per year following comprehensive exams. A tuition waiver is also included. Required qualifications include a minimum GPA of 3.5 on all undergraduate coursework and GRE scores exceeding the 50th percentile. Prior research experience is preferred.

Ph.D. ASSISTANTSHIP: The Ph.D. assistantship includes a stipend of $23,400 per year, increasing to $24,000 per year following comprehensive exams. A tuition waiver is also included. Required qualifications include a minimum GPA of 3.5 on all undergraduate or graduate (if entering with a M.S.) coursework and GRE scores exceeding the 50th percentile. Prior research experience is preferred. Priority will be given to applicants with an M.S. degree, but exceptional applicants at the B.S. level will also be considered.

The Division of Coastal Sciences is a research and graduate education unit within the School of Ocean Science and Technology, offering programs leading to the Doctor of Philosophy and Master of Science degrees. The Division is located at Gulf Coast Research Laboratory (Ocean Springs, MS), a marine laboratory featuring comprehensive basic and applied research programs in coastal and marine biological sciences (http://gcrl.usm.edu). Research program support includes state-of-the-art laboratory facilities and instrumentation; a fleet of small and large research vessels, including the R/V Point Sur; the GCRL Museum collection; the Center for Fisheries Research and Development; NSF I/UCRC Science Center for Marine Fisheries, and aquaculture facilities including the Thad Cochran Marine Aquaculture Center. Additional information on graduate programs in the Division of Coastal Sciences can be found here: http://gcrl.usm.edu/coastal_sciences/index.php . Interested students should contact Dr. Zachary Darnell (zachary.darnell@usm.edu). Please include a copy of your CV (including GRE scores), unofficial undergraduate and graduate transcripts, and contact information for three professional references. Review of applicants will begin immediately. For full consideration, submit all materials prior to January 2, 2018.

Zachary Darnell <zachary.darnell@usm.edu>

USussex BehaviourConservation

Insect behaviour, life history and environmental change

A Ph.D. studentship (42 months) is available from September 2018 under the supervision of Dr Wiebke Schuett, Department of Evolution, Behaviour and Environment, School of Life Sciences.

Deadline: 6th January 2018

Environmental, including anthropogenic, change has vast consequences on individuals, population dynamics and communities. Behaviour is often the first response to such change. Thus, understanding individuals' behavioural response to environmental change is important for identifying which individuals or species are likely to persist in or disappear from altered habitats. Individuals of many species consistently differ in their behaviour (i.e. show personality differences). Such personality differences are often closely linked to life-history, physiological and/or morphological traits, forming suits of correlated traits (i.e. pace-of-life syndromes, POLS). Unravelling how environmental conditions influence POLS structure would make an important contribution to understanding responses to and (ecological and evolutionary) consequences of environmental change.

A fully-funded Ph.D. studentship is offered in this research area. Topics that the successful candidate could pursue include the influence of environmental change (e.g. urbanization, climate change) on behaviour, and other POL traits, as well as their (co)variance. This might involve the evolution of personality differences, information use and decision-making under unpredictable environmental conditions, causes and consequences of POLS and impacts of environmental conditions on individuals, populations and communities. We offer the opportunity to work on insects, but work on other invertebrates might also be possible. Experimental work can be conducted in the field, in enclosures (preferably on ground beetles) and/or in the laboratory (several taxa).

Please submit a formal application using our online application system at http://www.sussex.ac.uk/study/phd/apply, including a cover letter (headed with project title), a short potential project outline (ca. 300-500 words), CV (max 2 pages), BSc/MSc degree transcripts and certificates, IELTS certificate (if non-UK) and names of two academic referees.

Candidates must hold/expect to obtain minimum 2:1 in BSc Biology or relevant subject. An MSc degree will be advantageous. We expect a highly motivated, talented, well-organised and meticulous candidate with strong quantitative skills. The candidate will have background in Behavioural Ecology, Field Ecology, Conservation, Evolution and/or Experimental Ecology. Previous experience in collecting data in the field, working with insects, behavioural observations, physiological analyses, statistical modelling (preferentially in R) is advantageous. 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. A driving license is desirable.

Contact Anna Izykowska for application enquiries (a.izykowska@sussex.ac.uk)

Contact Dr Wiebke Schuett for enquiries about the project (wiebke.schuett@uni-hamburg.de)

Wiebke Schuett <wiebkesch@googlemail.com>

UVermont QuEST

QuEST @ the University of Vermont:

https://www.uvm.edu/quest *The Quantitative and Evolutionary STEM Training (QuEST) provides doctoral students with the skills, knowledge, and competencies needed to solve environmental and global health problems in an ever changing workforce and research environment.*

The University of Vermont NSF Research Traineeship (NRT) program is an innovative and evidence-based model for transforming STEM graduate education training. Emerging infectious diseases, antibiotic and pesticide resistance, reduced crop yields caused by climate extremes and shifts, and the loss of biodiversity affect environmental and global health and food security. In each case, identification of successful solutions to these global challenges requires fundamental knowledge of evolutionary principles. QuEST trains these problem-solvers.

Research

Research activities will center around three topical areas and their intersection: evolutionary and ecological impacts of rapid environmental change, global change and disease dynamics, and modeling for prediction. Study systems will reflect the research expertise of over 30 faculty across eight academic units at the University of Vermont and will span diseases, pests, and species invasions in plant, insect, marine, amphibian, and human systems. Learn more about QuEST research < https://www.uvm.edu/node/248274 >: https://www.uvm.edu/quest/research-internships-experience *Faculty*

The QuEST program is unique among other interdisciplinary, big-data programs across the country in our emphasis on evolutionary training, modeling for prediction, and culturally sensitive teamwork. Meet QuEST faculty < https://www.uvm.edu/node/248272 >: https://www.uvm.edu/quest/participating-faculty *Career*

Meaningful internships drive career connections. QuEST internships are designed to develop continued partnership with industry and non-academic institutes and centers. Students will identify possible internship partners by end of the first year and during second year include the internship as part of dissertation research proposal including deliverables resulting from work. Learn about internships < https://-

www.uvm.edu/node/248274 >: https://www.uvm.edu/quest/research-internships-experience "C. Brandon Ogbunu" <chike.brandon@gmail.com>

UVienna PlantPhylogeography

The Research Group Plant Systematics of the Department for Botany and Biodiversity Research at the University of Vienna (https://plantsystematics.univie.ac.at/), Austria is recruiting a

PhD student in Plant Evolution & Phylogeography (m/f)

Transcontinental or even world-wide distribution of plants is a common phenomenon on the levels of families and genera. However, there are very few cases of world-wide distribution of plant species, that do not result from direct or indirect human aided dispersal. The tufted hair grass (Deschampsia cespitosa) occurs in (semi-)natural habitats worldwide in temperate zones (incl. tropical high mountains) and is thought to have achieved its present day distribution essentially without human assistance. We study the pathways and the chronology of long distance dispersal leading to its present world-wide distribution by investigating the biogeographic patterns, i.e. the relationships among the Eurasian, North and South American (including Antarctica), African, and Australasian populations and the evolution of polyploid variants in various regions. Using molecular (cpDNA) and genomic tools (Restriction site Associated DNA markers = RADseq) we aim to identify source populations and their derivates. The cpDNA data are expected to provide a global picture of relationships and dispersal routes within and between geographical regions and continents. Single Nucleotide Polymorphism (SNP) patterns gained from RADseq data will deliver more precise information on divergence among populations within regions and among them. These data will also provide information on genetic structure and diversity, and help in revealing population history, for instance possible phases of very small founder populations following arrival after long-distance dispersal. This study using the combination of the above introduced and several additional tools (e.g. cytogenetics) in this grass species will provide new insights into the history of plant dispersal and the evolution of grassland ecosystems in the temperate regions on a global scale.

The candidate should have - an MSc in evolutionary biology or related fields, such as evolutionary genetics, molecular ecology, bioinformatics, etc; - high motivation and enthusiasm; - an excellent academic track record; - a demonstrated computer literacy, including some knowledge of Unix (e.g., from a course); - preferred: experience with NGS methodology (wet lab or bioinformatics); - excellent organization and communication skills; - fluency in English (NB German knowledge is not essential)

We are an international team with English as the working language. The position offers a salary according to Austrian Science Fund standard (including health insurance), and the opportunity to attend international conferences. To be considered please send your application as a single pdf file to josef.greimler@univie.ac.at, including a motivation letter with a statement of research interests (max. 2 pages), your CV and if applicable publication list, university certificates including grades, and the names and contacts of three referees. Please note: Incomplete applications will not be considered. Screening of applications will begin immediately and will continue until the position is filled. The latest preferred start date is April 1st, 2018.

AssProf Dr Ovidiu Paun Department for Botany and Biodiversity Research University of Vienna Rennweg 14, A - 1030 Vienna http://plantgenomics.univie.ac.at ovidiu.paun@univie.ac.at

UWestAlabama BaikalSculpinEvolution

MS position in Conservation Biology Stipend: up to $22,000/yr Tuition waiver approved for students who instruct introductory biology lab sections

The Laboratory of AQuatic Evolution (LAQE) at the University of West Alabama is dedicated to research involving the evolution and conservation of aquatic biodiversity. We have an opening for one Master of Science student to assist with ongoing projects including, but not limited to: 1) Speciation in ancient lakes (Lake Baikal, Siberia); 2) Adaptation to extreme aquatic environments; 3) Functional genomics of mitochondria.

The University of West Alabama is a small, public Master's-granting institution located within commuting distance of Meridian, MS and Tuscaloosa, AL. The University offers an attractive benefits package and competitive salaries. Affordable housing is available in Livingston, Alabama, within walking distance of campus.

Duties and responsibilities: - Conduct independent and collaborative research on fishes of Lake Baikal. - Maintain a small live fish facility. - Travel to Siberia (Russia) in summer 2018. - Participate in lab meetings. - Help train new lab members. - Instruct undergraduate biology laboratory sections (optional).

Qualifications: - Bachelor of Science degree in biology or a related field. - Interest in/experience with phylogenetic systematics and NGS bioinformatics. - Experience with general molecular biology techniques (DNA extraction, PCR, electrophoresis). - Proficiency with Microsoft Excel (required) and R (preferred). - Organized and detail-oriented.

Benefits: The stipend for this research assistant position is $14,000 per year. This may be supplemented by up to $8,000 and a full tuition waiver if the student agrees to teach laboratory sections of general zoology or introductory biology.

Interested candidates should build an application containing; 1) cover letter; 2) curriculum vitae including GPA and GRE scores; 3) contact information for three professional references. Official transcripts will be required prior to candidate selection.

Complete applications (pdf) should be attached to an email with the header "Graduate student application" and sent to: msandel@uwa.edu

Michael Sandel, PhD Assistant Professor & Coordinator of Conservation Programs Department of Biological and Environmental Sciences The University of West Alabama 205-652-3475 msandel@uwa.edu

The University of West Alabama does not discriminate on the basis of race, color, national origin, gender, religion, age, disability or sexual orientation in employment, or the provision of services. Applications from members of minority groups are encouraged.

"Sandel, Michael" <msandel@uwa.edu>

UWisconsin Madison InvasiveInsectAdaptation

University of Wisconsin-Madison MS and PhD positions on molecular adaptation of invasive insects

Position Description: MS and/or PhD research assistantships are available to assess how invasive insects adapt to novel environments in the Molecular Ecology Lab at UW Madison. Insect pests can be viewed as model systems in which to explore fundamental concepts in ecology and evolutionary biology. They are especially promising candidates to study mechanisms of rapid evolution at the genetic level, as many insect pests have shown a remarkable ability to cope with pesticides, novel climatic space, and novel host plants. While there are significant challenges in determining adaptation at the genetic level and in finding ways to forecast future changes, there are strong incentives (ecological, economic and social) to do this research. Students will combine population genomics approaches with field ecology and manipulative experiments to understand the evolutionary mechanisms of adaptation. Training will focus on the use of population genomics and physiological approaches to relate spatial and temporal variation in the environment to adaptive genetic variation.

Information on University, Department, Lab, and City: The University of Wisconsin-Madison is one of the major research universities in the United States. This project will be supported in the Department of Entomology and under the supervision of Dr. Sean Schoville.— Madison consistently ranks as one of the best places in the United States to live, work, and study. It is Wisconsin's capital city, with a vibrant population of approximately 230,000 that combines small town charm with a variety of leisure and cultural opportunities.

Stipend/Salary: Current annual stipend levels are $22,081 per year before taxes, plus tuition remission and health care benefits.— Financial support is available for two years.— The start date for the project is September 2018.

Qualifications: A BS or BA degree in entomology, biology or a related discipline is required.

We are looking for motivated students interested in pursuing a MS or PhD degree at UW-Madison. Students with an MS degree will be given preference in admissions to the PhD program. The preferred candidate will have prior research experience and have some knowledge of population genetics. Candidates should have interests in entomology, evolutionary ecology, and working in both the field and laboratory. Excellent writing and verbal communication skills are expected, as well as the ability to work collaboratively.

Application Process: Applications will be reviewed upon receipt and review will continue until candidates are chosen.— The application deadline is Jan 9, 2018. The University of Wisconsin-Madison is an equal opportunity/affirmative action employer. We promote excellence through diversity and encourage all qualified individuals to apply.

Interested applicants are asked to e-mail the following documents listed below to our Student Services Coordinator Sara Rodock (rodock@wisc.edu) (in ONE PDF file please).— Please specify in your letter when you would be available to start.

Required Documents: -The "Entomology; University of Wisconsin-Madison Graduate Application Cover Sheet" which can be found at: http://www.entomology.wisc.edu/sites/default/files/schoville_coversheet.doc - A well-crafted cover letter outlining research interests, academic and professional backgrounds - Resume/CV - Copies of transcripts (unofficial copies acceptable at this point) - GRE scores if available - Names and contact addresses of three references

– Sean Schoville University of Wisconsin-Madison Department of Entomology 1630 Linden Drive 637 Russell Labs Madison, WI 53706 Office phone: 608-262-2956 http://labs.russell.wisc.edu/molecularecology sean.schoville@wisc.edu

Jobs

AuburnU EvoDevo

Faculty Position Evolution of Developmental Mechanisms Department of Biological Sciences, College of Sciences and Mathematics Auburn University

The Department of Biological Sciences at Auburn University invites applications for a tenure-track, 9-month faculty appointment at the level of Assistant Professor, beginning Fall, 2018. We seek applicants exploring the evolution of developmental mechanisms in marine systems who will contribute to our marine biology program. We particularly encourage those working on marine invertebrate systems to apply. The successful candidate is expected to establish an extramurally funded, internationally recognized research program. Instructional responsibilities include development of graduate and/or undergraduate courses on topics that include the evolution of developmental mechanisms, developmental biology, larval biology, evolution, or related fields. This position is the first of three hires in the broader area of development.

Applicants must have a Ph.D. in biology or a related discipline and must demonstrate excellent written and interpersonal communication skills and collegiality. Qualifications include postdoctoral or professional experience, a strong publication record, and evidence of potential for funding. The candidate selected for this position must be able to meet eligibility requirements for work in the United States at the time the appointment is scheduled to begin and continue working legally for the proposed term of employment. Applicants must submit a cover letter describing specific qualifications and interest in this position, a curriculum vitae, a description of research focus, a statement of teaching philosophy and experience, and the names and contact information of three professional references. Additionally, applicants should have an established Google Scholar profile. Review of applications will begin January 1, 2018, and will continue until a suitable candidate is found.

Applicants must apply online at: http://-aufacultypositions.peopleadmin.com/postings/2575 More information can be found at: www.auburn.edu/-biology Questions should be directed to Ken Halanych at ken@auburn.edu.

Auburn maintains high levels of research activity and high standards for teaching excellence. Its 2017 enrollment of 29,776 students includes 23,964 undergraduates and 5,812 graduate and professional students. Organized into twelve academic colleges and schools, Auburn's 1,450 faculty members offer more than 200 educational programs. The newly hired faculty member will be able to participate in University-wide initiatives including the Auburn University Cellular and Molecular Biology Peaks of Excellence program (AU CMB) and the Omics and Informatics Cluster. The University has formal ties to HudsonAlpha Institute for Biotechnology and Dauphin Island Sea Lab, which offer opportunities for new faculty to build research connections

Auburn residents enjoy a thriving community, recognized as one of the "best small towns in America," with moderate climate and easy access to major cities or to beach and mountain recreational facilities. Situated along the rapidly developing 1-85 corridor between Atlanta, Georgia, and Montgomery, Alabama, the combined Auburn-Opelika-Columbus statistical area has a population of over 500,000, with excellent public school systems and regional medical centers.

Auburn University is an EEONet/Disability Employer

Paula Norrell <pkn0001@auburn.edu>

AuburnU EvolutionaryAdaptation

Faculty Position in Global Change Biology

Department of Biological Sciences, College of Sciences and Mathematics

Auburn University

The Department of Biological Sciences at Auburn University invites applications for a tenure-track faculty position beginning Fall 2018 at the rank of Assistant Professor in Global Change Biology of Marine Systems and/or Plant Systems. The successful candidate is expected to establish an extramurally funded, internationally recognized research program focused on local, regional, or global impacts of anthropogenic environmental changes. We seek candidates who will complement a University initiative focused on climate change and who will position us to address problems of global anthropogenic changes as they relate to biotic diversity. The newly hired faculty member will be able to participate in University-wide initiatives including the Climate, Human, and Earth Systems (CHESS) Cluster

The University has formal ties to Dauphin Island Sea Lab, which offers opportunities for new faculty to build research connections. The candidate will have teaching responsibilities in undergraduate Ecology and will be expected to develop or contribute to a graduate course in their research specialty.

Applicants must have a Ph.D. in Biological Sciences or a closely related discipline, and may have relevant postdoctoral experience. The successful candidate must demonstrate excellent written and interpersonal communication skills and collegiality. Desired qualifications include a strong record of publication, teaching experience, and demonstrated (or potential) ability to acquire extramural funding. The candidate selected for this position must be able to meet eligibility requirements to work in the United States at the time the appointment is scheduled to begin and to continue to work legally for the proposed term of employment.

Review of applications will begin January 1, 2018, and will continue until a suitable individual is hired. Applicants should submit curriculum vitae, a description of research interests, a statement of teaching philosophy and experience, and the names and contact information of three professional references. Applicants must submit their materials online at:

http://aufacultypositions.peopleadmin.com/postings/-2596 More information about the department and its programs can be found at the following web site:

http://www.auburn.edu/cosam/departments/biology/-index.htm Auburn maintains high levels of research activity and high standards for teaching excellence. Its 2017 enrollment of 29,776 students includes 23,964 undergraduates and 5,812 graduate and professional students. Organized into twelve academic colleges and schools, Auburn's 1,450 faculty members offer more than 200 educational programs.

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Paula Norrell <pkn0001@auburn.edu>

AustralianNationalU 2 AnimalEvolutionaryPhysiology

Two academic positions in the Division of Ecology and Evolution, Research School of Biology, The Australian National University, Canberra.

The Australian National University is consistently ranked among the top universities in the world. The Division of Ecology and Evolution in the Research School of Biology is a high performing whole organism department with a strong international reputation for developing theory that transcends specific taxa. We are internationally recognised in a number of areas including evolutionary, behavioural and molecular ecology, phylogenetics and population genetics, macroevolution and macroecology and physiological ecology. We are home to a large population of postdoctoral and postgraduate researchers from around the world. Our research is underpinned by outstanding equipment, infrastructure and support staff, and funded by an extensive range of external grants.

To sustain and grow the scale and impact of our research and teaching, we seek to make two new continuing or fixed term (with a pathway to continuing) appointments at Academic Levels B or C (Lecturer or Senior Lecturer, equivalent to Assistant Professor) to complement and build on our research strengths, one each in the following themes: Position 1: Animal evolutionary/ecological physiology; Position 2: Population ecology. Outstanding candidates in other closely related areas also are encouraged to apply. Successful applicants will have received their PhD (or equivalent) no more than 15 years the time of their appointment, taking into account career interruptions and non-traditional career paths.

The successful applicants will be, or have the potential to become, international research leaders with their own strong, independent research programs, and be open to collaboration with existing faculty. We are keen to recruit people with a strong field program and/or those who will take advantage of our extensive live animal and plant facilities. We are also interested in theoreticians, but they must be capable of supervising field and/or lab-based empirical projects. The successful applicants must be able to win external research funding. We are interested in people who can develop collaborative grants with our existing staff, and can diversify our funding portfolio. The Division teaches a range of whole-organism courses at all year levels, with every member of academic staff involved in high-quality undergraduate teaching. The successful applicants will have a clear commitment to teaching excellence. We expect that the successful applicants' research and teaching will reflect the latest theoretical, quantitative and experimental advances in their field. We will only appoint people who are collaborative, collegial and community minded, and accessible to colleagues, research students and undergraduates, and keen to be engaged in the workings of the school.

ANU has committed to the SAGE Pilot of Athena SWAN Charter, and we expect that at least one of the candidates appointed will be a woman.

ANU values diversity and inclusion and believes employment opportunities must not be limited by socioeconomic background, race, religion or gender. The University actively encourages applications from Aboriginal and Torres Strait Islander people. For more information on employment opportunities, contact our Indigenous Employment Consultant on indigenous.employment@anu.edu.au. For information about staff equity at ANU, visit http://hr.anu.edu.au/staff-equity . For further information please contact Professor Scott Keogh, Head, Division of Ecology and Evolution E: Scott.Keogh@anu.edu.au

Application information.

In order to apply for this role please make sure that you upload the following documents:

* A statement addressing the selection criteria * A one-page statement of your research vision for the next 5-10 years * A one-page statement of your teaching philosophy * A half-page statement on where you see potential for collaborations within RSB. * Current curriculum vitae (CV) which includes the names and contact details of at least three referees (including a current or previous supervisor). If your CV does not include referees, you can complete these online when prompted in the application form.

Applications which do not address the selection criteria may not be considered for the position.

Full details can be found at this link: http://-jobs.anu.edu.au/cw/en/job/519012/lecturer-senior-lecturer scott.keogh@anu.edu.au

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AustralianNationalU 2 PopulationEcologist

NOTE: For both of these positions we are interested in people who have a strong background in evolutionary biology

Two academic positions in the Division of Ecology and Evolution, Research School of Biology, The Australian National University, Canberra.

The Australian National University is consistently ranked among the top universities in the world. The Division of Ecology and Evolution in the Research School of Biology is a high performing whole organism department with a strong international reputation for developing theory that transcends specific taxa. We are internationally recognised in a number of areas including evolutionary, behavioural and molecular ecology, phylogenetics and population genetics, macroevolution and macroecology and physiological ecology. We are home to a large population of postdoctoral and postgraduate researchers from around the world. Our research is underpinned by outstanding equipment, infrastructure and support staff, and funded by an extensive range of external grants.

To sustain and grow the scale and impact of our research and teaching, we seek to make two new continuing or fixed term (with a pathway to continuing) appointments at Academic Levels B or C (Lecturer or Senior Lecturer, equivalent to Assistant Professor) to complement and build on our research strengths, one each in the following themes: Position 1: Animal evolutionary/ecological physiology; Position 2: Population ecology. Outstanding candidates in other closely related areas also are encouraged to apply. Successful applicants will have received their PhD (or equivalent) no more than 15 years the time of their appointment, taking into account career interruptions and non-traditional career paths.

The successful applicants will be, or have the potential to become, international research leaders with their own strong, independent research programs, and be open to collaboration with existing faculty. We are keen to recruit people with a strong field program and/or those who will take advantage of our extensive live animal and plant facilities. We are also interested in theoreticians, but they must be capable of supervising field and/or lab-based empirical projects. The successful applicants must be able to win external research funding.

We are interested in people who can develop collaborative grants with our existing staff, and can diversify our funding portfolio. The Division teaches a range of whole-organism courses at all year levels, with every member of academic staff involved in high-quality undergraduate teaching. The successful applicants will have a clear commitment to teaching excellence. We expect that the successful applicants' research and teaching will reflect the latest theoretical, quantitative and experimental advances in their field. We will only appoint people who are collaborative, collegial and community minded, and accessible to colleagues, research students and undergraduates, and keen to be engaged in the workings of the school.

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Applications which do not address the selection criteria may not be considered for the position.

Full details can be found at this link: http://jobs.anu.edu.au/cw/en/job/519012/lecturer-senior-lecturer Scott Keogh <scott.keogh@anu.edu.au>

BrownU ResAssist EvoDevo

Brown University Research Assistant position for Developmental Biology

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

We are looking to hire an excellent full-time research assistant who is encouraged to conduct her/his independent research under PI's supervision. The area of research includes developmental biology, molecular biology, evolutionary developmental biology, live imaging, proteomics, and RNA-IP-seq. Basic skillset and knowledge in molecular biology (e.g. cloning, PCR) and a good accomplishment in her/his undergraduate work is prerequisite. Other necessary trainings (e.g. microinjection, confocal imaging, proteomics) will be provided by the PI. The successful individuals will be given own projects to conduct and finish (hopefully with lead author publications) within two-three years of appointment. This is an excellent job opportunity for individuals who seek to proceed to graduate school or medical school with a good record of research accomplishment in near future.

Any interested individuals should contact me via e-mail: mamiko_yajima@brown.edu. Please enclose your CV, title of your thesis, and name of your thesis advisor. Reviews will begin immediately and continue until position is filled. To be noted, the University does not support a Visa for this position. Desired start date is after March 1, 2018.

Mamiko Yajima <mamiko_yajima@brown.edu>

ColumbiaU TeachingEvolution

Lecturer in Ecology, Evolution and Environmental Biology

Columbia University invites applications for a Lecturer in Discipline position in the Department of Ecology, Evolution and Environmental Biology (E3B). This is a full-time appointment with multiyear renewal contingent on successful review. E3B represents broad interests in ecology, evolution, behavior, conservation biology, and environmental science. We seek a candidate with a serious commitment and proven record in teaching, advising (ideally at a graduate level), and research. S/he will serve as Program Director for E3B's Master's program in Ecology, Evolution and Conservation Biology, and will teach four to five classes annually including a student research development seminar and other graduate and advanced undergraduate courses. Appointment will begin July 1, 2018. Candidates should submit a cover letter, CV, 2-page teaching/mentoring statement (including philosophy, experience and plans), a two-page statement outlining prior research accomplishments and contact information for three references by January 15, 2018 to academicjobs.columbia.edu/applicants/Central?quickFinde579.

For additional information, see e3b.columbia.edu.

Applications from women and minorities are especially encouraged. Columbia University is an Equal Opportunity/Affirmative Action employer – Race/Gender/Disability/Veteran.

Jae McFadden Administrative Coordinator, Assistant to: Prof Shahid Naeem, Chair, Department of Ecology Evolution and Environmental Biology Columbia University 1200 Amsterdam Avenue 1014 Schermerhorn Ext New York, NY 10027 Tel: 212-851-5833 Fax: 212-854-8188

Jetaime E McFadden <jm3416@columbia.edu>

CornellU DiseaseEvolution

The *Department of Entomology* < https://entomology.cals.cornell.edu/ > at Cornell University seeks to fill a tenure-track faculty appointment in Vector Biology and Vector-Borne Disease. This is a nine-month, tenure track position with 60% research/40% teaching responsibility. Assistant or early Associate Professor preferred, but rank is open. The new faculty member will sustain a strong, internationally recognized, and well-funded research program emphasizing infectious diseases of humans and/or other animals that are transmitted by arthropods such as flies, ticks and mosquitoes. Focus should be on the interaction between an arthropod vector and the disease-causing microbes they transmit. Particular areas of focus may include genetics, physiology and biochemistry of the vector and/or microbe related to infectivity and transmission. We expect that the appointed faculty member will exhibit campus leadership and will synergize with current faculty with related interests. This hire is associated with the Cornell Institute of Host-Microbe Interactions and Disease (CIHMID) and is consistent with a campus-wide emphasis on expanding research and teaching in Infection Biology. Potential exists for intellectual connections and collaborations across multiple units at Cornell, including the Departments of Molecular Biology and Genetics, Ecology and Evolutionary Biology, Microbiology, and Biological Statistics and Computational Biology, as well as with Cornell's College of Veterinary Medicine and Weill College of Medicine.

The appointment will carry a teaching responsibility of approximately one course per year, with the courses to be taught determined by the interests and abilities of the applicant. There will be opportunities to contribute to the Master of Public Health Curriculum, the Global and Public Health Sciences major, and the MS program of the Northeast Regional Center for Excellence in Vector-Borne Diseases (NEVBD).

QUALIFICATIONS: Applicants are required to have a Ph.D. in Biology or a related discipline by the time of appointment and should exhibit demonstrated and prospective excellence in research and teaching.

APPLICATION PROCEDURE: Start Date: July 2018 or as negotiated. Applicants should submit a cover letter, research description (not more than 5 pages), statement of teaching philosophy and experience/interests (not more than 3 pages), and up to three representative publications at < https://academicjobsonline.org/ajo/jobs/10524 >. Applicants should also include contact information for three individuals who can provide references. Review of applications will begin January 30, 2018 and will continue until the position is filled. Inquiries may be directed to the Chair of the search committee, Dr. Brian Lazzaro, at *bplazzaro@cornell.edu*.

Brian P. Lazzaro, Ph.D.

Liberty Hyde Bailey Professor

Director, Cornell Institute of Host-Microbe Interactions and Disease (CIHMID)

Departments of Entomology and Ecology & Evolutionary Biology Cornell University Ithaca, NY, 14853, USA

tel: +1-607-255-3254

em: bplazzaro@cornell.edu

http://www.lazzaro.entomology.cornell.edu http://cihmid.cornell.edu Brian Lazzaro <bplazzaro@cornell.edu>

GeorgiaSouthernU Genetics

The position we are advertising for includes someone who does landscape genetics, which looks at the evolution of populations as it correlates with their physical landscape. The advertisement is a bit broader, but we would like to encourage someone with a strong population genetics background fill the position.

—– Landscape Ecologist/ Assistant

Professor Search #67499 College of Science and Mathematics / Biology - Statesboro Campus The Department of Biology in the College of Science and Mathematics invites applications and nominations for the position of Assistant Professor of Landscape Ecology. This position will be located on the Statesboro campus. In January 2017, the University System of Georgia Board of Regents voted to consolidate Armstrong State University and Georgia Southern University. The new, 27,000-student university will be named Georgia Southern University with campuses in Savannah, Statesboro, and Hinesville. The expected timeline for the first entering class will be fall 2018. Complete details are available at http://consolidation.georgiasouthern.edu/. Within this setting, the Department of Biology consists of a diverse faculty of teacher-scholars involved in a wide spectrum of activities from molecular to ecological studies on the coastal plain and throughout the world. The Department provides undergraduate and graduate students with a challenging education that is research-based and technology-oriented. We provide a foundation for lifelong learning and appreciation of biological processes and biological diversity through teaching, research and outreach. The Department of Biology on the Statesboro campus is housed in three buildings, including a new 158,000-square-foot Biological Sciences Building.

Position Description. Reporting to the department chair, the position of Assistant Professor of Landscape Ecology requires research, teaching and service responsibilities as well as a doctoral degree in the Biological Sciences or other relevant field. The successful candidate will develop an externally funded research program in any area of landscape ecology, including, but not limited to, geospatial modeling, landscape genetics, and ecological and evolutionary processes on a landscape scale. The successful candidate will also teach undergraduate and graduate courses. The position is an academic 9-month, tenure-track appointment, and the salary is competitive and commensurate with qualifications and experience.

Required Qualifications: - Earned doctorate in the Biological Sciences or other relevant field by 31 December 2017 - Demonstrated excellence in research in landscape ecology - Potential to attract extramural funding - Expertise and commitment to teaching excellence - The ability to teach courses at multiple levels within the disciplines of ecology and evolution, and develop a course in landscape ecology

Preferred Qualifications: - Postdoctoral experiences - Student-centered research and/or teaching experience Screening of applications begins January 31, 2018, and continues until the position is filled. The preferred position starting date is August 1, 2018.

A complete application consists of a letter addressing the qualifications cited above; a curriculum vitae; statement of research interests and teaching interests/philosophy; and three letters of reference. Applications must be sent electronically as a single PDF attachment (include applicant name in file name). Letters of recommendation in PDF format should be sent separately via email to the search chair. Other documentation may be requested. Only complete applications and applications submitted electronically will be considered. Finalists will be required to submit to a background investigation.

Applications and nominations should be sent to: Dr. Checo Colon-Gaud, Search #67499 Electronic mail: jccolongaud@georgiasouthern.edu Telephone: 912-478-5487 More information about the institution is available through http://www.georgiasouthern.edu or http://www.bio.georgiasouthern.edu.

Georgia Southern University seeks to recruit individuals who are committed to working in diverse academic and professional communities and who are committed to excellence in teaching, scholarship, and professional service within the University and beyond. The names of applicants and nominees, vitae, and other non-evaluative information may be subject to public inspection under the Georgia Open Records Act.

Georgia Southern University is an Affirmative Action, Equal Opportunity institution. Individuals who need reasonable accommodations under the ADA to participate in the search process should contact the Vice Provost.

John J. Schenk, Ph.D. Assistant Professor of Plant Biology Georgia Southern University Herbarium (GAS), Curator Department of Biology 4324 Old Register Road Georgia Southern University Statesboro, GA 30460-8042

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

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HarvardU 2ResTech AncientDNA

Two Research Technicians in Ancient DNA at Harvard

We are look for two people to join a team of technicians working in an Ancient DNA laboratory at Harvard University and the Howard Hughes Medical Institute in Boston, Massachusetts, USA. The successful applicants will study DNA from human remains over the last 20,000 years. Please visit our website for more information about our research (https://reich.hms.harvard.edu/).

We have two positions available. This is an ideal opportunity for candidates with one of three possible backgrounds:

(1) Experienced research technicians with a background in sterile technique and and/or genomics who seek longer term employment in an exciting and rapidly moving field.

(2) Undergraduates who anticipate completing their studies in Spring 2018 and are interested in a career in the field of Ancient Biomolecules and seeking experience in a world-class ancient DNA lab.

(3) Physical anthropologists with experience in analyzing skeletal material who would specialize in sample preparation and acquisition.

We are looking for candidates intending to stay for at least three years.

Principal Responsibilities:

Experimental Work (80% of responsibilities) - Sample preparation in a clean room environment to prepare for DNA extraction - Extracting of DNA and preparation for sequencing in a clean room environment - Amplification of DNA, cleanup and enrichment of libraries - Sequencing the DNA, and help to identify the best samples for further analysis - Working with liquid handling robots - Keeping a meticulous record of experiments and analyses in a lab book and database - Decontaminating equipment and work surfaces after every experiment - Cleaning the clean rooms and equipment on a regular basis - Frequent discussions with laboratory colleagues working on ancient DNA - Occasional sample preparation in non-cleanroom environment such as museums

Documentation, Administration and Meetings (20% of responsibilities) - Preparing, ordering, and maintaining stocks of necessary consumables, reagents, and supplies - Documenting, compiling, and analyzing experimental data - Updating supervisors by presenting oral and written reports - Reading relevant scientific literature - Working well in a team of research technicians with identical duties

Preferred Qualifications:

- Bachelor's degree in the life sciences with hands-on research experience in basic laboratory techniques and understanding of molecular biology principles, or a bachelor's degree in physical anthropology or archaeology. - Familiarity with genomics (library preparation and sequencing) and sterile techniques, or alternatively skeletal analysis. - Meticulous work habits including keeping a detailed and accurate lab notebook - Skilled at troubleshooting experiments and critical thinking about experiments and results - The ability to multi-task to take care of the general well-being of the laboratory

Additional Qualifications:

- Previous work in an Ancient DNA laboratory - Familiarity with genetics and next generation sequencing. - Medical Diagnostics or Microarray Fabrication (either in academic or industry) - Cell Culture with training in sterile techniques - Excellent written, documentation and oral communication skills. - Computer skills, including familiarity with Microsoft Word and Excel and ideally UNIX - Extremely strong organizational skills

Please apply through the following website. We will interview candidates on a rolling basis, and hope to make decisions in January 2018. https://hhmi-openhire.silkroad.com/epostings/index.cfm?fuseaction=app.j obInfo&version=2&jobidi0

David Reich <reich@genetics.med.harvard.edu>

Job:MonashU ResOfficer EvolutionaryGenomics

Research Officer position in evolutionary genomics / evolutionary ecology mitochondria, male infertility and pest control

Monash University Melbourne Australia

Research in Damian Dowling's laboratory is focused on the role the mitochondrial genome plays in evolutionary adaptation and population fitness. Maternal inheritance of the mitochondrial genome renders the mitochondrial DNA vulnerable to the accumulation of mutations that are harmful to males, but neutral or beneficial to females.

In collaboration with partner organisations in New Zealand (AgResearch, Landcare Research, and the University of Otago), we aim to harness these male-harming mtDNA mutations as a novel resource for pest control. Our approach is called the Trojan Female Technique; and its goal is to insert mtDNA mutations into pest populations, which render the males sterile, but have no effects female reproductive success. These Trojan Female mutations can then spread through the pest population, and cause a crash in pest population numbers.

We are seeking a talented and highly-motivated Research Officer to join our laboratory group, to help develop the Trojan Female Technique, in the fruit fly Drosophila melanogaster. The project will integrate a variety of techniques, spanning molecular biology and evolutionary biology. As the successful candidate, you will play a lead role in creating genetic strains of flies, each carrying different sets of mtDNA mutations. You will screen each strain for fertility (using standard methods in evolutionary biology), and then sequence the complete mitochondrial genomes of the strains exhibiting lowest male fertility.

As the successful candidate, you will have an undergraduate degree, with a successful track record of research experience (either via undergraduate or Masters level research projects, or via previous employment as a Research Assistant).

The position is a full-time, fixed-term appointment available for 12 months. Flexible working arrangements may be negotiated.

For further details, including full position description, see

http://careers.pageuppeople.com/513/cw/en/job/-571456/research-officer-biological-sciences Your application must address the selection criteria. Please refer to “How to apply for Monash jobs”

Information about Monash University

Currently ranked 80th in the Times Higher Education World University Rankings, Monash University is a member of Australia’s “Group of Eight” a coalition of research-intensive universities, and is internationally recognized for excellence in research and teaching. The School of Biological Sciences (http://monash.edu/-science/about/schools/biological-sciences/) is home to a collegial and world class research environment, with key strengths in evolutionary ecology and genomics.

Melbourne

Monash is located in Melbourne, a vibrant cultural and recreational centre, and is consistently rated one of the world’s most liveable cities (http://en.wikipedia.org/-wiki/World’s_most_livable_cities)

Enquiries to: Dr Damian Dowling, Associate Professor, damian.dowling@monash.edu

“damian.dowling@monash.edu”
<damian.dowling@monash.edu>

LMU Muenchen ResAssoc EvolBiol

Research Associate Position

Akademischer Rat auf Zeit (A13)

A research associate position is immediately available in the Department of Evolutionary Ecology at the Ludwig-Maximilians-Universitat Munchen (LMU) with a payment scale comparable to a Senior Lecturer/Reader salary in the UK.

The position. We seek a highly motivated, mature researcher with a proven publication record in evolutionary developmental biology, comparative genomics, transcriptional regulation, or a combination of these fields. Research interest relating to Drosophila are preferred, but not mandatory. For candidates actively seeking funding, this position provides a great opportunity to develop an independent research agenda and to start a research group. Scientific cooperations within and outside the chair are explicitly encouraged (hRp://www.en.biologie.uni-muenchen.de/-forschung/topics/index.html). The position comes with 5 hours of teaching duties during the semester (approx. 145 hours per annuum) including lecturing, course administration and student supervision. With multiple local master and graduate programs, you will meet a group of interna.onal and highly mo.vated students, open to interdisciplinarity.

The environment. The successful candidate will be based in the Department of Evolutionary Ecology (www.evolu.onary-ecology.bio.lmu.de), and affiliated to the chair of Nicolas Gompel, who studies the genetic origin of evolutionary changes (www.gompel.org). A main focus of the group is to characterize the molecular changes resulting in new gene regulation and phenotypic evolution. We combine enhancer dissection with reporter constructs in transgenic Drosophila with quantitative imaging and statistical modelling to understand the molecular bases of regulatory changes. We examine these changes at the level of closely related Drosophila species as well as populations, and adapt classical Drosophila melanogaster genetics to these different species to test evolutionary hypotheses.

Munich University (LMU) and Munich Technical University (TUM) are both recognized among Europe's premier academic and research institutions being consistently ranked among the top Universities worldwide. In particular the life science branch with its newly inaugurated campus offers excellent technical facilities and many interaction possibilities including the Gene Centre, several Max-Planck-Institutes and the Helmholtz Centre (www.campusmar.nsried.de/en/ 336-2/). The Campus Martinsried where the LMU Biocenter is located offers state-of-the art computing facilities for genome-scale analyses, high-end imaging facili.es, and an exci.ng mul.disciplinary environment. Munich is Bavaria's capital, a vibrant, yet relaxed city with many traditions still alive and a high quality of living.

In contrast to the current funding climate in many other European and non-European countries, funding rates are relatively high in Germany, and there are several sources to apply from, see e.g. hRp://www.research-in-germany.org/-en/research-funding.html or hRp://www.dfg.de/en/-research_funding/programmes/index.jsp. In addition, transnational European funding schemes offer aRrac.ve opportuni.es (hRps://erc.europa.eu).

How to apply. Applicants holding a PhD with a proven publication record are encouraged to apply. Teaching experience is beneficial. Applications including a statement of motivation including relevant expertise and scientific objectives, a CV and the contact details of at least two references should be sent as a single .pdf file to gompel@bio.lmu.de, subject term 'research associate'. The position is immediately available and remains open until filled. Start date is negotiable depending on the applicant's situation.

Please feel free to contact me if you have any further questions.

Best regards,

Sheren Leung

Ms. Sheren Leung Office Evolutionary Ecology Faculty of Biology Ludwig-Maximilians-Universitat Munchen Großhadernerstr. 2 82152 Planegg-Martinsried Tel.: +49(0)89-2180-74203

"Leung, Sheren" <leung@biologie.uni-muenchen.de>

McGillU EcolEvolutionaryInformatics

The Department of Biology at McGill University invites applications for a tenure-track position in ECOLOGICAL/EVOLUTIONARY INFORMATICS. Applicants with strength in the development and/or application of quantitative (computational and mathematical) approaches to the analysis and interpretation of large evolutionary/ecological datasets, from genomes to ecosystems, are encouraged to apply. We anticipate filling this position at the Assistant Professor level. Applicants must have a Ph.D. or equivalent degree, and a substantial record of research excellence. Postdoctoral experience is preferred. The successful applicant will be expected to conduct a vigorous program of independent, externally funded research, to communicate research findings in both professional and public forums, and to contribute to teaching at both undergraduate and graduate levels. A competitive startup package as well as access to a wide range of shared research facilities are available. Salary negotiable, according to qualifications and experience.

Applicants should forward a curriculum vitae, short statements of research and teaching interests, and 3 representative publications in a single PDF file (filename = lastname-firstname-ECOEVOINFO.pdf) to: ecoevoinfo.biology@mcgill.ca.

Applicants should also arrange to have 3 letters of reference submitted directly to this email address. All correspondence should include Ecological/Evolutionary Informatics Search and the applicant's name in the subject line.

The application deadline is December 18, 2017

dan.schoen@mcgill.ca

MichiganStateU Bioinformatician-ComputationalScientist

Bioinformatician at Michigan State University

Several faculty in the Department of Integrative Biology at Michigan State University are looking to collectively hire a highly motivated bioinformatician/computational scientist with a biology background for a full-time position. Typical research projects will use RNA-sequencing, RAD-sequencing, whole genome sequencing and assembly, and targeted capture sequencing to address questions in ecology, evolution, comparative genomics, and developmental biology. We are looking for an enthusiastic and organized individual to join our team, who is skilled at working for multiple people and on different projects. The position will be based in East Lansing, MI on the MSU campus and comes with a competitive benefits package.

Primary duties will include: 1. Curating sequence data (10%) 2. Analyzing sequence data (65%) 3. Producing tables and figures and writing data analysis methods and results (10%) 4. Mentoring students on bioinformatics methods (10%) 5. Reading scientific literature to stay up to date on newest analysis methods (5%)

Required Qualifications: The job requires knowledge equivalent to that which normally would be acquired by completing a four-year college degree in bioinformatics or related field and up to six months of related and progressively more responsible or expansive bioinformatics experience; or an equivalent combination of education and experience. The candidate should be well- versed in unix/linux, as well as at least one other programming language (e.g. R, python, perl). Applicants should have extensive experience analyzing large 'Â¥'Vomic'Â datasets.

Desired Qualifications: A Master'Âs or PhD degree in bioinformatics or related field. Experience in at least some of the following key areas: 1. Analyzing complex RNA-seq experimental data sets for differential gene expression 2. Analyzing RAD-seq datasets'Xaligning to reference and creating de novo assemblies, SNP discovery, genotyping, etc. 3. Genome assembly and annotation 4. Genome comparisons 5. Phylogenomics 6. Epigenomics

Required applicant materials: 1) Brief cover letter describing research and data analysis experience and career goals 2) CV 3) Names and email addresses for 3 references

How to apply Interested candidates should apply through the MSU Applicant Page at careers.msu.edu (job ID 480028). If you have questions, email Dr. Mariah Meek (mhmeek@msu.edu), with "Bioinformatics position" in the subject line. DO NOT EMAIL APPLICATION MATERIAL TO DR. MEEK.

Review of application material will begin on January 8, 2018. Position is open until filled.

"Braasch, Ingo" <braasch@msu.edu>

NOAA NWFSC Seattle ConservationBiology

Senior Scientist to Assess Persistent Organic Pollutant Transfer from Female Southern Resident Killer Whales to their Calves - Seattle, WA Need to fill by Jan 12, 2018 for work to start Feb 12, 2018

Lynker has an opening with the NOAA Fisheries, Northwest Fisheries Science Center (NWFSC), Conservation Biology Division (CB) to support research into the impacts of persistent organic pollutant data from serum, milk and blubber samples to quantify the transfer of these pollutants from female delphinids to their calves during gestation and lactation. Results shall be used by managers to update models that predict changes in contaminant levels in Southern Resident killer whales as well as identify periods of higher risk from circulating contaminants for female killer whales and their calves.

Key responsibilities include: * Calculate variables from chemistry (lipid concentrations and persistent organic pollutant concentrations in milk, serum, and blubber) and body mass data from delphinids for reports on contaminant transfer dynamics during gestation and lactation in delphinids. * Use statistical and graphical software to analyze data and prepare figures for reports per instructions from the project leader. * Final reports will be prepared by the project leader, but the contractor shall contribute some literature review summaries, statistical analysis of data, and figures depicting data trends for inclusion in the reports.

Must Have Skills and Requirements:

Bachelor's degree, or higher, from an accredited college or university with a major directly related in a field of study as related to the requirements of specific task order with emphasis in fisheries, oceanography, social science, natural science, mathematics, or hydrology, plus three (3) years of experience in related field or combination of such totaling seven (7) years combined education and experience. Master's Degree may be substituted for experience.

Additional required qualifications include:

Strong math and data processing skills

Proficiency using Microsoft Excel software to manipulate data

Proficiency using Microsoft Word software

Experience constructing figures from data and summarizing results from data analyses

Experience searching and summarizing peer-reviewed scientific literature

Additional preferred qualifications include:

Familiarity with scientific research on marine mammals, particularly delphinids in human care

Science writing ability satisfactory for peer review Let me know if this is doable and what additional information you may need from me. Thanks! Liz - Elizabeth J. Tarquin Director, Marine Sciences Division Lynker Technologies LLC (808) 747-3065 ltarquin@lynkertech.com www.lynkertech.com Lynker - a HubZone- and ISO-certified company

Liz Tarquin <ltarquin@lynkertech.com>

NorthCarolinaMuseum InvertCollectionsManager

North Carolina Museum of Natural Sciences: Collections Manager for Non-Molluscan Invertebrates

Salary: $35,474.00 - $57,292.00 Location: Wake County, NC Job Type: Permanent Full-Time Department: Dept of Natural and Cultural Resources Closing: 1/5/2018 5:00 PM Eastern

Description of Work The N.C. Department of Natural and Cultural Resources (NCDNCR) is the state agency with a vision to be the leader in using the state's natural and cultural resources to build the social, cultural, educational and economic future of North Carolina. NCDNCR's mission is to improve the quality of life in our state by creating opportunities to experience excellence in the arts, history, libraries and nature in North Carolina by stimulating learning, inspiring creativity, preserving the state's history, conserving the state's natural heritage, encouraging recreation and cultural tourism, and promoting economic development.

The North Carolina Museum of Natural Sciences' mission is to illuminate the natural world and inspire its conservation. The Museum enhances the public's understanding and appreciation of the natural environment in ways that emphasize the biodiversity of North Carolina and the southeastern United States and relates the region to the natural world. The mission is accomplished by maintaining the state's zoological and geological collections; conducting statewide biological survey research and environmental studies; offering exhibits that feature plants and animals of North Carolina; presenting natural history programs for children and adults; providing experiential workshops in the natural sciences for teachers; and producing and disseminating publications about nature and environment.

The Museum's Research & Collections (R&C) section includes research scientists, collections curators, collections managers and support professionals. The major responsibilities of the R&C section are to maintain and expand the Natural Sciences research collections of the Museum, conduct original research, disseminate research results, participate in science communication, public outreach, and education, and assist other Museum sections, in programming and exhibit development. R&C staff and facilities are spread across three Museum buildings: The Nature Exploration Center (NEC), the Nature Research Center (NRC), and the Research Laboratory. This position is located primarily in the Research Laboratory facility.

This position will be primarily responsible for the management and maintenance of the Museum's Non-Molluscan Invertebrate Collection and associated curatorial duties (databasing, specimen inventory and management, managing loan activity, collection expansion, participating in funded collections grants, seeking additional collections stewardship funding, etc.). This position will be responsible for coordinating, training, and supervision of volunteers and others who might work with this Collection. This position will be expected and encouraged to participate in active research projects in invertebrate biology, taxonomy, and/or ecology, leading to publication of results in peer-reviewed scientific journals and popular media outlets. The position will participate in various educational and outreach activities of the Museum, including (but not limited to): annual signature events; regular, short science presentations offered to the public; and 'behind-the-scenes' tours of the Collections facilities. This position might also be called upon by other state agencies or external organizations to provide collections information, training and other assistance.

Knowledge, Skills and Abilities / Competencies:

1. Demonstrated knowledge of invertebrate taxonomy and/or biology. 2. Demonstrated experience with microscopy, scientific illustration, and/or other methodological skills related to working with invertebrate specimens. 3. Ability to learn computer languages. 4. Ability to converse using professional interpersonal and public communications skills. 5. Ability to organize and work independently to accomplish assigned tasks in a timely manner.

Minimum Education and Experience Requirements

Graduation from a four-year college/university with a degree in biology, zoology, or a science curriculum related to the area of expertise and two years of experience in specialty area; a master's degree in natural science area may be substituted for experience; or an equivalent combination of education and experience. Management Preferences: * Master's degree * Demonstrated experience managing or curating natural sciences

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NTNU Trondheim Norway EvolutionaryEntomology

The NTNU University Museum, Department of Natural History (Trondheim, Norway) seeks a highly motivated entomologist to perform biosystematic research in one or more of the large insect orders, preferably Lepidoptera, Coleoptera or Hymenoptera, and to be curator of parts of our terrestrial invertebrate collection.

Please see this page for more information: https://www.jobbnorge.no/ledige-stillinger/stilling/145378/associate-professor-in-biological-diversity Best regards Torbjørn

– Torbjørn Ekrem, PhD Professor of biosystematics NTNU University Museum, Department of Natural History http://www.ntnu.edu/employees/torbjorn.ekrem Coordinator Norwegian Barcode of Life (NorBOL < http://www.norbol.org >) Co-editor Chironomus Journal of Chironomidae Research < http://www.ntnu.no/ojs/index.php/chironomus/index >

Torbjørn Ekrem <torbjorn.ekrem@ntnu.no>

OceanU China BioinformaticsEvolution

TENURE TRACK PROFESSOR IN BIOINFORMATICS AND/OR EVOLUTIONARY BIOLOGY

Ocean University of China (OUC) is one of the leading research institutions in marine science and technology in Asia. It is located in the coastal city Qingdao in northern China. Detailed information about the university could be found at: http://eweb.ouc.edu.cn/weneralwnformation/list.htm Positions to be filled by the Institute of Evolution and Marine Biodiversity (http://web.ouc.edu.cn/iemb/gywwww/list.htm), which was founded in 2010 and particularly strong in biodiversity and developmental biology research. We are now expanding to bioinformatics and evolutionary biology. TWO junior-level positions are open. Working environment is bilingual (English + Chinese). Duties$B!'(B

The candidate should be able to develop a research program in bioinformatics or evolutionary biology or related fields, especially in relation to marine organisms. The candidate is competent in the application of population genetics, functional genomics or environmental genomics to issues related to life processes. The candidate should also be interested and serious in providing technical support for other lab$B!G(Bs research falling in his/her scope. We are also building a computation cluster, which would need involvement from the candidate, so any past experience in this is plus. Previous experience in guiding undergraduate/graduate students is welcome. Teaching is usually no more than one course per semester. Requirments: Ph. D. in Population Genetics, Bioinformatics, Biology, Ecology and Evolution, etc., with postdoc experience in related topics;

A strong publication record;

Excellent knowledge of written and spoken English;

Contact information of two referees

Work location: Yushan Campus of OUC, Yushan Rd. (old downtown), 266003 Qingdao, China Duration of contract: 5 years (tenure-track position, could be continued) Salary: Salary is based on the qualifications and experience of each candidate. Enquiry is welcome. Application: Please include detailed curriculum vitae, contact information of two referees, and a brief statement describing your interest in the position, teaching philosophy, future research plan, etc. All applications will be treated confidentially. Interested candidates must submit their complete application package before March 10th, 2018, to the attention of: Dr. Hongan Long,

Contact email: 2018iembhire@gmail.com

Institute of Evolution and Marine Biodiversity,

Ocean University of China, Qingdao

H Long <longhongan@gmail.com>

SanDiegoZoo Bioinformatics

Bioinformatics Scientist - Genetic Rescue - San Diego Zoo

The Conservation Genetics group at the San Diego Zoo Institute for Conservation Research is seeking an experienced bioinformatics scientist to join the effort for genetic rescue of the critically endangered northern white rhinoceros.

The Bioinformatics Scientist will work in the Conservation Genetics group at the San Diego Zoo Institute for Conservation Research as part of the multi-institution team utilizing induced pluripotent stem cells (iPSCs) as a method for genetic rescue of the northern white rhinoceros (NWR). This position is for someone who enjoys using bioinformatics as a tool to understand the biological relevance of gene expression and genomic differences. Areas of focus may include whole genome sequencing analysis and annotation, transcriptomics, gene networks, epigenetics and CRISPR gRNA design for reporter lines.

The northern white rhinoceros genetic rescue project is a collaborative venture designed to prevent the otherwise certain extinction of this form of rhinoceros. A white paper describing the scope of the project is available in an open access paper: Saragusty, et al., 2016; Rewinding the Process of Mammalian Extinction. Zoo Biology 35:280-292. Previously, in collaboration with the laboratory of Jeanne Loring at the Scripps Research Institute, the reprogramming of fibroblast cells from northern white rhinoceros, producing induced pluripotent stem cells was reported. More recently, this ongoing collaboration has resulted in the reprogramming of fibroblasts from additional northern white rhino individuals using non-integrating vectors as described in this preprint.

Please share this information with others who may be interested. Applications close on January 15, 2018. Additional information and directions on submitting an application may be found via this link. -

https://www.hrapply.com/sandiegozoo/AppJobView.jsp?link=3D8305&page=3DAppJobList.jsp&skimSessionName=com.hrlogix.view.tags.bootstrap.table.JobListTable&skimName=requisition.requisition_id&skimNdx&op=reset Oliver A. Ryder, PhD Director of Conservation Genetics oryder@sandiegozoo.org

oryder@ucsd.edu

SGN Frankfurt MolecularBiosystematics

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

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

PhD Position in Molecular Biosystematics (part-time, 65%) The project Lecanomics new ways of species detection and recognition in a ubiquitous group of lichens aims to connect both ends of the taxonomic work-flow: field exploration and verification of potential new species by genomic methods. Based on reference genomes we want to develop genomic and genetic markers for species identification and delimitation that will be tested on samples from underexplored regions of the world. Worldwide sampling and feedback to collectors is organized by a team of, at present, 20 international specialists through a self-developed webbased work-flow management system. The platform also enables participation of amateur (citizen) scientists. Insights from this project are supposed to streamline the taxonomic work-flow for inconspicuous organisms.

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

Specific tasks will include: - generating draft reference genomes and developing novel genetic markers for species delimitation in lichens - using genome-wide datasets to study species delimitation in selected groups of the lichen genus Lecanora - assisting in the administration of our web-based communication and workflow management system and cooperate with an international team of specialists Your profile: - a Masters degree or equivalent in a field related to biodiversity research - experience in molecular genetic lab methods (preferably including library preparation and genome reduction techniques) - basic programming skills in and experience with databases (these assets are desirable but not mandatory) - good command of English (oral and written)

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

Salary and benefits are according to a part-time public service position in Germany (TV-H E 13, 65%).

The position is a 3-year fixed-term post, starting April 1st, 2018.

The Senckenberg Gesellschaft fuer Naturforschung supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference.

The place of employment will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft fuer Naturforschung.

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

Please include a cover letter outlining your motivation, a detailed CV, your full transcripts and grades, contact details of two potential references, a summary of your Master/Diploma thesis, and, if available, a list of publications to the address below: Senckenberg Gesellschaft fuer Naturforschung Senckenberganlage 25 60325 Frankfurt am Main E-Mail: recruiting@senckenberg.de, cc to: christian.printzen@senckenberg.de For scientific enquiries please contact Dr. Christian Printzen, christian.printzen@senckenberg.de.

Mit freundlichen GruÃen / Best regards

Isabel Gajcevic, M.A.

Personalsachbearbeiterin

SENCKENBERG

Gesellschaft fur Naturforschung (Rechtsfahiger Verein gemaÃ - 22 BGB) Senckenberganlage 25 60325 Frankfurt am Main

Besucheradresse: VoltastraÃe 1, 60486 Frankfurt am Main (5.

Obergeschoss)

Telefon/Phone: 0049 (0)69 / 7542 -

Leiterin Personal & Soziales

- 1458 Loke, Uta

Stellv. Leiterin Gruppe Personal & Soziales

- 1319 Elsen, Carina

Mitarbeiter/in Personalbeschaffung (Recruiting)

- 1313 di Biase, Maria

- 1313 Helm, Jessica

- 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1467 Mail: recruiting@senckenberg.de

Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Bohning-Gaese, Prof. Dr.

Uwe Fritz, Prof. Dr. Ingrid Kroncke Prasidentin: Dr. h. c. Beate Heraeus Aufsichtsbehorde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

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UBath 2 2yr PrizeFellowships

== University of Bath Prize Fellowships in the Faculty of Science, Evolutionary Biology

== Our Prize Fellowships offer early-stage researchers the opportunity to join a cohort of like-minded rising research stars. These two-year research fellowships in our priority research areas are part of a scheme intended to fast-track fellows to a permanent appointment at Bath. As a member of this elite group, you will be on track to become a key member of our research community with a permanent academic position. Our supportive community successfully nurtures ambitious early stage researchers and provides for the requirements of their developing research programme. In the Faculty of Science we will appoint a total of seven Fellows to further strengthen and develop areas of existing research excellence. One appointment will be made within the Evolutionary Biology theme of the Milner Centre for Evolution and the remaining six within the other priority areas.

== The Milner Centre for Evolution welcomes applicants in all ares of evolution research but applicants with interests in experimental evolution, statistical approaches to evolution and evolutionary ecology/genomics are especially welcome to apply.

== Closing date for applications is 31/12/17; Interview dates are 15th - 26th January 2018 for first stage interviews (via Skype or telephone), and week commencing 5th February for second stage interviews.

==Further details can be found at https://-www.bath.ac.uk/jobs/Vacancy.aspx?ref=SF5354 —–

== University of Bath Prize Fellowships in the Faculty of Science, Bioinformatics

== Our Prize Fellowships offer early-stage researchers the opportunity to join a cohort of like-minded rising research stars. These two-year research fellowships in our priority research areas are part of a scheme intended to fast-track fellows to a permanent appointment at Bath. As a member of this elite group, you will be on track to become a key member of our research community with a permanent academic position. Our supportive community successfully nurtures ambitious early stage researchers and provides for the requirements of their developing research programme. In the Faculty of Science we will appoint a total of seven Fellows to further strengthen and develop areas of existing research excellence.

== Driven by technological advances, the modern life sciences have been transformed by the availability of ever larger datasets. These include huge archives of population data such as patient records, high resolution images of cells, tissues and organs, and the almost incalculable variety of genes, genomes and metagenomes that make up natural biological diversity. The opportunities opened up by these 'Big Data' bring several challenges and have led to the growth of the interdisciplinary field of bioinformatics that combines computer science, statistics and mathematics to analyse and interpret biological data. Nowhere is this better exemplified than in the field of comparative genomics where analysis of high-throughput sequencing data has already made a considerable impact in understanding the diversity and evolution of organisms and the genomics underlying phenotype variation.

The University of Bath has made significant advances in enhancing bioinformatics within several departments. The Prize Fellow can be drawn from multiple disciplines and will have expertise in developing big data tools and interfaces for: querying, manipulating and mining big data; software development; contextualization and integration for hypothesis driven research.

== Closing date for applications is 31/12/17; Interview dates are 15th - 26th January 2018 for first stage interviews (via Skype or telephone), and week commencing 5th February for second stage interviews.

== Further details can be found at https://-www.bath.ac.uk/jobs/Vacancy.aspx?ref=SF5354; For informal enquires please contact Prof Sam Sheppard (s.k.sheppard@bath.ac.uk)

Tiffany Taylor <T.B.Taylor@bath.ac.uk>

UBielefeld 2Tech Individualisation

SFB Transregio 212: 9 Postdoc, 16 PhD, 2 Technician positions

A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3)

A collaborative research centre (SFB) has recently been funded by the German Research Foundation for the period 2018 to 2021 to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology and evolution. As part of this collaborative research centre, a total of 9 Postdoc positions (E13), 16 PhD positions (E13/65%) and 2 half-time technician positions (E8 or E9/50%) are available at Bielefeld University, the University of Muenster and the University of Jena from 1st of February 2018 or as soon as possible thereafter across 19 Projects (see below for more details). The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programmes. Full details of the SFB can be found at www.uni-bielefeld.de/biologie/crc212 . Thematic background

Individuals differ. This seemingly trivial statement has nevertheless led to paradigm shifts, as three different fields of organismal biology have seen a marked change in key concepts over the last years. In behavioural biology, it has been realised that there are profound differences between individuals and that these can be stable over time and across contexts, giving rise to the concept of animal personalities. In ecology, an increasing focus is likewise on the considerable variation in the ecological niche realised by species, populations, and even individuals. In evolutionary biology, where individual variation has always been central, there is an increasing awareness of the complexity with which genotypes interact with the environment to produce unique phenotypes. Therefore, a concept of an individualised niche is needed, rather than focusing only on a mean value for a given population.

The central research goal of the collaborative research centre is to redefine the niche concept on the individual level. In pursuing this conceptual goal, the CRC relies on a collaboration of empirical biologists, theoreticians, and philosophers of science. We want to gain a comprehensive, empirically adequate and philosophically reflected understanding of how individual phenotypes interact with their environment and what the ensuing consequences for ecological and evolutionary processes are. We hypothesise that, across taxa, the interaction between the individualised phenotype and the environment results in individualised niches via three mechanisms of adjustment and adaptation: niche choice, niche conformance and niche construction.

Profile

We seek bright and highly motivated postdoctoral researchers, biological technicians and students with very good Master (or equivalent) degrees who ideally have ample experience in relevant topics (e.g. animal behaviour, behavioural ecology, chemical ecology, population ecology, evolutionary ecology, evolutionary genomics, theoretical ecology, philosophy of science). Ideal candidates will be able to work both independently and as part of a multidisciplinary team.

To apply for any of the positions, please provide: (i) a letter of motivation including a statement of your research interests, how you would contribute to the particular project, relevant skills and experience;(ii) a CV including publication list; (iii) names and contact details of two referees willing to write confidential letters of recommendation. All materials should be emailed as a single PDF file to the respective PI of the project.

The application deadline is 07th of January 2018 or as otherwise specified for specific projects. Interviews will take place in January 2018. The preferred start date is 1st of February 2018 but is flexible and will depend on the timeframe of the most qualified applicant. The SFB-webpage (www.uni-bielefeld.de/biologie/crc212), or Oliver Kruger (oliver.krueger@uni-bielefeld.de) provide further details. PhD programmes exist in Muenster (www.uni-muenster.de/Evolution/mgse) and Bielefeld (www.uni-bielefeld.de/(en)/biologie/phd).

The Universities of Bielefeld, Munster and Jena are equal opportunity employers. We particularly welcome applications from women and disabled people. Given equal suitability, qualifications and professional achievement, women or disabled people will be given preference, unless particular circumstances apply.

Project A01: Fitness consequences of niche choice and conformance in a marine mammal

What are fitness consequences of breeding under high vs. low social density? Can pups adaptively conform to their social environment? Is a

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UCambridge FieldAssist EvolutionButterflyLearning

The Evolution of Brains and Behaviour Lab (http://shmontgomery.co.uk/index.html) at the University of Cambridge is seeking a field assistant to help with behavioural studies of Heliconius butterflies in Gamboa, Panama. The successful candidate will spend approximately three months in Panama, beginning in early February 2018. The position is open to all students with a background in zoology and interest in animal behaviour or neurobiology.

The studies will form part of a project investigating the learning capabilities of Heliconius butterflies. Unique amongst the Lepidoptera, Heliconius butterflies actively feed on pollen which is collected from a limited number of a rare plants. In utilising these plants, Heliconius establish “traplines”; routes through the forest connecting several plants which are used with a high degree of spatial and temporal regularity. This behaviour suggests pollen feeding is dependent on an enhanced, visual orientated spatial memory and sophisticated learning ability.

As part of this project, we will investigate the learning ability of Heliconius in non-spatial contexts. We will conduct colour, shape and olfactory associative learning experiments on Heliconius, as well as closely related non-pollen-feeding species, at the Smithsonian Tropical Research Institute in Gamboa, Panama (STRI). Field assistants will be involved in collecting wild butterflies from surrounding forests, tending to stock butterfly populations and assisting with behavioural experiments. This is an excellent opportunity for a recent graduate to gain experience in behavioural experimentation, experimental design and field collecting.

Dates: starting and finishing dates are flexible, but ideally the successful candidate will be available for three months, beginning in early February 2018.

Funding: the successful applicant will receive 800 USD per month, which comfortably covers living costs while in Panama. STRI requires that all researchers have health insurance, this is not provided but can be purchased through STRI. Financial assistance with transport to Gamboa will be available if required.

Accommodation: application can be made for accommodation through the Smithsonian Tropical Research Institute or arranged privately. Accommodation costs are approximately $250-300 per month. Gamboa is a small town with all facilities within comfortable walking distance.

Interested applicants should have training in biology or a related field, and should send a CV and brief statement of research interests to Fletcher Young (fletcherjyoung@gmail.com). Applicants will be interviewed via Skype in early January.

Applications will close December 29^th 2017.

Fletcher Young <fjy22@cam.ac.uk>

UCollege London PlantOrFungalEvolutionaryBiol

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>

UGeorgia PlantEvolution

MAJOR RESPONSIBILITIES: The incumbent will address fundamental ecological and evolutionary questions in plant ecology with an emphasis on plant roots and their interactions with the soil environment, specific soil organisms, and/or the root microbiome. Field-based research should be integrated with other approaches (e.g. modeling, computational, molecular, genomic). The successful candidate will be expected to maintain a high-impact, externally funded research program in belowground plant ecology; mentor undergraduate students, graduate students, and/or postdoctoral scholars across relevant disciplines; and teach undergraduate and graduate-level courses.

QUALIFICATIONS: Candidates must have a PhD in Plant Biology, Plant Pathology, Ecology, or related field. Candidates to be considered for Associate Professor must have an established extramurally-funded research program.

SALARY: Salary commensurate with qualifications and experience.

APPLICATION PROCEDURE: Inquiries about the position should be directed to Dr. Jim Leebens-Mack, Chair of the Search Committee (jleebensmack@uga.edu). All application materials must be submitted via the university's faculty job portal at https://facultyjobs.uga.edu/postings/3265. Materials to be uploaded include: a) cover letter, b) resume/vitae, c) statement of research accomplishments and goals, d) statement of teaching accomplishments and philosophy that relate to NSF-AAAS Vision and Change, e) 3 highest impact publications combined into 1 PDF, and f) names and e-mail addresses of four referees who will receive an online link for submitting letters of reference. Review of applications will begin on February 28, 2018, and continue until the position is filled.

INSTITUTIONAL INFORMATION: UGA, a Land/Sea Grant institution located 90 miles northeast of Atlanta, is ranked 16th among public universities in the U.S. News & World Report's 2018 edition of America's Best Colleges. The Departments of Plant Biology and Plant Pathology encompass a broad range of disciplines and have historical strengths in plant ecology, evolutionary biology and plantassociated microbiology. UGA offers a vibrant research environment with potential collaborations with faculty across the plant sciences (https://plantcenter.uga.edu/), the Odum School of Ecology, and the Complex Carbohydrate Research Center, among others. Opportunities for off-campus interactions include the Savannah River Ecology Lab, the Coweeta Hydrologic Lab, the Sapelo Island Microbial Observatory, and several research farms and Research and Education Centers in the College of Agricultural & Environmental Sciences. Athens, GA, is consistently ranked highly for its quality of life and vibrant culture (https://www.visitathensga.com).

UGA is an EEO/AA/Vet/Disability Institution. As such, we are especially interested in candidates who can contribute to the diversity and excellence of the academic community. We not only strongly encourage women, minorities and other diverse candidates to consider applying for this position, but we also maintain that all candidates should share our commitment to diversity and inclusion. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, gender identity, sexual orientation or protected veteran status. Persons needing accommodations or assistance with the accessibility of materials related to this search are encouraged to contact Central HR (facultyjobs@uga.edu). Please do not contact the department or search committee with such requests.

"jleebensmack@uga.edu" <jleebensmack@uga.edu>

UHohenheim Bioinformatics

The Faculty of Agricultural Sciences invites applications for the position of a

Full Professor (W3) of Bioinformatics

at the Institute of Animal Science to be filled as soon as possible.

The successful candidate will teach management and analysis of omics-data in agriculture in the Faculty of Agricultural Sciences' degree programs. Participation in teaching in the Faculty of Natural Sciences and the Faculty of Business, Economics and Social Sciences is also required. The candidate should be able to teach both in German and in English.

The research focus of the Professorship should be on the development of bioinformatic methods and algorithms and the analysis of massive DNA and RNA data sets from livestock and associated microorganisms. This includes assembling and functional annotation of sequenced genes and transcripts as well as taxonomic and functional classification of data from microbiological multi-omics projects. Interdisciplinary collaboration with associated research groups of the University of Hohenheim is expected.

The position offers attractive conditions for first-time full professor appointees. Scientists with interest in the research focus and excellent methodological skills in Bioinformatics are encouraged to apply. Prerequisites for applicants are habilitation or an equivalent research and teaching record which may have been established during a Junior or Assistant Professorship.

The advertised position is tenured. If appointed as full professor for the first time, the University of Hohenheim reserves its right to probationary employment. With equal qualifications, preference will be given to candidates with disabilities.

The University of Hohenheim seeks to increase the proportion of women in research and teaching, and strongly encourages female scientists to apply.

Please attach the following documents to your application: a statement of your future research interests, a curriculum vitae, a documentation of academic achievements (copies), a list of publications, a list of third-party funded projects, a teaching record, information on teaching evaluations, and three key publications.

Please apply online at www.uni-hohenheim.de/prof-appt-portal before the 31 st of January 2018.

Questions regarding the position may be directed to Prof. Dr. Reiner Doluschitz (Reiner.Doluschitz@uni-hohenheim.de). University of Hohenheim Faculty of Agricultural Sciences 70593 Stuttgart | Germany

– Dr. Karl Schmid Professor of Crop Biodiversity and Breeding Informatics Institute of Plant Breeding, Seed Science and Population Genetics (350) University of Hohenheim Fruwirthstrasse 21, D-70599 Stuttgart Tel: +49 711 459-23487 Email: karl.schmid@uni-hohenheim.de Web: evoplant.uni-hohenheim.de

Karl Schmid <karl@minzer-schmid.de>

UMaine PlantEvolutionaryBiol

I am excited to announce a job listing for an Assistant Professor of Plant Evolutionary Biology and Systematics at my department at the University of Maine:

http://bit.ly/2A2WcsQ As chair of the search committee, I welcome questions about the position, our department, or the university of Maine.

Jacquelyn L. Gill Assistant Professor of Paleoecology & Plant Ecology School of Biology & Ecology Climate Change Institute 134 Sawyer Research Labs University of Maine Orono, ME 04469 (207) 581-2305 (office) contemplativemammoth.wordpress.com (blog) @JacquelynGill (Twitter)

Jacquelyn Gill <jacquelyn.gill@maine.edu>

UMassachusetts Amherst ResFellow CellMovementEvol

RESEARCH FELLOW, University of Massachusetts Amherst

The Fritz-Laylin Lab (fritzlaylinlab.org) at the University of Massachusetts Amherst is recruiting a highly motivated Research Fellow. The Fritz-Laylin lab studies cell motility at the interface of evolutionary biology and quantitative cell biology to define minimal requirements for cell movement, and to trace the evolutionary history of this complex behavior. These efforts require developing molecular tools for little studied organisms with unique evolutionary relationships and cell behaviors.

The initial responsibilities of the Research Fellow will focus on establishing protocols for molecular transformation and genetic manipulation of microbial eukaryotes, as well as measuring changes in gene expression during life stage transitions. Experience working with non-model organisms is NOT required but the successful candidate will be able to quickly learn how to apply their knowledge of common experimental techniques to new systems. The successful candidate will have the opportunity to work closely with the PI but is also expected to be proactive and independent, and able to work both individually and collaboratively with a team.

Dr. Fritz-Laylin is committed to helping all lab members build the skills needed to achieve their long-term career goals. Such skills include biological knowledge, molecular and cell biology techniques, project management, as well as science communication in the form of oral presentations, scientific publication, and grant writing. Dr. Fritz-Laylin meets with lab members weekly to discuss research progress and training needs. Enthusiastic applicants with diverse perspectives who wish to join a dynamic research group are encouraged to apply

Required Qualifications

Bachelor's degree in Biology or related discipline with a minimum of 2 years laboratory experience.

Preferred Qualifications

Preference may be given to candidates with experience in molecular biology (cloning, gels, western blot). Candidates with previous experience in gene expression and/or CRISPR technology would be highly competitive.

This is a non-benefited, full-time position. Salary is commensurate with experience. Initial appointment is for one year; reappointment beyond the first year is contingent upon availability of funding and job performance. Primary responsibilities will include, but are not limited to: molecular cloning, translating gene expression technologies to non-model organisms, and measuring gene expression. Active participation in laboratory meetings is required of all lab members.

Candidates must apply online by submitting a cover letter, CV, and the contact details of three references willing to provide letters of recommendation to:

http://umass.interviewexchange.com/-jobofferdetails.jsp?JOBID=92404 Review of applications will begin January 9, 2018 and continue until the position is filled. Applications received by January

9, 2018 will be given priority consideration.

The University of Massachusetts Amherst is an Affirmative Action/Equal Opportunity Employer of women, minorities, protected veterans, and individuals with disabilities and encourages applications from these and other protected group members.

Lisa Barry <lisak@bio.umass.edu>

UMissouri StLouis PlantSystematics

Nominations and applications are invited for the E. Desmond Lee Endowed Professorship in Botanical Studies to be filled by an outstanding scientist in an area of research that incorporates molecular and genomic approaches to the study of plant diversity, including phylogenetics and systematics. The appointment may be made at either the associate or full professor rank. This tenured position was established to enhance the partnership between the University of MissouriÂ'St. Louis and the Missouri Botanical Garden, where the endowed professor will have research associate status. The professorship is one of 36 endowed professorships comprising the Des Lee Collaborative Vision (DLCV), which are distinct from more traditional academic positions in having a primary responsibility for community outreach and engagement.

The University of MissouriÂ'St. Louis is a leader in partnerships with key institutions in the St. Louis Region. Alliances and programs have resulted from collaborations with the Missouri Botanical Garden, Saint Louis Zoo, St. Louis Science Center, Danforth Plant Science Center, and many others. The partnership with the Missouri Botanical Garden includes collaboration with the Whitney R. Harris World Ecology Center at UMSL, which promotes research and education in tropical biology and conservation, and participation in our outstanding graduate program in ecology, evolution, systematics, and conservation that attracts top scholars from all over the world. The Department of Biology also has an active research group in cell and molecular biology and participates in a joint program in biochemistry and biotechnology. The Missouri Botanical Garden, with more than 45 Ph.D. scientists, has a renowned research program, an outstanding library, and a world-class herbarium with more than 7 million plant specimens.

The Des Lee Endowed Professor in Botanical Studies will be expected to pursue an active program of research in botanical studies and oversee a laboratory at the University that facilitates the training of students in molecular techniques. Areas of particular interest are plant systematics and evolution, biodiversity studies, population genetics, ecology and conservation. In keeping with existing strengths in our program, research emphasis on tropical organisms, communities or floras is particularly welcome. The endowed professor will be actively engaged in community outreach and will have teaching responsibilities similar to other tenured, research-active faculty in the department. The professor is expected to take an active and integrative approach and exhibit, in his or her scholarship, both intellectual rigor and accessibility to wide range of diverse audiences. In keeping with the Des Lee Collaborative Vision, the successful candidate will have demonstrated interest in, and skills relevant to, engaging scholars outside his or her focused research specialty, and in engaging a public outside the academy. Therefore, we seek a broadly interactive colleague who is interested in crossing disciplinary boundaries within science and from science to the larger community. Laboratory and office space at the University, in addition to all research facilities at the Missouri Botanical Garden, will be available to the successful candidate. The position includes an annual budget in support of the collaboration between the University and the Garden.

The application review process is ongoing and will continue until the position is filled. The position will be available beginning Fall 2018, but the start date is negotiable. For full consideration, candidates must provide a cover letter outlining qualifications and interests, detailed curriculum vitae, statement of current and future research plans, statement of experience and plans in community outreach, along with names and contact information for three references from whom letters may be requested.

Address any questions to pparker@umsl.edu and ricklefs@umsl.edu. Formal submission of application materials must be done via the UniversityÂ^{1}s website: www.umsl.jobs. Click on the E. Desmond Lee Endowed Professorship in Botanical Studies, and follow the instructions provided. Job posting ID is 24884.

Christine.Edwards@mobot.org

UNevada EvolutionaryPhysiology

The School of Life Sciences at the University of Nevada, Las Vegas is searching for a new faculty position. The position is for a Neurophysiologist and other research areas may be considered. Preference will be given to those who complement current strengths in the School. The School of Life Sciences is highly integrative with a strong ecology and evolutionary biology program. Please encourage those with an interest in evolutionary neurophysiology to apply.

https://www.higheredjobs.com/details.cfm?JobCode6615075 Review of Applications will begin on January 15, 2018

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.

PROFILE of the UNIVERSITY

Founded in 1957 < https://www.unlv.edu/about/history >, UNLV is a doctoral-degree-granting institution of approximately 29,000 students and 3,000 faculty and staff < https://www.unlv.edu/about/glance/facts > that is classified by the Carnegie Foundation for the Advancement of Teaching as a research university < https://www.unlv.edu/research > with high research activity. UNLV offers a broad range of respected academic programs < https://www.unlv.edu/academics/degrees > 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 < https://www.unlv.edu/campuslife/las-vegas >, driving economic activity through increased research < https://www.unlv.edu/research > and community partnerships < https://www.unlv.edu/service/community-partners >, and creating an academic health center for Southern Nevada that includes the launch of a new UNLV School of Medicine < https://www.unlv.edu/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.

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 January 15, 2018 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 Donald K. Price, Ph.D. Director and Professor School of Life Sciences University of Nevada, Las Vegas donald.price@unlv.edu

Donald Price <donald.price@unlv.edu>

UQAT Quebec ForestPopulationGenetics

"Date : December 21st 2017 TENURE TRACK PROFESSOR IN MOLECULAR BIOLOGY OF SPECIES ASSOCIATED WITH FOREST ECOSYSTEMS Competition no 2017-63

The Université du Québec en Abitibi-Témiscamingue (UQAT) is a human sized institution that operates primarily in Abitibi-Témiscamingue, in the Nord-du-Québec, in the Hautes-Laurentides and with aboriginal communities. For more than a quarter of a century, UQAT has distinguished itself on several levels: teaching, research and creation, and service to the community. Thanks to its recognized expertise, UQAT plays an increasingly significant role not only at the regional scale, abut also at the provincial, national and international scales. The university's unique development model builds on partnerships in all its territories and thus ensures accessibility to university training. UQAT has been able to develop in several fields of which it is now renowned, creation and new media, human and social development, education, forests, engineering, management, mining and the environment, health and aboriginal communities.

Since the creation of UQAT, forest research has always been part of the institution's development plans. Strategic developments, including a partnership with UQAM, have enabled the establishment of a critical mass of interdisciplinary experts in "ecology and sustainable forest management" and in "valorisation, characterisation and transformation of wood". Consequently, UQAT has a well-established reputation in training, research and technology transfer in forest research, an expertise that is now recognised across Quebec, Canada and the international community. With the creation of the Forest Research Institute (IRF) in 2011, UQAT developed a structure that increases its contribution to forest science and technology. To date, the IRF relies on a team of eleven researchers, an Industrial Chair, two Canada Research Chairs, several specialised laboratories, and an extensive network of partnerships locally and around the world. The Institute attracts over $ 3 million annually in research, publishes more than 50 articles per year in recognised scientific journals, contributes to the training of a large contingent of highly qualified personnel, and is well known for a commitment to technology transfer as it organises a large number of dissemination activities. Renewed in 2014, the NSERC-UQAT-UQAM Industrial Chair in Sustainable Forest Management confirms the importance of developing and implementing innovative strategies and practices for ecosystem-based sustainable forest management. The IRF is active in both Abitibi-Témiscamingue and Nord-du-Québec, with significant spin-offs for Québec and Canadian society as a whole.

Position to be filled by the Forest Research Institute :

TENURE TRACK PROFESSOR IN MOLECULAR BIOLOGY OF SPECIES ASSOCIATED WITH FOREST ECOSYSTEMS

FUNCTION :

The candidate must be able to develop a research program in molecular biology, more especially in relation to species associated with forest ecosystems. The candidate should be interested in the application of population genetics, functional genomics or environmental genomics to issues related to forest ecology and forestry. The candidate must demonstrate excellence in the proposed field of research in order to be eligible for the major granting agencies, including the John R Evans Leaders Fund. It should be noted that IRF has a state-of-the-art laboratory in molecular biology that allows the candidate to quickly start his research program. The candidate should also have an interest in doing research in partnership with companies and government agencies associated with forestry, wildlife management, as well as ecological restoration. The candidate must be able to work in a small university in a region whose mission is, among other things, to contribute to the socio-economic development of the community. The professor will supervise graduate students in the Master's Degree in Ecology and the Doctoral Degree in Environmental Sciences, two of the graduate programs offered at UQAT.

REQUIREMENTS :

. Ph. D. in Ecology, Environment, Genetics, Biology, Forestry or a related discipline with expertise in molecular biology; . Candidates who have submitted their doctoral thesis could be considered. The candidate will have to commit to all the steps leading to graduation; . A research file demonstrating significant scientific productivity; . Excellent knowledge of written and spoken French (language of teaching), or the intent to acquire it.

OTHER CRITERIA CONSIDERED AS AN ASSET:

. A postdoctoral fellowship as well as experience in industry or government

PRIMARY WORK LOCATION: Rouyn-Noranda

START DATE: June 1st, 2018

DURATION OF CONTRACT: 2 years (tenure-track position)

SALARY: Salary is based on the qualifications and experience of each

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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

UTexas ElPaso CollectionManager

Natural History Collection Manager

Job ID: 3575 Location: El Paso, TX Full/Part Time: Full-Time Regular/Temporary: Regular

FLSA Status

Exempt Posting End Date

Review of applications will begin immediately and will continue until February 15, 2018. Monthly Salary

$3,106

$37,277/year + benefits Hours per Week

40.00 Standard from 800AM to 500PM Hiring Department

Biological Sciences Please Note

This position is grant funded continued employment is contingent on the availability of funds. Required Application Materials

A cover letter, academic curriculum vitae, collections Experience Statement (1-2 pages), including any experience with Arctos and a list of 3 professional references are required in order to apply.

Please upload all documents in one file. Purpose of Position

The collection manager for the University of Texas at El Paso Biodiversity Collections (UTEP-BC, natural history collections) will administer a world-class collection of specimens. The collections consist of fluid-preserved specimens, study skins, herbarium specimens, invertebrate collections, Cenozoic fossils, frozen tissues, wet and dry skeletons, acoustical recordings, digital and film-image archives, and extensive library holdings. The collections have an historical strength in Chihuahuan desert extant and extinct invertebrate and vertebrate specimens, and recent collections have focused on this region, Central and South America, and Central Africa. University curators and students, and national and international scholars use the collections extensively for research and education. The collections manager is responsible for day-to-day activities in the collection and reports to the director. Essential Functions

Collections management and conservation: * Ensure long-term integrity and preservation of collections and collection-storage environment. * Maintain and improve collection-care protocols. * Develop and maintain collection database (Arctos database). * Maintain and organize records of collection activity, use, and status for annual reports, grant submittals, and other documentation.

Acquisition and collection development: * Oversee the preparation and staging of newly acquired specimens for their integration into the collection. * Organize and prepare documentation necessary for specimen accession, including national and international permits and associated documentation. * Electronically catalog specimens and their associated information. * Participate in acquisition of specimens for the UTEP-BC by facilitating donations and by occasional fieldwork and expeditions at the direction of the curatorial staff.

Museum operational service: * Process all specimen loans, exchanges, and gifts; incorporate received specimens into the collection; maintain appropriate records of such activities. * Collaborate with curators to plan and implement divisional goals, priorities, and programs. * Collaborate with other museum collections managers to achieve high quality collections care and economy of scale in all collections-related activities. * Work proactively to place specimens from the UTEP-BC collection into the hands of qualified researchers for study. * Assist and supervise users of the collections. * Respond to inquiries from scientists, governmental and consulting agencies, the public, and other users. * Participate in the museum's public programming by providing information and specimens and assisting in exhibit design; assist in museum public functions. * Conduct tours for visiting scholars, students, and the public.

Supervision: * Hire, train, and supervise undergraduate assistants. * Train and supervise volunteers working in the collection.

Professional development: * Work closely with the curators to ensure consistency of practice. * Participate in collection management training and development through professional societies. * Undertake research in area of expertise when not in conflict with collection management duties. * Participate in professional scientific societies.

Knowledge of all Microsoft Office software and able to learn and use institutional software systems.

Complies with all State and University policies.

Other duties may be assigned.

Required Qualifications

A Master's degree or Ph.D. from an accredited university in museum studies, systematics, botany or invertebrate/vertebrate zoology or bachelor's degree plus a minimum of 2 years experience working with museum collections in a position with similar responsibilities.

Familiarity with biodiversity informatics, including the database Arctos, web-based applications, and distributed networks.

Demonstrable knowledge of care and management of natural history collections, with a special emphasis on preventative conservation,

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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

UToronto BioinformaticsTech

The University of Toronto Centre for Analysis of Genome Evolution & Function (CAGEF, http://www.cagef.utoronto.ca/) is searching for a Bioinformatics Technician. This is a long-term staff position for an individual interested in both data analysis as well as bioinformatics training & education. The individual will be responsible for analyzing client data, assisting with client experimental design, and developing and presenting bioinformatic training workshops, courses, and online tutorials to enable bench scientists to take a more engaged role in the analysis of their own data.

Candidates should have a bachelor degree in bioinformatics, computational biology, biostatistics, or an equivalent combination of education and experience, and at least three years of recent and relevant post-graduate experience in the field. They should also have practical experience with bioinformatics, biostatistics, genome analysis, next-generation genome data management and analysis, Unix, Python, R & Bioconductor.

Direct experience and interest in developing and presenting bioinformatics workshops, programs, and material is strongly desired.

The individual will have the opportunity to actively engage in major research projects, obtain co-authorship on scientific publications, and have the potential to perform independent research.

CAGEF is an independent unit within the University of Toronto Faculty of Arts & Science that provides genomics, proteomics, and bioinformatics services. Our mandates includes the promotion of interdisciplinary research, education, and training.

More information can be found https://utoronto.taleo.net/careersection/10000/jobdetail.ftl?job=1702268&tz=GMT-05%3A00 Questions can be sent to david.guttman@utoronto.ca

David S. Guttman Director, Centre for the Analysis of Genome Evolution & Function Professor & Associate Chair for Research, Department of Cell & Systems Biology University of Toronto 25 Willcocks St. Toronto, ON M5S 3B2 Canada

416-978-6865 office david.guttman@utoronto.ca guttman.csb.utoronto.ca www.cagef.utoronto.ca David Guttman <david.guttman@utoronto.ca>

WhitmanC Washington LabTech MolecularEvolution

Seeking a full-time laboratory technician to carry out research on the molecular basis of repeated evolution:

Funding is available for a 20-month position. During that time, the technician will work with me to design and implement functional 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 - attention to detail and ability to work independently - excellent organizational and communication skills

Understanding of or experience with transgenic techniques is preferred; we use Agrobacterium-mediated transformation.

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. 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, starting at $25,000 annual salary. Starting date is flexible but should be summer or fall 2018.

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 / résumé, including names and contact information for three references

Questions may be directed to: Dr. Arielle Cooley cooleya@whitman.edu

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Arielle Cooley, Assistant Professor Whitman College Biology Department Walla Walla, WA 99362

Arielle Cooley <cooleya@whitman.edu>

Other

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)

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"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>

AMNH NewYork HelenFellowship

Dear Colleagues,

The BridgeUP: STEM program at the AMNH is excited to announce that the application for the Helen Fellowship is now open. This fellowship is a one-year residency for post-baccalaureate women to devote time immersed in computational scientific research and educational outreach at the AMNH. This fellowship is an initiative at the AMNH dedicated to increasing the diversity of the talent pipeline by providing underrepresented students access to the skills and tools required for the 21st Century.

Please share this great opportunity with any female student or advisee who might be interested. To learn more about the fellowship and the application process, visit < http://www.amnh.org/bridgeup/helen > https://www.amnh.org/learn-teach/adults/bridgeup-stem/helen-fellowship .A colorful PDF flyer can be downloaded at this website.

Who is eligible to apply? The fellowship is intended for recent college graduates with a conferred bachelor's or master's degree in computer science, natural sciences, applied mathematics, computational science, or other relevant majors prior to the fellowship start date in September.

What are the benefits? Fellows will receive an annual salary of $70,000 plus generous benefits. Funding is also available for research, travel and equipment expenses.

How do I apply? The online application is now open and is due by January 21, 2018. To learn more about application requirements, visit https://www.amnh.org/learn-teach/adults/bridgeup-stem/helen-fellowship . With Regards,

The BridgeUP: STEM Team

Email: bridgeupstem@amnh.org

bridgeupstem@amnh.org

Kluane RedSquirrelAssistants

Field Assistants Required 2018 Kluane Red Squirrel Project, Yukon, Canada

We are looking for field technicians to assist with fieldwork for three different time periods: (a) 1 March-15-May (b) 1 May-15 August, and (c) 1 September - 15 October.

The positions are part of a long-term study of red squirrel ecology, evolutionary biology and physiology. As a member of the study, technicians will be involved with monitoring the reproduction and survival of individual squirrels. Fieldwork will involve live-trapping and handling of squirrels, radio-telemetry, behavioural observation, and locating young in their nests. Some positions will also require additional handling for physiological assays (e.g., blood sampling). This is an excellent opportunity to gain experience working with a collaborative research team on a long-term study of a wild mammal.

All fieldwork is carried against the beautiful backdrop of southwestern Yukon, Canada. We will be staying at a rustic field station two hours from Whitehorse, and ~30 min to the nearest town (Haines Junction). All food and accommodation are provided and technicians are provided with transportation (within reason) to and from the field site either through airfare or vehicles.

Training will be provided and no experience is necessary. Candidates should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal behaviour. The field camp is remote and low tech (no showers, cell phone service, or internet), so successful applicants must enjoy the outdoors and be able to remain a positive and responsible team member under relatively isolated and demanding conditions. Candidates must be in good physical condition and have an enthusiasm for learning. We work on 'squirrel time', which often involves long work days; as such, applicants must have a strong work ethic. The atmosphere at squirrel camp is friendly and inclusive and all nationalities are welcome.

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 kluaneredsquirrels@gmail.com by January 5 2018. Please also indicate the time period(s) you are interested in.

“jeffrey.lane@usask.ca” <jeffrey.lane@usask.ca>

MountainLakeBiologicalStation GrantWriting Jul29-Aug3

Six-day hands-on grant writing workshop at Mountain Lake Biological Station

Grant Writing Workshop July 29 - August 3, 2018 Registration Deadline: July 13, 2018

Location: Mountain Lake Biological Station 240 Salt Pond Cir., Pembroke, VA 24136.

Join NSF program director Dr. Leslie Rissler for a six-day hands-on grant writing workshop for junior scientists who want to learn strategies, styles, and structures to improve their grant proposals. The experience is geared toward early career proposal writers including early stage faculty, postdocs, and senior graduate students and will include direct discussions and writing sessions based on participants’ own proposal ideas. Limited enrollment (12) will enable close interaction.

Cost: $250 registration, plus room and board ($262.50 double occupancy or $285.25 private accommodation if available).

For More information: About workshop structure and content: Contact Leslie Rissler, Leslie.Rissler@gmail.com

About registration, travel logistics, and the field station: Contact MLBS, mlbs@virginia.edu, (540) 626-7196, or visit mlbs.org

esn8n@virginia.edu

OmmenPrize EvolutionMedicine

“Now open for nominations! Omenn Prize ($5000) for best scientific paper published in 2017 on a topic related to evolution in the context of medicine and public health - nominate at https://evolutionarymedicine.org/funding-and-awards/gil-omenn-prize/” Cheers, Sean

Sean Byars <seangbyars@gmail.com>

Phyloseminar CecileAne Dec13

Next on http://phyloseminar.org: >From reconstructing to using phylogenetic networks Cécile Ané University of Wisconsin-Madison Wednesday, December 13, 2017, 9:00 AM PST

I will first highlight why network reconstruction is worth the effort, and then explain some of the challenges of network reconstruction and network intepretation. These challenges include identifiability issues, difficulties to summarize network uncertainty, and interpretation issues related to network-thinking. Finally, I will describe new phylogenetic comparative methods that can be applied to phylogenetic networks, and are implemented in the PhyloNetworks Julia package.

Frederick “Erick” Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ Erick Matsen <ematsen@gmail.com>

SMBE CallForAwardsNominations

Nominations Due for Prestigious SMBE Awards

Dear SMBE Members: In 2015, SMBE instituted four new awards for: Early-Career, Mid-Career, and Lifetime Research Achievements, and Service to the SMBE Community. We are now calling for nominations for these awards and ask you to consider nominating your colleagues.

The nominations will be due on January 19, 2018.

Briefly, the Junior Award for Independent Research is intended for nominees in tenure-track positions at the Assistant Professor level or equivalent; the Mid-Career Award is for the research contributions of faculty nearing promotion to Full Professor or in the early stages as a Full Professor; the Lifetime Contribution Award is for exceptional contributions to the published literature in the field of molecular biology and evolution; and the Community Service Award recognizes outstanding efforts on behalf of the Society and the broader scientific community. Awardees will receive a cash prize and a trip to the upcoming SMBE Annual Meeting in Yokohama, Japan (July 8-12, 2018).

Here are links to the pages describing these awards:

*Allan Wilson Junior Award for Independent Research * http://www.smbe.org/smbe/AWARDS/FacultyAwards/AllanWilsonJuniorAwardforIndep endentResearch.aspx < https://t.e2ma.net/click/l8jxm/duvmg1/diehze >

Margaret Dayhoff Mid-Career Award http://www.smbe.org/smbe/AWARDS/FacultyAwards/MargaretDayhoffMidCareerAward .aspx < https://t.e2ma.net/click/l8jxm/duvmg1/tafhze >

Community Service Award http://www.smbe.org/smbe/AWARDS/FacultyAwards/CommunityServiceAward.aspx < https://t.e2ma.net/click/l8jxm/duvmg1/92fhze >

Motoo Kimura Lifetime Contribution Award http://www.smbe.org/smbe/AWARDS/FacultyAwards/MotooKimuraLifetimeContributio nAward.aspx < https://t.e2ma.net/click/l8jxm/duvmg1/pvghze >

Nominations require a nomination letter, which should clearly indicate the award under consideration and also serve as a recommendation letter; a separate one-page summary of the nominee's qualifications for the award; a CV of the nominee; and an additional letter of recommendation.

Self-nomination is not allowed. The nominator need not be an SMBE member, but the nominee must be a member of SMBE to be considered for the award. The materials should be compiled into a single PDF file, and should be emailed to tleatherman@allenpress.com.

Best Regards, George Zhang SMBE Awards Committee Chair Society for Molecular Biology & Evolution smbe@allenpress.com

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

Software IQTree version 1 6 0

Dear Community,

We are pleased to announce the major release 1.6.0 of the IQ-TREE software for phylogenomic reconstruction (http://www.iqtree.org). Among others, notable new features include:

- Many new realistic models of sequence evolution: Heterotachy, Lie Markov and Polymorphism-aware Models. - Three new empirical protein models mtMet, mtVer, mtInv for mitochondrial evolution. - Improved ModelFinder allowing to test all above models. For partitioned analysis ModelFinder now supports edge-linked partition model selection and fast relaxed clustering algorithm (-rclusterf option) like PartitionFinder2. - A fast tree search option to match the speed of FastTree while still obtaining better trees (-fast option). - Ancestral sequence reconstruction (-asr option). - An option to reduce the impact of model violation for the ultrafast bootstrap (-bnni option). - Xeon Phi Knights Landing (AVX-512 instruction set) support.

Kind regards,

IQ-TREE development team

Bui Quang Minh Center for Integrative Bioinformatics Vienna (CIBIV) Campus Vienna Biocenter 5, VBC5, Ebene 1 A-1030 Vienna, Austria

minh.bui@univie.ac.at

Software NeEstimator v2 1

Hi Folks

We are pleased to announce a major upgrade to the NeEstimator software.

The new version (2.1) implements some major improvements particularly for the linkage disequilibrium (LD) method of estimating genetic effective population size (Ne) from diploid genotypes. These improvements facilitate the use of SNP data for LD estimates of Ne.

The changes include

1. Faster capacity to estimate Burrows r, 2. An option to estimate r between loci on separate chromosomes or linkage groups (with user-supplied linkage data), 3. An improved method of estimating jacknifed confidence intervals, and 4. Improvement to the handling of low frequency alleles.

The new software can be downloaded here < http://www.molecularfisherieslaboratory.com.au/neestimator-software/ >.

(http://www.molecularfisherieslaboratory.com.au/neestimator-software/)

Best wishes,

NeEstimator development team (Chi Do, Robin Waples, David Peel and Jenny Ovenden) "j.ovenden@uq.edu.au" <j.ovenden@uq.edu.au>

SouthAfrica StripedMouse ResAssistResManager

First call :

Position as research assistant (March - October 2018)

and as research manager (November 2018-November 2019

at the striped mouse project in South Africa,

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

As research assistant, you will help the postdoc Pauline Vuarin during her studies on the extinction risk of different sub-populations in Goegap.

As research manager you will work closely together with the station manager and both managers will share responsibilities. However, each will have specific main duties, but should also be able to deal with all other duties (for example when the other manager is on leave, or when a new manager has to be trained). Our current research manager will leave the project in October 2018. The new research manager will be instructed by the present research manager.

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

Great opportunity: This is a great opportunity to spend 1.5-3 years in Africa, acquiring important skills in field biology and project management, while improving your CV. These skills will become valuable whether you later continue with a PhD or other jobs. It will be very hard and demanding, but also a once in a life time experience! You must be hard-working, highly motivated, able to work independently, good in communicating with people, able to supervise others, and not afraid of snakes. You should love to live at a remote place in nature, without regular internet and cell-phone reception. Most importantly, you are fascinated by nature and science!

Job description: Five working days a week (Mo, Tue, Thu, Fr, Sat), with Wednesday being used for a shopping trip to town (not counted as working day) and Sundays being free. Included are four weeks of holiday for 12 months, which has to be taken outside the main breeding season (August to November) during periods when other students are present at the research station.

Primary duties research manager / secondary duties station manager

. Data:

o Weekly data entry

o Weekly data check

o Monthly data backup

o Monthly data report

o Training and supervision of field assistants

o Training of students and postdocs

o Support for students and postdocs

o Management of transmitters

o Management of field and laboratory supplies

Primary duties station manager / secondary duties research manager

. Technical support research station:

o Water system incl. sewage system

o Solar system

o Gas bottles replacement

o House and furniture

o Running of the respirometry laboratory

o Management of the captive colony

o Management of the research station car

o Management of bank account and cash box

o Management of research station supplies

Compensation:

. Free accommodation.

* A monthly compensation of R 3 500, which is sufficient to pay all costs of living. This compensation will rise to R4 700 per month in November 2018, when the research assistant takes over the research manager position. *

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

Responsibilities:

. The manager has to cover the costs to get to the station, including travel costs and visa fees. For this, a refund can be paid (see above).

* The manager needs to arrange for a health insurance covering him / her during the stay. A copy must be sent to C. Schradin before travelling to the stations.

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

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SouthAfrica VolResAssist PhysiologyBehaviour

Volunteer Research Assistant Position We are looking for 3 volunteer research assistants to carry out exciting experiments with captive Damaraland mole-rats, Fukomys damarensis at the Kuruman River Reserve, in the South African Kalahari Desert.

Broadly, our research investigates the influence of genes, hormones and social factors on individual developmental, growth and behaviours.

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

Applicants should be available for a period of 6 to 12 months starting as soon as possible. They should be hardworking, enthusiastic, physically fit, and prepared for long hours in the laboratory. Successful applicants will be responsible to run experiments and will be involved in data collection and management (behavioural observations, collection of blood and urine samples). Other general tasks related to animal handling (hormone injections and implants) and husbandry and data handling will also be expected. Some applicants should feel comfortable with being involved in experiments requiring the sacrifice of experimental subjects. Working weeks will not exceed 45 hours.

This position is particularly suited, but not exclusively, for people aiming to carry on their academic education or a management position in a research project. Successful applicants can expect to gain invaluable experience in animal handling procedures and in conducting and managing experiments. They will also gain database skills (MySQL) and will be provided with the opportunity to work on a personal project using the data available in our existing database.

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

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

Shortlisted applicants will be invited for a Skype interview.

Deadline: 31st December 2017 (the position will remain open until filled)

philippe.vullioud@gmail.com

StonyBrookU GraduateOpportunities

DEADLINE EXTENSION: Due to uncertainties regarding the tax legislation currently before congress, the program in Ecology and Evolution at Stony Brook University has decided to consider applications for the PhD program submitted before Jan 15. Review of applications has already begun and there are limited spots available, so it is advisable to submit as soon as possible. Please see additional program information below.

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GRADUATE OPPORTUNITIES IN ECOLOGY AND

EVOLUTIONARY BIOLOGY

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

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

DEPARTMENTAL FACULTY

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

Nolwenn Dheilly - Evolution of Host-Parasite Interactions http://you.stonybrook.edu/dheilly/ Andreas Koenig http://www.stonybrook.edu/commcms/anthropology/faculty/akoenig.html David Matus - Evolution of Cell Invasion http://www.stonybrook.edu/commcms/biochem/research/faculty/matus.html# Janet Nye - Quantitative Fisheries Ecology https://you.stonybrook.edu/jnye/ Alistair Rogers - Plant Physiology and Climate Change www.bnl.gov/TEST Shawn Serbin - Plant Physiology and Remote Sensing www.bnl.gov/TEST Jeroen B. Smaers - Brain Evolution, Phylogenetic Comparative Methodology, Macroevolutionary Morphology https://smaerslab.com/ Leslie Thorne - Ecology and Behavior of Marine Birds and Mammals http://you.stonybrook.edu/thornelab/ Nils Volkenborn - Benthic Ecology and Sediment Biogeochemistry https://you.stonybrook.edu/voll/ Patricia Wright - Tropical Conservation and Primatology http://www.patwrightlab.net/pat-wright.html For more information regarding the Graduate Program in Ecology and Evolution, please see http://www.stonybrook.edu/ecoevo/index.html for general information. For specific information on the PhD and MA programs, please see http://www.stonybrook.edu/commcms/ecoevo/program/index.html and

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UTexas ElPaso REU ChihuahuanDesertBiodiversity

REU Opportunity Summer 2018: "Research Experience for Undergraduates in Chihuahuan Desert Biodiversity"

The University of Texas at El Paso (UTEP) Department of Biological Sciences invites applicants for the NSF sponsored Research Experience for Undergraduates (REU) in Chihuahuan Desert Biodiversity. This is a 10 week summer program. The goal of this program is to provide undergraduate students with experience in hypothesis-driven collaborative research utilizing field based and/or laboratory methods and fully engage students in projects associated with the ecology and evolution influencing Chihuahuan Desert biodiversity.

The program provides:

* High quality research experience in ecology and evolutionary biology in the field and/or lab * Research opportunities at the Indio Mountains Research Station (IMRS), a 40,000 acre facility controlled by UTEP * One-on-one and group mentoring from active research faculty in multidisciplinary fields * Training in bioethics and other relevant professional skills

The program includes:

* $5500 stipend for 10 weeks

* Housing in shared apartments and field station

* Travel reimbursement of up to $600

For more information on the program, research projects or to apply please visit: http://science.utep.edu/cdb-reu/ Enquiries: CDB-REU@utep.edu

"Moody, Michael L" <mlmoody@utep.edu>

WillametteU VolFieldPosition Coevolution

The Smith lab at Willamette University is soliciting applications for volunteers to participate in field research studying the pollination biology and coevolution of Joshua trees (*Yucca brevifolia*) and yucca moths (genus *Tegeticula*) from mid March to mid April of 2018. Volunteers will assist in the completion of pollination experiments in a plant hybrid zone located in central Nevada, which will involve collecting flower and leaf tissue samples, installing pollinator exclusion cages over Joshua tree flowers, collecting moths, and sorting insects to species.

All food and accommodation costs will be covered by the project. Travel within the United States will be paid by the project. International travel costs may potentially be covered, and will be considered on a case-by-case basis. However, participants traveling from outside the US must arrange travel documents and secure appropriate visas themselves.

Participation will require living at a remote field camp continuously for approximately five weeks. Meals are communal, prepared in a small RV kitchen, and evenings are typically spent around the camp fire. Many past participants have returned for additional years, and many have used the experience gained on this project to secure other positions in agency, private conservation organizations, and graduate programs in ecology, evolution, and entomology.

However, prospective participants should be aware that conditions in the field are challenging. The field site has no running water. Apart from personal tents and walks in the desert there is little opportunity for personal space and time, and there are no cell phone/internet services at the field site. (Wifi and cell service are available in the nearest town, a 30-minute drive away). Daily temperatures may drop below freezing or exceed 90 F, and windstorms are very common. So, it is important that prospective volunteers be enthusiastic about living and working closely with others in challenging conditions. Volunteers should also be capable of hiking up to 6 miles per day while carrying heavy and awkward loads, and able to climb a 6' ladder.

Prospective volunteers should submit a CV or resume, the name and contact information for one or more professional references, and a letter describing their interest in the project by email to csmith@willamette.edu . There is no degree requirement, but a familiarity with and an interest in ecology and natural history are necessary.

Please include the words 'Volunteer Field Assistant' in the subject line of your message.

Screening of applicants will begin on January 15th, 2018, and continue until all positions are filled.

More information about our research can be found here:

http://www.nsf.gov/discoveries/disc_summ.jsp?cntn_id=115956&org=NSF http://www.reviewjournal.com/news/water-environment/joshua-tree-yucca-moth-co-evolution-fascinates-researchers https://knpr.org/knpr/2013-01/joshua-tree-researcher-searching-citizen-scientists Christopher Smith <csmith@willamette.edu>

PostDocs

AmherstC MA EvolutionSexMatingChrs

AmherstCollege.EvolutionSexMatingChrs

2-YEAR POSTDOC IN EVOLUTIONARY GENOMICS SEX AND MATING-TYPE CHROMOSOMES

The Hood Lab (https://www.amherst.edu/people/facstaff/mhood) in the Biology Department at Amherst College is seeking to fill a 2-year Postdoctoral Research Associate position. The research addresses the evolutionary genomics of chromosomes determining reproductive compatibility and the consequences of recombination suppression. This project will involve collaborative work with participating laboratories, including with the Giraud Lab (http://www.ese.u-psud.fr/article211.html?lang=en), and a mixtures of molecular and bioinformatics approaches. Start date will be as early as spring, 2018.

Qualifications: A Ph.D. is required in evolutionary biology, genetics or related field and have research interests in the evolution of reproductive systems (particularly involving self-incompatibility systems), genome sequence analysis, chromosome dynamics and structural evolution and evolutionary genetics.

To apply online and for more information, please visit our web site at https://apply.interfolio.com/48016 or https://jobs.amherst.edu

About Amherst College: Amherst College, one of the premier liberal arts colleges in the nation, is located in Amherst, Massachusetts, a town of approximately 35,000 residents in the western part of the state that is also home of UMass-Amherst. The college's community is composed of about 1,800 students from 49 states, plus D.C., Puerto Rico and the Virgin Islands, and 54 countries around the world, and about 1,000 staff and faculty. The college's scenic 1,000-acre campus includes a 500-acre wildlife sanctuary and the Book & Plow Farm; three museums: Emily Dickinson Museum, Beneski Museum of Natural History and Mead Art Museum; and multiple educational and cultural venues and resources through the Five College Consortium. The town of Amherst offers an amazing variety of coffee shops, restaurants and entertainment, and a very active outdoor life. Our vibrant campus, diverse community and beautiful surrounding, makes Amherst College and the Town of Amherst a great place to work, learn and live!

Statement of Non-discrimination: Amherst College does not discriminate in admission, employment, or administration of its programs and activities on the basis of race, national or ethnic origin, color, religion, sex or gender (including pregnancy, sexual orientation, gender expression, and gender identity), age, disability, genetic information, military service, or any other characteristic or class protected under applicable federal, state, or local law. Amherst College complies with all state and federal laws that prohibit discrimination, including Title VII of the Civil Rights Act, Title IX, Section 504 of the Rehabilitation Act, the Americans with Disabilities Act, the Equal Pay Act and the Age Discrimination in Employment Act. Inquiries should be addressed to the Chief Diversity and Inclusion Officer, Amherst College, P.O. Box 5000, Amherst, MA 01002-5000.

Michael E. Hood Professor of Biology Amherst College Amherst, MA USA 01002-5000 ph (413) 542-8538 email: MHood@amherst.edu https://-www.amherst.edu/people/facstaff/mhood Michael Hood <mhood@amherst.edu>

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.

spfeife1@asu.edu

ArizonaStateU EvolutionaryMedicine

Evolution & Medicine Postdoctoral Research Fellowship

Salary:

$60,000

Job #12228

Full-time

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.

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, the CEM provides postdoctoral fellows with opportunities collaborate with faculty from a

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BielefeldU PinnipedEvolutionaryGenomics

Post-doctoral position: Pinniped ecological and evolutionary genomics With Dr Joe Hoffman (Bielefeld University, Germany), Prof Oliver Kruger (Bielefeld University, Germany) and Dr Jaume Forcada (British Antarctic Survey, UK)

An outstanding opportunity is available for a postdoctoral researcher to work on the ecological and evolutionary genomics of fur seals. The position is available in Joe Hoffman's research group (www.thehoffmanlab.com) in the Department of Animal Behaviour at Bielefeld University. It runs from early 2018 to the end of 2021 and is funded by the German Research Foundation (DFG) within the recently approved collaborative research centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

The project: The postdoc will exploit and continue to build upon an exceptionally detailed long-term study of Antarctic fur seals (Arctocephalus gazella) at Bird Island, South Georgia. High quality genome and transcriptome assemblies have already been generated and microsatellite and high density SNP data will be available for 'Ã7000 marked individuals spanning a time series from the mid 1980's to the current day. The aim of this project (sub-project A01 of the collaborative research centre) is to determine how fitness variation is shaped by interactions between individual genetic quality (inbreeding) and the social environment within breeding colonies. Highly detailed observational and biometric time-series data will be collected from mother-offspring pairs in two neighbouring colonies of high and low social density. The mechanistic underpinnings of fitness variation will then be dissected apart using a novel combination of endocrinological and immunological profiling, high-density SNP genotyping, transcriptomics and genome-wide methylation profiling. This will generate unprecedentedly detailed insights into fitness variation in a wild vertebrate, with major implications for understanding ecological and evolutionary dynamics as well as adaptation to climate change.

The applicant: We seek a bright and highly motivated postdoc with a strong PhD in a relevant topic (e.g. population genetics, behavioural, evolutionary or conservation genomics, bioinformatics, animal behaviour, behavioural ecology). A deep understanding as well as extensive practical experience of working with high-throughput sequencing data (including RADseq, transcriptomic and whole-genome resequencing data) is highly desirable, as is proficiency in writing custom scripts and working in Unix and R. Experience of working with large-scale, long-term datasets from wild animal populations would also be a bonus. As the postdoc involves two field seasons at South Georgia in the South Atlantic, experience of fieldwork with vertebrates and ideally large mammals would also be highly beneficial. The ideal candidate will also be able to work both independently and as part of a team. A very high standard of spoken and written English is required and a proven track record of publishing in high quality international peer-reviewed journals would be advantageous.

The working environment: The postdoc will join the Hoffman lab, a young and dynamic group comprising five PhD students and two postdocs. They will be based at the Department of Animal Behaviour at Bielefeld University (www.uni-bielefeld.de/biologie/vhf/index.html). The department is the oldest of its kind in Germany and currently hosts around six principal investigators, ten postdocs and twenty PhD students. It offers a stimulating international environment and an excellent research infrastructure including brand new molecular laboratories. The working language of the Department is English. The postdoc will also have the opportunity to interact closely with the cooperation partner (Dr Jaume Forcada) during two Antarctic field seasons and via placements at the British Antarctic Survey in Cambridge.

Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling and prevention programmes. Bielefeld University places great importance on a work?Cfamily balance for all its employees. Bielefeld is a city of 325,000 inhabitants with an attractive historical centre and easy access to the Teutoberger Wald for hiking and other outdoor pursuits. It offers a very high standard of living and is well connected to most major European cities.

The collaborative research centre: The postdoc will be embedded within a larger collaborative research centre (SFB) comprising 18 principle investigators, 8 postdocs and 16 PhD students based at Bielefeld

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BielefeldU ScientificCoordinator

Dear Prof. Golding, could you please circulate the job advert below via EvolDir and put it in the Postdoc section of EvolDir.

1 Postdoc (50%) position as a scientific coordinator

A half-time Postdoc position as a scientific coordinator is available at the Faculty of Biology at Bielefeld University, in the Department of Animal Behaviour (with Prof. Oliver Krueger, see http://www.uni-bielefeld.de/biologie/animalbehaviour). The position runs from early 2018 to the end of 2021 and is funded by the German Research Foundation (DFG) within the recently approved collaborative research centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

The tasks of the scientific coordinator are to assist the speaker of the collaborative research centre in all tasks related to the running of the centre.

The collaborative research centre: The postdoc will be embedded within a larger collaborative research centre (SFB) comprising 18 principle investigators, 9 postdocs and 16 PhD students based at Bielefeld University, the University of Muenster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programmes. Full details of the SFB can be found at www.uni-bielefeld.de/biologie/crc212 . Main responsibilities

- Organisational tasks (100%):

- Planning and coordination of meeting and conferences of the SFB/TRR 212

- Assistance to the spokesperson in communicating with members of the collaborative research centre

- Keeping the webpage of the collaborative research centre up to date

- Writing outreach material for dissemination to the public and the media

Applicant's profile

We seek a bright and highly motivated postdoctoral researcher with

- a university degree in a relevant discipline, e.g. biology,

- a completed PhD in a relevant field, ideally related to behavioural ecology or evolutionary ecology,

- experience with coordinating science projects,

- experience with organising scientific meetings and conferences,

- experience in public outreach and media activities,

- ability to work both independently and as part of a team, and

- excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage:

- experience in coordinating a group of people

- experience with large-scale research projects.

Remuneration

Salary will be paid according to Remuneration level 13 of the Wage Agreement for Public Service in the Federal States (TV-L).

Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling, and prevention programmes. Bielefeld University places great importance on a work-family balance for all its employees.

Application procedure

To apply, please provide: (i) a letter of motivation including a statement of your 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 emailed as a single PDF file to: oliver.krueger@uni-bielefeld.de. The application deadline is January 7th 2018 and interviews will take place shortly thereafter. After the decision, the position should start as soon as possible. For further information on the project and the department, please contact Oliver Krueger oliver.krueger@uni-bielefeld.de with any informal inquiries.

Bielefeld is a city of 325,000 inhabitants with all expected amenities and easy access to the Teutoburger Wald for hiking and other outdoor pursuits. It offers a high standard of living and is well connected to most major European cities.

Bielefeld University has received a number of awards for its achievements in the provision of equal opportunity and has been recognized as a family friendly university. The University welcomes applications from women. This is particularly true with regard both to academic and technical posts as well as positions in Information Technology and Trades and Craft. Applications are handled according to the provisions of the state equal opportunity statutes. Applications from suitably qualified handicapped and severely handicapped persons are explicitly encouraged. With best wishes, Oliver Kruger

Prof. Dr. Oliver Kruger Department of Animal Behaviour VHF

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BielefeldU TheoreticalEvolutionaryEcol

2 Postdoc positions in Theoretical Evolutionary Ecology at Bielefeld University, Germany (application deadline: January 7, 2018)

Two Postdoc positions in theoretical evolutionary ecology are available at the Faculty of Biology at Bielefeld University, one position in the Department of Evolutionary Biology (with Prof. Dr. Klaus Reinhold, see http://www.uni-bielefeld.de/biologie/Evolutionsbiologie) and one position in the Department of Theoretical Biology (with Jun.Prof. Dr. Meike Wittmann, see www.uni-bielefeld.de/biologie/theoreticalbiology). The positions run from early 2018 to the end of 2021 and are funded by the German Research Foundation (DFG) within the recently approved collaborative research centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC^3).

The aim of both Postdoc projects is to develop ecological and evolutionary theory to contribute towards a better understanding of intra-specific niche variation. One project is entitled “Local population density as a key dimension of the individualised niche: An eco-evolutionary modelling approach” (sub-project D03 of the collaborative research centre, with Meike Wittmann, http://www.uni-bielefeld.de/biologie/crc212/D03.html). This project will explore how individuals and populations respond to spatial variation in population density, and how the various response modes (genetic variation, phenotypic plasticity) feed back on patterns of population density and also influence the population’s ability to persist in the face of habitat loss or habitat fragmentation. This project involves collaborating with empirical groups in the collaborative research centre. The other project is entitled “Modelling adaptive individualised niches in behaviour” (sub-project D04 of the collaborative research centre, with Klaus Reinhold, http://www.uni-bielefeld.de/biologie/crc212/D04.html). This theoretical project will explore the conditions that favour the evolution of between-individual variation in behavioural niches. The aim is to focus on mate choice and exploration and examine to which extent phenotypic variation can be maintained based on genetic differences and variation in adaptive phenotypic plasticity.

The collaborative research centre: The postdocs will be embedded within a larger collaborative research centre (SFB) comprising 18 principle investigators, 9 postdocs and 16 PhD students based at Bielefeld University, the University of M?nster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programmes. Full details of the SFB can be found at www.uni-bielefeld.de/biologie/crc212 . Main responsibilities: * Research tasks (90%): - Development of eco-evolutionary models - Mathematical analysis of models - Implementation in a programming language, e.g. in R, C++, Python - Simulation studies - Collaboration with other research groups in the collaborative research centre - Writing scientific publications * Organizational tasks in the research group and collaborative research centre (10%)

Applicant’s profile: We seek bright and highly motivated postdoctoral researchers with * a university degree in a relevant discipline, e.g. biology, mathematics, physics or bioinformatics, * a completed PhD in a relevant field, ideally related to theoretical ecology, population genetics, or * evolutionary ecology, * experience with mathematical modelling, * programming skills in at least one programming language (e.g. R, C++, Python), * interest in both biological and mathematical questions, * ability to work both independently and as part of a team, and * excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage: * papers in peer-reviewed international journals, * experience in collaborations between empiricists and theoreticians, and * experience with high-performance computing.

Remuneration: Salary will be paid according to Remuneration level 13 of the Wage Agreement for Public Service in the Federal States (TV-L).

Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a

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BrownU EvoDevo

Brown University Postdoctoral Fellow position for Cell and Developmental Biology

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

We are looking to hire a talented full-time postdoctoral fellow who conducts her/his independent research under PI's supervision.

In our group, two major projects are currently undertaken:

(1) Cell and Developmental Biology: Identifying how germline factors contributes to cellular functions and development, using sea urchin embryonic cells and human cancer cells.

(2) Evolutionary Developmental Biology: Discovering how the molecular evolution alters the developmental program and contributes to species diversity, using multiple echinoderm embryos.

Both projects require skills in embryology and live imaging such as microinjection, optogenetic manipulations of a protein, and 4D-confocal imaging. Experience in Biochemical and bioinformatic approaches is also welcomed: these include Immunoprecipitation followed by proteomic analysis or by RNA-seq to broadly identify the targets.

A good accomplishment in her/his Ph.D. work with publications in the above relevant area is necessary. The PI will provide any other necessary training both in experiments and manuscript/grant writing. The successful individuals are strongly encouraged to apply for postdoctoral fellowships. The PI will guide her/him in this process.

We greatly appreciate one's independent thinking, creativity, curiosity, enthusiasm, and hard working. The successful individuals are expected to lead their projects in an independent manner. This is an excellent job opportunity for individuals who seek to develop their own research and eventually to proceed to a next step of their career in science in next 3~5 years.

Any interested individuals should contact me via e-mail: mamiko_yajima@brown.edu. Please enclose your CV, reprints of your representative works (or a Ph.D. thes is if appropriate), name of your thesis advisor. Reviews will begin immediately and continue until position is filled. Desired start date is after February 1, 2018.

Mamiko Yajima <mamiko_yajima@brown.edu>

CBGP Madrid PlantVirusCoevolution

Postdoctoral Position Available

We look for candidates to apply to the Spanish Programme "Juan de la Cierva 2017" to do post-doctoral research at the Plant-Virus Interaction and Co-Evolution Group, Centro de BiotecnologÃÂa y Genomica de Plantas UPM-INIA (CBGP) (www.cbgp.upm.es)

Research topics: The long-term goal of the group is to understand the evolution of plant-virus interactions. Within this broad field of research the post-doctoral scientist to be recruited will participate in a programme of research on Virus Emergence, specifically on how ecosystem simplification affects infection patterns, host range evolution and virulence of multihost plant viruses.

Conditions: Conditions and application procedures are specified at Ayudas para C ontratos Juan de la Cierva-Incorporacion 2017 at (http://www.idi.mineco.gob.es/portal/site/MICINN/menuitem. dbc68b34d1 1ccbd5d52ff eb801432ea0 /?vgnextoid Â50f421 5103f510VgnV CM1000001d0 4140aRCRD&vgnextchanne lga04939e6b 42410VgnVCM 1000001d041 40aRCRD)

Specific advantages offered by Universidad Politecnica de Madrid (UPM) can be found at (http://www.upm.es/Investigacion/Programa_Propio_UPM)

Requisites: Applicants should have a Ph D degree obtained between 1 January 2013 and 31 December 2015, with interests in evolutionary biology, genetics, molecular biology and /or ecology and should send their application and CV to

Prof. FERNANDO GARCÃÂïÂ¿Â½A-ARENAL fernando.garciaarenal@upm.es

BEFORE DECEMBER 31 2017

For further information about the group: http://www.cbgp.upm.es/index.php/es/informacion-cientifica/interaccion- de-las-plantas-con-el-medio-ipm/plant-virus

Recent publications of the group related to the above-specified topics:

Fraile A. et al 2014. Host resistance selects for traits unrelated to pathogenicity that affect fitness in a plant virus. Molecular Biology and Evolution 31: 928 - 939.

Hily J. M. et al. 2014. The relationship between host lifespan and pathogen reservoir potential: An analysis in the system Arabidopsis thaliana-Cucumber mosaic virus. PLoS Pathogens 10: e1004492.

Roossinck MJ, GarcÃÂa-Arenal F. 2015. Ecosystem simplification, biodiversity loss and plant virus emergence. Current Opinion in Virology 10: 56-62.

Fraile A, GarcÃÂa-Arenal F. 2016. Environment and evolution modulate plant virus pathogenesis. Current Opinion in Virology 17: 50-56.

Poulicard N. et al. 2016. Human management of a wild plant modulates the evolutionary dynamics of a gene determining recessive resistance to virus infection. PLoS Genetics 12: e1006214.

Bera, S. et al. 2017. Pleiotropic effects of resistance-breaking mutations on particle stability provide insight into life history evolution of a plant RNA virus. Journal of Virology 91: DOI : 10.1128/JVI.00435-17

McLeish, M. J. et al. 2017. Scale dependencies and generalism in host use shape virus prevalence. Proceedings of The Royal Society B. Biological Sciences (in press).

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Fernando GarcÃÂa-Arenal Catedratico de la Universidad Politecnica de Madrid Centro de BiotecnologÃÂa y Genomica de Plantas (CBGP, UPM-INIA) Universidad Politecnica de Madrid (UPM) - Instituto Nacional de Investigacion y TecnologÃÂa Agraria y Alimentaria (INIA) Campus de Montegancedo-UPM 28223-Pozuelo de Alarcon (Madrid) Spain Phone: (34) 91 336 4550/4539 Phone: (34) 91 715 77 21 Fax: (34) 917157721 fernando.garciaarenal@upm.es www.cbgp.upm.es Twitter: @CBGP_Madrid FaceBooK: @cbgpupm CBGP Severo Ochoa

Fernando GarcÃÂ'a-Arenal <fernando.garciaarenal@upm.es>

CharlesU CzechRep PollinationEcology

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 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@gmail.com

CIHMID Cornell DiseaseEvolution

The Cornell Institute of Host-Microbe Interactions and Disease (CIHMID) is soliciting applications for postdoctoral fellowships. Details can be found at http://cihmid.cornell.edu/postdoc.html . The CIHMID Postdoctoral Fellows Program is intended to support independent and innovative postdoctoral researchers working in affiliation with CIHMID labs at Cornell. Postdoctoral Fellows are expected to maintain intellectual ownership over their projects and will be provided with a modest discretionary allowance to support their research, in addition to a competitive salary and benefits package. Application to the program is competitive, and we anticipate 1-3 appointments per year.

Applications for appointments to begin in Summer or Fall 2018 will be due by February 26, 2018. Applicants are required to confer with prospective host labs prior to application.

Program Overview

- CIHMID expects to appoint 1-3 postdoctoral fellows this year, with each postdoctoral fellow supported for a 3 year appointment conditional on satisfactory performance. - CIHMID postdocs will be expected to develop an independent, interdisciplinary research program. CIHMID postdocs should have intellectual ownership of their projects and are expected to build bridges between different disciplines, fields, and departments. - Postdocs should be affiliated with one or more CIHMID labs (listed at < http://cihmid.cornell.edu/faculty-listing.html >) that can provide infrastructure and access to resources. Working across multiple labs may be seen as positive but is not a requirement. - Postdoctoral researchers in the program will be provided with a variety of professional development opportunities geared toward transition into permanent academic positions. - Appointments will be made at a salary of $50,000 per year with full health and retirement benefits, and will be provided with up to $10,000 per year to support expenses such as research costs, participation in conferences, and purchase of small equipment and computers. - The postdoctoral researcher will be encouraged to apply for external fellowships. If an external fellowship application is successful, the external fellowship will become the mechanism for support. CIHMID guarantees that the postdoctoral research will not suffer any decrease in salary or benefits from accepting an outside fellowship and will increase the discretionary spending allowance to $15,000 for each year of support on the external fellowship. The postdoc will remain part of the CIHMID program in order to take advantage of professional development and other opportunities.

Application Process

- Application consists of CV, plan of proposed research (3 pages maximum, excluding references), 2 letters of recommendation to be submitted directly by the recommenders, and a statement of support from the prospective advisor. - Project proposals should be developed by the applicant in consultation with the prospective associated host lab or labs. Preliminary conceptions of some potential projects will be posted on the CIHMID website in early Deceber, but proposals need not be limited to the listed projects. - Candidates will be selected based on applicant track record and career promise, merit of the proposed project, and fit to CIHMID objectives. - *Applications are due by February 26, 2018 *and can be submitted at < https://academicjobsonline.org/ajo/jobs/10542 >. Interviews will be conducted in March and awards will be announced in the first week of April. Appointments may begin as early as Summer 2018. - We welcome applications from candidates with diverse backgrounds, including those underrepresented in biological research science.

Eligibility

- Applicants should have been awarded a Ph.D. within the last 3 years or should be graduating imminently. Applicants must receive their Ph.D. before the postdoctoral appointment can begin. - Applicants who are already established at Cornell will be considered only if they are changing labs or substantially changing projects.

Brian P. Lazzaro, Ph.D.

Liberty Hyde Bailey Professor Director, Cornell Institute of Host-Microbe Interactions and Disease (CIHMID) Departments of Entomology and Ecology & Evolutionary Biology Cornell University Ithaca, NY, 14853, USA

tel: +1-607-255-3254 em: bplazzaro@cornell.edu http://www.lazzaro.entomology.cornell.edu http://cihmid.cornell.edu Brian Lazzaro <bplazzaro@cornell.edu>

ColoradoStateU 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>

Columbia NYC Computational Phylogenomics

Title: Post-doctoral Researcher in Computational Phylogenomics. Start Date: 2018 Flexible Department: Ecology, Evolution, and Environmental Biology (E3B). School: Faculty of Arts and Sciences, Columbia University. URL: http://eaton-lab.org A postdoctoral researcher position is available in the Eaton lab at Columbia University in New York City in the subject of Comparative Genomics and Computational Phylogenetics.

Generally, our group studies plant diversification with a focus on the ecological and evolutionary consequences of hybridization/admixture, and the development of genomic and bioinformatic tools for studying phylogeny. Projects often involve a combination of field work (e.g., China/Tibet, Latin America), genomics/bioinformatics, and programming.

Currently, one position is available to contribute to an NSF funded project: Replicated Evolution of Leaf Form in Neotropical Viburnum. This will involve analyzing large-scale RAD-seq data sets in combination with a reference genome to examine spatial variation in phylogenetic relationships across genomes and evolutionary time-scales in a reticulate clade of neotropical trees. Methodologically, a significant focus is on spatial variation across the genome, and inferring phylogenies from SNPs. Ideal candidates will have experience working with genomic data, an interest in phylogenetic comparative methods, and potentially in contributing to field work in Latin America. In addition to the designated project, the candidate will be encouraged to pursue independent and collaborative research related to additional areas of interest.

Additional postdoc positions for independent research are also available in the lab. For this type of position inquire about specific postdoctoral fellowships.

* How to apply: * To apply send your application to Deren Eaton (de2356@columbia.edu)with subject line “Postdoc application”. Please include a Cover Letter (2 pages max) describing your research, your CV, contact information for three references, and at least two relevant publications.

* Requirements: * – Ph.D. in Evolutionary Biology or related discipline. – Experience in computational genomics or bioinformatics. – A record of scientific publications. – English language writing and communication skills

Deren Eaton Assistant Professor Ecology, Evolution, and Environmental Biology (E3B) Columbia University 1200 Amsterdam Ave New York, NY, 10027 de2356@columbia.edu

“de2356@columbia.edu” <de2356@columbia.edu>

CSIC Madrid RodentEvolution

Postdoctoral position: Genotype-phenotype associations in the evolution of rodent sperm form and function.

The project deals with the evolution of morphology of rodent spermatozoa. Work developed so far concentrated on the role of sexual selection on the shape and size of spermatozoa and how these influence swimming patterns. Future studies will deal with changes in different lineages of muroid rodents (mice, voles and hamsters), paying attention to the appearance of novel traits and modifications of the sperm head bauplan. Research will focus on changes in sequence and regulatory evolution of protamines and other genes that control de formation of the sperm head in the final stages of sperm differentiation.

Candidates should have a PhD degree, which should have been obtained between 2013 and 2017. A good publication record in high-impact journals is essential.

Duration of contract is 2 years.

Recent publications on this and related areas: Lüke L, Campbell P, Varea Sánchez M, Nachman MW, Roldan ER (2014) Sexual selection on protamine and transition nuclear protein expression in mouse species. Proc Royal Soc, B. 281:20133359.

Lüke L, Vicens A, Tourmente M, Roldan ERS (2014) Evolution of protamine genes and changes in sperm head phenotype in rodents. Biol Reprod 90:67.

Lüke L, Tourmente M, Dopazo H, Serra F, Roldan ERS (2016) Selective constraints on protamine 2 in primates and rodents. BMC Evol Biol 16:21.

Lüke L, Tourmente M, Roldan ERS (2016) Sexual selection of protamine 1 in mammals. Mol Biol Evol 33: 174-84.

Vicens A, Tourmente M, Roldan ERS (2014) Structural evolution of CatSper1 in rodents is influenced by sperm competition, with effects on sperm swimming velocity. BMC Evol Biol. 14:106.

Tourmente M, Villar-Moya P, Rial E, Roldan ER (2015) Differences in ATP generation via glycolysis and oxidative phosphorylation and relationships with sperm motility in mouse species. J Biol Chem 290: 20613-26.

And see also: https://www.researchgate.net/profile/Eduardo_Roldan/contributions Please send CV before 2 January 2018 to: Eduardo Roldan, Reproductive Biology and Evolution Group, Dpt of Biodiversity and Evolutionary Biology National Museum of Natural Sciences (CSIC), Madrid, Spain Email: roldane@mncn.csic.es

roldane@mncn.csic.es

DalhousieU MarineGenomics

Support is available for a postdoctoral position at Dalhousie University (Halifax, Nova Scotia, Canada) for research on the genomics of commercially exploited marine fishes. The successful candidate will have a background in bioinformatics and genomics, including genome assembly, and will be co-supervised by Paul Bentzen (paul.bentzen@dal.ca) and Daniel Ruzzante (daniel.ruzzante@dal.ca; http://ruzzante.ca). The project will involve collaboration with Fisheries and Oceans, Canada (DFO).

The position is available for 2 years, starting as soon as a suitable candidate is found. The successful candidate will be hired for one year, renewable for the second year pending satisfactory performance. Applicants please send a statement of research interests, CV, copies of up to 4 publications and the names and e-mail addresses of two people willing to act as academic references to: Daniel Ruzzante (daniel.ruzzante@dal.ca) and Paul Bentzen (paul.bentzen@dal.ca).

Review of applications will start January 1.

Informal inquiries are welcome.

Dr Daniel E Ruzzante, Killam Professor Canada Research Chair in Marine Conservation Genetics (2002-2012) Department of Biology, Dalhousie University, Halifax, NS, Canada - B3H 4R2 ph:(902)494-1688 fax:(902)494-3736 http://ruzzante.ca/ Daniel.Ruzzante@Dal.Ca

DukeU SocialMammalGenomics

Post-doctoral position in social mammal behavior and genetics

A postdoctoral position in social mammal behavior and genetics is available in the Tung lab < http://www.tung-lab.org/index.html > at Duke University. Our current research < http://www.tung-lab.org/research.html > focuses on the biological consequences of social relationships and social stressors in primates and other social mammals, using genomic and computational tools. Open project areas involve the functional genomic analysis of life history trade-offs in wild meerkats and gene regulatory signatures of social experience in wild baboons and captive rhesus macaques. Applicants are also encouraged to be creative in developing their own projects, as long as they fit within the lab's general interests.

Postdoctoral applicants should have a strong background in evolutionary biology, behavioral ecology, and/or functional/computational genomics. Strong data analysis skills, including programming and statistical modeling experience, are essential. Familiarity or experience with mammalian behavior or genetics is a plus.

The Tung lab offers a congenial research environment that fosters strong interdisciplinary training and collaborative exchange. The lab is based in Duke's Department of Evolutionary Anthropology < http://evolutionaryanthropology.duke.edu/ >, and is affiliated with the Duke Department of Biology < http://biology.duke.edu/ >, the Center for Genomic and Computational Biology < https://genome.duke.edu/ >, and the Duke Population Research Institute < https://dupri.duke.edu/ >. Depending on research project, the successful may work under the co-mentorship of Dr. Luis Barreiro < http://luis-barreirolab.org/ > at the University of Chicago.

To apply for the position please send an email to Jenny Tung (jt5@duke.edu) including a cover letter, current CV, and contact information for at least two references.

Duke University is an Equal Opportunity Employer dedicated to building a diverse academic community.

Jenny Tung Associate Professor Departments of Evolutionary Anthropology and Biology Duke Population Research Institute jt5@duke.edu 919-668-4912 www.tung-lab.org "Jenny Tung, Ph.D." <jenny.tung@duke.edu>

Harvard MalariaParasiteFunctionalGenomics

Position: Postdoctoral Fellow

The Neafsey Lab at the Harvard T.H. Chan School of Public Health is seeking a Postdoctoral Associate to contribute to our research program in the evolutionary genomics of malaria biology and disease (https://sites.sph.harvard.edu/neafsey-lab/). The successful candidate will work collaboratively with other group members to develop innovative empirical approaches for exploring the functional consequences of Plasmodium parasite polymorphisms that may contribute to drug resistance and/or immune evasion. Approaches may include but are not limited to CRISPR/Cas9 genome editing and transcriptomics (bulk and single cell). Our lab has a strong tradition of generating and analyzing large genomic datasets from malaria parasites and vector mosquitoes to understand mechanisms of disease evolution, transmission, population dynamics, drug resistance, immune evasion, and host-pathogen interactions. We are now looking to extend that work into the phenotypic realm to functionally validate parasite polymorphisms that may impact public health.

Ideal applicants will have a PhD in a relevant field, with strong background in molecular biology and/or molecular genetics, ideally in the context of malaria or other infectious diseases. The successful candidate will join a diverse group with expertise that spans molecular epidemiology, computational biology, and evolutionary genomics and transcriptomics. Applicants will be expected to develop a research program that is original but fits within the general priorities of the team, taking into account the relevant literature, own experience, and advice from other scientists. Candidates are required to have a Ph.D. in biology/molecular biology/molecular parasitology or equivalent. Strong molecular biology laboratory skills are essential, previous experience with in vitro culture and manipulation of Plasmodium or other eukaryotic parasites strongly desired.

Additional experience in CRISPR/Cas9 and RNAseq would be advantageous. Candidates should demonstrate a track record of consistent publication, have strong organizational, written, and oral communication skills, and be able to work both independently and as part of a team.

Please contact Daniel Neafsey by email: neafsey@hsph.harvard.edu with CV, letter of interest, and names of at least three references.

We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability status, protected veteran status, or any other characteristic protected by law.

neafsey@hsph.harvard.edu https://sites.sph.harvard.edu/neafsey-lab/ https://twitter.com/dneafse Daniel Neafsey <neafsey@broadinstitute.org>

Ifremer France MarineBiodiversity

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

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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 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

References

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2.S. Creer et al., Molecular Ecology 19, 4-20 (2010).

3.M. Hajibabaei, S. Shokralla, X. Zhou, G. A. C. Singer, D. J. Baird, Plos One 6,(2011).

4.J. Pawlowski et al., Plos One 6,(2011).

5.F. Sinniger et al., Frontiers in Marine Science 3,(2016).

6.D. A. Cowart et al., PLoS ONE 10, e0117562 (2015).

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11.I. Bista et al., Genome 58, 197-197 (2015).

12.F. Lejzerowicz et al., Scientific reports 5, 13932 (2015).

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Sophie Arnaud Haond <Sophie.Arnaud@ifremer.fr>

ImperialC London ProteinEvolution

Hi all,

a 3-year postdoctoral position is available at Imperial College London and the MRC London Institute of Medical Sciences (LMS) to work in the Molecular Systems group headed by Dr Tobias Warnecke. You will also closely interact with the Computational Protein Biology group led by Joe Marsh at the MRC Human Genetics Unit, University of Edinburgh.

We are looking for an outstanding postdoctoral scientist to work on an exciting project at the intersection of medical population genetics, molecular evolution, and protein structural biology. The project is aimed at modelling and predicting the joint impact of two or more amino acid variants on protein structure and protein complex formation, using globinopathies as a model system. We want to explore how naturally occurring variants, obtained from large population cohorts, interact at the structural level when combined on a single genetic background, to obtain view of population-wide epistatic potential and to allow individualized disease predictions that can be tested experimentally.

The project requires extensive computational modelling of protein structure and interactions so advanced working knowledge of state-of-the-art modelling software is highly desirable. You should be proficient in at least one programming/scripting language (java, python, etc.) as well as R or Matlab and comfortable with carrying out large-scale analysis in a computing cluster environment. Candidates must have a strong publication record, excellent verbal and written communication skills, and a track record of addressing scientific problems in an innovative, thoughtful and systematic manner. Prior knowledge of haemoglobin and/or red blood cell biology is a bonus.

You will hold a UKRI Innovation Fellowship (UK nationals) or a Rutherford Fund Fellowship (non-UK nationals) and be part of a national cohort of fellows funded by the UK Government's Industrial Strategy fund. Locally, the fellow will be part of a diverse computational/experimental research team with expertise and wide-ranging interest in epigenetics, systems biology, and molecular evolution (molsys.lms.mrc.ac.uk). In addition, the fellow will benefit from close interaction with the Marsh group in Edinburgh (ed.ac.uk/mrc-human-genetics-unit/research/marsh-group). Dedicated support and career advice will be available through Imperial's Postdoc Development Centre.

Please contact Dr Warnecke for further information about the post (tobias.warnecke@lms.mrc.ac.uk).

For full details of this post and to complete an online application, visit https://mrc.tal.net/vx/lang-en-GB/-appcentre-1/candidate/postings/802 and upload your CV, names and contacts of two scientific references along with a covering letter stating why you are applying for this role (providing evidence against the requirements of the job as per the job description and person specification). Please quote reference number LMS - 733.

Closing date: 11 January 2018 Final appointment will be subject to pre-employment screening

*Salary quoted is inclusive of London weighting. Additional allowances comprise a 1,000 lump sum Settlement Allowance plus a yearly Training Allowance of 850 in the first year, paid in monthly instalments. The Training Allowance increases to 1,300 in year two, and 1,800 in the third year.

Tobias Warnecke Group Leader Molecular Systems Group MRC London Institute of Medical Sciences (LMS) & Imperial College London http://molsys.lms.mrc.ac.uk

"Warnecke, Tobias" <tobias.warnecke@lms.mrc.ac.uk>

IowaStateU SnakeEvolutionaryGenomics

Postdoc: Evolutionary Genomics of Garter Snake Life-history Strategies

Postdoctoral Research Associate Department of Ecology, Evolution, and Organismal Biology Iowa State University

The Bronikowski lab is recruiting a Postdoctoral Research Associate to study the evolutionary genomics - including population, quantitative, and molecular selection analysis - of garter snakes (Thamnophis elegans) from the Eagle Lake basin in California. Populations of garter snakes in this vicinity are arrayed along a slow-to-fast continuum of life history strategies, with upper elevation populations comprised of individuals that grow slowly, mature late, reproduce infrequently, and live longer relative to lower-elevation populations. The successful applicant will collaborate with myself and colleagues on an NSF-supported project to analyze allelic-time series for signatures of population genomic response to recent extreme environmental change. Additional projects could include quantitative genetic analysis of life-history traits, and molecular evolutionary selection analyses of genomic regions, according to the successful applicants interests. We will also leverage the past 40 years of data on meta-population demography, life-history evolution, stress-response evolution, and behavior to test for population- or ecotype-specific characters and alleles that correlate with population persistence and through extreme environmental events. We envision the principal duties will be 80% genetic, computational and project management, plus some time for supervising basic molecular lab work. There is also opportunity for field work if interested. Collaborators on the project include Drs. Anne Bronikowski and Nick Serao (Iowa State University), Dr. Stevan J. Arnold (Oregon State University), Dr. David Miller (Penn State University), and Dr. Amanda Sparkman (Westmont College). Required qualifications, terms of employment and application instructions follow below.

Required Qualifications

Education: A PhD degree in evolutionary genetics or bioinformatics, or acceptable equivalent combination of education and experience.

Experience/Skills: Experience with population genomic/transcriptomic data; demonstrated experience working in a Linux/Unix shell environment; competency with at least one scripting language (e.g., Perl, Python, R). Demonstrated experience with population genomic analyses for complex demography, admixture, and local adaptation. Preferred experience or willingness to help with annotation of the Thamnophis elegans genome. Well-developed organizational and time management skills, and leadership ability to direct (with the PIs) a large and productive project.

Terms of Appointment

Starting salary is dependent on previous post-doctoral experience, (https://www.grad-college.iastate.edu/-post_doc/policies.php) plus benefits. The position of renewable for up to two years, pending satisfactory progress. Start date is flexible.

Application Instructions

For full consideration, applicants should apply by Jan 15, 2018. Informal inquiries are encouraged prior to formal application. For formal application, please send 1) a cover letter, 2) a curriculum vitae, 3) a brief statement of research experiences/interests, and 4) names and contact information for three references to Dr. Anne Bronikowski at broniko-job@iastate.edu.

Iowa State University is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, age, religion, sex, sexual orientation, gender identity, genetic information, national origin, marital status, disability, or protected veteran status, and will not be discriminated against. Inquiries can be directed to the Director of Equal Opportunity, 3350 Beardshear Hall, (515) 294-7612.

Please contact Anne Bronikowski if you have any questions about this postdoctoral position.

Anne Bronikowski, Professor Email: broniko-job@iastate.edu https://www.eeob.iastate.edu/people/-anne-bronikowski "Bronikowski, Anne [EEOBS]" <abroniko@iastate.edu>

JacksonLaboratory Maine EvolutionaryGenomics

The Dumont Lab at The Jackson Laboratory is seeking a Postdoctoral Associate in the field of mammalian evolutionary genomics. Our group uses both wet-bench and computational tools to understand the genetic mechanisms and evolutionary processes that govern observed patterns of DNA diversity. On-going projects in the lab are investigating (i) inter-genomic conflict and sex-specific recombination rate divergence; (ii) the biological basis of sex ratio distortion; (iii) patterns, causes, and implications of mutation rate variation; and (iv) the interplay between genetic variation and chromosomal function at rapidly evolving loci like the pseudoautosomal region and centromeres.

The successful candidate will be encouraged to develop an independent research program that leverages the mouse model system, extensive JAX resources, and institutional expertise to address basic questions about where genetic diversity comes from, how it is maintained in populations, and how the mechanisms that generate genetic variation evolve over time.

The Jackson Laboratory (http://www.jax.org) in Bar Harbor, Maine, USA, is recognized internationally for its excellence in research, unparalleled mouse resources, outstanding training environment characterized by scientific collaboration, and exceptional core services - all within a spectacular setting adjacent to Acadia National Park. Translational research collaborations in genomics-based, personalized medicine are fostered through our JAX Genomic Medicine campus in Farmington, CT. In addition to lab-based training, JAX has developed a unique program for trainees to expand their professional skills in science communication, entrepreneurship, teaching, mentoring and laboratory management to best prepare postdocs for future career opportunities.

Required qualifications include a recently obtained PhD or MD in Genomics, Evolutionary Biology, Genetics or a related field, and a genuine enthusiasm for basic biological research. Expertise with mouse genetics, computer programming, and large-scale data analysis is strongly desired, but not required. Ability to plan, execute and analyze an independent research project is essential, as well as exceptional verbal and written communication skills. Preference will be given to self-motivated and career oriented individuals.

To apply, please submit (1) a cover letter describing past research accomplishments, research interests, and career goals, (2) a current CV, and (3) the contact information of three references, as one PDF file. Apply online at http://www.jax.org/careers/postdoc.html. Select link for Bar Harbor position #6757.

All qualified applicants will receive consideration for employment without regard to race, color, religion, age, mental disability, physical disability, medical condition, sex, sexual orientation, genetic information, ancestry, marital status, national origin, veteran status, and other classifications protected by applicable state and local non-discrimination laws.

Beth Dumont <Beth.Dumont@jax.org>

KansasStateU FishMicrobiomeEvolution

Postdoctoral Researcher Position at Kansas State University: Fish Microbiomes in Extreme Environments

We are searching for a motivated and independent postdoctoral scholar interested in developing a research project investigating how microbiomes of fish vary along environmental gradients, how genetic and environmental factors interact to shape microbiomes, and how variation in microbiomes may shape the ecological function of individuals and populations. The postdoctoral scholar's research is expected to be integrated with our studies of phylogenetically-independent lineages of livebearing fishes that have colonized and adapted to toxic, hydrogen-sulfide-rich springs in Mexico. A core objective of the project is to use comparative analyses and experimental approaches to understand how microbe-animal interactions may facilitate adaptation to extreme environmental conditions.

The position will be available in the laboratory of Dr. Michi Tobler in the Division of Biology at Kansas State University in Manhattan, KS (http://sulfide-life.info). The Division of Biology provides a highly interdisciplinary research environment, with focal strengths in genomics, ecology, and evolution. Our division provides excellent opportunities for collaborative networking with microbial ecologists, particularly through recently funded initiatives that bring together researchers from different universities in the state of Kansas to study microbiomes of plants, soils, and aquatic environments. In addition, candidates can leverage collaborative ties with the laboratory of Dr. Joanna Kelley at Washington State University (https://labs.wsu.edu/genomes/), which will provide added expertise in bioinformatics. Beyond research, we will provide additional professional development opportunities, emphasizing improvement of teaching and mentoring skills, grant writing, and obtaining skills for getting a permanent job.

Candidates are expected to have completed or be completing a PhD degree, to have strong written and oral communication skills, and to be able to work both independently and as part of a collaborative team.

Our lab provides a diverse and inclusive environment for students and researchers, and we particularly welcome applications from candidates with diverse backgrounds. First and foremost, we are interested in recruiting creative minds that have an interest in developing and leading independent projects. Ideal candidates will also have at least two of the following core competencies: (1) experience with the analysis of microbiomes or a background in microbial ecology; (2) bioinformatics skills relevant to the analysis of next-generation sequence data; (3) experience with fish/aquatic biology in an experimental or field setting.

The appointment will be for up to two years, with an initial appointment of one year and an extension based on performance. Salary will be commensurate with experience, and full benefits are included.

Interested applicants should email Michi at tobler@ksu.edu if they have any questions. Applications have to be submitted directly through Kansas State University (http://careers.k-state.edu/cw/en-us/job/-502903/fellow-post-doc-biology) and include a curriculum vitae, a cover letter that includes a statement of research interests that explicitly describes professional qualifications for the position in the context of research goals, and contact information for three references.

The preferred start date is February 2018. Review of applications will begin immediately and will continue until the position is filled.

Michi Tobler Division of Biology Kansas State University 116 Ackert Hall Manhattan, KS http://sulfide-life.info
Michi Tobler <tobler@ksu.edu>

Lausanne Switzerland ExperimentalEvolutionDrosophila

Postdoctoral Position:— Experimental evolution in response to chronic malnutrition in Drosophila

A postdoctoral position is available in Tad Kawecki's group at the Department of Ecology and Evolution, University of Lausanne, Switzerland. We are looking for a qualified and motivated researcher to study genomic and molecular/physiological bases of evolutionary adaptation to nutrient-poor diet in Drosophila. The project will take advantage of a long-term evolutionary experiment, in which replicate populations have been maintained on an extremely poor larval diet for over 230 generations. These populations have evolved a variety of life history, physiological and behavioral adaptations to this nutritional stress, as well as modified interactions with pathogenic and beneficial bacteria. Genome resequencing and gene expression profiling point to candidate genes and pathways that may mediate these evolutionary changes. The general aim of the project is to verify some of these candidates and gain a deeper insight into the underlying mechanisms. Possible approaches include genetic mapping, detailed analysis of gene expression and molecular phenotypes and manipulative experiments using Drosophila genetic toolkit. For more information see Erkosar et al. (2017) mBio 8:e01496-01417 and Vijendravarma et al. (2015) Ecology Letters 18:1078-1086.

The project requires a combination of experimental and statistical/genomics skills, interest in adaptive evolution, and independence in designing and carrying our experiments. Experience with Drosophila or knowledge of insect physiology are a plus but are not required. The research group is English-speaking and no-preexisting knowledge of French is required, but learning basic French would make living in Lausanne easier. In addition to work on the project, the holder of the position is expected to contribute up to 25% of the working time to teaching activities, including supervision of master students.

The candidate is expected to start within the first four months of 2018. The position is at 100% (lower rate is negotiable e.g. for family reasons), with the annual salary of about CHF 80,000 (about US$ 80,000 or Euro 68,000). The position is initially offered for one year; a possible extension for additional two years will depend on the funding situation and the progress of the project.

Lausanne is a medium-sized city on the shores of Lake Geneva, surrounded by a wine growing region recognized as a UNESCO World Heritage Site, and within one hour of the Alps. It offers a great variety of cultural, recreational and outdoor opportunities. The Department of Ecology and Evolution (www.unil.ch/dee) is a vibrant research community, with 20 research groups, over 100 graduate students and over 40 postdocs.

To apply, submit a motivation letter, your cv, a description of your research experience and interest, and the names and contact information of 2-3 referees. The application material must be uploaded through the UNIL online recruitment platform at http://bit.ly/2BFXdUP (you may have to create an account in the system first). For questions concerning the position, please send an email to Tadeusz.Kawecki@unil.ch. The review of applications will start on December 15 and will continue until a suitable candidate is found.

Tadeusz Kawecki <tadeusz.kawecki@unil.ch>

LosAlamosNatlLab ComputationalBiol

Job title: Postdoc position in computational biology When: Starting January 2018 or later for a 2-3 year appointment Org name: T-6, Theoretical Biology & Biophysics, and CNLS Description: A postdoctoral position is available at Los Alamos National Laboratory to investigate the connection between virus genetic evolution and epidemic spread. Many viruses evolve rapidly and differently during various modes and rates of spread. This project will elucidate how the genetic evolution is linked to different spread patterns. The main virus to be studied is HIV, but other pathogens may become included in the project. We are looking for candidates with expertise in computational biology, evolutionary biology, and/or phylogenetics with interests in mathematical epidemiology. The successful candidate will develop models connecting evolution and epidemiology with the ultimate goal to predict and prevent human epidemics.

This position may be jointly associated with the Center for Nonlinear Studies depending on the candidate and how the specific project is formulated.

Job Requirements Minimum Job Requirements: Experience with computer modeling. Experience with genetic evolution modeling and phylogenetics. Demonstrated ability to publish peer-reviewed papers, effective written and oral communication skills, willingness to work in a team environment, and a Ph.D. pending or received within the last five years.

Desired Skills: Software development experience: R, perl, Python, C, or other appropriate language for analyses and model development. Understanding of virus systems and pathogenesis. Experience in mathematical epidemiology, ecology, population genetics or similar.

Education: PhD in related field completed within the past five years or soon to be completed.

Notes to Applicants: Please contact Dr. Thomas Leitner (tkl@lanl.gov) for more information.

Candidates may be considered for a Director's Fellow or Metropolis Fellow, and outstanding candidates may be considered for the prestigious Distinguished Fellows positions.

"Leitner, Thomas Kenneth" <tkl@lanl.gov>

McGillU PopulationGenetics

Postdoc and PhD projects in *mathematical and statistical population genetics at McGill University in Montreal, Canada*.

The projects aim to develop mathematical, statistical, or computational models to better understand human genetics, human history, and disease. Sample projects are outlined below. The positions are fully funded, and the candidates should expect to work on theoretical ideas in statistics, machine learning, algorithms, and stochastic systems as well as applications.

Candidates should have:

- a strong background in mathematics, statistics, programming, or related fields;

- demonstrated interest in biology, evolution, or medical research;

- a curious and creative mind.

Applications and queries should be sent to Simon Gravel gravellab@gmail.com. Please include a statement of interest (1 page or less), a CV, contact information for three references, and a low-resolution scan of transcripts (for prospective PhD students).

Project 1: Genetics, Human history, and health

Goals: to develop mathematical and statistical models of human genetic diversity; to refine our understanding of human history, demography, and disease risk; and to improve our ability to diagnose and treat individuals in diverse populations

Project 2: Tumor heterogeneity

Goals: to build models of tumor heterogeneity in primary and metastatic tumors through simulation and mathematical models; to answer fundamental questions about cancer progression and resistance to treatment; and to help interpret the latest generation of tumor sequence data.

Project 3: Genetics, Genealogies, and Evolution

Goals: to develop statistical models that combine genetic and genealogical data to learn about the transmission history of alleles over generations and identify evidence for selection or disease-causing alleles.

simon.gravel@gmail.com

NorthDakotaStateU EvolutionaryGenomics

Position: Postdoctoral Research Associate

Location: North Dakota State University, Department of Biological Sciences, Fargo, ND

Research Area: Evolutionary Genomics of non-model Allopolyploids

A highly motivated and talented postdoctoral fellow is sought to join the lab of Dr. Jill Hamilton in the Department of Biological Sciences at North Dakota State University (NDSU). The position is a 2 year fellowship, renewable upon satisfactory performance following the first year, and may be extended further as funding permits. The anticipated start date is flexible with possible start date of early 2018 or soon after hiring approval. The successful candidate will develop research in plant evolutionary genomics, focusing on the role whole genome duplications have played in plant evolution. The postdoctoral fellow will interact with the Hamilton Lab at NDSU and collaborators using a combination of whole-genome sequencing and transcriptomics data to test hypotheses regarding the evolution of duplicate genes across heterogeneous environments in a non-model allopolyploid, Geum triflorum. The postdoctoral fellow will be expected to analyze large datasets and lead preparation and publication of peer-reviewed manuscripts and present findings from the research project. In addition, there will be ample opportunity to pursue research questions besides those of the particular study. Salary is commensurate with experience.

Candidates must have 1) a Ph.D. in biology, evolution, genetics, or related area from an accredited university, 2) demonstrated experience working with next-generation sequence data and large genomics data sets, 3) strong oral and written communication skills, and 4) demonstrated ability to work independently and as part of a collaborative team.

Preference will be given to candidates with experience or demonstrated interest in 1) plant evolution and ecology, 2) quantitative genetics and statistical modeling, 3) documented ability to successfully publish, including first-author publications 4) mentoring graduate and undergraduate students, 5) grant writing, 6) promoting a culture of safety in the laboratory, and 7) laboratory management skills.

Applicants must submit a cover letter, a curriculum vitae, a description of research experience (2 pages maximum), and contact information for three professional references. All application materials must be submitted online at: www.jobs.ndsu.edu Review of applications will begin January 5, 2018 and continue until the position is filled.

Questions regarding the search may be sent to jill.hamilton@ndsu.edu. Additional position information can be found at: https://jobs.ndsu.edu/postings/8815 Jill Hamilton Assistant Professor Department of Biological Sciences North Dakota State University Fargo, ND, USA 58102

“Hamilton, Jill” <jill.hamilton@ndsu.edu>

NYU AbuDhabi MangrovePopulationGenomics

Post-doctoral Researcher Opening: Mangrove Genomics

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’Â 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 will be contingent on experience. In addition, 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 and benefits are 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 'Â¥MANGROVE APPLICATION'Â in the subject line. Only short listed candidates will be contacted for an interview.

John Burt <john.burt@nyu.edu>

Omaha NGS Conservation

Omaha's Henry Doorly Zoo & Aquarium Department of Conservation Genetics (OHDZA-CG) based in Omaha, Nebraska, is seeking a postdoctoral researcher with interest/expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

omahazoo.com | madagascarpartnership.org

RESPONSIBILITIES AND DUTIES include the following (other duties may be assigned):

The successful applicant will be proficient in the construction of genomic libraries and in-solution hybridization methodologies for high-throughput sequencing as well as all relevant analyses of large datasets, and management of next-generation sequence (NGS) workflows. Interested candidates should be highly motivated, organized, independent, and have extensive experience with molecular genomics and bioinformatics, and be able to efficiently write and revise manuscripts. This individual, in collaboration with a staff bioinformatician, will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and other taxa from Madagascar. Assembly of whole genomes is in-progress, but will likely require additional analyses pertinent to specific research projects. Data from a variety of species have already been generated, thus candidates will be able to quickly start analysis and manuscript preparation.

Travel to Madagascar to support the field programs of OHDZA-CG is required for a minimum of five-week intervals twice a year.

WORK SKILLS: * Strong people skills * detail-oriented * willingness to learn and contribute * follow directions * meets deadlines.

BASIC QUALIFICATIONS: * Applicants should hold a PhD in bioinformatics, computer science, molecular genomics or related field and have more than one year of experience in high-throughput genome sequence analysis.Applicants should be experienced at software related to NGS data and be able to manipulate genomic data for phylogenetics and phylogeography. Our group's focus is large-scale sequencing for phylogenetics, phylogeography and evolutionary studies of lemurs, tortoises and other taxa from Madagascar. * Thus, previous experience in genome assemblies, annotation, and analysis of a variety of NGS pipelines is preferable. * The ideal candidate will be independent, highly motivated, productive, have outstanding written and verbal communication skills and be able to work effectively in a team with members from diverse backgrounds. * The successful applicant must be interested in interdisciplinary science and field research and have a solid publication record that illustrates the ability to conduct novel, independent research.

PREFERRED QUALIFICATIONS:

Candidates should have 3+ years of experience in molecular biology, genetics, or bioinformatics. The position requires proficiency in programming (Perl or Python) and knowledge of Bash scripting using Linux systems, while familiarity with R is a plus. Proficiency in C, C++, Go, or similar systems language will warrant additional consideration. Applicants are also expected to be familiar with bioinformatics tools, able to implement complex computational pipelines, incorporate genomics databases and have extensive and creditable laboratory experience with constructing genomic libraries. The applicant will need to work closely with two full-time technicians to manage NGS lab work, as well as with a full-time bioinformatician. While in Madagascar, the applicant will work with many Malagasy graduate students on a variety of projects to assist with completion of their degrees and peer-reviewed manuscripts. These above duties require a candidate with excellent interpersonal skills, and the ability to train and teach both national and international audiences. The candidate must also be able to jump between a variety of projects, based on needs of the research group.

TIME FRAME:

These positions will be part of an on-going team of rotating postdoc fellows. One of the positions is expected to begin in January 2018, while the second is expected to start approximately May 2018. The initial appointment will be for two years, with the possibility to extend to three years.

HOW TO APPLY

Applicants should submit their curriculum vitae, a statement of research interests and career goals, and a few publications. Please send materials to genetics(at)omahazoo.com.

Genetics Department <genetics@omahazoo.com>

Paris TheoreticalEvolutionaryEcology

Postdoc position in theoretical evolutionary ecology in Paris (France)

A postdoc position, funded by the French National Research Agency (ANR), is available to work with Florence Débarre and François Blanquart in Paris (Centre Interdisciplinaire de Recherche en Biologie, UMR CNRS 7241, Collège de France). We work in an interdisciplinary research group gathering biologists, probabilists, and bioinformaticians; the lab is located in the Latin Quarter in Paris.

We are looking for a highly motivated postdoc interested in developing mathematical and computational models of evolution, to explore various aspects of the effects of environmental heterogeneity and population subdivision on local adaptation and diversification. Depending on the postdoc's interest, these models may also be tailored to describe the evolution of infectious diseases. Background (or a strong interest) in evolutionary biology / ecology and strong quantitative skills are required for the position.

The position can start on 1st March, 2018 or later, but note that the funding runs out on 30th November, 2019. Duration and salary are commensurate with experience (see table below).

To apply: If you are interested in this position, please send a CV, a 1-page description of your research interests and motivation, and the contact details of potential references (all in one single pdf) to Florence Débarre (florence.debarre@college-de-france.fr) and François Blanquart (francois.blanquart@college-de-france.fr). Review of applications will start on 22nd January 2018, but will continue until the position is filled.

Feel free to contact us if you have any questions about the position.

F.Débarre and F.Blanquart

Salary and postdoc duration

Experience | Duration | Monthly Salary (before tax)

<2y after PhD | 18 months | 2500 between 2 and 4y after PhD | 16 months | 2800 â¥5y after PhD | 14 months | 3200

Our websites FD: http://www.normalesup.org/~fdebarre/ FB: https://sites.google.com/site/francoisblanquart/ Team: http://www.lpma-paris.fr/smile/ Unit: http://www.college-de-france.fr/site/en-cirb/index.htm flo.debarre@gmail.com flo.debarre@gmail.com

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SanFranciscoStateU HIVEvolution

Position Type: NSF funded postdoc position at San Francisco State University to work with Dr Pleuni Pennings in the CoDE lab on fitness costs of mutations in HIV.

Lab website: https://pleunipennings.wordpress.com/ Position Description: I am looking for a postdoc to work on a project funded by NSF, in collaboration with Dr Adi Stern (Tel Aviv University) and Dr Robert Shafer (Stanford University). The goal of the project is to estimate the fitness costs of mutations in HIV, which will help us understand how the virus evolves and which parts of the HIV genome are most important for the functioning of the virus. All wet lab work for this project will be carried out in Tel Aviv, so in San Francisco I am looking for someone who is interested in doing the programming, the statistics and the writing.

Requirements: PhD in Biology or related field.

Other preferred qualifications:

I am looking for someone with experience and interest in several of the following domains: evolution, virology, bioinformatics and statistics.

The preferred candidate will also have an interest in / experience with one or more of the following: teaching, working with students from groups who are traditionally underrepresented in research, outreach (e.g., writing, social media, video).

The preferred candidate will have experience with writing clear / understandable scientific prose as evidenced by a writing sample.

Why this is a great opportunity:

You will be part of an extremely diverse department of biology.

You will be working on an exciting project that bridges virology and evolutionary genetics.

You will be able to contribute to training of students of diverse backgrounds.

You will get the opportunity to work with people at Stanford and Tel Aviv University (including trip to Tel Aviv).

If you are interested to collaborate with people at Stanford, UCSF or UC Berkeley, I will encourage that and help set up contacts.

In the CoDE lab, you will work in a supportive environment where research is important, but papers are never more important than people.

Appointment:

Funding is available for at least three years. Appointment will be for one year initially, but will be extended for up to three years if expectations are met.

How to apply:

Send a 1-2 page cover letter, your CV, a recent paper (or draft) written by you, and names and email addresses for three references to pennings@sfsu.edu. Only pdf's please!

Deadline: I will start looking at applications from January 4th 2018 and hope to hire as soon as possible after that.

– Pleuni Pennings Assistant Professor Department of Biology, San Francisco State University

Website: http://pleunipennings.wordpress.com/ My office hours are 3-4 on Tuesday and 2-3 on Friday in HH763.

Pleuni Pennings <pspennings@gmail.com>

StockholmU MarineMetabarcoding

Hi all,

We have just announced a 2-year Post Doc position in Baltic Sea Ecology at Stockholm University, Dept. Ecology, Environment and Plant Science; This position is associated with the project "The role of cross-community interactions between benthic above- and below-ground organisms for ecosystem functioning" that aims to understand how interactions between infauna and epibenthic organism (primarily macroalgae and their associated fauna) influence ecosystem process rates in Baltic Sea coastal areas. Of particular interest will be cross-community interactions in coastal terraces; an understudied habitat where drift macroalgae accumulate. This project will investigate how terraces influence abiotic sediment conditions, three major parts of the benthic community and their interactions: sediment microbiota (bacteria, meiofauna), macroinvertebrate infauna, and epibenthos (algae and associated invertebrates). The successful candidate will focus on molecular ecological workflows, including DNA sequencing techniques, to assess benthic microbial biodiversity, bioinformatics and ecological modelling. The candidate should have previous experience of field sampling, molecular ecology, high-throughput sequencing, bioinformatics and ideally statistical network modeling or causal (piecewise) modeling. More info at:

http://www.su.se/english/about/working-at-SU/-jobs?rmpage=job&rmjob=4290&rmlang=UK The positions are part of a strategic initiative at strengthening Baltic Sea research at Stockholm University; three tenure-track professorships are also advertised (based at Dept. Physical Geography and Dept. Geological Sciences). We particularly seek scientists interested in collaborative research related to different aspects of the Baltic Sea environment. While each position has a home department, the employees will enjoy being a part of an interdisciplinary research team at the Stockholm University Baltic Sea Centre. Deadline for applications: January 15, 2018.

More information about the other positions, departments and application procedure can be found at su.se/english/vacancies.

Best regards,

– Best regards

Francisco Nascimento

Dept. of Ecology, Environment and Plant Sciences Stockholm University

Francisco Nascimento <francisco@ecology.su.se>

TelAvivU BacterialSocialEvolution

The Eldar lab at Tel-Aviv University is looking for a highly motivated post-doc for a 3-4 years' period, to work on an ERC funded project on the evolution of cooperation and communication in bacteria. The post-doc will take place in Tel-Aviv University in Israel.

Background: bacterial cooperation is often regulated by cell-cell communication systems known as quorum-sensing. Some bacterial mobile elements also code for their own signaling systems and use it to regulate their transfer or to manipulate their host behavior. The aim of the project is to analyze the interplay between bacterial and mobile-element quorum-sensing systems and understand their impact on the evolutionary divergence of quorum-sensing systems and mobile element life-history strategies.

The proposed work combines:

1) Modeling the implication of a variety of processes on selection for cooperation and conflict between bacteria and its mobile elements.

2) Analysis of data coming from a variety of sources, including high throughput fitness landscape data, time-lapse microscopy and genomic data.

3) Active participation in the design (and preferably implication) of experimental work.

Requirements: The applicant should ideally have

* A strong mathematical background

* Previous experience in evolutionary or systems biology modeling approaches

* An interest (and preferably experience) in microbial physiology, ecology and evolution.

*A good publication track record

Fellowship will depend on the applicant's record.

The work will be done at the faculty of life sciences in Tel-Aviv University, the largest university in Israel located at the heart of the city of Tel-Aviv.

avigdor@gmail.com

Tel-AvivU BatBehavioralEvolution

The Yovel lab: www.yossiyovel.com is searching for a post-doc interested in different aspects of bat behavioral ecology including echolocation, navigation, social behavior and the brain.

Candidates must be U.S citizens.

Preferences will be given to candidates that have good programming skills in Matlab, R or Python.

Applicants should send their CV to:

Yossi Yovel yossiyovel@gmail.com

Yossi Yovel <yossiyovel@gmail.com>

TempleU Phylogenomics

Multiple Postdoctoral Positions Temple University

Multiple postdoctoral positions are available in the computational laboratory of Dr. Sudhir Kumar at Temple University in Philadelphia, USA. Applicants are encouraged to apply if they are interested in one or more of the following areas: (1) Development of methods for estimating divergence times from multigene and genome-scale datasets. (2) Empirical analysis of available large molecular datasets to test biological hypotheses related to species divergence times. And/or (3) Development of software for estimating divergence times and timetrees.

Applicants should submit their detailed curriculum vitae and a summary of research interests by e-mail to s.kumar@temple.edu (send a single PDF file). It is advised that applicants survey our recent publications online at http://www.kumarlab.net/publications/all (e.g., #142, #146, #149, #151, #154, #156, #158, and #159). Priority will be given to applications received by January 15, 2018, and applications will be reviewed as long as funding is available. Positions are available immediately. Please contact Sudhir Kumar by email (s.kumar@temple.edu) with questions regarding these positions.

Kumar laboratory is part of the Institute for Genomics and Evolutionary Medicine (iGEM; http://-

igem.temple.edu). iGEM provides an intellectually stimulating, sophisticated, and multi-dimensional research environment for young scientists. Temple University located is in the heart of historic Philadelphia, and is the sixth largest provider of graduate education in the USA. Situated in close proximity to New York City and Washington DC, Philadelphia is home to a large biotech industry as well as many outstanding academic and research institutions.

Contact: Sudhir Kumar (s.kumar@temple.edu)

Sudhir Kumar <s.kumar@temple.edu>

TempleU TumorEvolution

Multiple Postdoctoral Positions

Multiple postdoctoral positions are available in the computational laboratory of Dr. Sudhir Kumar at Temple University in Philadelphia, USA. Applicants with expertise in molecular evolution and interest in somatic evolution of tumors are encouraged to apply. We are equally interested in applicants with expertise in cancer genomics and an interest in expanding their skills in evolutionary analysis. Successful applicants will contribute to the development of methods and tools for the analysis of data from bulk and single cell sequencing of tumors. They will also analyze large tumor genome datasets to test biological hypotheses relating to the evolution, persistence, and adaptation of clones in tumors. This is a new research area with opportunities to make fundamental contributions with a strong potential for clinical relevancy. Applicants are encouraged to contact us directly to learn more about current (unpublished) research in our laboratory.

Applicants should submit their detailed curriculum vitae and a summary of research interests by an e-mail to s.kumar@temple.edu (send a single PDF file). Priority will be given to applications received by January 15, 2018, and applications will be reviewed as long as funding is available. Positions are available immediately. Please contact Sudhir Kumar by email (s.kumar@temple.edu) with questions regarding these positions.

Our computational laboratory is located in the Institute for Genomics and Evolutionary Medicine (iGEM; http://igem.temple.edu). iGEM provides an intellectually stimulating, sophisticated, and multi-dimensional research environment for young scientists. We have collaborations with Fox Chase Cancer center and other laboratories studying cancer evolution experimentally. Temple University located is in the heart of historic Philadelphia, and is the sixth largest provider of graduate education in the USA. Situated in close proximity to New York City and Washington DC, Philadelphia is home to a large biotech industry as well as many outstanding academic and research institutions.

Contact: Sudhir Kumar (s.kumar@temple.edu)

Sudhir Kumar <s.kumar@temple.edu>

Toulouse EvolutionaryBiology

IAST Research Fellowships in Evolutionary Biology,

The Institute for Advanced Study in Toulouse (IAST; www.iast.fr) invites applications for post-doctoral research fellowships in Evolutionary Biology, with a start date of September 1, 2018.

We welcome applications from researchers with research interests in any of the following areas: theoretical models of evolution (applied to family structure, strategic interactions, plasticity, cognition, learning, cultural evolution); related empirical work.

We seek candidates with a strong research background in their own discipline, but willing and able to develop research projects drawing on IAST's substantial interdisciplinary resources, including particularly the proximity of strong groups in economics (Toulouse School of Economics, TSE). We are open to a variety of research methods, including theory, field and laboratory experiments, observational field work, and the analysis of large secondary data sets. All research interests relevant to the broad study of human behavior are welcome, but interests close to those already developed at IAST will be given special consideration.

Eligible applicants Active researchers who have or will have completed their PhD after January 2015 and before September 2018. The IAST offers its researchers an opportunity to devote themselves full time to their research at the start of their careers. Motivated applications will be considered from candidates whose PhDs were completed in 2014 or earlier; please explain your reasons in your cover letter.

Conditions Fellows are provided with office space, computer facilities and a contract for two years, renewable for a third year.

All applications need to be sent through our website: http://www.iast.fr/apply before December 31, 2017

Cynthia Diaz <cynthia.diaz@tse-fr.eu>

UBielfeld BehaviouralGenomics

Postdoc position in Behavioural Genetics and Genomics

A Postdoc position in behavioural genetics and genomics is available at the Faculty of Biology at Bielefeld University, in the Department of Animal Behaviour (with Prof. Oliver Kruger, see http://www.uni-bielefeld.de/biologie/animalbehaviour). The position runs from early 2018 to the end of 2021 and is funded by the German Research Foundation (DFG) within the recently approved collaborative research centre (SFB/TRR 212) entitled: A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

The aim of the Postdoc project (sub-project C03 of the collaborative research centre) is to test whether common buzzard (Buteo buteo) chicks respond in their gene expression to different levels of blood parasite infection. Additionally, the project aims to develop a SNP-approach to find loci associated with fitness variation in this species. The project builds on a long-term study of individually marked birds that by now lasts for thirty years across over 2500 marked individuals. Fitness data of adult buzzards as well as many other phenotypic traits are routinely measured and should be linked to genetic or transcriptomic data of buzzard chicks.

The collaborative research centre: The postdoc will be embedded within a larger collaborative research centre (SFB) comprising 18 principle investigators, 9 postdocs and 16 PhD students based at Bielefeld University, the University of Muenster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programmes. Full details of the SFB can be found at www.uni-bielefeld.de/biologie/crc212 . Main responsibilities

- Research tasks (90%):

- Development and analyses of genomic and transcriptomic data sets

- Analyses of microsatellite data sets

- Participation in field work activities from April to June each year

- Collaboration with other groups in the research centre

- Writing scientific publications

- Organizational tasks in the research centre (10%)

Applicant's profile

We seek a bright and highly motivated postdoctoral researcher with

- a university degree in a relevant discipline, e.g. biology, genetics or bioinformatics,

- a completed PhD in a relevant field, related to behavioural genomics, population genetics, or evolutionary ecology,

- experience with genomic and transcriptomic approaches and data,

- experience with relevant software packages,

- interest in both behavioural and genomic questions,

- ability to work both independently and as part of a team, and

- excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage:

- papers in peer-reviewed international journals,

- experience in collaborations between field biologists and -omics-people, and

- experience with large-scale research projects.

Remuneration

Salary will be paid according to Remuneration level 13 of the Wage Agreement for Public Service in the Federal States (TV-L).

Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling, and prevention programmes. Bielefeld University places great importance on a work-family balance for all its employees.

Application procedure

To apply, please provide: (i) a letter of motivation including a statement of your research interests and skills and experience relevant to the position; (ii) a CV including publication list; (iii) names and contact details of two referees willing to write confidential letters of recommendation. All materials should be emailed as a single PDF file to:

oliver.krueger@uni-bielefeld.de. The application deadline is January 7th 2018 and interviews will take place shortly thereafter. After the decision, the position should start as soon as possible. For further information on the project and the department, please contact Oliver Kruger (oliver.krueger@uni-bielefeld.de) with any informal inquiries.

Bielefeld is a city of 325,000 inhabitants with all expected amenities and easy access to the Teutoburger Wald for hiking and other outdoor pursuits. It offers a high standard of living and is well connected to most major European cities.

Bielefeld University has received a number of awards for its achievements in the provision of equal opportunity and has been

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UCaliforniaIrvine EvolutionaryGenomics

The Emerson lab at UC Irvine (http://emersonlab.org) is soliciting candidates for an NIH funded postdoctoral position on evolutionary genomics in Drosophila. The project aims to understand how genome structure evolves, including traditionally challenging mutations like tandem duplicate arrays and transposable element insertions. We accomplish this by comparing genetic variation within and between species on a genome-wide scale discovered in reference-grade genomes comparable in completeness and contiguity to the FlyBase assembly of D. melanogaster. We are also functionally characterizing structural mutations. Candidates joining the lab will have access to dozens of cutting edge reference grade genomes, including D. mauritiana, D. sechellia, D. simulans, and D. teissieri as well as population samples from D. simulans and D. melanogaster. Candidates will ideally have interests broadly relevant to the theme of structural variation but will also be offered opportunities to pursue their own interests and collaborations in evolutionary genetics. For more information about the project see the following: http://emersonlab.org/jobs/sv_postdoc_2017.html The Emerson lab is very collaborative and offers ample opportunities for interacting with other evolutionary genetics labs at UCI (http://emersonlab.org/collaborators/). The successful candidate will have a PhD in one of the following or related fields: evolutionary genetics, bioinformatics, computational biology, statistics, or experimental genomics (especially high throughput sequencing and/or functional genomics). The Emerson lab is affiliated with the department of Ecology & Evolutionary Biology, the Center for Complex Systems Biology, and the Center for Evolutionary Genetics at UCI as well as the Southern California Evolutionary Genetics Meeting. Interested applicants should apply here:

https://recruit.ap.uci.edu/apply/JPF04423 Review of applications will begin on January 5th and will continue until the job is filled. Consistent with UCI policy, the duration of the position is dependent upon performance (annual appointments, with potential for renewal), and salary will be commensurate with experience. Applications should include: a CV; a research statement explaining the candidateâ euro s previous research experience and future research objectives; and contact information of two or more references. For more about the Emerson lab and academic and professional environment at UCI, visit: http://emersonlab.org/ Sincerely,

J.J. Emerson | Assistant Professor Ecology & Evolutionary Biology | Center for Complex Biological Systems University of California Irvine

"jje@uci.edu" <jje@uci.edu>

UCalifornia Riverside DataVizPhylogenomics

Postdoc: Interactive and Exploratory Data Visualization Tools for High-Throughput -Omics Datasets

2.5 year postdoctoral position at the University of California, Riverside focused on the development of new data visualization tools within the prototype Phinch framework.

Phinch (http://phinch.org) is an open-source framework for visualizing biological data, funded by a grant from the Alfred P. Sloan foundation. This project represents an interdisciplinary collaboration between Pitch Interactive (http://pitchinteractive.com/ - a data visualization studio in Oakland, CA) and the Bik Lab at UC Riverside (https://biklab.github.io). Typical user applications for Phinch include environmental rRNA amplicons or shotgun metagenomic data, although this framework is being expanded to support any type of sample/observation data represented in a standard format (RNA-seq, gene variants, phenotype character matrices, etc.). The appointed candidate will work with the Pitch Interactive studio to implement novel and interactive visualization features, develop statistical tests as visual plugin tools (e.g. via R shiny apps), and implement new phylogenetic visualizations for microbial ecology datasets. The postdoctoral scholar will also contribute to software documentation and end user training workshops as needed.

Prospective applicants should review project aims outlined in the funded grant proposal (https://doi.org/10.6084/m9.figshare.5471809.v1) as well as these other related resources:

* Phinch GitHub Wiki https://github.com/PitchInteractiveInc/Phinch/wiki * Bik HM, Pitch Interactive (2014) Phinch: An interactive, exploratory data visualization framework for -Omic datasets, bioRxiv, doi: http://dx.doi.org/10.1101/009944 (preprint)

Minimum Qualifications:

Postdoctoral applicants should possess a Ph.D. in a biological or computational discipline, demonstrate a strong publication record and ability to conduct independent research. All applicants are expected to develop strong written and verbal communication skills, as well as assist in mentoring undergraduate and graduate students.

Desirable Qualifications:

Proficiency in a standard programming language (Python or Javascript preferred), experience in biological data visualization (e.g. using RStudio or D3.js), and knowledge of common -Omics data types and workflows (e.g. analysis of rRNA amplicon datasets in QIIME, experience with binning/assembly/functional analysis of shotgun metagenomes, large phylogenomic analyses, etc.). Applicants with expertise in phylogenomics, comparative phylogenetics, and/or statistical analysis in R or Python are especially encouraged to apply.

Application and Appointment:

All appointments are initially for one year, and renewable based on performance. Salaries are commensurate with experience and based on minimums set by the University of California postdoctoral union. To apply, submit a curriculum vitae, a 1-page statement of research interests, and contact details for 2-3 academic references to holly.bik@ucr.edu. Review of applications will begin immediately, and will continue until the position is filled.

Please contact Holly Bik (holly.bik@ucr.edu) if you have any questions about this postdoctoral position.

– Holly Bik Assistant Professor Department of Nematology University of California, Riverside 3401 Watkins Drive Riverside, CA 92521 Email: holly.bik@ucr.edu Phone: (+1) 951-827-4230

Web: http://biklab.github.io Twitter: https://twitter.com/hollybik holly.bik@gmail.com

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UCambridge ComparativeGenomics

POSTDOCTORAL RESEARCH ASSOCIATE: COMPARATIVE GENOMICS

We invite applications for a postdoctoral Research Associate position in the Department of Zoology in Central Cambridge on Downing Street with Dr Stephen Montgomery's research group. It is funded for up to 36 months by the ERC and should start on 1st February 2018 or soon after.

The PDRA will study comparative genomics and the genetic basis of mushroom body expansion in Heliconius butterflies. We have recently confirmed previous reports that Heliconius have massively expanded mushroom bodies, an insect learning and memory centre (see Montgomery et al. 2016 J. Comp. Neurol. 524 (9):1747-1769). This provides a novel case study for investigating the genetic basis of volumetric expansion of 'higher order' brain regions. We are interested in using comparative genomics and transcriptomics, in combination with extensive phylogenetic, neuroanatomical and developmental work, to identify genes that contribute to changes in mushroom body size, structure and function.

DUTIES WILL INCLUDE: - Designing and building bioinformatics pipelines to carry out de novo genome and transcriptome assemblies, using a combination of sequencing technologies; - Designing and executing genome/transcriptome assembly, orthology detection; - Performing evolutionary analyses to investigate gene-phenotype associations, adaptive molecular evolution and gene duplication, differential expression and regulatory evolution; - Data management; - Analysing and writing up the results; - Contributing to the wider research environment.

There is scope for the nature of the analyses to be shaped by the interests of the candidate.

REQUIRED SKILLS AND QUALIFICATIONS: - PhD in an appropriate subject (e.g. comparative/evolutionary genomics, computational biology or bioinformatics, etc.).

- An enthusiasm for comparative genomics and an excellent understanding of key methodologies and challenges of the field; - Experience with large genome/transcriptome datasets; - Excellent programming and data management skills; - An interest in brain and behavioural evolution, or phylogenetic tests of gene-phenotype associations; - Ambition and drive, strong work ethic and good interpersonal skills and a strong publication record for their career stage; - Enthusiasm to interact with colleagues; - Ability to organise time and work effectively, independently and responsibly in a research team setting.

FIXED-TERM: - The funds for this post are available for up to 36 months in the first instance. - The University values diversity and is committed to equality of opportunity. - The University has a responsibility to ensure that all employees are eligible to live and work in the UK.

FURTHER INFORMATION: http://www.jobs.cam.ac.uk/job/16043/ RESEARCH GROUP: http://www.shmontgomery.co.uk Dr. Stephen Montgomery

NERC Independent Research Fellow Dept. of Zoology, University of Cambridge Downing St. Cambridge, CB2 3EJ Tel: 01223336678 Email: shm37@cam.ac.uk Twitter: @eohomo Departmental webpage Personal webpage

Stephen Montgomery <shm37@cam.ac.uk>

UChicago ComputationalGenomics

Post-doctoral positions in computational genomics

Two postdoctoral positions in computational genomics are available in the Barreiro Lab. Our lab is currently located at the University of Montreal but in June 2018 we will be moving to the Section of Genetic Medicine at the University of Chicago.

Our group studies the genetic basis of variation in the human immune response, as well as the evolution of differences in the immune response between humans and other primates. ?The exact projects for prospective postdocs are flexible and applicants are encouraged to propose their own projects, as long as they fit within the lab's general interests.? Current work includes (i) characterization of population differences in the immune response in humans, (ii) testing the functional impact of variation in social status on vaccine responses in rhesus macaques (close collaboration with Dr. Jenny Tung at Duke University), (iii) comparative studies of innate immune responses in mammals, and (iv) the role of epigenetic changes in the regulation of innate immune responses. More details on some of our ongoing projects and past work can be found on our website: http://luisbarreirolab.org/ Postdoctoral applicants should have demonstrated experience with genomic data analysis. Strong programming and bioinformatics skills are essential. Candidates with experience in gene expression data analysis, eQTL mapping, epigenetic profiling, and/or co-expression network analysis are strongly encouraged to apply.

Our lab offers a congenial research environment complemented by the rich academic milieu of the University of Chicago, particularly in the departments of Genetic Medicine, Human Genetics, and Ecology and Evolution. Postdocs in our lab are encouraged to develop collaborations with other groups and to start developing an independent research program. To apply for the position please send an email to Luis Barreiro (luis.barreiro@umontreal.ca) including a cover letter and your resume/CV together with contact information for at least two references. Informal inquiries are also welcome. Start dates are negotiable.

Luis Barreiro Associate Professor

The University of Chicago is an Affirmative Action/Equal Opportunity/Disabled/Veterans Employer and does not discriminate on the basis of race, color, religion, sex, sexual orientation, gender identity, national or ethnic origin, age, status as an individual with a disability, protected veteran status, genetic information, or other protected classes under the law.

Luis Barreiro, PhD. *Assistant Professor * *CHU Sainte-Justine/University of Montreal* *Canadian Research Chair in Functional and Evolutionary * *Genomics of the Immune System. * 3175, Côte Sainte-Catherine, *Phone# : 514-345-4931 ext. 2544* *e-mail: luis.barreiro@umontreal.ca

Luis Barreiro <lbbarreiro@gmail.com>

UCologne EvolutionAntibioticResistance

Postdoc position in modeling the evolution of antibiotic resistance

We seek a postdoctoral researcher for a collaborative project between the groups of Prof. Joachim Krug (Theoretical Physics, University of Cologne) and Prof. Arjan de Visser (Genetics, Wageningen University) on predicting evolutionary pathways to beta-lactam resistance. The project combines theory and experiments and is part of the new Collaborative Research Center 1310 "Predictability in Evolution" funded by Deutsche Forschungsgemeinschaft (DFG) and coordinated at the University of Cologne. The aim of the project is to identify key predictors of the evolution of beta-lactam resistance across time scales and levels of organization. The postdoc will develop mathematical models that link bacterial resistance and fitness to underlying phenotypes and implement them in a dynamical context to quantify the predictability of evolutionary trajectories. This will be done in close collaboration with an experimental postdoc, who will be appointed within the same project.

Profile: We seek a highly motivated person with a PhD in statistical physics or quantitative biology. We expect the successful candidate to have acquired a broad repertoire of numerical and analytic methods for the modeling of complex systems; previous experience with population genetic theory and microbial systems is an asset but not a requirement. The initial appointment is for two years with the possibility for extension up to four years. Salary will be paid according to level E13 of the German public service salary scale (TV-L). The project can start as soon as we have found a suitable candidate.

Applications: Submit enquiries and applications (including CV, letter of motivation and names and contact information of two references) before January 15, 2018 to Joachim Krug. The University of Cologne is one of the leading German institutions in Molecular and Evolutionary Genetics. Wageningen University is a leading university in the field of the life sciences. The University of Cologne is an equal opportunity employer in compliance with the German disability laws. Women and handicapped persons are therefore strongly encouraged to apply.

Prof. Joachim Krug Institute for Theoretical Physics Zülpicher Strasse 77 50937 Köln Germany P: (+)49 221 470 2818 M: krug@thp.uni-koeln.de W: www.thp.uni-koeln.de/krug/ "arjan.devisser@wur.nl" <arjan.devisser@wur.nl>

UCopenhagen AntEvolution

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Postdoctoral Fellowship in Evolution and Eco-Physiology, Department of Biology, U Copenhagen, Denmark

A two-year postdoctoral fellowship on the evolution and eco-physiology of fungus-farming ants is available from June 1, 2018 in the Section for Ecology and Evolution within the Department of Biology at the University of Copenhagen in Denmark.

The fellowship will be part of a 5-year research project financed by an ERC Starting Grant. Led by Assistant Professor Jonathan Shik (www.jonathanshik.com), the project will be based in the thriving research environment of the Centre for Social Evolution (http://socialevolution.ku.dk/home/), and will involve fieldwork in the Panamanian tropical rainforests at the Smithsonian Tropical Research Institute (http://www.stri.si.edu/). The successful applicant will have experience and interest in ecology, evolution, physiology, microbial ecology, and molecular techniques.

Project Overview

The project will focus on the remarkable lineage of leafcutter ants (genus *Atta*) that harvest fresh vegetation and use it as compost to produce domesticated fungal crops in huge underground nests that feed massive super organismal colonies with millions of workers. We will explore how leafcutter ants have managed to grow a single cultivar lineage from Texas to Argentina, thriving across extreme contemporary rainfall and temperature gradients and across diverse climates over millions of years. Projects will combine field experiments in Panamanian rainforests and integrative laboratory studies of cultivar gene expression to resolve the mechanisms governing the resilience of industrial-scale fungus farming in ants within diverse tropical insect communities.

The deadline for applications is February 15, 2018 at 11:59 PM CET. For further details and information about how to apply, visit: http://employment.ku.dk/faculty/?show=146492 – Assistant Professor Centre for Social Evolution Department of Biology University of Copenhagen Universitetsparken 15 2100 Copenhagen, Denmark (+45) 31 15 21 40 Email: jonathan.shik@gmail.com Website: j < http://faculty-staff.ou.edu/S/Jonathan.Z.Shik-1/Site/Home.html > onathanshik.com

J Shik <jonathan.shik@gmail.com>

UCopenhagen IndoPacificBirdPopGenomics

*Population genomics of Indo-Pacific birds, postdoc *

A 2-yearpostdoc (with a possible extension for up to a year) in Population Genomics is available from 1 April 2018 or as soon as possible thereafter.

Section for Biosystematics at the Natural History Museum of Denmark

Faculty of Science

University of Copenhagen

The successful candidate will work on population genomics of Indo-Pacific birds aspart of a larger ongoing Villum Foundation funded project that aims to elucidate the underlying mechanisms of how species form, disperse, adapt and interact and how this leads to the species distributions we see today.

Work in the group includes phylogenetics, phylogeography and systematics and we have a strong field component (currently we work mostly in Papua New Guinea), with the aim of collecting additional data (molecular and ecological) as well as fitting satellite transmitters to monitor annual movement of sedentary bird species.The candidate is mainly expected to work on the generation of genomic data and downstream analyses but is also encouraged to be part of the field efforts.

The work will be in close collaboration with other group members as well as with other staff and students at the Natural History Museum of Denmark (notably withthe Evogenomics group led by Professor Tom Gilbert) and the Swedish Museum of Natural History (notably members of the Department of Bioinformatics andGenetics). We seek applicants who have intimate knowledge of and interest in population genomics and phylogeography irrespective of organisms. This research builds on a large collection of freshtissue material from two elevational gradients on Indonesian islands (Buru and Seram) and two elevational gradients in Papua New Guinea and aim to shed light on movement along the gradients and across the barriers and how populations differentiate and adapt over time.

The postdoc's duties will include research as well as teaching. The post may also include performance of other duties.

*Qualifications: *

- A strong background in population genomics
- Excellent analytical skills within population genomics
- Excellent written and verbal communication skills
- Ability to effectively work independently and in multidisciplinary teams

Furtherinformation on the Department is linked at *http://www.science.ku.dk/english/about-the-faculty/organisation/Inquiries about the position can be made to Associate ProfessorKnud Jønsson, Section forBiosystematics, Natural History Museum of Denmark, Universitetsparken 15, DK-2100 Copenhagen , Denmark,Email: *kajonsson@snm.ku.dk

The position is open from 1 April2018 or as soon as possible thereafter.

The University wishes our staff to reflect the diversity of society and thus welcomes applications from all qualified candidates regardless of personal background.

*Termsof employment *

The position is covered by the Memorandum on Job Structure for Academic Staff.

Terms of appointment and payment accord to the agreement between the Ministry of Finance and The Danish Confederation of Professional Associations on Academics in the State.

The starting salary is currently up to DKK 413.717 including annual supplement (+ pension upto DKK 70.746). Negotiation for salary supplement is possible.

*The application, in English, must be submitted electronically. *

*Please include *

- Curriculum vita
- Diplomas(Master and PhD degree or equivalent)
- Research plan - description of current and future research plans
- Complete publication list
- Separate prints of 3 particularly relevant papers

*The deadline for applications is 28 January 2018, 23.59 GMT + 1. *

After the expiry of the deadline for applications, the authorized recruitment manager selects applicants for assessment on the advice of the Interview Committee.

You can read about the recruitment process at *http://employment.ku.dk/faculty/recruitment-process Interviews will be held in the the first weeks of March

*Apply https://candidate.hr-manager.net/ApplicationInit.aspx?cid=1307&ProjectId=146392&DepartmentId=18977&MediaId=4642&SkipAdvertisement=true Part of the International Alliance of Research Universities (IARU), and among Europe's top-ranking universities, the University of Copenhagen promotes research and teaching of the highest international standard. Rich in tradition and modern in outlook, the University gives students and staff the opportunity to cultivate their talent in an ambitious and informal

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UEastAnglia 2 AgeingLifeHistoryEvolution

Up to two three-year postdoc positions and a technician position are available in my lab.

Contact me for questions/queries: A.Maklakov@uea.ac.uk

To apply click here : https://goo.gl/PdnH2J pounds 32,548 to pounds 38,833 per annum Why do we age: linking evolutionary causes with proximate mechanisms We are seeking highly motivated and enthusiastic postdoctoral Senior Research Associates for ERC-funded project on the evolution of ageing in the Maklakov lab in the School of Biological Sciences at University of East Anglia.

Understanding ageing is one of the big unsolved problems in biology.

Recent progress in the study of ageing has challenged the current paradigm that ageing results from energy trade-offs between survival and reproduction. In this project, we will work at the interface of evolutionary biology and bio-gerontology towards the goal of explaining the mismatch between this paradigm and the empirical findings. We will focus on i) uncovering potentially missing parts of the classic survival/reproduction trade-off; and ii) testing an emerging new theory of ageing that aims to replace the classic view.

You will help setting up the new lab, conduct experimental work using Caenorhabditis nematodes as the model organism, help supervising and training new lab members and actively participate in the research life of the lab and the School, such as seminars and journal clubs. Funding is available for further training and professional development by attending national and international conferences and workshops.

Research Environment The successful candidate will become a part of the growing lab that will soon include two postdocs, a senior laboratory engineer and a research technician.

The lab is part of the Organisms and the Environment theme at the School of Biological Sciences at UEA. There several world-class labs with similar interests at the theme, including Prof. Tracey Chapman (ageing, diet, sexual conflict, Drosophila), Prof. Andrew Bourke (social evolution and ageing in social insects), Prof. David Richardson (telomere biology, ageing in birds), Dr. Simone Immler (germline/soma interactions, zebrafish and mathematical modelling).

Furthermore, there are three world-leading research institutes (John Innes Centre, Earlham Institute and Quadram Institute) that together with UEA comprise Norwich Research Park, and provide great opportunities for collaboration. Finally, PI has strong ties with Uppsala University in Sweden and there are opportunities for doing projects together with an established nematode lab there. In our lab, we encourage dynamic collaborative atmosphere and promote joint projects and discussion clubs both within and outside the immediate research group.

The School The School of Biological Sciences benefits from close interactions with other Schools within UEA, including the Schools of Chemistry and Pharmacy and the Norwich Medical School. UEA is also part of the Norwich Research Park that includes the Norfolk and Norwich University Hospital, the Institute of Food Research and the John Innes Centre.

Please apply here: link to UEA HR advert: https://goo.gl/PdnH2J Dr. Alexei A. Maklakov Lecturer and ERC Fellow School of Biological Sciences University of East Anglia Norwich Research Park Norwich, NR4 7TJ UK

Tel: +44 1603 591150

Our Lab page: http://alexeimaklakov.com Google Scholar: http://scholar.google.com/citations?user=-8aCng7oAAAAJ&hl=en&oi=ao Research Gate: https://www.researchgate.net/profile/Alexei_Maklakov Alexei Maklakov <A.Maklakov@uea.ac.uk>

UHalle BeeViralEvolution

1 year 5 month postdoc on viral evolution in bees

A postdoctoral researcher is sought for a project on the evolutionary ecology of viruses in bees within Robert Paxton$B!G(Bs lab at the University of Halle, Germany. The overarching goal of the research is to understand the role of viral epidemiology and evolutionary change for pathogen emergence and host switching; the project is embedded within the DFG$B!G(Bs priority program: Ecology and Species Barriers in Emerging Viral Diseases (SPP 1596). Requirements sought: a highly motivated individual; experience in, or knowledge of, evolutionary modelling and bioinformatics; an interest in host-parasite interactions. Opportunities exist to develop the research through lab and field-based experiments as well as molecular genetic analysis of bees and their viruses in the lab.

The working language of the lab is English. The neighboring group of Robin Mortiz makes for a strong profile in bee biology and genetics at the University of Halle. The position is available for 1 year and 5 months and, though the start date is flexible, we seek a person to commence research during spring 2018. Halle is a delightful, historical city approximately 1.5 hours SW of Berlin. The salary is on the standard German postdoc scale E13, which translates to approximately Euro 51-57 K per annum (dependent on experience).

Further details of the position can be obtained from Robert Paxton (robert.paxton@zoologie-uni-halle.de), to whom applications should be sent by 15 February 2018 as a single pdf file to include: cover letter referring to $B!H(Bposition 5-12596/17-D$B!I(B, cv, list of publications, a statement of research interests and goals (maximum 1 page), and contact details of two referees. Interviews are planned for March 2018, with a start date in April or as soon as possible thereafter.

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

UHelsinki Bioinformatics

Research group SpecIAnt (Speciation in ants) at the University of Helsinki, Finland is looking for outstanding candidates for a position of:

POSTDOCTORAL RESEARCHER OR BIOINFORMATICIAN IN EVOLUTIONARY GENOMICS AND SPECIATION for a fixed term of 2 years starting from 1.3.2018, or as soon as the best applicant is available.

The group SpecIAnt is a new Academy of Finland and Horizon2020 funded research group at the department of Biosciences and HiLIFE. Our team investigates the genomic and epigenetic basis of speciation using wood ants as a model system. Previously, we have discovered widespread hybridization between wood ant species in Southern Finland with unique consequences. Female hybrids are favoured by natural selection but male hybrids are selected against and die during development. Using large-scale genomic and transcriptomic data we have mapped candidate genomic regions and genes underlying reproductive isolation.

Now our aim is to compare genomic regions underlying reproductive isolation over multiple hybridization events.

The candidate will assemble reference genomes and investigate the patterns of divergence and population differentiation using newly acquired full genome and re-sequencing data. The project is executed in collaboration with Prof. Roger Butlin (University of Sheffield), Prof.

Michel Chapuisat (University of Lausanne) and Dr. Heikki Helantera (University of Helsinki). Collaborators offer opportunities for knowledge exchange and visits.

The candidate should have a Master's or a Phd degree. The successful candidate should be self-motivated and responsible with excellent team working, problem solving, and analytical skills. Previous experience in analysing data from high-throughput sequencing and working in Unix/Linux environment is required. A background in population genetic data analysis or speciation genetics is a plus.

For a bioinformatician, without PhD qualifications, the starting salary will be 2200 - 2500 euros/month, depending on the appointee's qualifications and experience. For a post doc the starting salary will be 3 100 euros/month, depending on the appointee's qualifications and experience. A four-month trial period will be applied.

To apply, please submit your application by 15.1.2018 using the University of Helsinki electronic recruitment system: https://www.helsinki.fi/en/open-positions/postdoctoral-researcher-or-bi oinformatician-in-evolutionary-genomics-and-speciation Upload a single pdf-file containing a one-page letter with a personal statement outlining your research interests and relevant work experience, your CV (including publication list), as well as contact information for 2 references.

For additional information, please contact Dr. Jonna Kulmuni by email: jonna.kulmuni(at)helsinki.fi. For further information about the research group see https://jonnakulmuni.wordpress.com/ References:

Beresford J, Elias M, Pluckrose L, Sundstrom L, Butlin R, Pamilo P, Kulmuni J. (2017) Widespread hybridization within mound-building wood ants in Southern Finland results in cytonuclear mismatches and potential for sex-specific hybrid breakdown. Molecular Ecology. 15:4013-4026.

Kulmuni J & Pamilo, P. (2014) Introgression in hybrid ants is favored in females but selected against in males. Proc Natl Acad Sci USA. doi: 10.1073/pnas.1323045111.

Kulmuni J, Seifert B & Pamilo, P. (2010) Segregation distortion causes large-scale differences between male and female genomes in hybrid ants. Proc Natl Acad Sci USA. 107(16): 7371-7376.

"Kulmuni, Jonna K" <jonna.kulmuni@helsinki.fi>

UMaryland SOM GenomicsBioinformatics

POSITION: Postdoctoral Fellow

The Dunning Hotopp Lab at The Institute for Genome Sciences at the University of Maryland School of Medicine is seeking a Postdoctoral Fellow to make significant contributions in genomics. Currently funded projects in a well support lab focus on understanding DNA integrations in human cancer genomes (NCI-TR01), bacterial DNA integrations in other animal genomes (NSF-ABI), and the genomics of filarial nematodes (NIAID-U19).

The ideal applicants must have experience in genomics and/or bioinformatics with a background in microbiology, cancer biology, and/or molecular evolution. Applicants should have demonstrated experience in applying laboratory and computational experimental approaches to generate and analyze large datasets. Preference will be given to applicants who are excellent writers, highly-motivated, independent yet able to work as part of a team, and have a strong publication record.

The successful candidate will have a doctoral degree in Microbiology, Genetics, Evolution, Biology, Computer Science, or a related ï. Experience with statistical analyses and/or programming in Perl, Python, C/C++ and R is desired, but not required.

The Dunning Hotopp Lab is located in a brand new building with state of the art sequencing facilities and a bioinformatics core. It is a demanding yet very supportive lab environment. In addition to basic genomics and big data research, the Dunning Hotopp group creates scicomm videos, develops novel software for the identification of lateral gene transfers, and does research as part of multi-institute, interdisciplinary teams. http://www.igs.umaryland.edu/labs/hotopp/projects/ TO APPLY: submit a cover letter, CV, and contact information for 3 references via the UMB jobs portal: https://umb.taleo.net/careersection/umb_faculty+and+post+docs/jobdetail.ftl?job=170001UF&lang=en "Bromley, Robin" <RBromley@som.umaryland.edu>

UMinnesota SoybeanPopGenetics

Position: Postdoctoral Research Associate

Location: University of Minnesota, Department of Agronomy and Plant Genetics, St. Paul, MN

Research Area: Soybean quantitative genetics and population genomics

Qualifications: PhD in quantitative genetics, population genetics, evolutionary genetics, plant breeding, or related field. Proficiency in the statistical programming language R, Perl, Python, or other programming languages. A demonstrated ability to publish original research in peer-reviewed journals is preferred.

We are seeking a postdoctoral research associate in the area of soybean quantitative genetics and population genomics. The successful candidate will have the opportunity to conduct studies at the interface between population genomics, genomic prediction, and plant breeding. Possible areas of research include integration of variant annotation into genomic prediction models; genetic determinants of variation in recombination rate; and the genetic basis of local adaptation and its prediction for soybean improvement. To address these questions, the successful candidate will use publicly available data in combination with internally developed databases and datasets, and have the opportunity to seek additional funding to conduct follow-up studies to test hypotheses developed throughout the course the preliminary analyses.

There are opportunities to improve your biocomputing skills through tutorials hosted by the Minnesota Supercomputing Institute https://www.msi.umn.edu/tutorials and the Biocomputing Discussion Group https://morrelllab.github.io/compute/. On the St. Paul campus there are a number of faculty with research programs in quantitative genetics (including Rex Bernardo, Yang Da, and Ruth Shaw) and evolutionary genetics (including Yaniv Brandvain, Emma Goldberg, Suzanne McGaugh, David Moeller, and Peter Tiffin). In additional to the activities of individual lab groups, you can participate in reading groups, including the P.R.O.S.T. evolutionary genetics discussion https://brandvainlab.wordpress.com/p-r-o-s-t/ organized by Yaniv Brandvain.

To apply, send a cover letter and curriculum vitae to Aaron Lorenz (lore0149@umn.edu) and Peter Morrell (pmorrell@umn.edu). Review of applications will begin on Dec 15, 2017 and continue until the position is filled.

– Aaron J. Lorenz Associate Professor Soybean Breeding and Genetics Department of Agronomy and Plant Genetics University of Minnesota Office: 307 Hayes Hall Office phone: 612-625-6754 Email: lore0149@umn.edu Mailing address: 411 Borlaug Hall 1991 Upper Buford Circle St. Paul, MN 55108

Aaron Lorenz <lore0149@umn.edu>

UNewHampshire BeeEcolEvolution

Wild Bee Behavior and Community Ecology Postdocs (2 positions)

The Rehan Lab (www.rehanlab.com) is hiring 2 postdoctoral research associates to study behavioral and community ecology of wild bees. The Rehan lab is a collaborative group of more than 12 researchers, staff, and students focusing on bee behavior, ecology and evolution. We are located at the University of New Hampshire in the Department of Biological Sciences. The postdoctoral researchers will join a vibrant team of integrative biologists passionate about all things bee.

*Behavioral Ecology Postdoc *

This postdoc will examine nutritional ecology of wild bees to determine pollen preference and nutritional requirements of native pollinators. There is increasing evidence that bee health is mediated not only by the quantity, but also quality of food provided during development. This researcher will conduct field and lab experiments to determine optimal diets for bee nutrition and pollinator health. We are also interested in the effects of maternally provisioned diet and mother-offspring interactions on social behavior. We encourage the postdoc to develop research projects on the social evolution and behavioral ecology of wild bees.

The successful candidate will have a PhD in a relevant area, and a strong background in behavioral ecology and evolution. Analytical and writing skills will need to be demonstrated with a history of first authored publications.

*Community Ecology and Taxonomy Postdoc *

This postdoc will develop taxonomic reference material and field guides for the wild bees of eastern North America. UNH is home of the Insect Collection of over 700,000 insect specimens and 20,000+ bees. We have databased this material and are actively working to develop status assessments of wild bees in the northeast as well as understanding habitat requirements and floral hosts using a mix of historic reference data and ongoing field surveillance. This researcher will help manage a field crew, analyze complex ecological data, write manuscripts and field guides, and engage in public outreach and educate events across New England.

The successful candidate will have a PhD in a relevant area, and a strong background in community ecology and bee taxonomy. Analytical and writing skills will need to be demonstrated and a background in GIS is highly desirable for this project.

The University of New Hampshire is an Equal Opportunity Employer and encourages applications from women and underrepresented groups. If interested, please send a CV, names of three references, and a short statement of interests to Sandra Rehan sandra.rehan@unh.edu by December 20, 2017. Postdoctoral Fellowship positions are available for one year and renewable up to three years with successful progress and performance.

Sandra Rehan, Assistant Professor Department of Biological Sciences University of New Hampshire Durham, NH, USA 03824 (603) 862-5310 www.rehanlab.com sandra.rehan@gmail.com

UNorthCarolina PopulationGenomics

The Schrider Lab (https://www.schriderlab.org/) in the Department of Genetics at the University of North Carolina at Chapel Hill is hiring a postdoctoral research associate. The successful candidate will perform computational research addressing problems in population and evolutionary genomics which may include but are not limited to the following:

1) The application of machine learning tools to problems in evolutionary/population genetics 2) Inferring populations' selective and demographic histories 3) Elucidating the population genetics of adaptation via simulation 4) The evolutionary consequences of genomic structural variation (e.g. duplications, deletions, inversions)

The postdoctoral research associate will have wide latitude in selecting/devising projects in these and related areas. Most of our research is conducted in humans, Drosophila melanogaster, and the malaria mosquito Anopheles gambiae, though candidates wishing to study another system will still be considered.

This a multidisciplinary position and candidates from a variety of backgrounds will be considered and receive training to address deficits as needed. A PhD in Evolution, Genetics, Bioinformatics, Computer Science, or a related field must be completed prior to the postdoc's hire.

Those interested should email Dan Schrider (drs@unc.edu) and include their CV as an attachment.

The University of North Carolina at Chapel Hill is an equal opportunity and affirmative action employer. All qualified applicants will receive consideration for employment without regard to age, color, disability, gender, gender expression, gender identity, genetic information, race, national origin, religion, sex, sexual orientation, or status as a protected veteran.

Dan Schrider <drs@unc.edu>

UOstrava ComputationalBiol

We are looking for a postdoc at the University of Ostrava, Czech Republic. Our team lead by Pavel Flegontov focuses on using computational methods, ancient DNA, and large autosomal datasets for investigating the history of human populations from an interdisciplinary perspective. We currently work mainly on the settlement of the American Arctic (see our preprint: https://www.biorxiv.org/content/early/-2017/10/13/203018) and on Eurasian steppe nomads of the first millennium CE. We also investigate the relationship of language families and ethnic groups around the Bering Strait, ancient populations of Chukotka, Jewish population history, Indian and negrito ancestry across Southeast Asia, and explore admixture models for diverse Papuan populations. We are collaborating closely with leading researchers in the field: David Reich (Harvard Medical School, Boston, MA), Johannes Krause and Stephan Schiffels (Max Planck Institute for the Science of Human History, Jena, Germany).

The postdoc will receive a net salary of 1200 EUR per month for 3 years. The cost of living is low in Czechia, and average net salary is below 1000 EUR. Depending on success of further grant applications, the salary may be increased in the 2^nd and 3^rd years.

The applicant should have experience in genetics and/or computer programming and at least one publication. To apply, please send an email with a CV attached to pflegontov[at]gmail.com until January 15, 2018. The selection process will consist of an interview and possibly a test assignment. Funding for the position is available since February 1, 2018, but the postdoc may start working a bit later.

Please see a full list of our publications at the following link: http://www1.osu.cz/~flegontov/ Pavel Flegontov, PhD http://www1.osu.cz/~flegontov/ Department of Biology and Ecology, Faculty of Science, University of Ostrava, Ostrava, Czech Republic

Pavel Flegontov <pflegontov@gmail.com>

UPennsylvania HumanGenomics

Human Evolutionary/Functional Genomics Postdoctoral Positions at the University of Pennsylvania

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

The ideal functional genomics candidate would have expertise in using cutting edge techniques for characterizing gene regulation and chromatin structure (e.g. massively parallel reporter assays, chromosome conformation capture, DNA acetylation and methylation analyses). The ideal computational candidates will have skills in computer programming (PERL/Python/C++) and using statistical environments (R/MATLAB) as well as expertise in population genetics theory and/or quantitative analyses of complex traits. Experience with large genome-scale datasets is a plus. Candidates working with non-human or model organisms who want to obtain experience working with human data are encouraged to apply. Salaries are commensurate with qualifications and experience.

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

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

Sarah Tishkoff, Ph.D. David and Lyn Silfen University Professor Departments of Genetics and Biology University of Pennsylvania Tel: 215-746-2670 tishkoff@pennmedicine.upenn.edu http://www.med.upenn.edu/tishkoff/ "Tishkoff, Sarah" <tishkoff@pennmedicine.upenn.edu>

UPittsburgh MicrobiomeOrganization

POSTDOC: Spatial organization of the microbiome (University of Pittsburgh)

The Wright Lab (http://wrightlabscience.com) is seeking an enthusiastic postdoctoral associate to lead a multi-disciplinary project aimed at understanding the spatial structuring of microorganisms within the microbiome. The successful candidate will develop and apply methods for dissecting the 3D organization of environmental and clinical microbiome samples. The project will involve combining multiple technologies, including robotics and high-throughput sequencing, to map microbial consortia at the sub-millimeter scale. This research provides the opportunity to test theories about how spatial structuring shapes the ecology and evolution of microbial communities.

The Wright Lab is a rapidly growing experimental evolution and comparative genomics hybrid wet/dry lab at the University of Pittsburgh. We are affiliated with the

Department of Biomedical Informatics, and collaborate closely with other experimental evolution and microbiology labs on campus. Our lab offers opportunities to gain experience giving presentations, lecturing, mentoring students, & writing proposals and papers. We are part of a broader effort to make the University of Pittsburgh a leader in applying evolution to the improvement of medicine. The university consistently ranks in the top 10 nationally for biomedical research funding. Pittsburgh, PA is often voted the most livable city in the US featuring eclectic neighborhoods, diverse culinary and entertainment opportunities, as well as easy access to natural areas (http://www.coolpgh.pitt.edu/).

QUALIFICATIONS: Qualifications for this position include a PhD in microbiology, ecology, evolutionary biology, or a related field. Ideal candidates would have experience in metagenomics or amplicon sequencing, be excited to learn new bioinformatics skills, and be willing to engineer new experimental devices. The candidate should 1) be fluent in written and spoken English, 2) be able to work independently and as a member of a team, 3) be hard-working, motivated, and eager to learn, & 4) have an interest in the microbiome.

TO APPLY: Please email applications (including cover letter, curriculum vitae, & names and email addresses for 3 professional references) to Dr. Erik Wright (eswright@pitt.edu). The position is available starting as early as February 2018 for 1 year, renewable up to 3 years contingent upon satisfactory performance. Salary is commensurate with experience and includes a comprehensive benefits package. Review of applications will begin immediately and continue until the position is filled.

Erik Wright Assistant Professor Department of Biomedical Informatics University of Pittsburgh Pittsburgh, PA (412) 383-4458 http://www.dbmi.pitt.edu/person/erik-s-wright-phd-ms "Wright, Erik Scott" <ESWRIGHT@pitt.edu>

USheffield Speciation

Postdoctoral Research Associate, University of Sheffield

2 years in the first instance, closing date 17 January 2018

You will work with Professor Roger Butlin to advance an ERC-funded project on the genetic basis of adaptation and speciation in the coastal gastropod, Littorina saxatilis. The project is focused on the evolution of reproductive barriers, starting with divergent adaptation in the face of gene flow and progressing towards completion of speciation. We focus on analysis of contrasting contact zones in Sweden and Spain, which we are analysing with intensive phenomics and genomics approaches. You will be expected to have a strong commitment to research in evolutionary genetics and a special interest in processes of speciation. Analysis of large sequencing data sets will be a key component of the role but you will also participate in sampling and experimental work as part of a large collaborative team.

You will have a PhD or equivalent experience in evolutionary genetics and experience of research in evolutionary genetics. You will have experience of analysing high-throughput sequence data sets and experience of constructing bioinformatics pipelines.

For informal enquiries, contact Roger on r.k.butlin@shef.ac.uk

To apply, go to www.shef.ac.uk/jobs using reference UOS018001

– Roger K Butlin

Professor of Evolutionary Biology Guest Professor Animal and Plant Sciences Centre for Marine Evolutionary Biology The University of Sheffield Department of Marine Sciences Western Bank University of Gothenburg Sheffield S10 2TN Gothenburg UK Sweden

r.k.butlin@shef.ac.uk

+44(0)114 2220097

"r.k.butlin@sheffield.ac.uk" <r.k.butlin@sheffield.ac.uk>

UTexasAustin EvolutionaryComputationalGenomics

Postdoctoral positions in evolutionary genomics, UT Austin

The research groups of Nancy Moran and Howard Ochman (Department of Integrative Biology, UT Austin) are seeking two postdoctoral research associates with experience in evolutionary biology, bioinformatics and genomics. Possible projects include the genomics of host-symbiont interactions in insect systems, genomics of bacterial populations, evolution and metagenomics of microbiomes. We are especially interested in candidates with expertise in bioinformatics and programming, and experience working with large genomic datasets.

Projects may be strictly computational or may include experimental lab work. Successful applicants would play a role in defining their own projects within this span of topics.

The Moran and Ochman research groups interact closely and address questions in evolutionary biology, genomics including functional genomics, insect biology and microbiology. More information is available at http://web.biosci.utexas.edu/moran/ and http://web.biosci.utexas.edu/ochman/ . UT Austin offers a very stimulating research environment and outstanding facilities and infrastructure. Austin is a progressive, vibrant city with many options for recreation and cultural activities.

Start date is flexible, within calendar year 2018. Salary would be $47000-$50000 per year depending on experience, and full benefits package is included. Initial appointments would be for 1 year, with potential to extend to 2 or 3 years.

If interested, please send a resume and brief statement of research interests and career goals to Kim Hammond: kim.hammond@utexas.edu. Please include names and contact information for three references familiar with your scientific work. We will begin reviewing applications on January 20 2018.

“Moran, Nancy A” <nancy.moran@austin.utexas.edu>

UUppsala WolfGenomics

Postdoc in population genomics of wolves We are looking for a competitive post-doc to join Hans Ellegren’s lab group of about 10 post-docs, PhD students, and bioinformaticians working with evolutionary and population genomic approaches to speciation, adaptation, molecular evolution and conservation genomics (http://www.ieg.uu.se/evolutionary-biology/ellegren/). The announced position is on an exciting project dealing population genomics and molecular evolutionary analyses of wolves. The position is for two years, with possibilities for two years extension.

The Scandinavian wolf population is a striking example of the impact of isolation on genetic diversity and survival. Wolves were once extinct in Scandinavia, but in the early 1980s two individuals re-entered the peninsula and successfully reproduced. Cut off from the larger Finnish-Russian metapopulation by the Reindeer husbandry area to the North, the population remained very small (less than 10 individuals) for a decade. However, in 1991 a single male immigrant entered the population and reproduced, resulting in genetic rescue through an increase in both genetic diversity and population size (VilÃ et al 2003 Proc R Soc Lond B 270:91-97). To this day the population remains characterised by prolonged periods of isolation with rare immigration events. Inbreeding is extensive.

We are sequencing the genomes of hundreds of wolves from both Scandinavia and the Finnish-Russian metapopulation. This dataset provides an ideal opportunity to study the genomic consequences of population isolation and genetic rescue, as well as providing critical conservation information for the long-term viability of the population. It also provides unique possibilities to study the distribution of fitness effects in an inbred population and the accumulation of deleterious mutations in gene sequences. We have recently demonstrated how inbreeding translates into extensive arrays of runs of homozygosity in individual wolves, with some having entire chromosome that are identical-by-descent (Kardos et al 2017 Genomic consequences of intensive inbreeding in an isolated wolf population. Nature Ecology and Evolution 2:124-131).

There are several possible lines to pursue depending on interest and background of the successful candidate/s. These include assessment of how genomic diversity varies over time and in relation to inbreeding, identification of candidate genomic regions for inbreeding depression, assessment of gene flow between populations, and molecular evolutionary analyses of large-scale sequence data.

A strong background in computational analyses of sequence data is required. Strong skills in population genomic and/or molecular evolutionary analyses are desirable.

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. It is a most 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.

Informal inquiries can be directed to Hans Ellegren (hans.ellegren@ebc.uu.se).

Applications will only be accepted when submitted through the Uppsala University web portal no later than Jan 20 2018, using this link: http://www.uu.se/en/about-uu/join-us/details/?positionId=185491 Hans Ellegren <hans.ellegren@ebc.uu.se>

UWMilwaukee PopulationGeneticsPedigrees

The Latch Lab at the University of Wisconsin-Milwaukee is recruiting a Postdoctoral Fellow in population genetics, to work at the intersection of captive population management and wildlife conservation. The fellow will design and conduct computational research focused on pedigree-based management. The fellow will have considerable flexibility in the selection of specific projects, and successful candidates are encouraged to be creative in developing their own projects that utilize simulations or modeling approaches related to resolving incomplete pedigrees and utilizing pedigrees in wildlife conservation and management. The work will have important implications for the conservation and management of wildlife both in situ and ex situ, and I anticipate that the fellow could make meaningful contributions to either or both of these fields.

A PhD in molecular ecology, population genetics, computational biology or related discipline is required. Applicants should have a strong publication record, demonstrable experience in molecular data analysis and computer modeling (C++ or C# preferred), and competency with at least one scripting language (e.g., Perl, Python, R). The position is funded for up to three years, has a salary of $47,476, and may begin as early as February 2018.

To apply, please submit a brief cover letter, a one-page description of your research experience/interests, and a CV with the names and contact information for three references to Emily Latch (latch@uwm.edu). Please see https://people.uwm.edu/latch/ to learn more about our group and send any questions or informal inquiries regarding the position to latch@uwm.edu. UW-Milwaukee is an equal opportunity/equal access/affirmative action employer fully committed to achieving a diverse workforce. Applicants from groups traditionally underrepresented in science are especially encouraged to apply.

Emily Latch <latch@uwm.edu>

Emily K. Latch Associate Professor Dept. of Biological Sciences University of Wisconsin - Milwaukee 3209 N. Maryland Ave. Milwaukee, WI 53211

Email: latch@uwm.edu Tel: 414-229-4245 Web: http://www.uwm.edu/ ~ latch Emily K Latch <latch@uwm.edu>

UZurich Bioinformatician EvolutionaryGenomics

Open Position: Bioinformatician in Evolutionary Genomics (80-100%)

A postdoctoral fellowship in evolutionary bioinformatics is available in Andreas Wagner's Laboratory at the University of Zurich, which is a member of the Swiss Institute of Bioinformatics (SIB). The lab is collaborating with multiple research groups as part of the University Research Priority Program (URPP) "Evolution in Action: From Genomes to Ecosystems". The candidate of choice would contribute to a range of collaborative projects on the evolutionary genomics of animals, plants, and microbes, whose common thread is the analysis of high-throughput sequencing or functional genomic data. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and life's fundamental organizational principles.

Requirements: We are looking for an individual with a PhD, who is highly self-motivated and independent, yet willing to support the computational research of his collaborators in a team-effort. Strong data analysis experience using R/Bioconductor and fluency in a major scripting language such as Python/perl is required, and experience in software development is a plus. The successful candidate will have experience with computational analyses of high-throughput sequencing data in genomics or population genomics. Only applications with a demonstrated interest and research history in evolutionary biology can be considered further. The working language in the laboratory is English. German skills, although helpful, are not essential.

Offers: We offer a friendly, international, dynamic and team-oriented scientific environment at the UZH. Zurich is an attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities. The position offers a highly competitive salary and is funded until December 31, 2020 (with possibility of extension). Part-time work is possible.

Contact: For informal enquiries please contact Stefan Wyder: stefan.wyder@evolution.uzh.ch, +41 44 634 82 44

Application: Please send a single (!) PDF file merged from the following parts to coordination@evolution.uzh.ch: CV including publication list, a statement of research interests not exceeding three pages, and three academic references. The application deadline is Jan 21, 2018. Starting date is March 2018 or upon agreement.

University of Zurich, URPP Evolution in Action

Mira Portmann Coordination Office URPP Evolution in Action University of Zurich c/o Department of Plant and Microbial Biology Zollikerstrasse 107 CH-8008 Zurich Tel.: +41 44 634 82 19 mira.portmann@uzh.ch

"mira.portmann@evolution.uzh.ch" <mira.portmann@evolution.uzh.ch>

Wageningen AntibioticEvolution

Postdoc position in experimental evolution of antibiotic resistance

We seek a postdoc for a collaborative project between the groups of Prof. Arjan de Visser (Genetics, Wageningen University) and Prof. Joachim Krug (Theoretical Physics, University of Cologne) on predicting evolutionary pathways to beta-lactam resistance. The project combines theory and experiments and is part of the new Collaborative Research Center 1310 "Predictability in Evolution" funded by Deutsche Forschungsgemeinschaft (DFG) and coordinated at the University of Cologne. The aim of the project is to identify key predictors of the evolution of beta-lactam resistance across time scales and levels of organization. The postdoc will perform experiments with E. coli and TEM-1 beta-lactamase to develop and test predictions of the probability of fixation of new resistance-enhancing mutations and their interactions, and quantify effects from various constraints on the repeatability of evolution. This will be done in close collaboration with a theoretical postdoc, who will be appo inted within the same project.

Profile: We seek a highly motivated person with a PhD in molecular evolutionary biology, microbial genetics or enzyme engineering. Experience with microbiological and molecular genetic protocols, including genome analysis, are absolute requirements; experience with evolutionary theory and quantitative models are an asset. Experimental work will be carried out at Wageningen University and at the University of Cologne. The initial appointment is for two years with the possibility for extension up to four years. Salary will be paid according to level E13 of the German public service salary scale (TV-L). The project can start as soon as we have found a suitable candidate.

Applications: Submit enquiries and applications (including CV, letter of motivation and names and contact information of two references) before 15 January 2018 to Arjan de Visser or Joachim Krug. The University of Cologne is one of the leading German institutions in Molecular and Evolutionary Genetics. Wageningen University is a leading university in the field of the life sciences. The University of Cologne is an equal opportunity employer in compliance with the German disability laws. Women and handicapped persons are therefore strongly encouraged to apply.

Prof. Arjan de Visser Laboratory of Genetics Wageningen University, Radix building Droevendaalsesteeg 1 6708 PB Wageningen The Netherlands P: (+)31 317 483144 M: arjan.devisser@wur.nl W: https://arjandevisserlab.wordpress.com Prof. Joachim Krug Institute for Theoretical Physics Zülpicher Strasse 77 50937 Köln Germany P: (+)49 221 470 2818 M: krug@thp.uni-koeln.de W: www.thp.uni-koeln.de/krug/

"arjan.devisser@wur.nl" <arjan.devisser@wur.nl>

Wissenschaftskolleg Berlin Fellowship

GAIN TIME TO THINK! 2018/19 COLLEGE FOR LIFE SCIENCES FELLOWSHIPS DEADLINE: — JANUARY 7, 2018 Call for Applications https://cfls-application.wiko-berlin.de/

The College for Life Sciences, a junior program of the Wissenschaftskolleg zu Berlin (Institute for Advanced Study), offers young life-sciences scholars from around the world an opportunity to take a break from the lab and gain time to work and develop their own projects and immerse themselves in an intellectually and culturally diverse environment.

Each year the Wissenschaftskolleg welcomes internationally recognized senior as well as promising junior scholars in all fields of knowledge, including the humanities, the social sciences and the arts and we invite you to become part of this "learning community". Our goal is to promote a kind of science that transcends disciplinary boundaries and goes beyond established issues and approaches.

Through the College for Life Sciences we promote scientists at the beginning of their career, i.e. postdocs, junior group leaders, lecturers, assistant, associate and junior professors.

The fellowships are intended for residencies of 3-6 months during the academic year 2018/19, i.e. September 2018 June 2019.

BENEFITS OF THE FELLOWSHIP * Three to six months' residency at the Wissenschaftskolleg in Berlin * A full stipend based on your previous salary * Studio accommodation on campus * Freedom to pursue a project of your choice * Insight into new areas of knowledge and research cultures * Integration into a unique international community of Fellows * Access to Berlin's excellent scholarly and scientific community * Access to the Wissenschaftskolleg's outstanding library and IT services We do not offer any lab space. For more details please visit: www.wiko-berlin.de/cfls APPLICATION AND REQUIREMENTS Please apply by January 7, 2018 with a project outline (about 1000 words), a letter stating your motivation for wishing to obtain a fellowship (about 500 words), your complete curriculum vitae, and a list of your publications here: https://cfls-application.wiko-berlin.de/ You are completely free to choose the project that you will pursue at the Wissenschaftskolleg; we impose no thematic presettings whatsoever.

You must have obtained your doctorate by the start of your fellowship, and we also require that you have at least one lead-author publication in a peer-reviewed journal. There are no restrictions regarding your discipline of origin in the life sciences, nationality, or age etc. Applications from scientists working at institutions in Berlin cannot be taken into consideration. If you have been a principal investigator for longer than five years, though, you are advised to apply for a regular fellowship at the Wissenschaftskolleg.

Dr. Ulrike Pannasch Wissenschaftliche Koordinatorin Academic Coordinator College for Life Sciences ulrike.pannasch@wiko-berlin.de

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Dr. Ulrike Pannasch Wissenschaftliche Koordinatorin/Academic Coordinator College for Life Sciences Wissenschaftskolleg zu Berlin / Institute for Advanced Study Wallotstr. 19, 14193 Berlin Tel. +49 - 30 - 89 001 - 255http://www.wiko-berlin.de/institution/college-for-life-sciences/ Ulrike Pannasch <paul@wiko-berlin.de>

WorkshopsCourses

Berlin GenomeAssemblyAndAnnotation Feb12-16 LastCall

Dear all, we have the last 5 spots left for the course "Assembly and Annotation of genomes" [https://www.physalia-courses.org/courses-workshops/course20/]

12-16 February 2018, Berlin (Germany)

Application deadline is: January 12th, 2018.

Instructor:

Dr. Thomas D. Otto (University of Glasgow, UK; [https://www.physalia-courses.org/instructors/t28/)]

Assistant instructors: Dr. Marcela Uliano da Silva (Begendiv, Germany; [http://bit.ly/2o3ImRb])

Mr. Maximilian Driller (Begendiv, Germany; [http://bit.ly/2zcwmQT])

Overview This course will introduce biologists and bioinformaticians to the concepts of de novo assembly and annotation. Different technologies, from Illumina, PacBio, Oxford Nanopoor and maybe 10X will be used mixed with different approaches like correction, HiC scaffolding to generate good draft assemblies. Particular attention will be given to the quality control of the assemblies and to the understanding how errors occur. Further, annotation tools using RNA-Seq data will be introduced. An outlook of potential analysis is given. In the end of the course the students should be able to understand what is needed to generate a good annotated genome.

Targeted Audience & Assumed Background The course is aimed at researchers interested in learning more about genome assembly and annotation. It will include information useful for both the beginner and the more advanced user. We will start by introducing general concepts and then continue to step-by-step describe all major components of a genome assembly and annotation workflow, from raw data all the way to a final assembled and annotated genome. There will be a mix of lectures and hands-on practical exercises using command line Linux. Attendees should have a background in biology. We will dedicate one session to some basic and advanced Linux concepts. Attendees should have also some familiarity with genomic data such as that arising from NGS sequencers.

Session content

Monday 12th 'V Classes from 09:30 to 17:30 - "get it starting" Session 1: Introduction (morning) In this session I will kick off with an introduction lecture about genome assembly and annotation - the past, the present and the future. I will use this introduction to motivate the five-day course. Next, I will explain the use of the virtual machine (VM), and the use of cloud computing. This is followed by short introduction to Linux. Through the morning we will kick off our first assembly and put it through an annotation tool (Companion).

Session 2: Visualization (half afternoon) During this afternoon, we are going to visualize the assembled and annotation genome from this morning in Artemis. The aim is to use the viewer to inspect the annotation, correct annotation and write out files. Next, we are going to perform a comparative exercise, (comparing the genome from the morning with a close reference) to understand the concept of syntheny, breakpoint or errors.

Session 3: Mapping In this module, I will teach the basics of read mapping. We will map reads with bwa mem onto a reference and will examine duplications and errors through not proper mapped read pairs. This is important to exanimate the correctness of assemblies and will be used later the week.

Tuesday 13th 'V Classes from 09:30 to 17:30 - "learn it the old way" Session 4: De Brujin graph and PAGIT This module is dedicated to short read assembly. Although it might be superseded due to long reads, understanding the concept of short reads and De Brujin graph is crucial. After a seminar about this subject, we will assemble the same genome as before, but this time with Illumina: de novo assembly with velvet, contig ordering, error correction. Through comparative genomics we are going to look at errors in the assembly, and how they could be found with remapping short reads, and also split long reads. Last, we are going to compare the assembly to the assembly from Monday. This session will go into the afternoon of Tuesday.

Session 5: RNA-Seq In this session, we will analysis the transcriptome of the sample we assembled so far, motivated through a little talk. In the exercise, we will map RNA-Seq reads, (short and long reads) understanding first the basics of RNA-Seq, but then will use the reads to correct gene models. We will discuss the concept of alternative splicing. Finally, we will annotate our assembly with Augustus, using the mapped RNA-Seq data and some manually corrected genes.

Wednesday 14th 'V Classes from 09:30 to 17:30 - "do it yourself'Â Session 6: Large genome assembly First we are going to kick off an assembly of a larger genome, and let it run in the cloud over the day and the night. It will be important during the day to check if the assembly is still running.

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Berlin MetabarcodingMicrobialCommunities Apr16-20

Dear all,

registration is now open for the course "Metabarcoding of microbial communities"

16th-20th April 2018, Berlin (Germany)

Instructors:

Dr. Martin Hartmann (Senior Researcher at the Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Switzerland)

Dr. Livio Antonielli (Computational biologist and bioinformatician at the Health & Environment Department, Bioresources. AIT -Austrian Institute of Technology, Austria)

Overview

This course will provide a thorough introduction to the application of metabarcoding techniques in microbial ecology. The topics covered by the course range from bioinformatic processing of next-generation sequencing data to the most important approaches in multivariate statistics. Using a combination of theoretical lectures and hands-on exercises, the participants will learn the most important computational steps of a metabarcoding study from the processing of raw sequencing reads down to the final statistical evaluations. After completing the course, the participants should be able to understand the potential and limitations of metabarcoding techniques as well as to process their own datasets to answer the questions under investigation.

Format This course is designed for researchers and students with strong interests in applying novel high-throughput DNA sequencing technologies to answer questions in the area of community ecology and biodiversity. The course will mainly focus on the analysis of phylogenetic markers to study bacterial, archaeal and fungal assemblages in the environment, but the theoretical concepts and computational procedures can be equally applied to any taxonomic group or gene of interest.

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.

Learning Outcomes

1) Understanding the concept, potential and limitation of microbial metabarcoding techniques.

2) Learning how to process raw sequencing reads to obtain meaningful information.

3) Obtaining experience on how to statistically evaluate and visualize your data.

4) Being able to make informed decisions on best practices for your own data.

Session content

Monday from 09:30 to 17:30

Lecture 1 - Introduction to NGS in microbial ecology

- Key concepts (metabarcoding, metagenomics, single-cell sequencing) - Sequencing platforms (core concepts, read length, read numbers, error rates) - In-depth example of sequencing on Illumina (over-and under- loading, sequencing process) - Genetic markers for metabarcoding (markers, primer selection & evaluation) - Experimental design (library preparation, replication, multiplexing, covreage, costs) - Understanding data formats (FASTQ, FASTA, others) - Core concept of computational pipeline for amplicons - Core concepts of popular software tools (MOTHUR, QIIME, USEARCH)

Lab 1 - Introduction to compute lab

- Introduction to command line (e.g. basic UNIX commands, batch processing) - Check functionality of computational environment with demo data - Checking basic characteristics of datasets (number of reads, read length, read quality)

Tuesday from 09:30 to 17:30

Lecture 2 - Quality control of NGS reads

- Pre-PCR noise (under-sampling, DNA extraction bias, sample storage, contamination) - PCR-dependent noise (single nucleotide misincorporations, PCR chimeras, primer dimers, unspecific amplification, preferential amplification, template concentrations) - Sequencing-dependent noise (filtering/trimming poor base calls, dealing with substitution, insertion/deletion errors, index cross- talk, amplicon carry-over)

Lecture 3 - Binning into operational taxonomic units (OTUs)

- Core concept of OTUs and phylotypes - OTU binning strategies (de-novo vs. reference-based, impact of alignment strategies, hierarchical clustering algorithms, seed- based clustering algorithms, model-based clustering algorithms) - OTUs versus ESVs (exact sequence variants)

Lab 2 - Sequence quality control and clustering into operational taxonomic units - Denoising, OTU binning, and ESV calling (e.g. paired-end merging, sequence filtering, dereplication, OTU clustering, chimera removal, target verification) Tools: USEARCH, VSEARCH, DADA2 - Target verification and extraction of hypervariable regions Tools: Metaxa2, ITSx, V-Xtractor

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Berlin MolecularPhylogeniesInBiodiversity Apr9-13

Molecular phylogenies in biodiversity

https://www.physalia-courses.org/courses-workshops/course28/ Dates

9-13 April 2018

WHERE

Botanisches Museum, Königin-Luise-Straße 6-8, Berlin

Instructor:

Dr. Diego Fontaneto (CNR, ITA): https://scholar.google.de/citations?user=WO97K4QAAAAJ&hl=en OVERVIEW

This course will introduce ecologists interested in biodiversity to the use of molecular phylogenies to address questions that cannot be addressed by using only ecological data in their studies. After a short introduction on how to obtain reliable molecular phylogenies, the focus of the questions that could be addressed will be on taxonomy, community ecology, and comparative methods.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at early-career researchers (PhD students, early postdocs) in ecology interested in widening their analytical toolbox. The course is structured in a way that even an inexperienced and naïve attendee could take advantage of the possibilities offered by the inclusion of molecular phylogenies in its analyses. There will be a mix of lectures and hands-on practical exercises using freely available software and online resources.

Most of the steps will be performed in R, but no previous knowledge on this statistical platform is required. All scripts will be carefully explained to allow all attendees understanding the rationale and usage of the statistical approaches.

LEARNING OUTCOMES

- Understand how to read, interpret and obtain molecular phylogenies, with a focus on the concepts and rationale behind phylogenetic methods

- Learn tools from DNA taxonomy

- Learn how to include phylogenies in the analyses of community ecology and in comparative analyses

- Hand-on experience on all the steps

- Being comfortable with using R when including molecular phylogenies in ecological analyses

SESSION CONTENT

Monday - Classes from 09:30 to 17:30 - “Molecular phylogenies”

Session 1: Introduction (morning)

In this session I will kick off with an introduction lecture about the rationale of including molecular phylogenies in ecological studies. I will use this introduction to motivate the five-day course. Next, I will explain some theory on molecular phylogenies and which kind of data is needed to obtain phylogenetic reconstructions. Through the morning we will start obtaining our first phylogenies to be used in the following days.

Session 2: Molecular phylogenies (afternoon)

During the afternoon, we are going through some of the available and easy methods to obtain phylogenies with distance-based, maximum likelihood, and Bayesian methods. The aim is to understand the use, potentials, and limitations of molecular phylogenies, and to be comfortable with them.

Tuesday - Classes from 09:30 to 17:30 - “DNA taxonomy”

Session 3: Molecular phylogenies continues (morning)

We will finish some of the analyses that we started the previous day.

Session 4: DNA taxonomy (afternoon)

This module will introduce the rationale of using DNA sequence data and molecular phylogenies to delimit species. We will cover in detail DNA barcoding, Automatic Barcode Gap Discovery, K/theta, Poisson Tree Process, Generalised Mixed Yule-Coalescent model, haplowebs, and then move to more sophisticated multi-locus methods. The module will be a mix of theory and hands-on practical exercises for each approach.

Wednesday - Classes from 09:30 to 17:30 - “Phylogenetic comparative methods”

Session 5: Phylogenetic structure in comparative data (morning)

We are going to show how statistical analyses comparing traits between species can provide spurious results if the confounding factor of phylogenetic non-independence of the data is not included in the analyses. After going through the methods that are currently used to look for a phylogenetic signal in the data, we will move to statistical approaches that include such phylogenetic structure in the statistical analyses (e.g. Phylogenetic Independent Contrasts and Phylogenetic Generalised Least Squares).

Session 6: Phylogenetic structure of communities (afternoon)

This module will explore the possibilities that are available to understand if there is a phylogenetic structure in community datasets, and which consequences it could have in the interpretation of the results of analyses in community ecology.

Thursday - Classes from 09:30 to 17:30 - “Apply your knowledge to real world”

Session 7: Group Tasks (morning)

Students will work in groups on a specific question they choose to analyse. Then, they will explain to all the others what analysis they would do, which data is required, and why. Then, they will perform the analyses.

Session 8: Group Tasks continues (afternoon)

For the rest of the day, groups are going to finish the analyses, and

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Berlin Paleogenomics May7-11

Paleogenomics

https://www.physalia-courses.org/courses-workshops/course27/ Dates

7-11 May 2018

WHERE

Botanisches Museum, Königin-Luise-Straße 6-8, Berlin (Germany)

Instructors:

Dr. Claudio Ottoni (University of Oslo, Norway)

Dr. Dr. Amine Namouchi (University of Oslo, Norway)

Overview

This course will introduce biologists to the main bioinformatic tools for the analysis of Next Generation Sequencing (NGS) data from ancient samples. Through a series of theoretical and practical hands-on sessions, the main goal of this course is to provide a clear understanding of the most common bioinformatic methods adopted in a wide range of paleogenomics projects (from metagenomic screening of ancient samples, to NGS reads mapping and phylogenetic tree reconstruction). Particular attention will be given to quality control, DNA damage assessment and variants calling. A basic introduction to NGS platforms and the main file formats used in most common bioinformatics pipelines will be provided. Each day will consist of a mix of introductory lectures on the theoretical background of the programs that will be used, followed by hands-on exercises using command line tools performed by the participants under guided supervision.

Target Audience & ASSUMED BACKGROUND

The course is aimed primarily at researchers (MSc and PhD students, postdoctoral fellows, engineers) interested in learning the different steps from NGS raw data analysis to phylogenetic tree reconstruction in archaeological samples. The hands-on sessions are targeted to beginners and more advanced users alike. The practical sessions will cover the most common pipelines adopted in paleogenomics, and can be applied to a wide range of projects, from metagenomics to genome resequencing. Attendees should have a background in biology and some familiarity with genomic data.

STRUCTURE

The course material will be delivered over 5 days, in 10 half-day sessions. These lessons will build off of one another, and feature a mix of lecture and in-class exercises.

For more information about the course, please visit our website: https://www.physalia-courses.org/courses-workshops/course27/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/-courses-workshops/ Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR Email: info@physalia-courses.org

Web: http://www.physalia-courses.org/- http://www.physalia-courses.org/ Twitter: @physacourses Tel: +49 15771084054 https://-groups.google.com/forum/#!forum/physalia-courses Carlo Pecoraro <info@physalia-courses.org>

Edinburgh PrecisionMedicineBioinformatics Jul16-20

"Precision Medicine Bioinformatics: From raw genome and transcriptome data to clinical interpretation (PMBI01)"

https://www.prinformatics.com/course/precision-medicine-bioinformatics-from-raw-genome-and-transcriptome-data-to-clinical-interpretation-pmbi01/ Instructors, Dr. Malachi Griffith and Dr. Obi Griffith from Washington University.

This course will run from 16th - 20th July 2018 in Edinburgh

Course Overview: Precision medicine refers to the use of prevention and treatment strategies that are tailored to the unique features of each individual and their disease. Analysis of high throughput genome and transcriptome data is major component of new large-scale precision medicine efforts. This analysis involves the identification of specific genome or transcriptome features that predispose an individual to disease, predict response to specific therapy, or influence diagnosis and prognosis. During this course (PMBI01), students will perform an end-to-end precision medicine analysis of real human genome (WGS and Exome) and transcriptome (RNA-seq) data. Students will start with raw sequence data for a hypothetical patient, learn to use the tools needed to analyze this data on the cloud, and interpret results in a clinical context. The goal of the analysis will be to identify personalized therapeutic options for this patient as well as identifying any prognostic or diagnostic implications in the data. After completing the course, students should be in a position to (1) understand raw sequence data formats, (2) perform bioinformatics analyses on the cloud, (3) run complete analysis pipelines for alignment, variant calling, annotation, and RNA-seq, (4) visualize and interpret whole genome, exome and RNA-seq results, (5) leverage the identification of passenger variants for immunotherapy (e.g. personalized cancer vaccines) and disease monitoring applications, and (6) begin to place these results in a clinical context by use of variant knowledgebases. The data, tools, and analysis will be most directly relevant to human cancer genomics and bioinformatics. However, many of the skills and concepts covered will be applicable to other human diseases and even those studying non-human organisms. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically to participants.

Intended Audience This workshop is primarily aimed at researchers and technical workers with a background in biology who want to learn fundamental bioinformatics skills for genomics with a particular emphasis on medical research applications. The course is essentially a crash course in bioinformatics for next generation sequence data analysis. It would also be useful for students with a computational background who seek an introduction to genomics technology and analysis approaches. In general, it is suitable for anyone working with genome or transcriptome data in the context of disease research. Attendees are encouraged to bring their own data or project outlines for discussion. Some time during the course will be dedicated to consultation with a team of instructors from the McDonnell Genome Institute.

Full course schedule at https://www.prinformatics.com/course/precision-medicine-bioinformatics-from-raw-genome-and-transcriptome-data-to-clinical-interpretation-pmbi01/ Email oliverhooker@prinformatics.com with any questions.

Other up-coming courses include

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

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Greifswald MathematicsInEvolution Sep16-Sep22

GreifOlution: Greifswald Summer School for PhD-students, PostDocs and advanced graduate students from 16/09/2018 to 22/09/2018 in Greifswald, Germany

As part of the "Year of Mathematical Biology" we proudly announce GreifOlution, the 1st Greifswald Summer School on Mathematics of Evolution (kindly funded by the DAAD, the German Academic Exchange Service).

The main focus of this summer school will be on mathematical models and methods for reconstructing phylogenetic trees and networks, but upon request we might also include some sessions on other related topics, e.g. from population genetics.

So if you are a mathematician or computer scientist with a strong interest in biology or a biologist who aspires to a deeper understanding of mathematical or statistical methods and models, this summer school is what you need!

Greifswald University is one of the hotspots of mathematical phylogenetics and biomathematics in Germany - as the only German university which has been offering a biomathematics study program already for 20 years, the small town located directly at the Baltic Sea has attracted lots of renowned researchers over the years!

So why not benefit from the presence of all these experts? Come and spend a week in summer at the beautiful Baltic Sea and deepen your knowledge on mathematical phylogenetics!

This summer school aims at bridging the gap between mathematics and biology and providing both a broad introduction to various fields of biomathematics (e.g. biostatistics, bioinformatics and mathematical phylogenetics) as well as insights into state-of-the-art research.

We invite applications from PhD students, PostDocs and advanced graduate students of Mathematics, Computer Science or Biology (and related areas of study) who have a great interest in Biomathematics, in particular in Mathematical Phylogenetics.

The school is free of charge. There are also no costs for the social dinner, the excursions and lunch during the summer school, but participants must cover their own accomodation and travel expenses. Foreign participants, however, may be eligible for funding (see the below for the DAAD reglementation concerning foreign participants).

For more details, please visit https://math-inf.uni-greifswald.de/institut/ueber-uns/mitarbeitende/fischer/greifolution/ or contact us at greifolution@uni-greifswald.de

We would be pleased to welcome you in Greifswald in September 2018!

Kind regards, Mareike Fischer

Prof. Dr. Mareike Fischer

Biomathematics and Stochastics

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Mareike Fischer <email@mareikefischer.de>

HaGoshrim Israel SocialInsectEvolution Jul15-20

Save the date!

German-Israeli Minerva School 2018: New Frontiers in Sociobiology and Sociogenomics July 15-20, 2018 HaGoshrim, Israel

A workshop on the frontiers of social insect research in the 21st century, especially the application of omics (genomics, transcriptomics, proteomics) ≫ Phylogenomics and comparative genomics in the study of evolution of novelty ≫ Transcriptomics and regulatory networks in the study of SocioEvoDevo and indirect genetic effects ≫ Socio-physiology: hormones and neurons as links between genes and social behavior ≫ Emerging molecular technologies: CRISPR-Cas, epigenetics, miRNAs, microbiomes

Lectures will be accompanied with hands-on tutorials on the omics data analysis and a field trip. The School is primarily targeted at graduate students and postdocs. Travel and full board accommodations will be covered by Minerva for 20 students. German and Israeli students will be invited to apply in January. More details to come on the School website: https://sites.google.com/view/minerva2018 Organizers: Jürgen Gadau, Judith Korb, Eyal Privman, Guy Bloch Additional speakers to be announced

Eyal Privman <eprivman@univ.haifa.ac.il>

MountainLakeBiologicalStation SummerField May21-Aug3

2018 MLBS Summer Programs

Announcing 2018 Summer Programs Field-based courses are UVA Summer Session classes offered by nationally-recruited faculty, and offered at the undergraduate and graduate level. Our NSF REU undergraduate research internship program is now in its 26th year.

Field Courses

Field Biology of Fishes Summer Session I: May 21-June 15 Field Herpetology Summer Session I: May 28-June 15 Wildlife Disease Ecology Summer Session II: June 18-July 6 Stream Ecology Summer Session III: July 16-August 3

Financial aid is available. MLBS courses are field-intensive, research-based experiences. Courses earn 3 UVA Biology credits. Non-college students are welcome to enroll.

Learn More and Apply <

https://mlbs.us14.list-manage.com/track/click?udd2397558126f5ceb0c7824&idâc8be2f01&eKa1f3f3e0 >

Research Experiences for Undergraduates (NSF-REU)

Become a National Science Foundation REU. Join undergraduates from around the country for a unique 10-week learning and living research experience in the southern Appalachians. Students conduct independent research in field ecology, evolution, behavior, and physiology under the supervision of resident scientists. REUs are internships that include all station costs, travel, and a $5,500 stipend.

Program dates: May 28 - August 3 Application deadline: February 20

Learn More and Apply <

https://mlbs.us14.list-manage.com/track/click?udd2397558126f5ceb0c7824&idá4726d03e&eKa1f3f3e0 >

mlbs.org < https://mlbs.us14.list-manage.com/track/-click?udd2397558126f5ceb0c7824&idH47465450&eKa1f3f3e0 >

Printable copies of our materials are available here < https://mlbs.us14.list-manage.com/track/-click?udd2397558126f5ceb0c7824&id339a39b3&eKa1f3f3e0 >.

Our mailing address is: Mountain Lake Biological Station University of Virginia PO Box 400327 Charlottesville, VA 22904

"Nagy, Eric S. (esn8n)" <esn8n@virginia.edu>

Online LandscapeGenetics Jan17-May9

Online Landscape Genetics Graduate Student Course Available Jan 17 'V May 9, 2018, Wed 8:30 'V 10:30 PST (also can be taken at any time using taped lectures)

Cost $500 individuals, $1000 Groups

Course Organizers: Helene Wagner, Melanie Murphy, and Lisette Waits Co-Instructors: Niko Balkenhol, Jeff Bowman, Sam Cushman, Marie-Josee Fortin, Caren Goldberg, Nusha Keyghobadi, Erin Landguth, Stephanie Manel, Sean Schoville, Kim Selkoe, Steve Spear, and others

Course description This course on Landscape Genetics provides a unique opportunity for interdisciplinary training and provides an overview of the field of landscape genetics. The course caters to students in basic and applied ecology, conservation and population genetics, landscape ecology, evolutionary biology and conservation biology. A key objective of landscape genetics is to study how landscape modification and habitat fragmentation affect organism dispersal and gene flow across the landscape. Landscape genetics requires highly interdisciplinary specialized skills making intensive use of technical population genetic skills and spatial analysis tools (spatial statistics, GIS tools and remote sensing).

Landscape Genetics will be concurrently offered at multiple universities across the globe, giving students the opportunity to learn from international experts and work with peers from outside institutions. For students who are not members of the participating institutions, we are offering a web-based online course to reach a broader audience. Each course meeting will start with a live web-cast lecture (no special software required) by an expert on the topic that introduces foundations and methods and highlights points for discussion in local seminar groups.

After breaking out into local course group discussion (including a discussion group for online course students), a web-based discussion across campuses will wrap up the weekly topic. Students who are unable to make it to live- cast of lectures can view taped lectures. In addition, students can choose to participate in an optional lab section using R and/or interdisciplinary group term projects with web-based collaboration across institutions. The final two options are provided to help students develop analytical skills in Landscape Genetics. Students who participate in group projects will have the option of applying to attend a project synthesis meeting in Coeur d'ÂAlene, Idaho in May 2018.

Course website: https://sites.google.com/site/-dgs2018landscapegenetics/ How to register? Please register here by Dec 30th: https://goo.gl/forms/-iEMKsRSbkp8KN25l1. A link to the registration form can also be found on the course website.

Faculty who would like to add a local section of the course at their university can register as a group or multiple students at one institution can register as a group to decrease cost/student.

Lisette Waits, PhD Distinguished Professor Department Head Fish and Wildlife Sciences University of Idaho Moscow, ID 83844-1136 (208) 885-7823

lwaits@uidaho.edu

Panama Taxonomy when

http://www.stri.si.edu/sites/-taxonomy_training/future_courses/2018/-2018_Taxonomy_Biology_Nemerteans.html The course is aimed at graduate students, post-docs, or professionals who are interested in learning and applying knowledge about the biology, diversity and systematics of a fascinating and ecologically important but understudied phylum of marine invertebrates - the nemerteans (ribbon worms). The students participating in this course will:

* Learn how to collect nemerteans associated with shallow coral reefs, mangrove fouling communities, and macroalgae of the Bocas del Toro region * Learn general

biological characteristics of the group, major taxonomic subdivisions, and characters used for species identification and description * Learn to collect and identify planktonic larvae of nemerteans * Learn to preserve larval and adult nemerteans for subsequent morphological and molecular studies

Nemerteans are ubiquitous in marine communities worldwide; they are common and diverse, with ~1300 described species, ranging in length from a few millimeters to several meters (one species is officially the longest animal on Earth). Most are free-living predators, that attack and subdue their prey using an eversible proboscis and an impressive array of toxins. Some are parasites or egg predators of other marine invertebrates, including many commercially fished species of crustaceans. Nemertean larvae are very diverse and are commonly present in the plankton. Yet these beautiful and fascinating worms remain largely ignored even by invertebrate zoologists, in part because of their cryptic habits (many are nocturnal, and, in general, they are hard to find unless you know how to look), presence of numerous cryptic species (morphologically indistinguishable, but genetically distinct), and also because of the inherent difficulties associated with preservation and identification of soft-bodied organisms. The nemertean fauna of Bocas del Toro, Panama is very poorly known. Some 16 species are reported in the published literature (with many undescribed species), but recent sampling and DNA-barcoding suggests that the actual diversity is at least five times that number. This likely reflects the amount of undescribed diversity for this phylum worldwide.

This course will engage students in the real work of collecting, identifying and describing nemerteans. The course will last 10 days, with the first five days dedicated to collecting and learning about nemertean biology and the techniques to identify, preserve and characterize nemertean species (both in their larval and adult forms). Our time will be divided between field trips, lectures and laboratory exercises. Second half of the course will be dedicated to individual research projects (e.g. producing formal descriptions of local undescribed species, studying the embryonic and larval development, feeding habits or other aspects of biology, according to student interests). The course will conclude with student presentations of their research projects. For more information on nemerteans see: https://-bocasarts.weebly.com/nemertean-tools.html 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/ “megansc@uw.edu” <megansc@uw.edu>

Portugal EvolutionaryBiol Feb5-9

Subject: Portugal-cE3c-Course: four advanced courses with deadlines January 2018 cE3c 'V Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the two courses with closer deadlines. Additional informations at: http://-ce3c.ciencias.ulisboa.pt/training/?cat ——

Course Practical Course on Phylogenetics

organized by Octavio Paulo| February 5-9 2018 @ Lisbon, Portugal

Objectives: Phylogenetics is one of the scientific areas of Biology that has grown fast and evolved in methodological terms in the last years. Its applications go from the studies of the evolution of species and populations to the least expected, as the study of the origin of the AIDS virus or seasonal cycles of the flu. The course is aimed at students and professionals that intend to get started in phylogenetic analysis as well as researchers already with some experience wanting to deepen or update their knowledge in the field. The course consists of theoretical classes as well as hands-on practical sessions using software. Participants are encouraged to bring their own sequence data for analysis.

Course instructor

Octavio Paulo (octavio.paulo@fc.ul.pt)

Professor at the Faculty of Sciences of the University of Lisbon, researcher at the Centre for Ecology, Evolution and Environmental Changes (http://-ce3c.ciencias.ulisboa.pt/member/octaacutevio-s-paulo), Coordinator of the Computational Biology & Population Genomics Group (http://ce3c.ciencias.ulisboa.pt/-team/COBIG2)

Intended audience: This five days intensive course will be open to a maximum number of 20 participants, being directed to PhD or MSc students in Biology, Evolution, Genetics or related areas, and postdocs and other professionals working in related topics.

Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below)

Deadline for applications: January 12^th, 2018

Candidates should send a short CV and motivation letter to Octavio Paulo (octavio.paulo@fc.ul.pt)

For additional details about the course and to know how to register, click here:

http://ce3c.ciencias.ulisboa.pt/training/?cat For more information about the course, please contact:

octavio.paulo@fc.ul.pt

Course Biodiversity and Plant Evolution

organized by Helena Cotrim and Manuela Sim-Sim | February 5-9, 2018 @ Lisbon, Portugal Objectives: On completion of the course, the students shall have acquired the following knowledge and understanding:

- Describe the main evolutionary acquisitions on groups of the plant kingdom and its adaptive significance.

- Comprehend the modern plant phylogeny and its sources of information.

- Explain the underlying evolutionary mechanisms of diversity and speciation in the plant kingdom.

- Describe the variety of pollination syndromes, reproductive systems and population structures present in the plant kingdom, and explain the mechanisms underlying this diversity.

- Explain and critically analyse how the genetic diversity and evolutionary potential of plant populations are influenced by phenomena like phenotypic plasticity, seed banks, hybridization, polyploidy and postglacial colonization history.

- Formulate hypotheses and propose methods when studying evolutionary phenomena in wild plant species.

Course instructors

Helena Cotrim (hmcotrim@fc.ul.pt)

Assistant Professor at the Faculty of Sciences of the University of Lisbon, researcher at the Centre for Ecology, Evolution and Environmental Changes (http://ce3c.ciencias.ulisboa.pt/member/helenacotrim)

And

Maria Manuela Sim-Sim (msimsim@fc.ul.pt)

Assistant Professor at the Faculty of Sciences of the University of Lisbon, coordinator of the NHS research group at the Centre for Ecology, Evolution and Environmental Changes (http://ce3c.ciencias.ulisboa.pt/member/maria-manuela-pinheiro-sim-sim)

Intended audience: This five days intensive course will be open to a maximum number of 10 participants, being directed to PhD or MSc students in Biology, Evolution, Ecology or related areas, and postdocs and other professionals working in related topics.

Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and

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Poznan RNAseqAnalysis Feb8-11

Course: RNA-seq Data Analysis 8 - 11 February 2018, Poznan, Poland This is a crush course on a complete, standard RNA-Seq data analysis.

It includes quality control and filtering, read mapping, ab initio and de novo transcriptome assembly, estimation of gene expression values, differential expression analysis, small RNA identification and even more. We provide ready-to-use solutions and pipelines so that each participant should be able to perform similar tasks himself.

Target: This is an introductory course for anyone whose aim is to learn how to deal with large-scale RNA-Seq data and to obtain biologically relevant insights. It is tailored for those who work in the fields of biotechnology, molecular biology, bioinformatics, or any other biological sciences, yet anyone can participate. Prior knowledge of NGS data analysis is not essential, however it is advised that the participants know basics of molecular biology, such as what is splicing, splicing isoform, transcriptome, gene expression etc. Also, no programming skills are required.

Expected effects: Upon completion of the workshop, the participants should know about RNA-Seq data sources, their formats, and be able to perform data quality control, read mapping to reference sequences, estimate gene/transcript expression values, and perform differential expression analysis, including interpretation of obtained results. The participants will also learn about transcriptome assembly methods and small RNA analysis and should be able to apply analytical pipelines in their own projects.

Also, much emphasis will be put on data visualization, plotting, interpretation, and troubleshooting.

Requirement: No programming skills are required. Also, prior knowledge of NGS data analysis is not essential, however it's advised that the participants know basics of molecular biology, such as what is splicing, splicing isoform, transcriptome, gene expression etc.

Program overview: PART 1: Linux for bioinformatics (1 day) This module introduces a Linux operating system, a powerful - yet often discouraging - environment for bioinformatics applications, such as NGS data processing. We will learn about commands that help working on huge datasets, including search and browsing of NGS-related data. We will learn basics of scripting and exercise various commands that enable automatization and control of data flow during a bioinformatics application. After a single day you should feel quite comfortable using this operating system and be well prepared for the following bioinformatics applications.

PART 2: Introduction to NGS data analysis (1 day) This is an introductory course to NGS data processing: starting with raw sequencing results in a FASTQ format, through different methods for data quality check, filtering, adapter trimming and read mapping to finally assemble a transcriptome. In a single day, you will learn a complete, functional pipeline for NGS application. Additionally, NGS-related formats, databases and knowledge bases will be discussed.

PART 3: A practical guide to RNA-seq data analysis (2 days) Alternative approaches for RNA-Seq data processing will be discussed and excercised, including estimation of gene and transcript expression levels, and differential expression analysis - all this using two or three alternative approaches. Ab initio (with mapping to genome) and de novo (genome-independent) transcriptome assembly will be performed, followed by basic annotation of the results. Essential diagnostic plots and quality checks will be done. Also, smallRNA-Seq data analysis will be introduced, including identification of microRNAs and short read annotation.

About us: We have been on the market since July 2013 and since then we have organized dozens of bioinformatics workshops with almost one thousand of participants altogether. We have completed a number of NGS projects for our customers, which included model and non-model organisms, from bacteria to human. We are a part of consortium aiming at development of personalized medicine services for diagnosis and therapy of lung cancer.

We are also conducting academic research in the area of genomics and transcriptomics, which provides us with expertise on standard and up-to-date bioinformatics solutions.

Speakers: - Izabela MakaÃÂ^{1}â euro Âowska (Professor, CEO at ideas4Biology Ltd., Head of the Department of Integrative Genomics, Faculty of Biology, Adam Mickiewicz University in Poznan) - MichaÃÂ^{1}â euro Â SzczeÃÂ^{1}â euro Âo̲niak (PhD, Deputy CEO at ideas4biology Ltd., University Adjunct at the Department of Integrative Genomics, Faculty of Biology, Adam Mickiewicz University in Poznan) - Joanna Ciomborowska-Basheer (PhD, Deputy CEO at ideas4biology Ltd., University Adjunct at the Department of Integrative Genomics, Faculty of Biology, Adam Mickiewicz University in Poznan) - Maciej Osowiecki (BSc, Junior Data Scientist at ideas4biology Ltd.)

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Sweden InterplayParentalCareSexualSelection Feb26-Mar03

WORKSHOP INVITATION

INTERPLAY BETWEEN PARENTAL CARE AND SEXUAL SELECTION

Dear Colleagues,

We are glad to invite you to our Workshop that will take place between 26th February and 3rd March 2018 in Fiskebäckskil, Sweden.

The main goal of this workshop is to provide a relaxed atmosphere where researchers interested in different aspects of the interplay between parental care and sexual selection will exchange ideas, discuss the recent developments in the field, and propose in details future directions. We embrace diversity as a way to enrich scientific discussions and we will prioritize attendees with diverse backgrounds, at different career stages, and that use different organisms and methodological approaches to address their questions. Besides, the workshop will provide the perfect forum for researchers (especially young scientists) to network with other specialists in the field.

The event will start with a reception on Monday 26th February, will include 3 full days of talks from invited speakers and attendees, 1 night of poster exhibition, and a last full day of general discussion of relevant sub-themes in the field, conducted in small groups self-organized by the participants. We ask participants to present results or ideas from on-going research instead of already published papers, given that the main focus of the workshop is the discussion of fresh perspectives and initiatives.

Confirmed invited speakers include:

Professor Suzanne H. Alonzo

University of California - Santa Cruz, USA

Dr Lutz Fromhage

University of Jyväskylä, Finland

Professor Wolfgang Goymann

Max Planck Institute for Ornithology, Germany

Dr. Irja Ida Ratikainen

Norwegian University of Science and Technology, Norway

Professor Nick Royle

University of Exeter, UK

There are no registration fees. Accommodation and meals for 40 participants will be covered by the financial support of the Gothenburg Centre for Advanced Studies in Science & Technology *(GoCAS)* and the Royal Swedish Academy of Sciences (*KVA).* Participants will only be charged for the costs of their social events and the transportation to the event venue.

For more details, access: https://-parentalcaresexualselection.wordpress.com/ *Application deadline: Monday, 08th January 2018.*

We look forward to hearing from you.

Best regards,

Gustavo S. Requena

Postdoctoral Fellow

Universidade de São 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>

USheffield UK PopulationGenomics Jan29-31

POPULATION GENOMICS WORKSHOP

January 29th-31st 2018 University of Sheffield, UK

This course will be held at the NERC Biomolecular Analysis Facility at the University of Sheffield and introduce participants to a variety of population genomics analyses for large next generation sequencing (NGS) datasets. It will include discussion on single nucleotide polymorphism (SNP) calling and filtering options, an introduction to population genomics statistics using the PopGenome R package, examining genetic structure, Fst-based analyses such as outlier detection/genomic islands of divergence, and genome-wide association analysis (GWAS).

The majority of the course will comprise practical computer sessions, giving participants hands-on experience in these analyses. We will perform these on the high performance computing cluster at Sheffield and computers will be provided. Prior experience with the Linux environment and basic command line tools would be advantageous.

There is no charge for the course, and successful applicants will be provided with accommodation for two nights and up to 100 towards travel costs to Sheffield.

The application closing deadline is at 5pm on Monday 18th December.

Further details and how to apply can be found at: https://www.sheffield.ac.uk/nbaf-s/courses/popgen Helen Hipperson <helenhipperson@gmail.com>

WhiteSea EvolutionMarineInvertebrates Jul25-Aug19

What: Summer course "Evolutionary and Taxonomic Diversity of Marine Invertebrates"

Where: St Petersburg and White Sea, Russia

When: 25 July - 19 August 2018

Background

Expertise in biodiversity, a core of biological sciences, is becoming sparse. The demand for such expertise, however, is widely recognized, as many fields of biology rely on sound understanding of biodiversity. Department of Invertebrate Zoology (St Petersburg State University, Russia) has been maintaining traditions of zoological studies and, while adopting the innovations, has also preserved this expertise in biodiversity. Now we offer to learn with us.

Objective

The main objective of this course is to demonstrate evolutionary and taxonomic aspects of marine invertebrate biodiversity and the impact of ecological factors on adaptive radiation within different phyla. The students will get familiar with the current phylogeny of Metazoa, with main phyla of marine invertebrates and traits of their evolution. The course has a special emphasis on the invertebrate diversity in major types of marine communities. Lectures provide the general framework, while extensive field and lab activities will enable students to follow the patterns of invertebrate life strategies. This approach gives experience of implying general zoology to ecosystem studies.

Target audience

MSc and PhD biology students who, for their current research projects or future career plans, need to understand marine invertebrate biodiversity from the evolutionary perspecive

Registration

Registration deadline is February 15, 2018. For the detailed program, learning outcomes, and registration form, please visit our web page: http://zoology.bio.spbu.ru/Education/Biodiversity/r_biodiv.php Please contact Anna Gonchar if you have questions: a.gonchar@spbu.ru

Anna Gonchar, Department of Invertebrate Zoology Faculty of Biology St Petersburg State University zoology.bio.spbu.ru

Anya Gonchar <anya.gonchar@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.