EvolDir

January 1, 2012

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 Phylomedicine Mar23-24 TravelGrants 2

http://www.smbe.org/phylomed/ SMBE Satellite Symposium on Phylomedicine March 23-24, 2012 Arizona State University Tempe, Arizona, USA

Applications are invited for multiple Travel Grants

Eligibility: Students, Postdocs, and early career scientists

Support: $500 for US and $1000 for international selectees Apply by E-mail to phylomedicine@asu.edu

Attach PDF/DOC/DOCX files containing:

(1) a short abstract PLUS title.

(2) Your CV, including the name of your mentor (if appropriate)

(3) Filled out Registration form (see http://www.smbe.org/phylomed/registration.php)

Deadline: December 15th, 2011.

Decision: Early January, 2012

Each travel grant awardee will be required to present a poster on March 23, 2012.

s.kumar@asu.edu

Dublin SMBE2010 Jun23-26 EvoDevoSymposium

Dear colleague,

We invite you to submit an abstract to the symposium “Genomic basis of Evo-Devo” to take place at the meeting of the Society for Molecular Biology and Evolution in Dublin (23rd-26th June, 2012).

The deadline to submit an abstract is the 27th of January 2012, for more details please visit:

http://www.smbe2012.org/scientific-content/call-for-abstracts.html Symposium “Genomic basis of Evo-Devo”

Genomics and Evo-Devo have provided many of the most exciting advances in evolutionary biology in recent years. The functional study of animal and plant genomes, in terms of gene regulation and networks, is now linking these two fields. This has the potential to bridge the gap between adaptive and structural approaches to biodiversity, and participate in an extended evolutionary synthesis. Moreover, new genomic tools (e.g., cheap sequencing) mean that increasingly functional studies can be done in classical plant and animal models species in Evolutionary Biology. In this session, we will focus on the study of changes at the genome level, which affect development, and consequently morphology. We invite contributions from scientists working on the genomics of emerging model organisms (sponge, bee, orchid, amphioxus, moss, etc.), and on natural variation in established models of developmental biology (e.g., nematodes, fruit flies, Arabidopsis). Given this broad representation of speakers, we expect a stimulating exchange between students of molecular evolution, organismal evolution, genomics, and evolution of development.

Confirmed speakers: Günter Theissen (University of Jena), Walter Salzburger (University of Basel)

If you have any question regarding this symposium please do not hesitate to contact us:

Mariana Mondragón-Palomino (University of Regensburg, mariana.mondragon@biologie.uni-regensburg.de)
Marc Robinson-Rechavi (University of Lausanne, Marc.Robinson-Rechavi@unil.ch)

Mariana Mondragon <Mariana.Mondragon@biologie.uni-regensburg.de>

Dublin SMBE2010 Jun23-26 OrthologyParalogyFunction

Dear colleague,

We invite you to submit an abstract to the symposium “The complex relationship between orthology, paralogy, and function” to take place at the meeting of the Society for Molecular Biology and Evolution in Dublin (23rd-26th June, 2012).

The deadline to submit an abstract is the 27th of January 2012, for more details please visit:

http://www.smbe2012.org/scientific-content/call-for-abstracts.html Symposium “The complex relationship between orthology, paralogy, and function”

Orthology and paralogy have been central concepts in molecular evolution since the distinction was first proposed by Fitch in 1970. A long standing interpretation of this distinction has been that orthologs would be more similar in function than paralogs. Until recently, this interpretation was rarely tested, and in fact rarely explicitly articulated in a testable manner. Yet it has been widely used, from undergraduate teaching, to the practical application of orthology searches for genome annotation. There has been a recent increase of research, seeking to define and test this “ortholog conjecture”. Notably, a recent paper (Nehrt et al. 2011, PloS Comput. Biol.) has reported a higher functional similarity of paralogs than of orthologs. This paper has generated much attention and debate, while at the same time recent work on orthologs has shown the vitality and importance of this field to a broad range of applications and questions. Our symposium will feature speakers addressing the fundamental relationships between molecular evolution and biological function, focusing especially on the role of orthology and paralogy in modulating such relationships.

Confirmed speakers: Eugene V. Koonin, Jianzhi Zhang

If you have any question regarding this symposium please do not hesitate to contact us:

Toni Gabaldon <toni.gabaldon@crg.eu>, Matthew Hahn <mwh@indiana.edu>, Iddo Friedberg <idoerg@gmail.com>, Marc Robinson-Rechavi <Marc.Robinson-Rechavi@unil.ch>

marc.robinson-rechavi@unil.ch

Dublin SMBE2012 Jun23-26 AnalysisGeneExpression

CALL FOR ABSTRACTS

We would like to invite researchers of transcriptome evolution to submit abstracts to the SMBE symposium described below.

Note that the DEADLINE for abstract submission for SMBE 2012 in Dublin is JANUARY 27 (http://www.smbe2012.org/).

EVOLUTIONARY ANALYSIS OF GENE EXPRESSION

RNA-Seq has revolutionized the field of comparative biology by allowing molecular profiling across organisms, even those without a reference genome sequence, thereby enabling the study of transcriptome evolution within large taxonomic groups. Large-scale comparative expression datasets are now becoming available, motivating the development of models and analytical techniques to investigate the process of expression evolution. The field is now positioned to address fundamental questions passionately discussed within the past decade, such as: - What is the contribution of gene expression changes to phenotypic variation and divergence? - What are the most common mechanisms of gene expression divergence? - How do drift and selection contribute to gene expression divergence across species, tissues, and developmental stages? In this symposium we hope to bring together researchers with a variety of perspectives working on these questions using different models to debate and contrast findings, consider new directions for the field, discuss standardization of methods for sample collection, treatment, data processing, and data sharing.

Confirmed speakers: Henrik Kaessmann, Patricia Wittkopp

Organizers: Rori Rohlfs (rrohlfs@berkeley.edu), Mehmet Somel (somel@berkeley.edu)

Mehmet Somel <somel.mehmet@googlemail.com>

Dublin SMBE2012 Jun23-26 EvolutionaryNetworksSymposium

Dublin.SMBE2012.Jun23-26.EvolutionaryNetworks

Registration for the 2012 Society for Molecular Biology and Evolution

Meeting and Abstract Submission for the Evolutionary Networks: Proteins, Genomes, Organisms Symposium are now open. SMBE 2012 is taking place in Dublin 23-26 June.

Register at the early bird rate now through the SMBE 2012 website (www.SMBE2012.org). DEADLINE FOR SUBMITTING ABSTRACTS IS JANUARY 27th, 2012

Symposium on Evolutionary Networks: Proteins, Genomes, Organisms

Evolutionary biology is studied at various scales from genes to biochemical pathways, cells, organisms, and societies, and aims to identify the processes that generate and maintain the impressive diversity observed at all these levels. The vast amount of biological data generated from high throughput technologies in the last decade revealed that many of those systems are characterized by complex interactions between various entities such as proteins, genomes and organisms. Networks (graphs) offer a general model to the study of structure and evolution of complex systems as they support different levels of abstraction for the description of patterns in the data and enable testing various hypotheses regarding the system behaviour. For example, network approaches revealed that the number of interactions of a protein within the cell, or an organism within the society is correlated with evolutionary observables such as substitution rates or extinction probability. This symposium will include presentations of network approaches in the evolutionary study of proteins, genomes and societies, with an emphasis on the evolution of network topology and community structure.

Contributions from interested speakers are welcome, please apply :)

Organizers: Tal Dagan, Eric Bapteste

Confirmed speakers: Sune Lehmann; Gipsi Lima-Mendez; Miguel A. and Csaba Pal

ebaptest@snv.jussieu.fr

Dublin SMBE2012 Jun23-26 HostVirusEvolution

We invite you to submit an abstract to the "Evolution of host-virus interactions" symposium to take place at the Society for Molecular Biology and Evolution meeting in Dublin on the 23rd-26th June, 2012.

The deadline to submit an abstract is the 27th of January 2012, and further details can be found at http://www.smbe2012.org/ Symposium:

Viruses are a major cause of emerging diseases, at least in part due to their rapid evolution, and diseases such as HIV, SARS, Dengue, and H1N1 influenza have stimulated an enormous interest in viral evolution in recent years. Their high mutation rates and large effective population sizes also combine to make viruses remarkable models for evolution in general. They parasitize taxa throughout the tree of life and are locked in a coevolutionary dance with their hosts. The symposium seeks to explore host-virus coevolution, considering changes in virulence, prevalence, and host range by exploring intersections between molecular evolution, molecular epidemiology, and phylogenetics. The small genomes of viruses permit recovery of tremendous amounts of sequence data from natural populations, while the rapid evolution of viruses has made them favorites for experimental evolution. The results of this work have not only illuminated a range of fundamental questions in genetics and evolutionary biology, but also have direct medical relevance.

Organizers: Marta Wayne, Francis Jiggins

Confirmed speakers: Robin Bush, Derek Smith

"F.M. Jiggins" <fmj1001@cam.ac.uk>

Dublin SMBE2012 Jun23-26 MicrobialGenomeEvol

Registration for the 2012 Society for Molecular Biology and Evolution Meeting and Abstract Submission for the Microbial Genome Evolution Symposium are now open. SMBE 2012 is taking place in Dublin 23-26 June. Register at the early bird rate now through the SMBE 2012 website (www.SMBE2012.org). DEADLINE FOR SUBMITTING ABSTRACTS IS JANUARY 27th, 2012

Symposium on Microbial Genome Evolution High-throughput sequencing makes it possible for the first time to sequence hundreds of microbial genomes rapidly at low cost. These methods have huge potential to significantly improve our understanding of microbial evolution, so that many research projects have recently been set up to generate and analyze such data. This symposium will provide an overview of the progress made by such projects, as well as the many challenges they pose. It is now possible to identify the vast majority of SNPs within large population samples of microbial isolates. These datasets are illuminating the molecular, ecological and population-level dynamic processes occurring over short time scales in natural populations inhabiting a range of habitats from the clinic to the environment. We aim to explore these recent advances and the development of new methods of analyses required to fully exploit these extremely large sequence datasets. Relevant topics include quantifying the variation in the rates of recombination and mutation between closely related lineages, the evolution of base composition, the relative power of drift and selection, examining the acquisition of adaptive traits (e.g. antibiotic resistance, host adaptation, metabolic flexibility, regulatory changes) within a phylogenetic framework, and the distribution of variation over time and space (phylogeography). The role of phage and conjugative elements in structuring populations as both vehicles for gene flow and parasitic elements will also be considered. The symposium will focus on variation within natural populations rather than experimental evolution.

Organizers: Howard Ochman, Edward Feil, Eduardo Rocha, Xavier Didelot, Daniel Wilson

Confirmed speakers: Julian Parkhill, Jonathan Eisen, Peer Bork, Ruth Hershberg, Sebastien Gagneux

daniel.wilson@ndm.ox.ac.uk

Dublin SMBE2012 Jun23-26 MolecularGenomicPhenotypic

We are pleased to announce that the registration for the 2012 Society for Molecular Biology and Evolution Meeting, taking place in Dublin 23-26 June 2012, and the abstract submission for the Molecular, Genomic, and Phenotypic Evolvability Symposium, are now open.

Molecular, Genomic, and Phenotypic Evolvability

Symposium summary: Evolvability is the capacity of organisms to undergo adaptation by means of natural selection. More than merely the flip side of evolutionary constraint, evolvability is a key concept in its own right that extends the modern synthesis into new territory. In this symposium we will examine the concept of evolvability in depth. We have chosen world-class speakers who will present data bearing on evolvability at various levels (sequence, gene, gene network, gene family, genome, and phenotype) and sharpen the definitions of evolvability at each level. These talks will relate evolvability to its components including robustness, modularity, buffering, facilitated variation, developmental compartmentalization, and the relation between genotype and phenotype. A key question for evolutionary biology is whether the components of evolvability are themselves evolvable or whether they are emergent properties of complex biological systems evolving under natural selection in an ever-changing environment.

*Confirmed speakers: *Andreas Wagner, Mark Siegal

*Organizers: *Rita Ponce, Daniel Hartl

More information and registration at: www.SMBE2012.org DEADLINE FOR ABSTRACT SUBMISSION: January 27th, 2012

anaritaponce@gmail.com

Dublin SMBE2012 Jun23-26 NextGenPopulationGenetics

Dublin.SMBE2012.Jun23-26.NextGenPopulationGenetics

Registration for the 2012 Society for Molecular Biology and Evolution

Meeting and abstract submission for the 'Population Genetic Inference from Next-generation Sequencing Data' symposium are now open. SMBE 2012 is taking place in Dublin 23-26 June.

Register at the early bird rate now through the SMBE 2012 website (www.SMBE2012.org). DEADLINE FOR SUBMITTING ABSTRACTS IS JANUARY 27th, 2012

Symposium on Population Genetic Inference from Next-generation Sequencing Data:

Next-generation sequencing (NGS) technologies enable scientists to generate large-scale DNA sequence data sets for model or non-model organisms. These large sequence data sets have become an important resource for population genetic studies and empowered researches to address fundamental questions in molecular and evolutionary biology.

This new scientific environment creates new challenges. Are available population genetics methods applicable to these new generation data? How can we incorporate sequence errors, genotype uncertainty and ascertainment bias in data analysis? The scale of NGS data and the need to model sequencing errors and low sequence coverage have driven the development of new computational and statistical methods for data analysis and hypothesis testing. These methods range from genome scans to infer selection at single loci or at a combination of several loci to likelihood-based, Bayesian and Approximate Bayesian Computation methods for inferring demography.

This symposium will cover current research on the development and application of new algorithms and statistical models for population genetic analysis of large DNA sequence data sets. Specifically, the symposium will present recently developed methods for identifying variant sites, calling genotypes, estimating the site frequency spectrum, inferring past population demography and detecting selection.

Contributions from interested speakers are welcome, please apply.

Organizers [in alphabetical order]: Frederic Austerlitz, Matteo Fumagalli, Zachariah Gompert, Evelyne Heyer

Confirmed speakers: Dr. Laurent Excoffier, Dr. Mattias Jakobsson, Dr. Peter D. Keightley, and Dr. Michael Lynch

Zachariah Gompert <zgompert@uwyo.edu>

Dublin SMBE2012 Jun23-26 RNAi Evolution

RNA silencing and heterochromatin as genome defence: TE's, Viruses and Selfish Elements

We invite anyone working on an evolutionary or comparative aspect of RNA silencing to submit an abstract for this symposium, which will form a part of the SMBE meeting in Dublin on the 23rd-26th June 2012.

The deadline for abstracts is the 27th Jan 2012 (see http://www.smbe2012.org/ for more details)

Suitable topics include (but are not limited to): * Transposable-element related RNAi pathways (such as piRNAs) * Antiviral RNAi pathways (such as viRNAs, but also miRNAs) * Viral supressors of RNAi * RNA-directed heterochromatin * Molecular evolution / population genetics of RNAi * Phylogenetic origins / comparative genomics of related pathways * Experimental evolution of RNAi * Theoretical models of RNAi evolution

Symposium detail:

RNA silencing provides adaptive immunity against viruses and transposable elements, and its discovery has provided new insight into the co-evolutionary dynamics of hosts and parasites. In addition, the link between RNA silencing and heterochromatin suggests that these dynamics may have a broad influence on the evolution of gene expression, genome structure and reproductive isolation.

Although studies in diverse taxa ranging from protists and plants to fungi and animals show that genome defence by RNA silencing and heterochromatin is ancient, evolutionary studies show that this defence mechanism can also evolve quickly in an evolutionary 'arms race' context.

This symposium will bring together recent work seeking to describe the nature of these dynamics from both molecular and evolutionary perspectives, and talks will be drawn from a wide range of approaches (experimental, theoretical, comparative) and study systems (plants, animals, fungi, viruses)

Organizers: Darren Obbard, Justin Blumenstiel

Confirmed speakers: Brandon Gaut, Santiago Elena

darren.obbard@ed.ac.uk

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

Durham NC Phenotype Feb23-25

Phenotype RCN meeting announcement: Feb. 23-25, 2012 We would like to invite interested researchers to participate in the second annual summit meeting of the Phenotype Ontology RCN. The meeting will be held at the National Evolutionary Synthesis Center in Durham, NC, February 23-25, 2012.

The Phenotype Ontology RCN (http://phenotypercn.org) was funded by NSF to establish a network of scientists who need to use or develop phenotype ontologies. In contrast to the many well-established ontologies in the molecular community, the representation of morphology, behavior and other phenotypic traits using ontologies is in its infancy. Such ontologies, however, have the potential to integrate phenotype with data across all levels of the biological hierarchy. This RCN is building a community that, because of itsdomain expertise, sets the standards and best practices for the development of phenotype ontologies and a vision for their utility.

The main focus of this meeting will be introduce and establish communication between scientists from several different research backgrounds including comparative evolutionary biologists, model organism biologists, applied scientists, andontology developers and logicians. We will be introducing concepts involved in developing and coordinating ontologies as well as ontology annotation.

Although funding is limited for this meeting, we can help you reserve a room at the conference rate. Please contact one of us if you are interested in attending.

Sincerely,

Phenotype RCN PIs:

Paula Mabee (pmabee@usd.edu) Eva Huala (huala@acoma.stanford.edu) Andy Deans (andy_deans@ncsu.edu) Suzanna Lewis (suzi@berkeleybop.org)

"Mabee, Paula" <Paula.Mabee@usd.edu>

Evo-wibo2012 Apr20-22

EVO-WIBO 2012, a gathering of the evolutionary biologists of the Pacific Northwest, will be held April 20-22, 2012. Information is available at http://www.zoology.ubc.ca/evo-wibo/. Registration will open on that site sometime in January 2012.

Please mark your calendars, and if you are in the region, please let others at your institution know. A small poster is available on the web-page to help advertise.

Student participation at EVO-WIBO will be generously sponsored by the American Society of Naturalists.

Thanks, Mike Whitlock (whitlock@zoology.ubc.ca)

whitlock@zoology.ubc.ca

Glasgow ParasiteEvolution Apr2-5

Registration and abstract submission for the British Society for Parasitology spring meeting 2012 (April 2-5) at the University of Strathclyde, Glasgow.

The BSP is celebrating its 50 year anniversary and has a diverse and exciting program, including an evolutionary ecology theme with sessions on:

The ecology of microbial infections (Keynote: Brit Koskella, Oxford University, UK) Molecular ecology of infection (Keynote: Steve Paterson, University of Liverpool, UK) Integrating evolution and ecology into epidemiology (Keynote: Sebastian Bonhoeffer, ETH, Switzerland) The role of host and parasite behaviours in infection (Keynote: Jaap de Roode, Emory University, USA) and the first BES Parasites & Pathogens special interest group session on Ecology Meets Medicine (Keynote: Les Real, Emory University, USA).

Abstracts are now invited for contributed talks to the above sessions. The website for registration and abstract submission is live and can be found here:

http://live.bsp.netxtra.net/news-and-events/news/-register-for-bsp-2012/ In addition to the evolution and ecology theme, the BSP 2012 has a broad scientific programme including the biannual Trypanosome and Leishmania seminar, Malaria, Helminth Immunology, Molecular Helminthology, Veterinary Parasitology, Mapping and Imaging Parasitology themes and much more.

The Spring Meeting opens with annual Public Understanding of Science lecture by Professor Mike Barrett followed by a civic reception at Glasgow City Chambers on the 2nd April and a Gala dinner at the world famous Kelvingrove Museum.

We hope you will join us and especially support the ecology sessions.

Dr Sarah Reece Address until February 2012 Wissenschaftskolleg zu Berlin Institute for Advanced Study Wallotstrasse 19, 14193 Berlin http://www.wiko-berlin.de sarah.reece@wiko-belin.de

Dr Sarah Reece Centre for Immunity, Infection & Evolution. Institutes of Evolution, Immunology and Infection Research, School of Biological Sciences, Ashworth Laboratories, University of Edinburgh, Edinburgh EH9 3JT Scotland, UK

Tel +44 131 650 5547 Fax +44 131 650 6564

sarah.reece@ed.ac.uk http://reece.bio.ed.ac.uk/ http://reece.bio.ed.ac.uk/

Hawaii InsectEvolution Feb22-23

*Announcing the 14**th** Pacific Entomology Conference to be held on February 22 and 23, 2012. *

* *

http://www.hawaiianentsoc.org/HES/-Pacific_Entomology_Conference.html All are welcome! Since 1991, the Pacific Entomology Conference has been the premier forum for all aspects of entomology pertaining to the Pacific Basin, in its broadest sense. Speakers regularly come from all over the world to present their work at this two-day event.

Registration and Submissions for general session talks, posters and symposia are being accepted through January 7, 2012.

The 14th Pacific Entomology Conference will be held at the Outrigger Waiki≪i Ä≪< https://resweb.passkey.com/Resweb.do?mode=-welcome_ei_new&eventID=3926448&fromResdesk=-true >, a timeless institution and home of Duke's Waikiki < http://dukeswaikiki.com/ >. This classic Hawaiian location is right on the beach with gorgeous views and easy access to nearby hotels and attractions.

It's also close to tranquil off-Waikiki beaches and Diamond Head State Park. This is a gorgeous time to visit Hawaii with temperatures reaching the upper 70's and pleasant trade winds. Waikiki is a great spot for a before or after conference break and an easy jumping off point for travel to the neighbor islands.

Symposia already scheduled include:

Honeybee Health and Pollination in Hawai'i

Threats to Alpine and Subalpine Insect Species and Communities in Hawai'i

Tephritid fruit fly systematics and control

Current and Emerging Insect Pests in Hawai'i and the Pacific

Hawaiian and Pacific Insect Conservation and Evolution

Additional Symposium proposals are welcome and should be sent to the Executive Committee Chair (hientsoc@hawaii.edu).

You can register online at: http://a3.acteva.com/-orderbooking/bookEvent/A312229 . Early registration ends on January 7, 2012. Online registration ends on February 8, 2012. If you would like to register after this date, contact the organizers directly at hientsoc@hawaii.edu. Registration includes a banquet at The Hula Grill on February 22 and a buffet luncheon at Duke's Waikiki < http://dukeswaikiki.com/ > on February 23.

Special room rates have been arranged for the conference at the Outrigger Waikiki, -please follow this link < https://resweb.passkey.com/Resweb.do?mode=-welcome_ei_new&eventID=3926448&fromResdesk=-true >. The hotel provides *free* wireless internet in public areas *and* in rooms, free in-room safe, *free* local and long-distance calls to any-where in North America, in-room coffee and tea, and refrigerators/microwave upon request. Check this link for a full list of amenities < http://www.outriggerwaikikihotel.com/accommodations/amenities.cfm >. The Outrigger Waikiki is also home to the largest white sand beach in Waikiki, the Society of Seven, hosts daily Hawaiian cultural activities, and has an Expedia onsight to arrange your Oahu adventures.

Daniel Rubinoff <rubinoff@hawaii.edu>

JohannesGutenbergU Biodiversity Sept16-19

21st International Symposium "Biodiversity and Evolutionary Biology" of the German Botanical Society (DBG).

The Institut für Spezielle Botanik und Botanischer Garten of Johannes Gutenberg-Universität Mainz and the section "Biodiversity and Evolution" of the German Botanical Society invite you to participate in the 21st International Symposium "Biodiversity and Evolutionary Biology" of the German Botanical Society (DBG).

September 16th - 19th 2012 | Mainz (Germany)

The symposium is intended to provide opportunity for stimulating exchange for botanists interested in plant systematics, morphology, phylogeny and evolution. We are looking forward to interesting talks and posters on your latest research and to lively discussions, and hope to learn much about new developments in our field.

Venue The symposium will be held on the campus of Johannes Gutenberg-Universität Mainz. The Botanic Garden is located on the campus, and the city of Mainz with its many attractions (e.g., important Roman remains, impressive and influential churches, Gutenberg-Museum - good wine, too) is within walking distance.

Preliminary program The preliminary program includes eight symposia, to be opened by internationally renowned speakers, and three further plenary talks on topics of broad interest.

Symposia - Next Generation Sequencing in Plant Systematics and Evolution - Ontogeny: from Meristems to Phenotypic Diversity - Pollination and Dispersal Biology - Mechanisms of Speciation - Evolution of Tropical Floras - Evolution of Mediterranean and Arid Floras - Evolution of Mountain Floras - Open symposium (topics not specified)

Plenary talks - Access and Benefit Sharing - Biodiversity Data Bases - Ex situ Conservation

Call for Abstracts The contribution of oral or poster presentations is encouraged. More details will be provided in the 2nd circular.

Registration online Online registration will be open from 15 April until 15 June 2012.

Workshops, satellite meetings and excursions Additional workshops and satellite meetings (on Thursday, 20 September 2012) are welcome. If you want to organize a workshop or satellite meeting, please contact Prof. Joachim W. Kadereit (kadereit@uni-mainz.de) until 31 January 2012.

An excursion to the internationally renowned nature reserve "Mainzer Sand" (relict steppe flora) is planned for Sunday (afternoon) 16 September 2012.

Time Schedule and Deadlines - 01 March 2012 - 2nd circular with more detailed information - 15 April 2012 - Abstract submission and online registration opens - 15 June 2012 - Abstract submission and online registration closes - 16 - 19 September 2012 Congress

Organizing Committee - Regine Claßen-Bockhoff - Berit Gehrke - Gudrun Kadereit - Joachim W. Kadereit - Angelika Schmitt - Christian Uhink

Contact - Joachim W. Kadereit (kadereit@uni-mainz.de)

Our meeting will be followed (20th - 23rd September) by the "Jahrestagung des Verbands Botanischer Gärten" (annual meeting of the Association of Botanic Gardens in Germany).

gehrke@uni-mainz.de

KansasCity 2012ArthropodGenomics May30-Jun2

Please save the dates and plan to attend! Registration will open in January! Monitor our website, www.ksu.edu/agc and watch for the next announcement.

--* Sixth Annual Arthropod Genomics Symposium *-*-* MAY 31, 2012 (Thursday evening) to JUNE 2, 2012

Keynote Speaker: Gene E. Robinson, Entomology and Institute for Genomic Biology, University of Illinois at Urbana-Champaign

Featured Speakers (confirmed): +William E. Browne, Biology, University of Florida +Angela E. Douglas, Entomology, Cornell University +Giles Duffield, Biological Sciences and Eck Institute for Global Health, University of Notre Dame +Karl Kjer, Entomology, Rutgers University +Marc S. Halfon, Biochemistry, State University of New York at Buffalo +Michel R. Kanost, Biochemistry, Kansas State University +Subba Reddy Palli, Entomology, University of Kentucky +Additional speakers will be announced soon!

The symposium focuses on new insights gleaned from analyzing arthropod genomes and is designed for scientists interested in genomic studies of Arthropods, both model organisms and those of agricultural or health relevance. The program will include platform presentations, a welcome reception, a bioinformatics-related workshop and arthropod genomics-related poster sessions. A few poster abstract submissions will be selected for platform presentations. Postdoctoral, graduate, and undergraduate students are also encouraged to attend.Â Sessions conclude Saturday evening, followed by an optional banquet.Â

--*-*-* New this year: i5k Community Workshop*-*-*-*-*- MAY 30, 2012 (Wednesday morning) to MAY 31, 2012 (Thursday afternoon) i5k Community Workshop: An international effort to sequence 5,000 of the world's key arthropod species. The Workshop will aim to bring together biologists, informaticists, and policy-makers to discuss and advance planning for the i5k initiative. Plans for the i5k Workshop include presentations by top genomics and bioinformatics researchers and representatives from the primary sequencing centers, followed by training and breakout sessions focused on i5k and other successful insect genome projects. The Workshop will conclude with a discussion of white papers and programmatic steps needed to enact i5k projects.

POSTER ABSTRACT DEADLINES IN 2012: Wednesday, February 29 If you DO wish your poster abstract to be considered for a General Session talk.

Friday, March 30 - If you do NOT wish for your poster abstract to be considered for oral presentation during the General Session.

TENTATIVE PROGRAM for SYMPOSIUM & i5k WORKSHOP Wednesday, May 30 i5k Community Workshop - 7:15-8:15 am Registration - 8:30 am -5:30 pm Speaker sessions - 7:30 pm-10:00 pm Poster session Thursday, May 31, 8:30 am-5:00 pm i5k Workshop continues with breakout groups, common session, and report-backs

Thursday evening, May 31, 7:30 pm Arthropod Genomics Symposium begins with keynote presentation and welcome reception

Friday, June 1 Symposium Platform and Poster Sessions Friday, June 1, 5:30-7:30 pm - Symposium Workshop Friday evening, June 1 Dinner on your own Saturday, June 2 Symposium Platform and Poster Sessions Saturday evening, June 2 Optional Kansas City BBQ banquet at Fiorellas Jack Stack Barbecue, Freighthouse location

Saturday evening, June 2 - Meeting concludes

VENUE: The symposium will take place at the Kansas City Marriott on the beautiful Country Club Plaza in Kansas City, Missouri.

REGISTRATION: Registration will open in January! Monitor our website, www.k-state.edu/agc/-symposium.shtml and watch for the next announcement.

QUESTIONS: Contact Doris Merrill at dmerrill@ksu.edu .

If you would like to join the ArthropodNews to ensure receiving future notices, please send an e-mail with your name and e-mail address to dmerrill@ksu.edu .

PLEASE SHARE THIS ANNOUNCEMENT WITH COLLEAGUES AND STUDENTS!

SPONSORS: *Center for Genomic Studies on Arthropods Affecting Human, Animal and Plant Health, Kansas State University *American Genetic Association *Eck Institute for Global Health, University of Notre Dame *University of Illinois at Urbana-Champaign *USDA-Agricultural Research Service

CORPORATE SPONSORS: +Monsanto Company +Pioneer Hi-Bred International, Inc. +Syngenta If you would like to become a corporate sponsor, please contact Doris Merrill at dmerrill@k-state.edu .

Susan J. Brown, Professor and Director, Center for Genomic Studies on Arthropods Affecting Human, Animal and Plant Health, Kansas State University Robin E. Denell, Distinguished Professor Chair, AGC Symposium Organizing Committee Jay D. Evans, USDA-ARS Bee Research Lab Co-Chair, i5k Workshop Organizing Committee by Doris Merrill, Program Coordinator K-State Arthropod Genomics Center Division of Biology, Kansas State University 116 Ackert Hall, Manhattan, KS 66506-4901 dmerrill@k-state.edu , www.k-state.edu/agc

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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

LaSage Switzerland SexDeterminationEvolution Jun6-9

Conference/workshop Sex-determination systems: mechanisms and evolution.

La Sage, Switzerland, June 6-9, 2012

Theme: Sex determination can be achieved through an impressive diversity of mechanisms. Many species (including some fish and reptiles) display environmental sex determination (with a switch determined by e.g. temperature, age, social cues, etc). If genetic, sex determination may be polygenic (many genes on different chromosomes) or monogenic (one single master gene). The latter case may lead to the evolution of highly differentiated sex chromosomes (as observed in birds or mammals), but not necessarily so. What are the mechanisms underlying alternative sex determination pathways, what are their costs and benefits (in particular regarding sex-ratio production), what are their consequences in terms of demographic processes or genomic evolution? What selective forces drive transitions among systems, which seem frequent on an evolutionary time scale?

Form: Three-days conference/workshop in the Alps (http://www.hoteldelasage.ch/) with the following invited speakers: D.Bachtrog, C.Peichel, J.Mank, N.Valenzuela, M.Kirkpatrick, E.Haag, L.Beukeboom. Participants will have the opportunity to present and discuss their work.

Fees: Euros 350.- including registration, food and accommodation.

Inscription: limited to 30 participants. Please send a brief CV and motivation statement by the end of January 2012 to nicolas.perrin@unil.ch

Nicolas Perrin Dept Ecology & Evolution University of Lausanne Switzerland

Nicolas Perrin <Nicolas.Perrin@unil.ch>

Lisbon Ethology Apr12-13

We are pleased to announce that the next conference of the Portuguese Ethology Society will take place on 12-13 April 2012 in Lisbon, at the Faculty of Sciences and is organized by the Centre for Environmental Biology.

This meeting will bring together contributions from several related fields - Ecology, Evolution, Development, Physiology and Neuroscience - and several animal groups - unicellular, invertebrates, vertebrates, mammals, humans. The meeting aims to provide an integrative vision of the study of animal behaviour, to provide an updated overview of the research being conducted in Portugal in this field and to promote the interaction between researchers and students.

Submission deadline: 15 of January, 2012

For more information (including invited speakers) see:

http://spe2012.fc.ul.pt/EN/index.html Hope to see you there!

The organizing committee

Joana Jordão, CBA, FCUL

Rita Covas, CiBio, UP

Rita Ponce, CBA, FCUL

Sara Hagá, FP-UL

Susana Varela, CBA, FCUL

anaritaponce@gmail.com

LundU BehaviourEvolution Aug12-17 Registration

Dear EvolDir-readers;

The registration to the International Behavioural Ecology Congress (ISBE 2012), to be held in Lund 12-17 August 2012 is now open for registration. Contributions (talks, posters) can now be sent in until the deadline on March 15 2012 through this link:

http://www.isbe2012lund.org/registration/ There is also an opportunity to send in suggestions for so-called

"Post-conference symposia", around more or less well-defined topics related to behavioural ecology and related fields, which will take place after the ISBE, on August 2012, as an independent event. Deadline for suggestions for post-conference symposia is January 31 2012, and more information can be found here:

http://www.isbe2012lund.org/post-conference-symposia/ General questions regarding ISBE 2012, including ackomodation issues, costs of registration, child care facilities etc. can be found on the conference website:

http://www.isbe2012lund.org/ Sincerely,

Erik Svensson

Erik Svensson Professor (Evolutionary Ecology) Department of Biology, Lund University SE-223 62 Lund SWEDEN

Phone: +46 46 222 38 19 Fax: +46 46 222 47 17 E-mail: erik.svensson@zooekol.lu.se

Webpage: http://www.lu.se/o.o.i.s/26007 Lab blog: http://svenssonresearchlaboratory.blogspot.com/ Researcher ID: http://www.researcherid.com/rid/E-8324-2010 Erik Svensson <Erik.Svensson@biol.lu.se>

Neuchatel AdaptiveLandscapeGenetics Feb7-8 2

Conference: Adaptive landscape genetics, Neuchatel, Switzerland

We are happy to announce the symposium

?Adaptive landscape genetics: current insights and future directions?

on February 7th and 8th 2012 at the University of Neuchatel (Switzerland).

see: www.unine.ch/ALG2012 Landscape genetics is an integrative field of research, aiming at understanding microevolutionary processes across natural populations. It is developing in a rapid way due to advances in genomics technologies, environmental data acquisition and statistical methods to associate them.

During this symposium, we intend to foster exchange between researchers having complementary expertise in order to further explore the contributions of landscape genetics to the assessment of the interactions between environment and adaptive genetic variation in natural populations. Invited speakers and contributed talks will offer an overview of current trends in the field and perspectives on how it will grow and develop in the future.

Invited speakers are: Malika Ainouche (Univ. Rennes, F) Auréline Bonin (Univ. Grenoble, F) Laurent Excoffier (Univ. Bern, CH) Felix Gugerli (WSL Birmensdorf, CH) Stéphane Joost (EPFL, CH) Christian Lexer (Univ. Fribourg, CH) Christophe Randin (Univ. Basel, CH) Pierre Taberlet (CNRS, F)

Fees: 150 CHF, including coffee breaks, meals and conference dinner (free for CUSO PhD students). Details and registration forms can be found at www.unine.ch/ALG2012 The organizers: Christian Parisod and Rolf Holderegger

rolf.holderegger@wsl.ch

Perth EvolPlantSignalling Sep16-21

The meeting is especially relevant to evolutionary biologists and ecologists and I apologise if I didn't make this clear in my post. I have re-written the invite below.

Monica

It is my pleasure to invite you to the very 1st Symposium on Plant Signalling & Behaviour to be held in September 16th-21st, 2012 in Perth, Western Australia.

This inaugural meeting is an open invitation to all interested molecular geneticists, biochemists, physiological ecologists, behavioural ecologists, community ecologists, evolutionary biologists, mathematical modellers, and even philosophers. It will bring together the latest views and concepts on plants from very diverse perspectives (from molecular to evolutionary) as well as a wide range of approaches (experimental, theoretical, comparative). As such, the Symposium will cover themes such as Plant Cell Biology and Signalling, Plant Sensory and Behavioural Ecology, and Theoretical Botany.

Postdoctoral and graduate students are strongly encouraged to attend.

Please visit the web site of the meeting here http://spsb2012.com/ and book these dates in your diary!

I really look forward to seeing you in Perth next year.

Best wishes for a fantastic festive season to everyone!

Monica Gagliano

Dr Monica Gagliano Postdoctoral Research Fellow Centre for Evolutionary Biology | School of Animal Biology & Centre for Microscopy, Characterisation and Analysis The University of Western Australia | Crawley | WA 6009 | Australia ph: +61 8 6488 1361 website: http://www.uwa.edu.au/people/monica.gagliano Monica Gagliano <monica.gagliano@uwa.edu.au>

Prague PolyploidyBiodiversity May7-10 Registration

Dear colleages,

we are happy to announce that registration and abstract submission for the International Conference on Polyploidy, Hybridization and Biodiversity (7-10 May 2012, Pruhonice near Prague, Czech Republic) are open now. Abstract submission and early registration deadline is 31 January. http://icphb2012.ibot.cas.cz/-index.html Following the conference, a one day Practical Workshop on Plant Flow Cytometry will take place at the Institute of Botany in Pruhonice. The number of participants is limited to 10 per course. The first course is scheduled for Friday, May 11, 2012. Other courses can follow on Saturday 12.5. / Sunday 13.5., depending on the participant's interest. The organization of the workshop is independent of the ICPHB, but information can be found on the conference webpages.

We look forward to seeing you in May,

Judith Fehrer & Ales Kovarik Institute of Botany & Institute of Biophysics Academy of Sciences of the Czech Republic

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

ULiverpool YoungEvolBiologists Mar29-30

NEYEES : North Of England Young Evolutionary Ecologists Symposium 2012

University of Liverpool 29-30th March 2012

Dear Colleagues,

We would like to invite all non-tenured (post-grad - fellow) researchers currently working in the North of England to a one-off symposium held at the Institute for Integrative Biology, University of Liverpool. NEYEES aims to bring together early career researchers working in the Evolutionary Ecology field in order to promote the sharing of ideas and approaches between neighbouring institutions.

The symposium will span 2 days, with a total of 20 talks. As a guideline, sessions will be divided up into 5 themes; Molecular Evolution, Symbiont Evolution, Sex and Life Histories, Population Biology and Adaptation to changing environments

These themes are guidelines however, and any talks not fitting into these subjects will not be disadvantaged.

Confirmed speakers: Arpat Ozgul (Cambridge) Chris Wilson (Imperial College London)

All attendees are invited to submit an abstract, and registration and abstracts should be submitted by the 19th February. To register and for more details, please visit http://pcwww.liv.ac.uk/~eharriso/ To ensure that the symposium achieves it's aim of fostering communication, we have capped registration in order to maintain an intimate atmosphere. Registration will therefore be on a first come, first served basis.

We hope to see you there

Ellie Harrison and Ewan Minter

ellie.harrison@liverpool.ac.uk

UMassachusetts LynnMargulis ALifeInScience Mar23-25

Please Save the Dates

Lynn Margulis SymposiumXA Life in Science: in Memory and Celebration

Friday March 23 to Sunday March 25, 2012

The University of Massachusetts, in collaboration with the family and friends of Lynn Margulis (1938-2011), cordially invites you to a Symposium, March 23-25, 2012, celebrating her life and work. Although the Symposium is still in its early planning stages, we wanted to alert you and other interested parties you may know in order to provide the lead-time needed to save these dates and arrange for travel to and from Amherst, Massachusetts.

We are very excited about this opportunity to gather in memory of Professor Margulis, and to explore the history, importance, and future of her intellectual accomplishments.

As plans take shape, they will be posted to < www.geo.umass.edu/margulis_symposium.html >.

Preliminary Schedule of Events

Friday March 23, 2012 Welcome and Lynn Margulis Film Festival

Saturday March 24, 2012 Welcome followed by seminars on Gaia, astrobiology, symbiosis, and a tribute dinner with Peter Westbroek, William Irwin Thompson, and a new essay by James Lovelock

Sunday March 25, 2012 Community and colleague comments and an afternoon field trip in memory and celebration to Lynn's favorite swimming hole (and last research site), Puffers Pond

James MacAllister <jimmymac@geo.umass.edu>

UNottingham PopGenetics Jan4-7 LastCall

This is a final reminder that registration for Popgroup45*, to be held at the University of Nottingham, UK, January 4th-7th 2011, closes on FRIDAY 9th DECEMBER. So far, we have over 180 persons registered - remaining slots for talks will be dealt with on a first-come first-served basis. See http://www.populationgeneticsgroup.org . Registration fees include everything, except for accommodation which must be booked separately. Fees are £170 (full), £160 (full + Genetics Society member), £150 (student), £140 (student + Genetics Society member).

We would like this opportunity to thank confirmed sponsors including: The Genetics Society, The Royal Society and Oxford University Press, Roberts and Company, Cambridge University Press and Heredity/Nature Publishing Group.

The organisers: Angus Davison, John Brookfield, Sara Goodacre, and Tamsin Majerus.

– *PopGroup is an informal international meeting which annually brings together up to ~200 scientists working in all areas of population genetics and evolutionary biology. Talks and posters from early career scientists, including PhD students, are particularly encouraged. The conference is officially registered with the Genetics Society as a special interest group.

Dr. Angus Davison School of Biology University Park University of Nottingham NG7 2RD

0115 8230322 angus.davison@nottingham.ac.uk www.angusdavison.org Angus.Davison@nottingham.ac.uk

UOregon EvoDevo Feb10-12 scholarships

Evolution, Development & Genomics Symposium 2012 - Scholarships Available & Early Registration Deadline Approaching

The Future of Evo-Devo - Genomes in context: Systems, populations and environment February 10-12, 2012 The Nines in Portland, OR www.evodevo2012.org Dear Colleagues,

We are pleased to announce the availability of scholarships for travel to and attendance of our symposium: "The Future of Evo-Devo - Genomes in context: systems, populations and environment." The deadline for scholarship applications is December 16th, one week before the EARLY REGISTRATION DEADLINE of December 23rd. Register now to ensure you receive the early registration price. Scholarship applicants will receive the early registration price, regardless of selection for award.

The symposium is being organized by students and faculty affiliated with the University of Oregon's NSF IGERT program on evolution, development and genomics. It will be held February 10 - 12, 2012 in Portland, OR at the Nines Hotel. Previous IGERT symposia have featured talks from many leaders in the field and received good coverage in Science. We have every expectation that this symposium will be equally engaging and positively influence the future of the field. We have deliberately capped registration for this symposium in order to facilitate a more intimate environment and to encourage free discussion between attendees and speakers. As such, if you are interested in attending, please register soon to ensure that you will join us as we discuss the future of evolution, development and genomics. Confirmed speakers include:

Peter Andolfatto (Princeton) Bill Bradshaw & Chris Holzapfel (University of Oregon) Anna Di Rienzo (University of Chicago) Paul Hohenloe (University of Idaho) Alexander Johnson (UCSF) Michael Levine (Berkeley) Antonia Monteiro (Yale) Dave Parichy (University of

Washington) John Postlethwait (University of Oregon) Matt Rockman (New York University) Karen Sears (University of Illinois) Gunter Wagner (Yale) Jens Walter (University of Nebraska) Shozo Yokoyama (Emory)

For more information, please visit the symposium website (www.evodevo2012.org) or see the attached flyer. We hope that you can join us in shaping the future of this interdisciplinary field.

David W Anderson <danderso@uoregon.edu>

UOxford EcolEvolStudent Jan4-6 Deadlines

Dear Colleagues,

The deadline for the submission of abstracts for the 2012 Edward Grey Institute of Field Ornithology 'Ecology and Evolution' Student Conference has been extended to Monday 12th December. This is the final deadline and selected participants will be contacted the following day (Tuesday 13th December).

Registration for the conference will remain open for a further week, closing on Monday 19th December.

For those already registered, and those intending to, we look forward to seeing you in Oxford in January!

The EGI Student Conference Organising Committee

—–

Dear Colleagues,

We are pleased to announce that registration is open for the 2012 Edward Grey Institute of Field Ornithology 'Ecology and Evolution' Student Conference, to be held on 4th to 6th January 2012.

The conference will take place in the University of Oxford at the Department of Zoology, and it is the aim of the conference to provide a setting for students of various research areas within ecology and evolution to present and discuss their work in a constructive atmosphere composed mainly of their peers. In addition to student talks and posters, the conference will consist of a number of plenary talks given by distinguished investigators. This year will see the conference broaden its scope to embrace ideas derived from non-ornithological systems, offering the ideal opportunity for interaction and exchange of ideas with peers and experienced researchers from a wide variety of disciplines. There will also be opportunities for students to attend workshop sessions during the conference.

Confirmed Plenary Speakers:

Virpi Lummaa (University of Sheffield) Stuart West (University of Oxford) Ben Hatchwell (University of Sheffield) Gavin Thomas (University of Bristol) Patricia Brekke (Zoological Society of London)

For more information, and to register for the conference, please visit the conference website: http://www.zoo.ox.ac.uk/egi/newsevents/conference.htm The registration fee includes workshop attendance, refreshments, a wine reception and also lunch and an end-of-conference banquet in one of Oxford's most beautiful colleges, Trinity College.

If you would like to present at the conference, please submit an abstract of 100 words or less to egiconference@zoo.ox.ac.uk stating either talk or poster (indicating landscape or portrait).

The closing date for the submission of abstracts is 5th December 2011.

Please forward this information on to all those who may be interested in the conference, and we look forward to welcoming you to Oxford in the New Year!

Best wishes,

EGI Student Conference Organising Committee

christopher.cooney@keble.ox.ac.uk

Virrat Finland EMPSEB18 EvolBiol Sep25-30

Event: EMPSEB 18 Date: 25-30 September, 2012 Location: Virrat, Finland

This is an early announcement that the 18th EMPSEB meeting will take place from 25-30 September 2012 in Virrat, Finland. The event aims to bring together the European PhD students in Evolutionary Biology, let them present their research, get feedback from the top scientists in the field, and develop collaborations with their peers.

The meeting will consist of plenary sessions, symposia, and posters covering a variety of topics in evolutionary biology. More information will be available at www.empseb18.com by end of January 2012. Registration and abstract submission will be open in Spring 2012. Students will have a possibility to apply for travel grants.

Organization committee: Robert Hegna, Ossi Nokelainen, Philipp Lehmann, Venera Tyukmaeva, Gaia Francini, Janne Valkonen, Veronica Chevasco, Aapo Kahilainen and Anni Ormala

– Venera Tyukmaeva Evolutionary Genetics Department of Environmental and Biological Science University of Jyväskylä

venera.v.tyukmaeva@jyu.fi

GradStudentPositions

BlackHillsStateU IntegrativeGenomics

Black Hills State University - Masters of Science in Integrative Genomics

Several Masters Graduate Assistant (GA) positions are available for Fall 2012 in the Integrative Genomics (IG) Masters program at Black Hills State University, Spearfish, SD. GA positions are available to students interested in working with any member of the IG faculty (http://www.bhsu.edu/Academics/TheColleges/CollegeofArtsandSciences/DepartmentsandPrograms/Masters/Faculty/tabid/4950/Default.aspx). Application deadline for fall 2012 admission is April 15th, 2012.

Integrative Genomics is an interdisciplinary graduate program that combines genomics, ecology, evolution, and physiology. The program is designed to provide those seeking a Masters degree the necessary skills and concepts to work cooperatively with others in a research area that takes a systems-wide approach and incorporates an organism's history and natural environment to understand organization and expression at the genomic level. Exposure to modern techniques and instrumentation in the laboratory and field prepares students for success in both academic and other biotechnology-related pursuits.

Integrative Genomics GAs receive an annual stipend of $16,640 and additional funds for laboratory supplies and expenses.

For an overview of the IG program and application information please visit our website http://www.bhsu.edu/Academics/TheColleges/CollegeofArtsandSciences/DepartmentsandPrograms/Masters/tabid/2164/Default.aspx or contact

Research Interests of faculty with openings: Cynthia Anderson: fungal genetics and genomics, plant pathology Dave Bergmann: microbial genetics and genomics John Dixson: organic and biochemistry, antimicrobial and antimalarial properties of plant extracts David Siemens: plant ecology, ecological genomics Brian Smith: herpetology, ecology, and conservation Garth Spellman: ornithology, evolutionary genetics and genomics, biogeography, and systematics Ben VanEe: plant systematics, population genetics, biogeography

Garth Spellman, Ph.D. Assistant Professor and Director of MSIG Program School of Natural Sciences Black Hills State University 1200 University Street, Unit 9053 Spearfish, SD 57799-9053 Garth.spellman@bhsu.edu

Founded in 1883, Black Hills State University is located in beautiful Spearfish, SD, the hub of the Northern Black Hills with a population of more than 10,000. Located on I-90, 10 minutes from the Wyoming border, Spearfish is only 46 miles from Rapid City, 65 miles from Mount Rushmore National Memorial and is an hour drive from Devils Tower and the Badlands of South Dakota. Spearfish Canyon, one of the oldest and most scenic canyons in the west, is a local favorite for hiking, biking and sightseeing.

– Garth M. Spellman, Ph.D. Assistant Professor of Vertebrate Zoology MSIG Program Director 1200 University Street, Unit 9053 Biology Department Black Hills State University Spearfish, SD 57799-9053

ph:605-642-6043 garthspellman@bhsu.edu http://www.bhsu.edu/artssciences/asfaculty/gspellman/Welcome.html "Spellman, Garth" <Garth.Spellman@bhsu.edu>

ChicagoBotanicGarden PlantConservation

PLANT BIOLOGY AND CONSERVATION AT THE CHICAGO BOTANIC GARDEN AND NORTHWESTERN UNIVERSITY

The Graduate Program in Plant Biology and Conservation is a joint program between Northwestern University (NU) and the Chicago Botanic Garden (CBG). Both PhD and MS degrees are offered. The program offers a unique opportunity to study ecology, evolution, and environmental issues at the interface of basic and applied plant science. Students apply to the program through Northwestern University and take courses at both NU and CBG with faculty from both institutions. The Conservation and Science Center at CBG is a tremendous resource for students and the Chicago region provides an excellent community at the forefront of research in conservation and sustainability.

To learn more contact program director, Nyree Zerega (nzerega@chicagobotanic.org) or visit our websites: Graduate Program: http://www.plantbiology.northwestern.edu/ Plant Science Center: http://www.chicagobotanic.org/research/labs.php?expanddiv=plant_conservation Application deadlines: PhD: December 31, 2011 MS: February 15, 2012

nzerega@chicagobotanic.org

DurhamU Lynx PopulationDynamics

PhD Postion in the School of Biological and Biomedical Sciences, Durham University UK:

Holocene population dynamics and connectivity of top predator species in the context of environmental change

This project will focus on the lynx (Lynx lynx), but include comparator species as possible. Predators are sensitive to changes in habitat or prey distribution and abundance, and such changes may impact on their population dynamics, dispersal behaviour and distribution. The primary aims are to test the following hypotheses. 1) The distribution of diversity and pattern of connectivity has been impacted by environmental factors such as climate change and deforestation during the course of the Holocene for a top predator like the lynx. 2) There is a relationship between historical environmental change and the population dynamics of top predators in Europe such that habitat change or loss is reflected in periods of local demographic responses. Similar studies of e.g. bison and musk ox have shown that both climate change and anthropogenic factors have been important in driving population dynamics throughout the Holocene. Ancient DNA and coalescent methods will be used to determine mutation rate in the mtDNA control region. The mutation rate estimate will then be used in Bayes factor and Bayesian skyline plot analyses (a method that tracks coalescent points back through time; implemented in the program BEAST) to track regional population dynamics over time, and coalescent analyses will be used to assess directional migration rates at contemporary time periods in the past. This will be reinforced using complementary analyses (such as mismatch distributions, spatial autocorrelation and conventional F-statistics).

Application materials including a c.v., two letters of reference, a cover letter and University transcripts should be sent to Rus Hoelzel (project supervisor) at a.r.hoelzel@dur.ac.uk no later than February 3rd, 2012.

You will also need to apply online for admission to the University of Durham in advance of that date (https://banners.dur.ac.uk/blive_ssb/bwskalog.P_DispLoginNon).

A full studentship will be available comparable to that provided by British Research Councils, but not restricted to British nationals. Please contact Rus Hoelzel for more information.

“HOELZEL A.R.” <a.r.hoelzel@durham.ac.uk>

EastTennesseeStateU LakeBaikalZooplankton

EastTennesseeStateUniversity.LakeBaikalZooplankton

NSF-funded Master of Science position to study ecological and genetic diversity of endemic and invading plankton crustaceans in Lake Baikal. This is a collaborative project involving research labs from Michigan State University, University of California Â’ Santa Barbara, University of Texas Â’ Austin, Wellesley College and East Tennessee State University. Additional collaborators include Institute of Biology, Irkutsk State University and A. KondrashovÂ^{1}s lab in Moscow State University. Lake Baikal is the deepest, the oldest and the largest (in terms of volume) lake on Earth, home to 20% of planetÂ^{1}s unfrozen surface fresh water and to a unique assemblage of endemic species of algae, invertebrates and fish. During the last 50 years Baikal has seen a considerable increase in temperature, primary production and the frequency of non-endemic crustaceans in zooplankton. Funds are available to investigate the genetic structure of populations of endemic copepods and invading cladocerans. The student will participate in at least one field season on Lake Baikal. Familiarity with handling zooplankton organisms, population genetics, microsatellites and SNP genotyping is a plus, but not required. Likewise, ability to speak Russian is a plus, but not required. For further details on the project contact Lev Yampolsky, yampolsk@etsu.edu. To apply: http://www.etsu.edu/gradstud/admissions.aspx . – Lev Yampolsky

Associate Professor Department of Biological Sciences East Tennessee State University Johnson City TN 37614-1710 G-phone 646-926-7657 (646-YAMPOLS) Office/lab 423-439-4359 Fax 423-439-5958

YAMPOLSK@mail.etsu.edu

ErasmusMundus EvolutionaryBiology

Erasmus Mundus Master Programme in Evolutionary Biology (MEME)

MEME is a two-year research oriented master programme for talented and motivated European and non-European students who are interested in understanding evolution in all its facets. The MEME programme will address the driving forces of evolution at all levels of organismal organization (from cells and individuals to populations and ecosystems), and it will allow students to study all kinds of organisms (microorganisms, plants, animals) in all kinds of habitats (marine as well as terrestrial) with a diversity of approaches (field, lab, theory). The focus of the programme is not only on how evolution shaped life on our planet in the past, but also on how understanding the principles underlying evolution can provide new insights and help to cope with present-day challenges in a variety of fields, including ecology, epidemiology, physiology, immunology, genetics/genomics, bioinformatics, economics and the social sciences.

Only few universities in the world would be able to offer a programme of such broad scope without compromising scientific quality. For this reason, four European universities (University of Groningen (Netherlands); University of Montpellier II (France); Ludwig Maximilians University of Munich (Germany); Uppsala University (Sweden)), have joined forces with Harvard University (USA). Together, this consortium is able to put together an attractive multidisciplinary programme that meets highest standards. All students have to study at (at least) two partner universities, and they will receive a double degree from two partner universities they have attended.

Being financed by the European Community, MEME has to satisfy the high quality standards imposed the prestigious Erasmus Mundus Programme. Full scholarships are available for European and for non-European students and these will be awarded in a selective procedure.

Starting date: September 2012

Application deadline: January 15, 2012 for European and non-European students

Please alert your students to this great opportunity!

More information and how to apply - please see www.evobio.eu Questions about the contents of the programme: Franjo Weissing (f.j.weissing@rug.nl) Questions about the requirements and the application procedure?

Please conact: Dr Irma C. Knevel

Erasmus Mundus MEME Programme Manager

Theoretical Biology Group

Centre for Life Sciences

P.O. BOX 11103

9700 CC Groningen (The Netherlands)

Email: i.c.knevel@rug.nl

Dr Irma C. Knevel

Erasmus Mundus Masters Programme Manager

Office hours: 9.00-17.00h on Mon-Wed and Fri

CEMACUBE Programme (on Monday and Wednesday): Dept of Biomedical Engineering (BME) - University Medical Center Groningen Visiting address: A.Deusinglaan 1, 9713 AV Groningen (Building 3215, Room 11.29) Tel: 31 (0)50 363 2530 - Email: I.C.Knevel@rug.nl Please visit for more information: www.biomedicaltechnology.eu(http://www.biomedicaltechnology.eu/)

MEME Programme (on Tuesday and Friday): Theoretical Biology Group - Centre for Life Sciences Visiting address: Nijenborgh 7, 9747 AG Groningen (Building 5173, Room 05.04) Tel: 31 (0)50 363 8098 - Email: I.C.Knevel@rug.nl Please visit for more information: www.evobio.eu(http://www.evobio.eu/)

Postal address MEME and CEMACUBE: Irma Knevel Theoretical Biology Group Centre for Life Sciences University of Groningen Nijenborgh 7 9747 AG Groningen The Netherlands

i.c.knevel@rug.nl

IASMA Italy PhylogenyInsectBehaviour

Fem-Italy.Phylogenomics&Behaviour

We are seeking an enthusiast student to employ genomics and phylogeny to understand the molecular basis of behavioural innovation in insects.

The student will focus on fruit flies, in particular Drosophila suzukii, an emerging fruit pest which shows an unprecedented ecological behaviour when compared to other fruit flies. Other models will be grapevine specific insect parasites. The goal is to understand how and when this species developed their novel ecological behaviour. The student will employ bioinformatics (including molecular phylogenetics, clock studies, comparative genomics and transcriptomics) to study the evolutionary history of the above species and of some of their gene families. Depending on student attitude/interest there may be space for other work spanning from chemical ecology to evodevo, as well as for the development of student's own ideas.

Most of the training/work will be carried out at the Research and Innovation Centre of the Edmund Mach Foundation (FEM), an agricultural research institute located in the Italian Alps. Part of the training will be done at an external PhD school chosen by the candidate in conjunction with FEM. Supervision will be given by

Omar Rota-Stabelli (phylogenomics) and Gianfranco Anfora (chemical behaviour) as well as by one supervisor at host university. FEM pays the studentship as well as external fees. There will be plenty of interaction/training/collaboration with other labs both at FEM and abroad, particularly at the Swedish University of Agricultural Sciences.

We are ideally looking for a candidate with a MSc in biology, bioinformatics, agriculture or a related discipline. A successful candidate will have a background either in evolutionary biology or bioinformatics, with some programming skills.

Application deadline: 10 January 2012

For more info: http://www.fmach.eu/UploadDocs/-8433_088_ASB_DDS_Profile.pdf Send your cv and application form to: phd.fem [AT] iasma.it

For (scientific) questions: omar.rota[AT]iasma.it

Omar Rota Stabelli PhD Marie Curie - PAT postdoctoral fellow Chemical Ecology, Department of Sustainable Agro-ecosystems and Bioresources, IASMA Research and Innovation Centre, Fondazione Edmund Mach, San Michele all'Adige, (TN), Italy

tel: ++39 0461 615 509 fax : ++39 0461 615 500

Italian Society for Evolutionary Biology www.sibe-iseb.it The SYsytematic Association http://-www.systass.org/ What if the very idea of growth accumulating riches, destroying the environment and worsening social inequality is a trap? Maybe we need to aim to create a society that is based on quality not quantity, on cooperation and not competition. Serge Latouche

Omar Rota Stabelli <omar42@gmail.com>

InterU PopGenetics

13 PhD studentships

INTERCROSSING offers generously funded 3-year training - available to candidates from all over the world.

We are an EU funded ITN (see http://-cordis.europa.eu/fp7/mariecurieactions/itn_en.html)

We fund PhD studentships that will provide rigorous training in three disciplines hardly ever found together any one young scientist: population genetics, informatics and statistics. EU candidates are expected to apply for training in a different country.

The need for this supra-disciplinary combination of skills reflects the extraordinary new demands produced by technologies that allow us to sequence whole genomes, and to quantify their regulation and expression in many samples from the same species in multiple locations. This torrent of data overwhelms current computational, genetic and statistical approaches for distinguishing the biologically relevant patterns from the background noise.

The consortium behind INTERCROSSING - including 5 universities and 7 Small to Medium Enterprises spanning 9 EU countries - are all using the NGS technologies, but have found the recruitment of appropriate Early Stage Researchers (ESRs) a major obstacle to building on their innovations. This fundamental shortage in the EU research community is slowing the scientific and industrial exploitation of these groundbreaking new data streams; the shortage of key talent occurs worldwide. Students completing this training will therefore be in high demand.

Details of how to register an interest in these PhD projects see here: http://-intercrossing.wikispaces.com/ Richard Nichols Professor of Genetics http://webspace.qmul.ac.uk/-ranichols/research.htm

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LausanneU MultigeneFamilyEvolution

PhD studentship (3 years) on multigene family evolutionary history (MHC) at the University of Lausanne, Switzerland

We are looking for a highly motivated and enthousiastic Ph.D. candidate who would be involved in a project dealing with multigene family evolution and protein interactions. The project will concern the evolutionary history and molecular evolution of MHC class II genes in birds, and involve complex lab work and molecular evolutionary analyses including phylogenetics, recombination, selection and protein modeling. For further information and a list of publications, see: http://-www.unil.ch/dee/page9057.html . Start: March 2012.

Salary: according to the guidelines of the Swiss National Science Foundation.

The Department of Ecology and Evolution in Lausanne provides a lively and stimulating environment for research. It harbours research programs in evolution, conservation biology, ecology and bioinformatics, with an active program of seminars and discussion groups (in English), and has excellent facilities for molecular genetics and genomics; see http://www.unil.ch/dee/. The doctoral program includes activities organized with several other universities in Switzerland. Lausanne, situated on the northern shore of Lake Geneva, has a lively cultural life and is surrounded by spectacular mountain environments; see http://www.lausanne.ch/ . Candidates should have a masters degree in an appropriate discipline and a keen interest in molecular evolution, with good laboratory expertise. To apply, please send by e-mail only (Luca.Fumagalli@unil.ch) a cover letter describing your motivation for conducting research on the advertised topic, a complete CV and names and addresses of two people who could supply written references. The position will stay opened until 15th January 2012 or until filled.

Dr Luca Fumagalli, Laboratory for Conservation Biology, Department of Ecology and Evolution, Biophore, University of Lausanne, CH-1015 Lausanne (Switzerland)

Luca.Fumagalli@unil.ch

LouisianaStateU Phylogenetics MolEvolution

Ph.D. Students - Lab of Jeremy M. Brown - Louisiana State University

Phylogenetics, Phylogeography, and Molecular Evolution

Applications for doctoral students in the lab of Dr. Jeremy M. Brown at Louisiana State University (LSU) are now being accepted for Fall 2012 admission. Research in the Brown lab is broadly centered on the use of a phylogenetic perspective to understand organismal history and molecular evolution. We work on both methodological and empirical questions, often taking a computational approach. Recent and ongoing empirical work includes large-scale studies of vertebrate phylogeny, the use of phylogenies as forensic tools in criminal cases of HIV transmission, and investigations into somatic diversification during tumor development. Recent and ongoing methodological work focuses on the development and testing of statistical approaches for phylogenomics and phylogeography. Extensive opportunities exist for collaboration with other evolutionary genetics labs at LSU (including those of Bryan Carstens, Mike Hellberg, Chris Austin, Dave Foltz, Robb Brumfield, and Prosanta Chakrabarty). An interest in programming is encouraged, but no prior background is required.

Accepted students are guaranteed funding through a mixture of research and teaching assistantships. A research assistantship (funded by the National Institute of Justice) to work on forensic HIV phylogenomics is available for the 2012-13 school year. Some excellent fellowship opportunities are also available for highly qualified applicants through the Louisiana Board of Regents (http://web.laregents.org/programs/borsf-programs/graduate-fellows/).

LSU's Dept. of Biological Sciences has a particular strength in computational evolutionary genetics. LSU continues to invest heavily in the computational sciences, with a recent focus on computational biology. Outstanding resources are available through the Center for Computation and Technology (http://www.cct.lsu.edu/home) and the Louisiana Optical Network Initiative (http://www.loni.org/).

Baton Rouge is located in South Louisiana, one of the most culturally unique locations in the United States (http://louisianatravel.com/). The surrounding area has excellent food, music, festivals, and outdoor recreation. LSU's campus is just over an hour's drive from New Orleans and allows easy access to much of the Gulf Coast.

Informal inquires are welcomed and can be sent to: j e m b r o w n [at] l s u . e d u

Applications for full consideration are due Dec. 12th. For more information on applying, see: http://www.biology.lsu.edu/grad/prospective.html https://app.applyyourself.com/?id=3Dgradlsu For more information on the Brown lab, visit us on the web at: http://www.phyleauxgenetics.org/ For more information on LSU's Dept. of Biological Sciences, visit: http://www.biology.lsu.edu/ Jeremy M. Brown Assistant Professor Louisiana State University Dept. of Biological Sciences 202 Life Sciences Building Baton Rouge, LA 70803

(225) 578-1745

http://www.phyleauxgenetics.org/ jembrown@lsu.edu

MarieCurie ITN 13 Bioinformatics

Dear colleagues,

I would like to inform you of the launch of a new interdisciplinary Marie Curie ITN called EUROTAST. As part of the project, we are currently hiring 13 Early Stage Researchers to work on various projects relating to the history of the transatlantic slave trade. The successful applicants will be recruited from a wide range of disciplines including history, archaeology, social anthropology, genetics and bioinformatics and will be based at 10 partner institutions across Europe. For more information on the individual projects and the application procedure please visit our website at www.eurotast.eu or contact us at enquiries@eurotast.eu.

Kind regards, Hannes Schroeder

-- Dr Hannes Schroeder Centre for GeoGenetics The Natural History Museum Ãster Voldgade 5-7 DK-1350 Copenhagen

+45 35 32 13 46 (office) +45 42 52 36 14 (mobile)

www.eurotast.eu EUROTAST â A Marie Curie Initial Training Network on the History, Archaeology and New Genetics of the Transatlantic Slave Trade

13 PhD Fellowships (in history, archaeology, bioarchaeology, social anthropology, genetics and bioinformatics)

EUROTAST is a new European-funded research network that will bring together an unprecedented range of young researchers to examine the history of the transatlantic slave trade and to explore its long-term effects. As part of the project, we are currently hiring 13 Early Stage Researchers to work on various projects relating to the slave trade. Each Fellowship is equivalent to a 3-year fully funded PhD position and must commence on 1 May 2012. The successful applicants will be recruited from a wide range of disciplines including history, archaeology, social anthropology, genetics and bioinformatics and will be based at 10 partner institutions across Europe. By bringing together researchers from these various fields, we will generate new data that will add to our knowledge of how the slave trade operated and how it impacted the lives of millions of people. For more details on the individual projects please visit our website at www.eurotast.eu or contact us at enquiries@eurotast.eu.

Academic Requirements Eligible applicants for the ESR Fellowships (equivalent to a PhD position) must be in possession of a Masterâs or Bachelorâs degree, in a relevant field. However, individual departments and universities will have their own specific entry requirements. Eligibility criteria set by the European Union for Marie Curie ESR fellowships require that the applicants have no more than 4 years research experience prior to the envisaged starting date.

Marie Curie ITN mobility requirement Researchers can be nationals of any country other than the country of the premises of the host organisation where they will carry out their project. However, the ESR Fellowships only cover the fee levels for EU citizens, not those for students from outside the EU. At the time of the selection, applicants must not have resided or carried out their main activity (work, studies, etc.) in the country where their Fellowship is to be held for more than 12 months in the 3 years immediately prior to the starting date of the fellowship.

Application process Please note that applications are welcomed from any qualified applicants, regardless of gender, ethnicity or country of origin, but will only be considered if eligibility requirements are met and the application guidelines are strictly adhered to. Applicants should send a full CV, a short cover letter outlining briefly why they are suitable for the position(s), and the names of 2 referees to applications@eurotast.eu. For full details on how to apply please visit our website at www.eurotast.eu. Deadline for applications is 31 January 2012.

Hannes Schroeder <hannes.schroeder@gmail.com>

MasseyU HumanGenomicEvolution

PhD Scholarship in Human Genomic Evolution

I am looking for a motivated and productive PhD student to study spatial patterns of human migration and admixture using genome-scale data and cutting-edge computational and statistical analysis. There is scope to accommodate existing research interests, but broadly speaking the successful candidate will develop, implement and test new methods in statistical genetics, and apply these methods to genetic and cultural anthropology datasets.

This computational position requires solid quantitative skills, preferably including some background in statistics and programming. Training in biology and anthropology can be provided as needed, and candidates from non-standard research backgrounds are strongly encouraged to apply. Candidates must already hold a Masters or Bachelors degree with Honors.

Payment of fees and a tax-free stipend are guaranteed for three years, with a probation period of one year prior to full confirmation.

The PhD position will be based in the Computational Biology Research Group at Massey University, New Zealand. My research team has a strong high-impact publication culture, and is firmly embedded in the international scientific community, with extensive collaborative links to the United States, France, Australia and Indonesia. Nevertheless, this position also offers a rare opportunity to experience New Zealand's unique natural and cultural environment. Palmerston North, a university town with a large international community, offers a full range of social and cultural amenities. The city is located close to both mountains and the sea, and presents regular opportunities for hiking, skiing, surfing, and adventure sports.

Information about the Institute of Molecular BioSciences (http://imbs.massey.ac.nz/) and the Computational Biology Research Group (http://massey.genomicus.com/) is available online.

To apply for this position, send the following documents (in PDF format) to Dr Murray Cox (email m.p.cox@massey.ac.nz):

1. A brief statement of research interests, qualifications and experience. 2. A curriculum vitae, including a list of scientific publications (if relevant). 3. The names and contact details of three referees willing to provide a confidential letter of recommendation upon request.

Informal enquiries are welcome. Formal applications are due by 15 January 2012.

Dr Murray P. Cox Institute of Molecular BioSciences Massey University Private Bag 11 222 Palmerston North 4442 NEW ZEALAND

http://massey.genomicus.com/
M.P.Cox@massey.ac.nz

MiddleTennesseeStateU PlantPopGenetics

The Morris Lab at Middle Tennessee State University (MTSU) is recruiting PhD students interested in plant population genetics, phylogeography, and systematics.

Current projects in the lab include reproductive ecology and population genetics of American beech (Fagus grandifolia), and population genetics and systematics of Illicium, a group of basal angiosperms. More specifically, with beech we seek to understand the ecological and anthropological mechanisms that drive shifts in reproductive strategies at different spatial and temporal scales. This project involves molecular work and computer modeling techniques. With Illicium, goals include robust reconstruction of phylogenetic relationships, testing biogeographic hypotheses, and understanding the evolution of divergent floral forms within the genus. This project will include novel molecular approaches to population studies, as well as more traditional revisionary systematic approaches.

Recruited students must be accepted into the MTSU interdisciplinary Ph.D. program in Molecular Biosciences (http://www.mtsu.edu/graduate/mbsphd/). GTA stipends for Fall 2012 are currently available for candidates meeting program requirements. Decisions regarding assignment of these GTA positions are likely to be made by mid-spring, so interested students are encouraged to contact Ashley Morris (ashley.morris@mtsu.edu) soon with a brief description of research interests and a CV. Morris lab website: http://frank.mtsu.edu/~amorris/index.html The MTSU Department of Biology is relatively large (nearly 40 faculty) and supports a diversity of research directions. The university has the largest undergraduate enrollment in the state, with total enrollment of more than 26,000 as of Fall 2011. We are located in Murfreesboro, Tennessee, just a short distance south of Nashville, the fourth largest city in the southeast. We are within a quick drive of some of the most spectacular natural scenery east of the Mississippi River (http://www.friendsofscsra.org/; http://www.fallcreekfalls.org/).

Dr. Ashley B. Morris Assistant Professor Department of Biology Middle Tennessee State University Murfreesboro, TN 37132 (615) 494-7621 amorris@mtsu.edu http://frank.mtsu.edu/~amorris/index.html Adjunct Faculty Department of Biology University of South Alabama Mobile, AL 36688

Web Editor and EC Member-at-large Association of Southeastern Biologists www.sebiologists.org web_editor@sebiologists.org

Ashley Morris <Ashley.Morris@mtsu.edu>

MississippiStateU EvolutionBiology

The Department of Biological Sciences at Mississippi State University invites applications for MS and PhD assistantships in Ecology and Evolution.

Ecology and Evolution is one of three focal research areas in the Department of Biological Sciences at Mississippi State University. Our graduate students work toward either the Ph.D. or M.S. degree. The research interests of the Ecology & Evolution faculty < http://countermanlab.biology.msstate.edu/eebfaculty.html > include conservation biology, ecology of invasive species, evolutionary genomics, landscape ecology, molecular evolution, phylogenetics, plant systematics, population genetics, quantitative ecology, speciation and wetland ecology. MSU houses an array of resources for ecological and evolutionary research, such as extensive botanical collections in our herbarium and greenhouses, a large avian collection of local and exotic birds, the MSU Entomological Museum < http://mississippientomologicalmuseum.org.msstate.edu// > which houses thousands of cataloged specimens, books and journals, high power computing available through the HPCC < http://www.hpc.msstate.edu/ > , access to GIS experts and software through the Geosystems Research Institute < http://www.gri.msstate.edu/ > and ample departmental lab space for molecular work with access to next-generation DNA sequencers.

We urge those interested to visit us online at http://countermanlab.biology.msstate.edu/eeb.html And to contact members of the Ecology & Evolution faculty before applying at http://countermanlab.biology.msstate.edu/eebfaculty.html To submit an application please follow the instructions available for MSU < http://www.grad.msstate.edu/prospective/programs/ > and the Department of Biological Sciences < http://biology.msstate.edu/degrees/graduate/ > .

Brian Counterman <bcounterman@biology.msstate.edu>

NewZealand beetle evolution

Origin and Evolution of New Zealand Beetles

We are seeking potential Ph.D. students interested in a three-year programme to study the evolution and systematics of New Zealand beetles. The student would be part of a team of that will be DNA sequencing representative beetles from all major groups occurring in New Zealand and will also lead an independent study of a monophyletic group their choice to address questions about New Zealand biogeography, beetle systematics, and natural history. The research will involve field work throughout New Zealand, specimen sorting, management, imaging and identification, DNA sequencing and downstream phylogenetic analyses.

The project is based in the New Zealand Arthropod Collection, Landcare Research, Auckland. The DNA sequencing will be performed in the Ecological Genetics laboratory, also at Landcare Research. Enrolment will be through the University of Auckland. There will also be opportunities to interact with researchers at the University of Auckland and the Allan Wilson Centre for Molecular Ecology and Evolution.

Experience in molecular techniques, specimen management/identification, and fieldwork is required.

For further details, please contact

Richard Leschen, leschenr@landcareresearch.co.nz or Thomas Buckley, buckleyt@landcareresearch.co.nz

Thomas Buckley <BuckleyT@landcareresearch.co.nz>

QMULondon EvolutionaryEcol

Queen Mary University of London School of Biological & Chemical Sciences Ph.D studentship, starting September 2012

Ecological and genomic research to optimise the conservation of dwarf birch in Scotland. Supervised by Prof. Richard Nichols and Dr Richard Buggs (School of Biological & Chemical Sciences, QMUL)

You will combine high-throughput genetic sequencing with ecological field- studies to evaluate conservation threats to the rare Scottish montane species: Betula nana (dwarf birch). Training in genetics and statistics will be provided by biologists at QMUL; the CASE partners, conservation charity Trees for Life and consultancy group Highland Birchwoods, will provide training in field biology and conservation management. This study will provide a textbook example of how research can enhance the practical conservation of a rare species.

Dwarf birch is the subject of the studentship for three reasons. (1) The research will solve critical problems identified by Trees for Life and Highland Birchwoods who are actively planting thousands of trees with a recent grant from the Heritage Lottery Fund. (2) Dwarf birch is threatened by climate change, over-grazing and hybridisation â solutions to these problems may be extended to many other conservation projects. (3) We already have genomic sequencing and genome-wide marker development underway for this species.

You will assess whether dwarf birch populations show evidence of loss of genetic diversity using RAD-sequencing to genotype c. 5000 SNP markers in 10 individuals from 10 populations being considered as seed sources for the conservation programme. You will also scan SNP loci for signatures of selection using the method developed by Beaumont and Nichols, combined with analysis of morphological measurements to test the hypothesis that the populations are locally adapted. You will assess the threat from hybridization to dwarf birch by using the genetic data, which can reveal genetic introgression after many generations of back-crossing.

The project will involve at least 9 monthsâ fieldwork in Scotland, working closely with the CASE partners. As well as collecting samples for sequencing, you will survey many natural populations and new plantations of dwarf birch, collecting data on abiotic environmental factors, plant growth, and rare insect species associated with dwarf birch. This data will be analysed to understand the optimal growing conditions for dwarf birch and current threats. Field assessments of how hybridisation affects the natural regeneration of dwarf birch will complement the genetic analyses.

The funding for this studentship will cover College fees and an annual stipend (Â£15,590 in 2011/12) plus a Â£1,000 pa supplement from the CASE partners. Applications are invited from candidates with, or expecting to be awarded, at least an upper-second class honours degree in an area relevant to the project (e.g. Ecology, Biology, Biomedical Sciences, Plant Sciences, Conservation Biology, Bioinformatics).

Given the highly competitive nature of this studentship, we advise candidates to make informal enquiries about the project as soon as possible, by email to Dr Richard Buggs (r.buggs@qmul.ac.uk). To apply, please complete an online application form via the following link: http://www.sbcs.qmul.ac.uk/prospectivestudents/research/studentships . The formal deadline for applications is: 31st January 2012

– Richard Buggs MA, DPhil NERC Post-doctoral Research Fellow School of Biological and Chemical Sciences Queen Mary, University of London London E1 4NS United Kingdom

email: r.buggs@qmul.ac.uk website: http://www.sbcs.qmul.ac.uk/staff/richardbuggs.html office: +44(0)207 882 3058 mobile: +44(0)772 992 0401 twitter: @RJABuggs

Richard Buggs <r.buggs@qmul.ac.uk>

QueenMaryU PlantGenomeEvolution

Impact of polyploidy on plant genome evolution

Supervised by Professor Andrew R. Leitch (School of Biological and Chemical Sciences, email: a.r.leitch@qmul.ac.uk)

This proposal addresses the impact of polyploidy, or whole genome multiplication for the generation of genetic novelty. Polyploidy is a major driving force in the generation of plant biodiversity, indeed 15% of speciation events likely involve polyploidy and probably all plant species have polyploidy in their ancestry.

The project will combine cytogenetics, epigenetics and next generation sequencing (NGS) technologies to determine how polyploidy influences genome evolution. It takes advantage of a series of natural and synthetic polyploids in genus Nicotiana that we have elevated into key model systems. (cf. Leitch & Leitch 2008, Science 320, 481-483). The proposed project will reveal patterns and tempo of polyploid genome divergence and determine how epigenetic modifications modulate or control genetic change. The research output will be a wealth of genomic features of interest to those studying genome evolution, speciation and crop genetics. It will also shed light on the role epigenetics plays at different stages of polyploidy evolution, a hitherto unexplored area of research.

To reach our objectives, you will combine standard and cutting edge cytogenetics, molecular biology and innovative NGS (Illumina platform technology) to: [1] Track down and identify key DNA sequences involved in polyploid species evolution. [2] Determine the genomic organisation of the sequences. [3] Evaluate the extent of epigenetic repatterning with polyploidy. [4] Determine modes and tempo of polyploid-induced sequence divergence. [5] Uncover the key processes associated with polyploid species divergence.

You will receive training in: Bioinformatics - to analyse high volumes of DNA sequence data generated by NGS; experimental design V to conduct and design novel experimental approaches to determine the key sequence players in polyploid species evolution; Laboratory skills - to conduct fluorescence in situ hybridisation and molecular biology procedures (e.g. PCR, qPCR, PFGE) to characterise key repeats involved in polyploid-induced speciation processes; writing and conference presentations- to present your data at international conferences and in high impact journals.

The research will likely involve a research period of a few weeks in the Czech Republic.

To apply, please complete an online application form via the following link: http://www.sbcs.qmul.ac.uk/-prospectivestudents/research/studentships . The formal deadline for applications is: 31st January 2012.

Andrew Leitch <a.r.leitch@qmul.ac.uk>

QueensU Belfast Nutrition Fitness

DEL funded PhD position at Queen's University Belfast

You are what you eat: the nutritional ecology of reproduction and ageing

Supervisors: Dr Sheena Cotter, Prof. Jaimie Dick (Queen's University Belfast)

Dr Rebecca Kilner (University of Cambridge), Prof. Ken Wilson (Lancaster University)

Disparate organisms, from humans to slime moulds, can balance their intake of different nutrients to maximize fitness. However, it is unknown whether this balance changes as organisms age and it is unclear whether organisms can offset the costs of reproduction through selective resource intake. We propose to use the burying beetle as a model system for addressing these general issues. Burying beetles are ideal for such work because we already know that reproductive investment is modified with age (Cotter et al 2011) and that burying beetles experience fitness costs associated with reproduction (Ward et al 2009, Cotter et al 2010). This project will investigate the costs of reproduction and ageing in a nutritional context and determine whether individuals can modify their diet to balance the needs of reproduction and self-maintenance.

The aim of this PhD studentship is to understand how resources are partitioned between different traits that contribute to fitness. The student will use the geometric framework for nutritional analyses (Simpson & Raubenheimer 1995) to assess which nutrient intakes maximize fitness at different ages and reproductive stages. Dietary manipulations will be then be used to probe the costs of reproduction, and choice tests employed to test whether individuals can ameliorate costs through selective nutrient intake.

Training

The student will receive training in:

* Insect rearing, collection and pedigrees * Dietary manipulations * Immunity assays * Statistical analysis

Applications

Application procedure: Informal enquiries to Dr Sheena Cotter, Tel: 028 90972691, Email: s.cotter@qub.ac.uk

Applications via https://dap.qub.ac.uk/portal/user/-u_login.php Closing date 10/1/12

Eligibility

The DEL studentship (equivalent to a NERC studentship) is available in full to UK students only and on a fees-only basis to EU students. Students from outside the EU are not eligible for funding.

Sheena Cotter NERC Postdoctoral Fellow/Proleptic Lecturer in Ecology and Evolutionary Genetics

School of Biological Sciences Queen's University Belfast Medical Biology Centre 97 Lisburn Rd Belfast BT9 7BL

Tel: 028 9097 2691 Fax: 028 9097 5877 Email: s.cotter@qub.ac.uk Webpage: http://www.qub.ac.uk/-schools/SchoolofBiologicalSciences/Staff/-DrSCCotter/ Sheena Cotter <s.cotter@qub.ac.uk>

TowsonU ParasitismEvolution

Graduate Position: Towson University V North American Nylanderia Social Parasite Study

Seeking a masters-level graduate student to participate in a study of a recently discovered socially parasitic ant species in genus Nylanderia. This project offers the opportunity to investigate the evolution of social parasitism within ants generally, and specifically within the genus Nylanderia. This project will involve extensive fieldwork, coupled with lab rearing of ant colonies and molecular data collection and analysis. Potential students should be enthusiastic, highly motivated, capable of working independently, and committed to a graduate education. A teaching assistantship is available for this position, along with summer support. Experience with ants is not necessary if the student has the discipline and tenacity to learn about this fascinating group of animals. Interested students should contact Dr. John LaPolla at jlapolla@towson.edu. Interviews of potential students will begin in mid-January, 2012.

For further information about the Towson University Biology Graduate Program see: http://wwwnew.towson.edu/biologicalsciences/-graduate_program.html John S. LaPolla, Ph.D. Associate Professor of Biology Co-Director, Biology Graduate Program Dept. of Biological Sciences 8000 York Road Towson University Towson, MD 21252 USA

phone: 410-704-3121 fax: 410-704-2405

“Lapolla, John S.” <JLapolla@towson.edu>

TuftsU SpeciationBiology

Graduate Position: Speciation Biology at Tufts

The Dopman Lab at Tufts University is seeking a doctoral student for Fall 2012 with an interest in speciation biology. The long-range goal of our research program is to gain a better understanding of how genes evolve to restrict gene flow within the context of accumulating isolating barriers that ultimately produce new species. As most life on earth arises following the combined action of multiple isolating barriers, some our deepest insights will come by genetically dissecting barriers that are widespread across taxa and eliminate disproportionate amounts of gene flow between daughter lineages. Emerging research reveals that ecological and behavioral barriers satisfy both criteria.

The Ostrinia genus is well suited to studying speciation because we have information on genetics, ecology, and sexual communication for numerous species. One of the better known Ostrinia is the European Corn Borer (ECB) moth. The ECB is a commonly cited model for speciation biology because sympatric “strains” are at the early stages of divergence and therefore provide a window into the evolutionary process of speciation. Of 12 potential isolating barriers between ECB strains, seven significantly reduce gene flow and five are either behavioral or ecological in nature. Current efforts in our lab are dedicated to elucidating the genetic basis for phenotypes underlying relevant ecological and behavioral barriers between strains, and determining the consequences of this variation for gene flow.

We seek a creative and motivated graduate student to work on speciation using the ECB as a model, but the potential for developing new research directions is high. Students must have the ability to work with others and a sense of humor, both of which are needed to make science fun and worthwhile. A strong undergraduate background in evolutionary biology is required, as is prior research experience. Relevant and highly desirable experience includes application of molecular genetic techniques or computational analysis of gene or genome/transcriptome data.

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

Interested individuals should immediately contact Erik Dopman (erik.dopman@tufts.edu) and provide in PDF format the following documents: (1) a 1-2 page cover letter that includes a statement of research interests, relevant educational background, and prior research experience; and (2) a CV that includes GPA/GRE scores and the names and contact information of 2-3 references. Applications to the graduate program are due on 15 January, with departmental review occurring shortly thereafter. (http://ase.tufts.edu/biology/-graduate/index.asp).

Erik.Dopman@tufts.edu

UAntwerp BehaviouralEvolution

The Evolutionary Ecology Group at the University of Antwerp has a vacancy for TWO PHD STUDENT POSITIONS in the following project: The role of exploration and experience in the development of spatial behaviour: home ranges and dispersal in the Great Tit

Starting date: 1st March 2012 Application deadline: 3rd January 2012

Project description

This project is part of a larger research program on patterns and processes of mobility and dispersal in animal populations. It is also closely linked to our long-term studies on ecology and behaviour of great and blue tits in nest-box populations. The general aim of this project is to test two general hypotheses on spatial behaviour, using a combination of field data, behavioural experiments and quantitative genetics: (a) individuals build up spatial information in the course of their life which they use in subsequent movement decisions, and this creates carry-over effects between life stages; (b) individuals differ consistently in their use of spatial information, and this explains part of the within-population variation in mobility patterns.

Briefly, we will collect detailed information on dispersal, exploration movements and home-ranges of two full cohorts of great tits throughout their lifetime. This information will be linked to a number of behavioural tests on exploration behaviour in laboratory and semi-natural contexts, and to results of experiments manipulating spatial behaviour. The project has funding for two PhD students who will work closely together, but for their dissertation each will focus on different parts of the project.

The first PhD project will focus on individual variation in behaviour. The student's main task will be to design and perform experiments in lab and field to study exploration behaviour in different contexts, and relate this to lifetime spatial behaviour of the same birds. In addition the student will devise experimental field procedures aimed at manipulating spatial experience of birds.

The second PhD project will focus on the analysis of lifetime patterns of mobility, with particular attention to the roles of heritable variation and prior experience. The statistical analysis will involve both linear and discrete-choice models. This part of the thesis will be partly co-supervised by Peter Goos of the Statistics Core Facility. The student will also analyze pedigree data with Animal models to obtain quantitative genetic estimates of heritable variation in traits associated with spatial behaviours. Both students will participate in collecting field data on mobility as well as routine population data.

Requirements

We are looking for enthusiastic and broad-minded candidates with a Master degree in Biology, a specialization in behavioural ecology or evolutionary ecology, excellent study grades, and a particular interest in studying processes that shape animal movement patterns. For the first position we prefer a student with a particular interest in experimental approaches for testing behavioural hypotheses, both in the lab and the field. Affinity with studying birds, in captivity as well as in the field, is an advantage for both positions. For the second position, preference goes to a candidate with strong statistical skills and an interest in modelling complex data. An additional degree in statistics is a particular advantage.

What we have to offer:

- We offer a PhD-scholarship for a maximum of four years (with a net salary of ca 1800 euro/month) with the aim of defending a PhD-dissertation at the end of the fourth year. After one year, the performance of the candidates will be evaluated to decide whether the scholarship will be continued.

- You will enrol in the Antwerp Doctoral School training program (www.ua.ac.be/ads) allowing you to take part in various courses, training programs and conferences within and outside the University.

- You will work in a team of several PhD students, postdocs and technical staff involved in the long-term great and blue tit study

- You will be member of the Evolutionary Ecology group, a dynamic and internationally-oriented research group that combines field, lab and modelling approaches to study various questions in ecology and evolutionary research, mainly focusing on birds and mammals (www.ua.ac.be/eveco).

- Starting date is 1st March 2012

Application

Applicants should send their complete CV, a one-page statement of research interests and motivation for this project, and contact information of two referees who can supply letters of recommendation upon our request.

Please send applications by email before 3rd January 2012 to: Erik Matthysen (erik.matthysen@ua.ac.be)

For more information please contact Erik Matthysen at the same address,

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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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UBern InvasionPopulationGenetics

PhD position in

Molecular and organismic invasion ecology

We are looking for a PhD candidate merging population genetics and organismic ecology to gain a more mechanistic and evolutionary understanding of invasion ecology. The project focuses on Arion lusitanicus (Spanish slug) which is regarded as one of the hundred most invasive alien species in Europe, and a serious pest in agriculture and gardening. Genetic and ecological approaches will be combined for investigating the history and mechanisms of the ongoing invasion. The project aims at the identification of invasion and colonization routes of the slug, and at assessing the ecological and evolutionary consequences of the invasion for the native relatives and related ecosystem processes. The project will combine molecular marker development using high-throughput sequencing, DNA sequencing, microsatellite genotyping, as well as experimental approaches including laboratory breeding, competition and field experiments.

We are seeking a highly motivated, independent PhD candidate who is willing to perform fieldwork, molecular laboratory work, and state-of-the-art statistical modelling of genetic and ecological data. The ideal candidate has a strong background in ecology and evolutionary biology, especially population genetics and phylogeography, and experience with molecular laboratory work and fieldwork. Experience with bioinformatics is a plus but not essential. A degree equivalent to a biology diploma or M.Sc. and a valid driver's license is required. Good written and spoken English is expected. Some knowledge of German or French would be beneficial for living in Switzerland but it is not necessary. The working language in our institute is English.

You will be supervised by Gerald Heckel (population genetics) and Eva Knop (community ecology). We offer a stimulating research environment with excellent facilities for laboratory work, computational analyses and ecological experiments. Information on the institute, the University of Bern, or life here in general can be obtained from http://www.iee.unibe.ch and http://-/bern.ch/. For informal inquiries, please contact gerald.heckel@iee.unibe.ch.

The position is funded for three years (pending final approval), and the anticipated starting date is February 1st 2012 or soon thereafter. Please send your application including a letter outlining your past research, particular motivation for this position and specific experience (max. 2 pages), CV, list of publications (if available), abstract of Master or Diploma thesis and contact details of 2-3 referees in a single (!) pdf file to gerald.heckel@iee.unibe.ch.

PD 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 Fax: +41 31 631 48 88 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 "Heckel, Gerald (IEE)" <gerald.heckel@iee.unibe.ch>

UBielefeld NewtPopGenetics

PhD position Population genetics & demographic analysis of newt populations

University of Bielefeld, Dep.of Animal Behaviour, Unit Molecular Ecology and Behaviour & Institute of Evolutionary Biology and Environmental Studies, University of Zurich, Switzerland

Application deadline 18.12.2011

[printable version http://www.dzg-ev.de/-de/stellenboerse/ausschreibungen/2011/-phd_bielefeld2011d.pdf] 1 PhD Position in population genetics and demographic analysis of newt populations

Due to their limited dispersal ability amphibians are generally considered to be structured as metapopulations. However, new studies show that the dispersal propensity of amphibians has been vastly underestimated in the past, thus challenging this common view. Aimed as a case study on a typically pond-breeding amphibian species this research project analyses the population structure of crested newts (Triturus cristatus) in the north of Germany (Hamburg). By applying new and powerful molecular approaches to determine the spatial extent of crested newt populations without any a priori assumption on the level of three spatial scales this project will explore the real spatial extent of crested newt populations by overcoming potential biases of past approaches. The chosen study design will allow to identify the degree of population connectivity and gene flow between breeding sites of crested newts and to combine these genetic data with demographic parameters estimated from mark-recapture data (birth, death, immigration and emigration) of breeding sites on a local scale. The results of the study will provide new and deep insights into the population dynamics of a typically pond-breeding amphibian species in evolutionary and ecological terms without confounding past a priori assumptions on the structure of amphibian populations.

We are looking for a highly motivated PhD candidate who is willing to perform intensive field work (collection of genetic and mark-recapture data), molecular laboratory work and state-of-the-art statistical modelling of genetic and mark-recapture data. Field work will be performed near Hamburg, molecular laboratory work and analyses will be carried out in the group of Sebastian Steinfartz at the University of Bielefeld and analysis of demographic data will be done at the University of Zurich in cooperation with Benedikt Schmidt. While based in Hamburg a close cooperation with the groups of Jörg Ganzhorn (Department of Ecology) and Alexander Haas (section of Herpetology) at the Zoological Institute of the University of Hamburg is intended. We are searching for a candidate who is highly flexible and willing to challenge the successful integration of molecular and first hand collected field and ecological data on a high level. In order to achieve this goal the successful candidate will be based at the three different locations (i.e. in Bielefeld, Hamburg and Zurich) with excellent research conditions and groups of highly motivated people with a strong interest and research background in organismic ecology and evolution. The position (65% TV-L E13) will start at the beginning of February 2012 and is funded by the German Research Foundation (DFG) for three years.

Please send your application until December 18st, including a curriculum vitae, a letter of motivation why you are interested in the project and addresses for references (e-mail addresses and telephone numbers) of two referees as a merged PDF to:

Dr. Sebastian Steinfartz Assistant Professor in Molecular Ecology and Behaviour Department of Animal Behaviour University of Bielefeld Germany Telephone: +49 521 106 2653 Email: sebastian.steinfartz@uni-bielefeld.de

We expect to interview candidates in early January in Bielefeld.

Inquiries and requests on the project should be directed either to Sebastian Steinfartz or to

Dr. Benedikt Schmidt KARCH Passage Maximilien-de-Meuron 6, 2000 Neuchâtel, Switzerland Switzerland Telephone: +41 32 725 72 06

benedikt.schmidt@ieu.uzh.ch

UBristol Drosophila LifeHistoryEvolution

UK and UK resident EU applicants are invited for a competitively-funded BBSRC studentship to begin Sept 2012

Closing date 10th Feb 2012.

Divergence in life history along ecological gradients in Australian rainforest Drosophilia: how does early growth affect longevity and immunity?

Supervisors: Dr Jon Bridle (University of Bristol) and Dr Nick Priest (University of Bath)

Evolution is a multiple optimisation problem: selection to optimise one trait typically has negative effects on others. Classical trade-offs include egg size and number, development rate and competitiveness, and fecundity and longevity but we lack empirical data on how consistent these correlations are across populations of the same species. Quantifying correlations between fitness traits, especially where they act differently on different life stages or genders, is critical to understand longevity and health in natural populations.

This studentship will explore how insect life histories are shaped by local selection. We are currently testing adaptive divergence in Australian Drosophila birchii along four 2-10 km ecological gradients, and are measuring 400+ isofemale lines from different altitudes for stress resistance, female fecundity and male mating success. These lines show remarkable increases in laboratory productivity at higher altitudes, implying strong trade-offs in the field. The student will examine how these traits affect the rate of ageing and the ability to resist fungal infections. Previous analyses of such Drosophila traits have revealed consistent associations between immunity, behaviour, longevity, and temperature.

We are looking for a highly-motivated student with a passion for evolutionary biology and genetics. (S)he will receive training in life history evolution theory, quantitative genetics, and modern molecular techniques, and will measure genetic variation in life history traits in Drosophila, and (most crucially) how these correlations vary among sites. In addition, (s)he will assay genome-wide linkage disequilibria in SNPs, allowing exploration of the genomic basis for these trait correlations.

This a competitively-funded studentship; funding will only be awarded to those research projects that attract the brightest and most enthusiastic candidates.

For more details, and to apply see:

http://www.bristol.ac.uk/science/prospective/-sciencesdtp.html

For informal enquires, please contact Jon Bridle directly (jon.bridle@bristol.ac.uk)

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

UCapeTown PlumagePolymorphism

Plumage polymorphism, with different plumage morphs occurring in the same age and sex classes of a breeding population, occurs in around 3.5% of bird species and has fascinated evolutionary ecologists for many years. Polymorphism is common in raptors, with around 30% of species expressing more than one colour morph. The Black Sparrowhawk (Accipiter melanoleucus) is a polymorphic raptor that exhibits a common light morph and a rarer dark morph. This species has recently colonised the Cape Peninsula in the Western Cape of South Africa where we have monitored the population for over 10 years. In this population the frequencies of the morphs are reversed with around 80% being dark morph birds.

Throughout most of its traditional range in southern Africa the Black Sparrowhawk breeds in the dry winter months, however in the Western Cape the species breeds during the wet winter months. This PhD will test the hypothesis that there is a selective advantage to being dark in these conditions.

The project will seek to understand the origin, adaptive function and maintenance of plumage colour variation in this species through two key components: an ecological study, which will test whether the different morphs have a selective advantage in different habitats or under different climatic conditions, and a molecular study to i) establish the role of the melanocortin-1 receptor (MC1R) in the evolution of plumage morphs in Black Sparrowhawks, and ii) to test the alternative hypothesis that plumage polymorphisms are maintained through limited dispersal and genetic drift.

The successful applicant will have an MSc degree in Zoology (or equivalent), relevant ornithological field experience and be available to start in early 2012. Students with a good BSc Honours degree and experience may be considered for registration at MSc level, with the intention to upgrade to PhD level. Funding is secured for an annual R100 000 CoE bursary (R75 000 for MSc) for three years and for project running costs. To apply, please send a CV (including your academic record & names and contact details of three referees) and a short motivation for why you wish to undertake this research to Hilary Buchanan at hilary.buchanan@uct.ac.za. For more information on the project, please contact: Dr Arjun Amar (arjun.amar@uct.ac.za) or Dr Jacqueline Bishop (jacqueline.bishop@uct.ac.za).

Closing date: 10 January 2012

Dr Jacqueline M Bishop Department of Zoology University of Cape Town Private Bag, Rondebosch 7701 South Africa

email: jacqueline.bishop@uct.ac.za or jbishop.uct@gmail.com tel no. +27 (0)21 650 3631 fax no. +27 (0)21 650 3301

Jacqueline.Bishop@uct.ac.za

UCincinnati EvolutionaryGenomics

The Baucom lab at the University of Cincinnati is currently recruiting PhD students interested in Plant Ecological and Evolutionary Genomics.

Current projects in the lab are focused on the genetic basis of trade-offs in plant defense, the evolution of plant 'weediness' and invasiveness, the impact of the mating system and gene flow on the evolution of herbicide resistance, and the influence of the soil metagenomic community on the evolution of important plant traits. We focus on the model weed species *Ipomoea purpurea* (the common morning glory) for the majority of these questions, although the potential to work with other plant species exists. We utilize manipulative field and greenhouse experiments, coupled with various molecular and genomics techniques, such as RNA-seq and transcriptome analysis. Students who train in the Baucom lab will learn how to utilize and manipulate large genomic datasets and thus basic bioinformatics techniques.

The Department of Biological Sciences at the University of Cincinnati hosts a strong group of evolutionary ecologists and biologists that are organized into Environmental Change and Biological Resilience (ECBR) and Sensory Biology, Behavior and Evolution (SBBE).

The training environment thus has an emphasis on evolution, ecology, genetics and behavior. Cincinnati, or the Queen city, is a large metropolitan city home to ~400K, a professional baseball and football team, a world-renowned zoo and almost weekly beer festivals. There are many distinct neighborhoods in this river city, excellent restaurants, and yet also plenty of camping and hiking in nearby northern Kentucky.

Interested students should contact Gina Baucom at regina.baucom@uc.edu, including a brief description of research interests and a CV. Applications to the graduate program are due by January 1, 2012.

The Baucom Lab: http://homepages.uc.edu/~ baucomra/Baucom_Lab/Home.html UC Biological Sciences graduate program information: http://www.artsci.uc.edu/collegedepts/biology/grad/ – Regina S. Baucom Assistant Professor Dept of Biological Sciences 721 Rieveschl Hall University of Cincinnati Cincinnati OH 45221 (513) 556-9721 Baucom Lab < http://homepages.uc.edu/ ~ baucomra/Baucom_Lab/Home.html > gina.baucom@gmail.com

Regina Baucom <gina.baucom@gmail.com>

UEdinburgh VirulenceEvolution

Funded PhD position available (full funding only for UK residents), evolution of bacterial virulence. (for application details see http://www.findaphd.com/search/ProjectDetails.aspx?PJID=36260&LID=455)

Bacterial pathogens are overwhelmingly opportunistic and typically grow in distinct environments causing no harm to humans. The major challenge in this proposal is to build new theory for virulence evolution in opportunistic pathogens, with a focus on food-borne pathogens, in particular pathogenic strains of E. coli.

The evolution of virulence is a major focus in evolutionary biology, and has resulted in a large body of theory based on the assumption that virulence is a result of selection for virulence factors (VFs) that enhance within-host growth, survival or between-host transmission. While this theory has met with success for specialist pathogens (e.g. malaria), for many opportunistic pathogens these proposed countervailing growth/transmission benefits of VF expression are difficult to identify in hosts, casting a large body of theory into doubt. To answer this challenge, we will develop and test a novel theoretical framework for virulence dynamics across multiple environments (from farm to fork). This project promises to deliver a significant redirection of virulence evolution theory, to capture the environmental and regulatory complexity of virulence in bacterial opportunistic pathogens.

In addition to a core theoretical component, experimental investigations will also be encouraged, to foster an integrative training spanning molecular microbiology, systems biology, ecology and evolution.

Funding Notes: This project is eligible for the EASTBIO Doctoral Training Partnership. This opportunity is only open to UK nationals (or EU students who have been resident in the UK for 3+ years) due to restrictions imposed by the funding body.

Applications are accepted all year round but note that supervisors are asked to nominate their favoured candidates for our studentships competition by Jan 10th 2012. For application procedure, see http://www.findaphd.com/search/ProjectDetails.aspx?PJID=36260&LID=455). Interviews will be held week beginning 6th February 2012

Sam Brown Centre for Immunity, Infection and Evolution University of Edinburgh West Mains Road, Edinburgh EH9 3JT http://brown.bio.ed.ac.uk/ http://ciie.bio.ed.ac.uk/ sam.brown@ed.ac.uk

<sam.brown@ed.ac.uk>

sampaulbrown@gmail.com

UGlasgow EvolutionaryPhysiology

PhD studentship U Glasgow: Physiology of annual cycles / moult / climate change (UK residents)

A textbook example in evolutionary biology involves changing frequencies of colour morphs, e.g. of light and dark Peppered moths, due to selection. For some long-lived species, corresponding need for phenotypic colour-adjustment recurs periodically, for example to match the white of snow cover in winter. Because such changes must be finely coordinated with environmental seasonality animals may be vulnerable to currently observed rapid changes in phenology. At present, our understanding of the physiological mechanisms that regulate periodic processes is insufficient for predicting to which extent animals can adapt to changing seasonality. To address this deficit, we use interdisciplinary approaches to study annual cycles of birds in the context of climate change. We look for an open-minded student interested in joining a diverse supervisory team with strengths in physiology, evolutionary ecology and chronobiology. The project is positioned at the University of Glasgow, Institute of Biodiversity, Animal Health and Comparative Medicine

(http://www.gla.ac.uk/researchinstitutes/bahcm/).

Project details:

"Tracking the seasons: tissue-based memory for avian moult?"

Supervisory Team: Barbara Helm, Neil P. Evans, Michelle Bellingham,

Jane E. Robinson, Peter J. Sharp, and Gerald A. Lincoln

One of today's major scientific challenges is to understand the effects of global climate change on ecosystem health. For most wild organisms mismatches between seasonally timed activities and environmental conditions can result in fitness costs to the individual as well as the whole population. For example, in species that exhibit geographically fine-tuned seasonal colour dimorphism (eg Ptarmigan), changing weather patterns could lead to temporal colour mismatching that heighten predation risk. In response to changes in ambient temperature some species have adjusted their seasonal migration or breeding distribution and are now exposed to photoperiods that differ from those to which they had formerly adapted. We thus need a greater understanding and ability to predict the costs and consequences of climate change. Birds provide an ideal model to address this as their seasonal activities in the wild are relatively well-known. Avian moult is an easily measurable trait that affects locomotor performance, thermoregulation, ornamentation and camouflage, all of which are linked to fitness. Therefore, it can be used to study scheduling in evolutionary and ecological contexts, as well as for investigating regenerative, cyclical processes and how these can be affected by climate change. This PhD project will address mechanisms of annual timing, specifically of avian moult, from a physiological perspective, with the aim of establishing links to seasonal processes in free-living birds. Funding: The project is NERC-funded for a duration of 3 years (UK residents only; £13,590 pa + full fees).

Eligibility and application: Interested candidates must have been resident in the UK throughout the 3-year period preceding the date of application, not wholly or mainly for the purposes of full time education. Applicants should have received a grade of 2:1 (B) or equivalent in their undergraduate degree; applicants who do not meet this threshold but have completed other postgraduate training programmes might be considered.

Please send full CV, contact details of at least 2 referees, and cover letter indicating motives and qualifications to Lorna Kennedy (lorna.kennedy@glasgow.ac.uk).

Closing Date – January 20, 2012

Further Information - To obtain more detailed information about the project, please contact the primary project supervisor, Barbara Helm (helm@orn.mpg.de). Please also see details on the College of Medical, Veterinary and Life Sciences Graduate school website (http://www.gla.ac.uk/colleges/mvls/graduateschool/informationforprospectivestudents/).

Barbara Helm <helm@orn.mpg.de>

UGlasgow ParasiteResistanceEvolution

PhD Studentship: University of Glasgow

Applied evolution: an experimental approach to investigating how the interaction between parasite life history strategies and control measures affects rates of resistance evolution

Supervisory Team: Barbara Mable, Jan Lindström (Institute of Biodiversity, Animal Health & Comparative Medicine), Paul Johnson (Robertson Centre for Biostatistics)

Resistance management is a key concern in human and veterinary medicine and in agricultural production systems. Although theoretical population genetics models predict factors that might influence resistance evolution in pathogens, potential interactions among pathogen attributes (e.g. mating system, life history traits, rate of gene flow between resistant and susceptible genotypes) and specific control measures (e.g., frequency and dosage of chemical applications) remain unclear. This study will take an experimental evolution approach to understanding the influence of such interactions on rates of resistance evolution, using nematodes as a model. Due to the difficulty of manipulating parasites in wild hosts, resistance evolution previously has been studied in the free-living but hermaphroditic and selfing nematode Caenorhabditis elegans. However, since most parasitic nematodes are outcrossing, this study will use Caenorhabditis remanei, whose mating system is more similar to that of most parasitic nematodes. The rate of evolution of resistance will be evaluated by treating worms with anthelminthics, applied at different frequencies and dosages, under experimentally varied reproductive modes and population demographics. The project is interdisciplinary and the student will receive training in a wide range of approaches, including experimental design, statistical analyses, experimental evolution, life history and population genetics theory, resistance management strategies, host- pathogen interactions, basic molecular and genomic techniques, genetic manipulation through transformation, and microbiology.

There is much potential for the student to develop specific strategies and possibly to extend the scope of the project to consider rates of evolution of other traits (e.g., longevity) or to investigate the genetic basis of resistance evolution. However, initial focus will be on the following questions: 1) Does manipulation of the mating system (outcrossing vs inbreeding; single vs polygamous mating) of C. remanei affect the rate of resistance evolution to anthelminthics? 2) Do particular life history strategies (reproduction early or late) affect the rate of resistance evolution? 3) How does anthelminthic dosage or frequency of application affect the rate of resistance evolution? 4) How does gene flow between susceptible and resistant worms affect the rate of resistance evolution? 5) Is there an interaction between dosage, mating system and life history traits?

Funding Details -

NERC standard stipend (£13,590 pa + full fees)

Duration - 3 years

Who is eligible? The candidate must have been ordinarily resident in the UK throughout the 3-year period preceding the date of application for an award, not wholly or mainly for the purposes of full time education.

More details described here: http://www.nerc.ac.uk/funding/application/studentships/ How to apply -

Full CV + contact details of at least 2 referees

Cover letter indicating motives and qualifications for undertaking the proposed program

Please send applications to: Barbara Mable (Barbara.mable@glasgow.ac.uk)

Deadline: We are hoping to find a student who could start early in the New Year so applications will be reviewed as soon as received.

Relevant Publications by the Supervisory Team:

1. Johnson, P.C.D., J.D. Hadfield, L.M.I. Webster, A. Adam, B.K. Mable and L.F. Keller. 2010. Bayesian paternity analysis in a parasitic nematode, Trichostrongylus tenuis. Heredity 104: 573-582. 2. Webster, L.M.I., P.C.D. Johnson, A. Adam, B.K. Mable and L.F. Keller. 2008. Absence of three known benzimidazole resistance mutations in Trichostrongylus tenuis, a nematode parasite of avian hosts. Veterinary Parasitology 158(4): 302-310.

3. Webster, L.M.I., P.C.D. Johnson, A. Adam, B.K. Mable and L.F. Keller. 2007. Macrogeographic population structure in a parasitic nematode with avian hosts. Veterinary Parasitology 144(1- 2): 93-103.

4. Mable, B.K. and D.J. Pree. 1993. Comparison of assay techniques for measuring dominance effects of resistance to dicofol in European Red Mites (Panonychus ulmi Koch). J. Econ. Entomol. 86:275-282.

5. Mable, B.K. and D.J. Pree. 1992. Stability of dicofol resistance in European Red Mite, Panonychus ulmi (Koch) populations on apples in southern Ontario. J. Econ. Entomol. 85:642-650.

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UHalle HostParasiteEvolution

PhD position in host-parasite evolution at the University Halle (Germany)

We are looking for a highly motivated PhD student to work on the evolution of host parasite interactions with the honeybee and its parasites as model system. The doctoral student will contribute to the national research network FIT BEE. Research work will involve laboratory as well field work. The ideal candidate should have experience with standard molecular genetic methods (PCR, real time PCR etc.) and must be willing and able to work with living honeybees. Experiences with host parasite evolution would be an asset.

Work place is the Molecular Ecology Work Group (http://www.mol-ecol.uni-halle.de/) at the University of Halle-Wittenberg in Halle (Saale), Germany. The position is available for 2 years, annual salary is according to standard German PhD scale TV-L E13 (50%) and we aim for the 01.03.2012 as starting date.

Please send your application (giving-D 237/2011 as reference) in a single pdf file including CV, statement of research interests (maximum 1 page) and contact details of two referees to robin.moritz@zoologie.uni-halle.de until the first week of January 2012.

Bernhard Kraus <kraus@zoologie.uni-halle.de>

UHelsinki HostParasite

PhD position (four years): Multilevel selection and host-parasite interactions

The newly appointed Centre of Excellence in Biological Interactions funded by the Academy of Finland calls for applications for a PhD position focusing on multilevel selection and host-parasite interactions.

The key objective is to conduct a comparative analysis of immune functions and diversity of immune genes in social and solitary insects. The aim is to shed light onto life history trade-offs under multiple levels of selection. The approaches entail field work, laboratory experiments and molecular analyses.

A successful candidate will be highly motivated with MSc in the field of evolutionary biology, ecology, or a related discipline. The student will work in the field, on field-collected material, on laboratory experiments, immune challenges and assays as well gene expression analyses. Willingness and ability to work in the field is essential, and any prior experience in immune assays on insects, experimental design, and molecular techniques is a bonus. She/he will be given guidance especially in the beginning, but will be expected to become more independent towards the end of the PhD.

The partners of the Centre of Excellence are located at the University of Jyväskylä, Finland (Prof. Johanna Mappes and Prof. Jaana Bamford), University of Helsinki, Finland (Prof. Liselotte Sundström) and Australian National University (Prof. Hanna Kokko). We offer a stimulating, creative and international working environment, modern facilities, reliable funding, excellent career prospects and nice colleagues. This position is based at the University of Helsinki but some of the work will be carried out at the University of Jyväskylä.

Salary: 2000EUR-2600EUR (gross) monthly including health insurance and other benefits

Application deadline: 31 December 2011

Starting date: The position is available from 1 January 2012, starting date is negotiable

Application should include 1) a cover letter with a statement of research interests, 2) CV and 3) names and contact details of two references. Applications and informal inquiries should be addressed to Prof. Lotta Sundström liselotte.sundstrom@helsinki.fi

eira.h.ihalainen@jyu.fi

UHelsinki SocialInsect

PhD position (four years): When self becomes non-self: disruption of a cohesive social entity

A PhD position is open in the newly appointed Centre of Excellence in Biological Interactions funded by the Academy of Finland.

The PhD student will focus on morphological, behavioural and genetic traits promoting reproductive isolation, and consequently disruption of a cohesive social entity. The project will utilise incipient stages of social parasitism in Myrmica ants as a model system, and will include field work as well as morphometric and genetic analysis by using DNA microsatellites and mtDNA. Moreover, studies on recognition systems by analysing surface chemistry are included.

We are looking for a candidate with an MSc in evolutionary biology, ecology, or a related discipline. A successful candidate will have a strong background either in molecular ecology and/or social insect biology, because both field and laboratory studies will be essential parts of the project.

The partners of the Centre of Excellence are located at the University of Jyväskylä, Finland (Prof. Johanna Mappes and Prof. Jaana Bamford), University of Helsinki, Finland (Prof. Liselotte Sundström) and Australian National University (Prof. Hanna Kokko). We offer a stimulating, creative and international working environment, modern facilities, reliable funding, excellent career prospects and nice colleagues. This position is based at the University of Helsinki.

Salary: 2000EUR-2600EUR (gross) monthly including health insurance and other benefits

Application deadline: 31 December 2011

Starting date: The position is available from 1 January 2012, starting date is negotiable

Application should include 1) a cover letter with a statement of research interests, 2) CV and 3) names and contact details of two references. Applications and informal inquiries should be addressed to Dr. Perttu Seppä perttu.seppa@helsinki.fi

eira.h.ihalainen@jyu.fi

UHouston EcologyEvolution

GRADUATE OPPORTUNITIES IN ECOLOGY AND EVOLUTIONARY BIOLOGY

The Department of Biology and Biochemistry at the University of Houston (UH) welcomes applications for its graduate program in Evolutionary Biology and Ecology for Fall 2012. The following faculty in the area of Evolutionary Biology and Ecology have opportunities available for their labs:

Blaine Cole (bcole@uh.edu) - Evolution and social behavior Dan Graur (dgraur@uh.edu) - Theoretical molecular evolution Dan Wells (dwells@uh.edu) - Evolution of development and behavior Diane Wiernasz (dwiernasz@uh.edu) - Sexual selection Elizabeth Ostrowski (eostrowski@gmail.com) - Evolutionary genetics and multicellularity George Fox (fox@uh.edu) - Experimental evolution and origin of life Gregg Roman (gwroman@uh.edu) - Evolution of behavior Rebecca Zufall (rzufall@uh.edu) - Genome and molecular evolution Ricardo Azevedo (razevedo@uh.edu) - Evolutionary genetics Steve Pennings (spennings@uh.edu) - Community ecology Tim Cooper (tcooper@central.uh.edu) - Experimental evolution Tony Frankino (wafranki@central.uh.edu) - Evolution of complex traits Yuriy Fofanov (yfofanov@bioinfo.uh.edu) - Evolutionary bioinformatics

For more information regarding the Evolutionary Biology and Ecology graduate program at UH see:

http://www.bchs.uh.edu/graduate/prospective-students/index.php http://www.uh.edu/admissions/-graduate/ The deadline for application of prospective students is March 1st, 2012, but students are encouraged to apply as early as possible.

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

razevedo@uh.edu

UIllinois IntegratedGenomics

The School of Integrative Biology at the University of Illinois is recruiting PhD students through a newly funded IGERT training grant, Vertically Integrated Training With Genomics (VInTG). VInTG students will address two grand challenges in biology: 1. How do genomes interact with the environment to produce biological diversity? 2. How are biological systems integrated from molecules to ecosystems? Our training model uses a back to the future approach where students will integrate modern, genome-enabled biology with a traditional, taxon-based approach.

The Smithsonian Tropical Research Institute (STRI), one of the world's premier tropical research institutes, is a partner in the grant and all students will be co-advised by both STRI and Illinois faculty. In addition, VInTG students will have access to STRI's diverse study sites and databanks for a wide variety of organisms and ecosystems in Panama.

To be eligible for support from this training grant, students must first be accepted into a graduate program at the University of Illinois. Examples of participating graduate programs include (but are not limited to) the Department of Animal Biology, Department of Entomology, Department of Plant Biology, Department of Natural Resources and Environmental Science, and the Program in Ecology, Evolution and Conservation Biology.

For more information, please contact Andrew Suarez <avsuarez@life.illinois.edu> or Carla Caceres <caceres@life.illinois.edu>.

Sincerely, Becky Fuller

Becky Fuller <fuller@life.illinois.edu>

UIllinois IntegrativeGenomics

PhD and MS Positions in Integrative Evolutionary and Physiological Genomics at the University of Illinois

I am seeking talented and motivated PhD and MS students to join my newly established research group at the University of Illinois, Urbana- Champaign.

Research in the lab focuses primarily on addressing questions related to adaptation and speciation along environmental gradients. These questions range from mechanistic investigations of physiological adaptation and acclimatization responses to comparative analyses of the importance of environmental gradients in population divergence, speciation, and biodiversity conservation. We work primarily with birds and mammals that are distributed across broad elevational gradients in the Andes and the Rocky Mountains using integrative gene-to-whole-organism approaches that draw on techniques from functional genomics to physiological ecology.

Graduate students in the lab are welcome (and encouraged) to develop their own projects that relate to the lab's broad research themes, or they may contribute to ongoing research in the lab. More information on these projects can be found at http://web.me.com/zcheviron. There are also several new projects under development that will be shaped in collaboration with new lab members. A background in evolutionary biology, ecological physiology, functional genomics, bioinformatics, and/or population genetics is a plus.

Interested students should apply through either the Program in Ecology, Evolution, and Conservation (http://sib.illinois.edu/peec/) or the Department of Animal Biology in the School of Integrative Biology (http://www.life.illinois.edu/animalbiology/graduate_program.htm). The application deadline for both programs is Jan. 1, 2012.

Please email a CV and brief statement of research interests to zcheviron 'at' gmail.com before applying to either graduate program.

Thank you, Zac Cheviron

Zachary Cheviron Assistant Professor School of Integrative Biology Department of Animal Biology University of Illinois 286 Morrill Hall Urbana, IL 61801

http://web.me.com/zcheviron zcheviron@gmail.com

UJyvaskyla EvolutionBehaviour

PhD-student position: evolution of social control mechanisms.

Center of Excellence in Biological Interactions, University of Jyväskylä, University of Helsinki (Finland).

Cooperation among individuals is a ubiquitous phenomenon across taxa from microbes to humans. However, the stability of cooperative relationships presents an evolutionary problem because cheaters who reap the benefits of cooperation without contributing to its costs can destabilize the cooperative relationships. Several mechanisms that control cheating behavior and maintain cooperation have been described in different taxa. These include punishment in cooperatively breeding birds, worker policing in insect societies, and partner choice in legume-rhizobia mutualisms. However, the links between biological reality and theoretical models of social control evolution are poorly understood, as are the consequences of different social control mechanisms at the level of groups and populations. This project aims at comparing and synthesizing the different approaches and examining their evolutionary consequences through a combination of theoretical and empirical work. The successful candidate can engage with the following topics, but is also welcome to develop other research related to the topic of social control mechanisms:

1. Mechanisms of social control across taxa and evolutionary contexts: reviewing and synthesizing theoretical models.

2. Social control in human co-operation: empirical studies on the effectiveness and consequences of different social control mechanisms (e.g. punishment and exclusion) on group success.

3. Population consequences of social control: simulation studies on the effects of different social control mechanisms on the long term prospects of populations.

The appointed candidate will be a member of the newly appointed Finnish Centre of Excellence in Biological Interactions funded by the Academy of Finland. We offer a stimulating, creative and international working environment, modern facilities, reliable funding body, excellent career prospects and nice colleagues.

The successful candidate will defend his/her thesis at the University of Jyväskylä, Finland. The thesis supervisors are Dr. Mikael Puurtinen at the University of Jyväskylä and Dr. Heikki Helanterä at the University of Helsinki. The empirical studies on human co-operation will be carried out at the University of Jyväskylä using computer-mediated decision making experiments. Theoretical work will be jointly supervised by Dr. Mikael Puurtinen and Dr. Heikki Helanterä. Additionally, the appointed candidate will have the possibility of carrying out some of the work at the Theoretical Biology Group at the University of Groningen (lead by professor Franz J. Weissing) , or at the Australian National University at Canberra (with professor Hanna Kokko), as well as collaborating with other researchers of the Center of Excellence.

Requirements: MSc in biology (or physics/mathematics). Strong interest in evolutionary biology is a must. Interest/experience in mathematical approaches is a plus.

Salary: Four-year funding starting from ~2000 and rising to ~2600. Includes health insurance and other benefits.

Application deadline 31st December, 2011. Include in the application i) a cover letter with a statement of research interest, ii) a CV, and iii) names and contact details of two references. Send applications and informal questions to mikael.puurtinen@jyu.fi. Appointed candidate can start immediately, but starting date is negotiable.

Dr. Mikael Puurtinen

University of Jyväskylä

PO Box 35, 40014 Finland

tel. +358 50 3758975

email mikael.puurtinen@jyu.fi

http://users.jyu.fi/~hemipu mikael.puurtinen@jyu.fi

UJyvaskyla HostPathogen

PhD position (four years): Host-pathogen relationship using fish infection models

A PhD position is open in the newly appointed Centre of Excellence in Biological Interactions funded by the Academy of Finland. We are looking for a highly motivated student to study pathogenesis of Flavobacterium columnare using fish infection models (rainbow trout and zebrafish). Our research group studies bacterial virulence and species interactions using a wide range of methods (including whole genome sequencing, genetics, molecular biology, microbiology and experimental evolution). The PhD project involves performing infection experiments and manipulation of bacteria and infection conditions.

A successful candidate will have MSc in biology (or she/he should complete MSc studies soon). Experience in microbiology or molecular biology are essential.

The partners of the Centre of Excellence are located at the University of Jyväskylä, Finland (Prof. Johanna Mappes and Prof. Jaana Bamford), University of Helsinki, Finland (Prof. Liselotte Sundström) and Australian National University (Prof. Hanna Kokko). This position is based at the University of Jyväskylä.

Salary: 2000EUR-2600EUR (gross) monthly including health insurance and other benefits

Application deadline: 31 December 2011

Starting date: The position is available from 1 January 2012, starting date is negotiable

Application should include 1) a cover letter with a statement of research interests, 2) CV and 3) names and contact details of two references. Applications and informal inquiries should be addressed to Dr. Lotta-Riina Sundberg lotta-riina.sundberg@jyu.fi

eira.h.ihalainen@jyu.fi

UJyvaskyla HostPathogen Update

Update: Please note the extended application deadline!

PhD position (four years): Host-pathogen relationship using fish infection models

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Salary: 2000EUR-2600EUR (gross) monthly including health insurance and other benefits

Application deadline: Evaluation of the applications begins in January 2012 but applications can still be submitted until the end of January

Starting date: the position is available from January 2012; starting date is negotiable (April 2012 at the latest)

Application should include 1) a cover letter with a statement of research interests, 2) CV and 3) names and contact details of two references. Applications and informal inquiries should be addressed to Dr. Lotta-Riina Sundberg lotta-riina.sundberg@jyu.fi

eira.h.ihalainen@jyu.fi

ULausanne LizardEvolutionaryBiol

PhD position in Evolutionary Biology of Common Lizards (Lacerta vivipara) at the University of Lausanne, Switzerland.

A 3-year PhD position in evolutionary biology is available in the research group of Prof. Patrick S. Fitze (University of Lausanne, Department of Ecology and Evolution www.unil.ch/dee). The position is part of an SNF-funded project aimed at studying the link between experimental population dynamics, sexual selection and coloration in the common lizard (Lacerta vivipara).

The project will involve both field and laboratory work. Applied methodologies will include behavioural, paternity and colour analyses. Fieldwork will be conducted over several months (5-8 month: March to October) per year in Jaca, in the Spanish Pyrenees.

Our international laboratory has a wide range of research interests, ranging from behavioural analyses, to the study of experimental population dynamics, population genetics and phylogenetics. Please browse our group website for further details: http://www.unil.ch/-dee/page81903.html .We are seeking an enthusiastic, highly motivated and creative candidate with keen interest in evolutionary biology, and the capacity to work both independently and as a team member. Applicants must have a MSc in biological sciences with expertise in molecular biology and statistics (knowledge of the R statistical package is an advantage). Good English writing and organisational skills are essential. The ideal candidate will have prior experience in experimental design, behavioural and colorimetric analyses, experimental population dynamics, programming, modelling and reptile handling, as well as good communication skills. The working language of the laboratory is English. Knowledge of French and/or Spanish is useful, but not essential.

Applications should be sent by email to Prof. Patrick S. Fitze (Patrick.Fitze@unil.ch). The application should consist of a single pdf-file, including a CV, a letter outlining motivation and research interests (max. 1 A4 page), the names of three referees (including e-mail address and phone number), and a summary of the candidate's MSc or undergraduate project (max. 2 A4 pages). Where relevant, publications should be included at the end of the file. The deadline for application is January 20th 2012. Preferred starting date is March 1st 2012. Short listed candidates will be invited to Lausanne for interview at the end of January/ start of February 2012. The salary of the successful candidate will be determined in accordance with the guidelines of the Swiss National Science Foundation (www.snf.ch).

The successful candidate will join a bustling research department consisting of 19 research groups with diverse study interests, ranging from evolutionary biology and ecology to applied ecology and conservation biology http://www.unil.ch/dee/page6757.html For additional information, please do not hesitate to contact:

– Patrick S. Fitze, Assistant Professor SNF

Department of Ecology and Evolution (DEE) Biophore, University of Lausanne room: 3212 1015 Lausanne phone: + 41 (0) 216924154 Switzerland Fax: + 41 (0) 216924165

http://www.unil.ch/dee/page81901.html Patrick Fitze <Patrick.Fitze@unil.ch>

ULeuven ImprintingBioinformatician

PhD scholarship for a Bioinformatician for a project on the evolution of genomic imprinting in social bees

Title of project: Social bees as a model for testing evolutionary theories of genomic imprinting

Outline of project: In mammals and flowering plants, some genes are known to be expressed to a different extent depending on whether they are inherited from the mother or from the father. Mechanistically, it is thought that such "genomic imprinting" is based on differential DNA methylation or histone modifications in the parental germ lines. Evolutionarily speaking, however, the functional significance of imprinting remains highly controversial. One of the theories, known as David Haig's kin conflict theory of genomic imprinting, posits that parent-of-origin specific gene expression patterns are a reflection of the differing evolutionary interests of maternally and paternally inherited genes. In this project, we will use the honeybee and the bumblebee as two novel insect models to study the occurrence of genomic imprinting and test Haig's theory. In our study, imprinted genes will be searched for using cutting-edge high-throughput sequencing methods, which now allow genome-wide screens for differentially methylated and imprinted genes against a reasonable cost.

The main task for the PhD student will be to carry out bio-informatic analyses on these nextgen sequencing data (alignment to reference genome, identification of parent-specific SNPs, matching RNA sequencing data to identified SNPs). Prior experience in analysing nextgen sequencing data is a must. Experience with BioPerl, R/Bioconductor and Python is also desirable. The ideal candidate would have a master in Bio informatics.

Earliest possible starting date: March 1 2012, or until position is filled. Application deadline: January 31st 2012

Funding is available for 4 years, and matching funding for consumable costs (ca. 25 000 euro/year) is also available.

The project will be supervised by Prof. Tom Wenseleers from the University of Leuven. For more information on his group, see http://bio.kuleuven.be/ento/wenseleers/twenseleers.htm . Applications with a personal statement and detailed CV should be sent directly to him: tom.wenseleers@bio.kuleuven.be

Prof. Tom Wenseleers * Lab. of Entomology Dept. of Biology Zoological Institute K.U.Leuven Naamsestraat 59 B-3000 Leuven Belgium * +32 (0)16 32 39 64 / +32 (0)472 40 45 96 * tom.wenseleers@bio.kuleuven.be http://bio.kuleuven.be/ento/wenseleers/twenseleers.htm
Tom Wenseleers <Tom.Wenseleers@bio.kuleuven.be>

UNotreDame PopulationGenomics

Ph.D. Position in Population Genomics and Ecological Speciation:

The research group of Jeff Feder at the University of Notre Dame is seeking to add an interested Ph.D. student to the laboratory to start in the Fall 2012 academic year to investigate issues related to the genomic architecture of speciation and ecological speciation.

A summary of the lab's research can be found at: http://federlab.nd.edu/ Our research is directed at discovering the ecological basis for population divergence, in particular, with regard to the apple maggot fly, Rhagoletis pomonella, a model for speciation-with-gene-flow. We combine field work with next generation mass sequencing to investigate how flies shift and adapt to new host plants to initiate the speciation process. Current work in this area is focused on critical adaptations involved in the physiology of overwintering diapause and fly chemoreception of host plant fruit odors that generating ecologically based reproductive isolation. We are also actively studying the how genome architecture may facilitate the speciation process and how the consequences of fly host plant shifts may cascade across trophic levels and affect the community structure of parasitoid wasps that attack R. pomonella.

Interested students should contact the lab and discuss their interests with (feder.2@nd.edu; 574-631-4159)and apply to the Dept. of Biological Sciences at Notre Dame (deadline Jan 1 2012) to the Ph.D. program. Information can be found at the Department web site at http://biology.nd.edu/ . Scott.P.Egan.28@nd.edu

UOtago EvolutionSocialNetworks

Applications are being sought for the following PhD project at the Department of Zoology, University of Otago, Dunedin, New Zealand.

Theme: Animal personality and social networks in a species with variable mating systems, the dunnock (Prunella modularis).

Supervisor: Dr. Shinichi Nakagawa (shinichi.nakagawa@otago.ac.nz)

Project Description: So-called animal personality (i.e. individual consistency within behaviours and correlations among behaviors) has become a major area of research in Behavioural Ecology. However, the understanding of individual consistency and variation in behaviour within populations is still far from complete. Although statistical approaches termed social network analyses have been extensively used for human personality research, the application of this technique to animal personality research is still limited.

By employing social network analysis, we plan to investigate one of the most diverse and complex mating systems observed to date in the animal kingdom - i.e. those of Dunnocks (see the brilliant book by the father of Behavioural Ecology, Prof. Nick Davies - Dunnock Behaviour and Social Evolution. Oxford Press, 1992). Our group has established a study population of Dunnocks in the Dunedin Botanic Garden where most of the individuals are uniquely marked and have been monitored for a period of 3 years. Dunnocks were first introduced in New Zealand around 150 years ago and probably took an original evolutionary path compared to their source populations in the UK. We have discovered that many life-history aspects are different in this population in relation to the well-studied population from Cambridge (e.g., mating patterns and longevity).

Combining extensive field data, sophisticated statistical techniques and computer simulations, this study tries to understand the maintenance of consistent individuals variation in behaviours, especially mating and parental care behaviours. This PhD programme is demanding but comprehensive in a way that students are exposed to: 1) a variety of field skills, 2) diverse statistical skills, 3) basic molecular techniques, and 4) computer simulations using agent-based modeling. Students are encouraged to form their own questions within the framework of the research programme (visit our website: http://-sparrow.otago.ac.nz/). I expect that the candidate will come out of this PhD as a well-rounded scientist with a multitude of skills.

The Ideal Candidate: The ideal candidate will possess experience in field ornithology, behavioural ecology and molecular ecology. They will be motivated, organised and extremely hardworking, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research programme. They will be a competent field worker, with experience of mist netting, and should be computer literate with familiarity with database management and statistical analyses (computer programming experience is plus but not required). Minimum qualifications: B.Sc. (Hons) and/or M.Sc. in Biological Sciences or equivalent with and A- average or better (note that adjustments are applied to other grade systems around the world; see below).

Scholarship Funding: Financial support should be available for a high achieving student with an A- average or better via a University of Otago scholarship (see http://www.otago.ac.nz/study/scholarships/-). The scholarship provides NZ$ 25,000 stipend per year for a total of 3 years, and also covers tuition fees.

Eligibility: The University of Otago and Departmental scholarships are open to all nationalities. However, overseas candidates for whom English is not a first language must satisfy the English Language Requirements of the University to be eligible for study (see http://www.otago.ac.nz/international/postgraduate/-index.html#englishlanguage). Other eligibility criteria are detailed here http://www.otago.ac.nz/-international/postgraduate/otago002221.html . How to Apply: Interested applicants are encouraged to make informal enquiries to Dr Shinichi Nakagawa. Please send your Curriculum Vitae, a copy of your academic transcript, a sample of your written scientific work and the names of two referees with a cover letter (a letter of your motivation) to:

Dr Shinichi Nakagawa (shinichi.nakagawa@otago.ac.nz), Department of Zoology, University of Otago, 340 Great King Street, P. O. Box 56, Dunedin, New Zealand.

The position will remain open until filled, application for University of Otago scholarships are now available year round. It would be desirable, however, for the successful applicant to be able to start by July 2012.

Look forward to hearing from you.

Shinichi Nakagawa

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UppsalaU FloralEvolution

PhD position in Plant Ecology at Uppsala University

One PhD position in Plant Ecology is available at the Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, starting spring 2012.

The PhD student will work in a project studying the role of pollinators as drivers of floral evolution, using the orchid Gymnadenia conopsea as the study system. The aims of the project include (1) to quantify experimentally the contribution from pollinators to selection on floral traits that exhibit geographic differentiation, (2) to examine if targets of selection vary with geographical context, (3) to quantify experimentally costs of reproduction and (4) to integrate experimental studies with demographic data to determine the net outcome of pollinator-mediated selection.

For further information regarding the position and project, please contact Assistant Prof. Nina Sletvold, e-mail: nina.sletvold@ebc.uu.se, http://www.ebc.uu.se/-forskning/IEG/Plant/Research_groups/-Sletvold_group/ Read the full announcement and apply via: http://www2.personalavd.uu.se/-ledigaplatser/3266doceng.html Nina Sletvold Plant Ecology and Evolution Dept of Ecology and Genetics, EBC Uppsala University Norbyvägen 18 D SE-752 36 Uppsala Sweden

nina.sletvold@ebc.uu.se

USeffield FireAdaptation

PhD funding opportunity for research on: Response of C3 and C4 grasses to fire and herbivory

R95 000 yr-1 for 3 years.

A collaborative project between Rhodes University, and the Universities of Sheffield and Cambridge.

The future climate of southern Africa is likely to include an increased intensity of the monsoonal system accompanied by greater fire frequency. Fire in grassy ecosystems is not selective and species that are tolerant of burning increase in abundance. Recent research has demonstrated that C4 grasses are more tolerant of burning than closely related C3 species. The C4 species recover faster after fire and have traits including higher winter fuel loads and flammability that are likely to promote seasonal burning. In addition to these direct effects on grass performance, re-growth after fire increases leaf palatability, which compounds potential palatability differences between C3 and C4 species. Hence, an understanding of the interaction of fire and herbivory is essential to understanding the future community structure of grassy ecosystems.

This study proposes to investigate this interaction by comparing the response of a model species (Alloteropsis semialata) to fire and selective herbivory using a common garden plot experiment. Replicate plots coplanted with the C3 and C4 subspecies of A. semialata have been established at Rhodes University (Grahamstown, South Africa) and will be subject to fire and selective herbivory in a factorial design. The relative performance of C3 and C4 plants will be assessed using established techniques. Results are anticipated to make a significant contribution to our mechanistic understanding how C3 and C4 grasses respond differentially to fire.

Applicants interested should have graduated with an appropriate degree (ecology or ecophysiology) and are welcome to make enquires of either Prof. Brad Ripley (b.ripley@ru.ac.za) or Dr Colin Osborne (c.p.osborne@sheffield.ac.uk). Applicants can be of any nationality and should send a full CV, academic transcript and details of 3 referees to Prof. Brad Ripley, Botany Department, Rhodes University, Grahamstown 6140, or b.ripley@ru.ac.za . Closing date the 20th January 2012. The bursary is higher than the standard NRF rate, and will support a good standard of living for a graduate student in South Africa

Colin Osborne Dept. Animal and Plant Sciences University of Sheffield

tel: +44-114-222-0146 lab pages: http://web.me.com/-colin.osborne/lab/home.html ecological informatics: www.grassportal.org Colin Osborne <c.p.osborne@sheffield.ac.uk>

USheffield ClimateAdaptation

Applications are being accepted for the following PhD project at the University of Sheffield, Department of Animal and Plant Sciences, UK.

The molecular ecology of stress: developmental plasticity in the face of predators, pathogens and climate change. Supervisor: Dr. Andrew Beckerman (http://-www.beckslab.staff.shef.ac.uk/)

Developmental plasticity defines the capacity of organisms to respond to environmental change -“ natural changes such as disease and predation, and human induced change in climate. This project will focus on three forms of stress linked to environmental change: increased temperature, exposure to parasites and exposure to predation. These forms of stress represent the major axes of natural and human induced threat for most organisms.

The project will focus on how chitin, central to development and disease, mediates adaptation in a changing environment. The student will link sensory perception genes and neurotransmitters - responsible for signal detection and initiating cascades of development -” with special nuclear receptor genes that oversee and coordinate patterns of development and importantly chitin synthesis and degradation. The project will identify developmental mechanisms for coping with environmental change, using the model system of Daphnia magna and will leverage several advanced technologies including RT-qPCR and transcriptomics.

The following three objectives frame the project: 1) Evaluate the role of candidate sensory and regulatory genes in stress responses via rigourous experiments and RT-qPCR. 2) Leverage extensive natural genetic variation and experimental transcriptomic technology to reveal major sets of genes responsible for detection, development and regulation of stress responses under climate change. 3) Explore via network modelling, candidate regulatory networks mediating stress responses common to and unique to each form of stress.

The PhD will take advantage of collaborations between Sheffield, Edinburgh and the Daphnia Genomics Consortium (Indiana, USA)

Candidates must apply by Jan 20 2012. I will interview a shortlist by the end of January, in preparation for a mandatory departmental interview in Mid-February. Successful candidates will be funded by NERC- UK or the University of Sheffield.

Applications must be made through the following link:

http://www.sheffield.ac.uk/postgraduate/research/-apply Feel free to contact me with any questions. Non-UK/EU students with funding are encouraged to contact me as well.

Best wishes, Andrew

Dr. Andrew Beckerman Department of Animal and Plant Sciences, University of Sheffield, Alfred Denny Building, Western Bank, Sheffield S10 2TN, UK ph +44 (0)114 222 0026; fx +44 (0)114 222 0002 http://www.beckslab.staff.shef.ac.uk/ See our new R Book: http://www.r4all.org http://www.flickr.com/photos/apbeckerman/ http://-www.warblefly.co.uk a.beckerman@sheffield.ac.uk

USherbrooke SwallowEvolution

U. Sherbrooke: Ph.D. on tree swallows

I am looking for a Ph.D. student to explore the links between behaviour, immunity and parasites in Tree swallow (Tachycineta bicolor). This research is part of a long-term program in collaboration with Prof. Dany Garant at the Université de Sherbrooke, Qc, Canada. Since 2004, more than 8000 individually marked tree swallows have been monitored on 400 nest boxes. The Ph.D. candidate will have access to this long-term dataset and will also participate to field work during two or three seasons (May to July) and assist with capture, marking and measuring of the birds, as well as collecting samples for hormone and DNA analyses.

Assets for this position include a M.Sc. degree, publications, a knowledge of 'basic' French (or a strong willingness to learn it), fieldwork experience, strong quantitative skills. A tax-free scholarship is available for three years, and financing for travel, fieldwork and lab expenses has been secured. The project could start either in May or September 2012.

For information on my research, see http://-pages.usherbrooke.ca/fpelletier/ Interested candidates should send a CV, a brief statement of research interests and the e-mails of two referees before December 20th to Fanie Pelletier: fanie.pelletier@usherbrooke.ca

Fanie Pelletier, Ph.D.

Professeure Agrégée Université de Sherbrooke Département de biologie Faculté des Sciences Sherbrooke (Québec) CANADA J1K2R1

tel.: 819-821-8000 poste 61092 fax: 819 821-8049

fanie.pelletier@usherbrooke.ca

Fanie Pelletier <fanie.pelletier@usherbrooke.ca>

USouthFlorida EvolutionaryBiol

The Department of Integrative Biology is accepting applications for students to enter their integrative graduate education program in Ecology and Evolution, Environmental and Ecological Microbiology or Physiology and Morphology (deadline Jan 1 2012, see http://-biology.usf.edu/ib/grad/admission/). Our department is committed to train the next generation of graduate students to prepare them for professional success in the fields of biological sciences that mirror our faculty's expertise, which emphasizes organismal interactions and adaptations to the environment at all scales, from microorganisms to complex plants and animals. Our program of graduate study is designed to foster the development of technical and analytical skills used in existing and emerging fields of discovery. Increasingly, students are given opportunities to include an international experience in their research projects and also be involved in outreach activities. The research and training ongoing in the Department of Integrative Biology contributes to advancements in both basic science and applications to real world problems.

Application files must be complete and received by the Biology Graduate Office before January 1, 2012 to be considered for Fall 2012 Teaching Positions or the University Graduate Fellowship.

Students can pursue a M.S. or Ph.D degree in Biology. Each of the degrees requires a student to identify an area of concentration. The program offers:

- M.S. in Biology, Concentration in Ecology and Evolution (EEV) - M.S. in Biology, Concentration in Environmental and Ecological Microbiology (EVM) - M.S. in Biology, Concentration in Physiology and Morphology (PMY) - Ph.D. in Biology, Concentration in Ecology and Evolution (EEV) - Ph.D. in Biology, Concentration in Environmental and Ecological Microbiology (EVM) - Ph.D. in Biology, Concentration in Physiology and Morphology (PMY)

Faculty research interests include: biomechanics and functional morphology; ecology (marine and freshwater, conservation, restoration, population, community and ecosystem); ecological genetics and epigenetics; ecophysiology; ecotoxicology; environmental microbiology; evolution; gene transfer; genomics; microbial physiology; research synthesis; and response to climate change.

Faculty who are currently accepting students into their laboratories (more information at http://biology.usf.edu/ib/faculty/):

* Bell, Susan- Marine Ecology * Crisman, Thomas- Freshwater Ecology * Deban, Stephen- Physiology, Biomechanics, and Evolution * Fox, Gordon- Plant Ecology, Conservation Biology, and Population Biology * Harwood, Valerie- Microbial Water Quality * Lajeunesse, Marc- Ecology, Evolutionary Biology and Research Synthesis * Lewis, David- Ecosystem & Landscape Ecology, Biogeochemistry * Martin, Lynn- Ecological Physiology and Immunology * McCoy, Earl- Conservation Ecology * Motta, Philip- Functional Morphology * Mushinsky, Henry- Conservation Ecology * Pierce, Sidney- Cellular Physiology and Biochemistry * Richards, Christina- Plant Ecological Genomics and Epigenetics * Rohr, Jason- Ecology * Scott, Kathleen- Microbial Physiology and Biogeochemistry * Stiling, Peter- Ecology

Christina Richards, Ph.D. University of South Florida Department of Integrative Biology 4202 East Fowler Avenue SCA 127 NES 107 (shipping) Tampa, FL 33620 (813)974-5090 (813)974-3263 FAX http://www.ecologicalepigenetics.com clr@usf.edu

UtahStateU Conservation

Two MS Fellowships: Utah State University Wildland Resources Department Environment and Society Department

The College of Natural Resources at Utah State University invites applications for two MS Fellowships to begin Fall 2012

Natural resource professionals face ecological changes occurring at unprecedented scales and rates due to a combination of historical management activities and climate change. In the Interior West, many forest ecosystems are at, or near, tipping points with respect to ecological integrity. Phenomena such as large-scale insect outbreaks, rapid aspen die-offs, and geographically and temporally synchronized severe fires are occurring across the region. Impacts may exceed historical resilience limits of forests, resulting in irreversible ecosystem state changes with pronounced socioeconomic impacts. This situation creates an acute need for a new generation of forest resource managers and scientists skilled in a variety of emerging technologies, able to incorporate rapidly changing research and data into decision-making, and able to communicate effectively with a variety of stakeholders. In response to this need, we have initiated an integrated graduate training program and invite applications for two MS Fellowships to begin January 2012.

Our goal is to create a small cohort of graduate students whose research will be linked under the theme “Managing for Resilience in Forested Ecosystems of the Intermountain West”. This program will use emerging research tools, common coursework, seminars and specific shared extension projects to provide the student fellows with skills and knowledge necessary for effective science-based input to management decisions about forested landscapes undergoing or threatened with large-scale change. Current topics related to management, adaptation, resilience and human dimensions of forest ecosystems and their components in a changing climate will be emphasized. Student fellows will participate in several outreach projects in cooperation with USU Extension Forestry during their time at USU including the planning of a Restoring the West regional conference, and publication of at least one article each in the Utah Forest News. The student fellows will also benefit from coordinated mentoring by an Advisory Board of faculty members who have active research programs in dynamic forested landscapes.

Application: To apply for one of the MS Fellowships, please submit the following materials to Dr. Karen Mock via email

(karen.mock@usu.edu):

* A resume describing your education, employment, and publication/presentation history, * A list of three references (and their contact information), * A copy of your academic transcripts (unofficial) and GRE scores, * A cover letter describing your research interests, why you would be a good candidate for this Fellowship, and how you found the Fellowship advertisement.

We will begin screening candidates on March 5, 2012, and will continue until suitable candidates are found. Formal application to the USU graduate school will ultimately be required for selected candidates. For additional information please see http://www.cnr.usu.edu/wild/htm/available-ms-fellowships . karen.mock@usu.edu

UWyoming ShurblandConservation

We are recruiting a Ph.D. graduate student to study ecological genetic and landscape approaches to mountain mahogany shrubland restoration in the labs of Dr. Kristina Hufford and Dr. Pete Stahl at the University of Wyoming. Research will investigate genotype-environment interactions and molecular marker divergence along a latitudinal transect of the mountain mahogany (Cercocarpus montanus) range to test predictions for appropriate seed collection zones for restoration.

There will be opportunities for the Ph.D. student to develop novel research directions within the framework of the study program, and we encourage applications from prospective candidates with a background and interest in restoration ecology and population genetics. Evidence of excellent written and communication skills and enthusiasm for field and laboratory research are a plus.

Qualifications for the position include a strong academic record and an MS degree. The graduate assistantship includes stipend, tuition and research support for 2.5 years and opportunities will exist to apply for additional funding. Enhanced stipend funding may be available for applicants with a minimum GRE score of 1200 (310 under the new scoring system) and GPA 3.0 (BS)/ 3.3 (MS).

We are interested to fill this position as soon as possible and applications should be received by January 12, 2012 for full consideration. An opportunity to visit the University of Wyoming may be possible during the graduate recruitment period. The position will remain open until filled.

Please send application materials, including a cover letter and copies of transcripts, GRE scores, resume and contact information for 3 references to: khufford@uwyo.edu

Dr. Kristina Hufford Ecosystem Science and Management University of Wyoming Dept. 3354 1000 E. University Avenue Laramie, WY 82071 USA

Kristina Hufford <khufford@uwyo.edu>

UZurich ArabidopsisAdaptiveVariation

PhD position at the University of Zurich: Plant Sciences and Policy

The project offered, entitled " Adaptation and biodiversity in alpine habitats - integrating genomic and ecological perspectives" aims to combine both fundamental science, with policy and conservation strategy. The student will experience an interdisciplinary research environment (including molecular genetics and field ecological research) as part of two diverse research groups (spending approximately 50% time with each group), co-supervised by two PIs with different backgrounds:

(1) Prof. Dr Kentaro Shimizu, Institute of Evolutionary Biology and Environmental Studies / Institute of Plant Biology, University of Zurich (http://www.ieu.uzh.ch/research/evolbiol/ecogenomics.html, http://www.botinst.uzh.ch/research/genomics/shimizu.html) (2) Prof. Dr Alex Widmer, Institute of Integrative Biology, ETHZ (http://www.env.ethz.ch/people/professors/fullprofessors/awidmer)

Summary: Most climate models indicate that global warming will strongly impact alpine floras worldwide, causing alpine habitats to experience rapid and dramatic environmental changes. Understanding how plants are adapted to their environment and can persist under changing climatic conditions is therefore not only of prime interest from a fundamental scientific perspective, but also from a political and conservation perspective. Developing policies and implementing conservation strategies can only be done once a deeper understanding of the fundamental processes underlying survival and adaptation in alpine environments has been achieved. However, despite the great interest in alpine plants and their adaptations to extreme environmental conditions, little is known about the genetic and molecular basis of altitudinal adaptations, which is primarily a consequence of the lack of suitable study organisms with genetic and genomic resources.

Scientific objectives:

Here we propose to study altitudinal adaptation in several Arabidopsis relatives, allowing us to take advantage of the wealth of genomic and genetic resources available for this model organism. Key questions include: Which genes are responsible for altitudinal adaptation and what is the function of these genes? Are the same genes responsible for altitudinal adaptation in multiple species or in different geographical areas? What is the adaptive value of the studied candidate genes under contrasting environmental conditions?

Policy related objectives:

The work of scientists is often quite separate from the work of those bodies that develop policy, and while one party may influence the other, interaction is scarce. This PhD program offers an opportunity to bridge this gap, as the findings from this project will help in the development of efficient conservation policies in alpine ecosystems.

Specification:

A Masters level degree or equivalent in an appropriate field is essential, and some experience in molecular genetics would be distinctly beneficial. Proficiency in English is also required.

To apply:

Please send your CV (including a brief description of your practical experience and grades), a brief statement of scientific interests (no more than two pages) and the details of two academic references (preferably by email). The review of applications will commence in mid December, and will continue until the position is filled.

Contact: a.tedder@botinst.uzh.ch

Dr Andrew Tedder Institute of Evolutionary Biology and Environmental Studies / Institute of Plant Biology University of Zurich Zollikerstrasse 107, CH-8008 Zurich Switzerland

a.tedder@botinst.uzh.ch

Office: +41 44 634 8270

Prof. Dr. Kentaro K. Shimizu Institute of Evolutionary Biology and Environmental Studies / Institute of Plant Biology University of Zurich Zollikerstrasse 107, CH-8008 Zurich Switzerland Phone +41-44-634-8247, 8270 FAX +41-44-634-8204 http://www.ieu.uzh.ch/research/evolbiol/ecogenomics.html http://www.botinst.uzh.ch/research/Genomics/Shimizu.html http://www.sysbio.uzh.ch/index.html E-mail: shimizu@botinst.uzh.ch

University Research Priority Program of Systems Biology / Functional Genomics Evolutionary and Ecological Genomics

shimizu@botinst.uzh.ch

VirginiaCommonWealthU EvolBiol

GRADUATE STUDIES IN ECOLOGY AND EVOLUTION AT VIRGINIA COMMONWEALTH UNIVERSITY

The Department of Biology at Virginia Commonwealth University invites applications from prospective graduate students for Fall 2012. We have a diverse Ecology and Evolution faculty engaged in research in Virginia and around the world. Emerging research clusters include population and community ecology, evolutionary genetics, computational biology & river science. Graduate students may apply through our Biology Masters in Science or Integrative Life Sciences Ph.D. programs. Competitive funding and tuition waivers are available to qualified students in both programs, and may include fellowships, and research/teaching assistantships. Please visit www.has.vcu.edu/bio/ to find information about both programs.

VCU is the largest public university in Virginia. We are located in Richmond, within easy reach of the Virginia coastal plain, Chesapeake Bay, James River, Virginia barrier islands and Blue Ridge Mountains, providing excellent opportunities for research in diverse natural systems. VCU's Rice Center for Environmental Life Sciences, located 30 minutes from campus, encompasses 342 acres of aquatic and terrestrial ecosystems along the James River and provides an outstanding resource for field-based research by both faculty and graduate students in the department. Facilities include new office and lab space, conference center, and boat house. For more information, see www.vcu.edu/rice/. On campus research facilities include the Trani Center greenhouse, aquatics facility, and IACUC approved animal facility. A satellite lab of the Nucleic Acids Core Facility provides a broad range of support for molecular approaches. Access to several next-generation DNA sequencing platforms is also available. The Environmental Analyses Laboratory provides state-of-the-art analytical services to support research in the environmental sciences. The Bioinformatics Computational Core Laboratory supports several supercomputing clusters and a research laboratory with access to state-of-the-art genomics and proteomics software and databases for research applications.

Faculty in Ecology & Evolution include:

John E. Anderson, Remote sensing and environmental Biology Bonnie L. Brown, Ecological and conservation genetics Lesley Bulluck, Population ecology, ornithology, conservation Paul Bukaveckas, River and ecosystems ecology Rodney J. Dyer, Population genetics and phylogeography Andrew J. Eckert, Evolutionary genetics and genomics Michael L. Fine, Acoustic communication and ecology of fishes Rima B. Franklin, Microbial ecology and environmental microbiology Gregory C. Garman, Fish ecology Christopher M. Gough, Forest ecophysiology and ecosystem ecology Derek M. Johnson, Spatial population ecology, plant-insect interactions Karen Kester, Behavior, evolutionary ecology, plant-insect interactions Dan McGarvey, Fish ecology Leigh McCallister. Aquatic ecology and oceanography Stephen McIninch, Fish ecology Maria C. Rivera, Computational evolutionary biology and phylogenetics Leonard A. Smock, Stream ecology and aquatic entomology James M. “Clint” Turbeville, Animal systematics and evolution James R. Vonesh, Population and community ecology Donald R. Young, Plant physiological ecology Julie C. Zinnert, Remote sensing, plant physiology, plant ecology

Competitive students have GPAs >3.0 and combined GRE scores 1,100 or greater. Experience, reference letters, and rationale for applying to the program are important elements of the application. Prospective students must apply through VCU's graduate school (http://www.vcu.edu/graduate/ps/admission.html) or through the Office of International Education (http://www.vcu.edu/oie/). For full financial consideration, applications must be received by January 15. Applicants that have identified faculty sponsors are more likely to be accepted and to receive financial support. Interested students are strongly encouraged to contact prospective mentors directly for more information, or graduate studies directors Dr. Jennifer K. Stewart (Biology MSc; www.has.vcu.edu/bio/graduate/) or Dr. Robert Tombes (Integrative LS PhD; www.vcu.edu/lifesci/phd/).

AECKERT2@VCU.EDU

VirginiaTech SwallowEvolution

We are seeking a highly motivated graduate student to take part in an NSF-funded study on the role of glucocorticoids in mediating life history tradeoffs in tree swallows. The student will become a member of the Department of Biological Sciences at Virginia Tech in Blacksburg, Virginia, and will be co-supervised by Ignacio Moore and Fran Bonier. The project will require that the student spend approximately 3 months at the field site in Ontario, Canada every year, from late April until late July, working with a team comprised of undergraduate field assistants, a postdoc, and the PIs (Bonier, Moore, and Mark Haussmann of Bucknell University). The project will involve large-scale field experiments (manipulations of glucocorticoids, parasites, and reproductive effort) and measurement of effects on reproductive investment, parental behavior, immune function, and markers of oxidative stress. The student will have the opportunity to be involved in all aspects of the project, and thus will receive broad training in field and laboratory methods. Start date: August 2012, with potential for participation in the field project beginning in May 2012.

Qualifications: Must have a Bachelor's degree (prior to the start date), preferably in Biology, although highly qualified candidates with degrees in other disciplines will be considered. Previous field research experience and/or a Master's degree in Biology preferred. Strong academic record, written and oral communication skills, organizational skills, and teamwork ability required.

Interested candidates should send a cover letter describing their academic goals and research interests, a cv, and contact information for at least 2 academic references who can comment on the applicant's academic performance and aptitude for field and lab research to Fran Bonier (bonierf@queensu.ca). More information about ongoing research in the Bonier lab can be found at: http://post.queensu.ca/~bonierf/ and information on the Moore lab can be found at: http://www.faculty.biol.vt.edu/moore/ . Frances Bonier, PhD Banting Postdoctoral Fellow Queen's University Biology Department Biosciences Complex 3523 Kingston, ON K7L 3N6 Canada

Research Scientist Virginia Tech Department of Biological Sciences Blacksburg, Virginia

phone: 613-533-6000 x77024 email: bonierf@queensu.ca http://post.queensu.ca/~bonierf/index.html

fbonier@gmail.com

WageningenU AvianBehaviourEvolution

PhD position in Behavioural Ecology, Wageningen University, The Netherlands

We offer a PhD Position (1.0 FTE) to undertake research on personality and social networks in great tits within the newly established Behavioural Ecology chair group at the Animal Science Department of Wageningen University, the Netherlands (vacancy number ASG-DW-ETH-0001; the application deadline is 15.12.2011). This position is available within the framework of NWO funded project and will be conducted in close cooperation with the Animal Ecology Department of the Netherlands Institute of Ecology (NIOO-KNAW).

Project details

The aim of the project is to unravel the effects of personality on connectivity and its behavioural and fitness consequences in a social network. Within this project we will measure spatial movements of birds using modern automated tracking techniques in order to determine social network characteristics and their fitness consequences, complemented by playback experiments as short term challenges to a network and by experimental testing of the fitness effects of long-term changes in a network. We will track movements and encounters of a large number of personality-typed great tits (Parus major) during the breeding season. All data collection and experiments will be conducted using a well described colour-ringed population of personality-typed great tits at Westerheide, near Arnhem, the Netherlands. The project is embedded in larger projects on the causes and consequences of animal personality, as well as in broader cooperative projects on movement ecology and wildlife animal tracking.

We ask

- Candidates must have an MSc or equivalent degree in a behavioural ecology or related fields (e.g. Animal Behaviour, Animal Ecology), be enthusiastic about field work, have strong experimental and analytical skills, have good organizational and (written and spoken) communication skills, and a proven ability to collaborate with others, willingness to conduct to organize and extensive ornithological field work, willingness to travel internationally, to attend conferences and visit other institutes, a driver licence and a licence to carry out experiments with vertebrates (i.e. article 9 of the WoD) is a plus

We offer

Employment basis: temporary for specified period; duration of the contract: 1.5 + 2.5 years, maximum hours per week: 38. Additional conditions of employment: To begin with, a PhD appointment for a period of 18 months. Continuation of the appointment with another 30 months will be based on performance evaluation. Gross salary per month EUR 2042 in the first year rising to EUR 2612 per month in the fourth year, based on a full time appointment. Participation in the training program of the Graduate School 'Production Ecology & Resource conservation, see www.pe-rc.nl . An excellent opportunity to develop an international scientific network.

The organization

The successful candidate will join the stimulating and international research environment of Wageningen University. The work will be conducted under supervision of Prof. dr Marc Naguib and in close cooperation with the Department of Animal Ecology of the Netherlands Institute of Ecology (NIOO-KNAW). For further information, please contact Marc Naguib (marc.naguib@wur.nl; +31 (0)317 483856). Links: http://www.wur.nl/uk http://www.zod.wur.nl/UK ; http://www.nioo.knaw.nl/en/node/1061

The application deadline is 15.12.2011

Application You can apply until 15 December 2011. Interviews will take place in early January

Go to the website below for more detailed information and to apply for the position http://www.wur.nl/UK/work/Vacancies+New To access the advertisement use the link above and enter the vacancy number ASG-DW-ETH-0001 into the “vacancy field”. Then follow the further links. Contact Marc Naguib at marc.naguib@wur.nl for or any questions regarding the position or the application procedure.

Prof. Dr. Marc Naguib Department of Animal Ecology, Netherlands Institute of Ecology (NIOO-KNAW) Wageningen, The Netherlands, Tel. +31 (0)317-473442 m.naguib@nioo.knaw.nl ; http://www.nioo.knaw.nl/users/mnaguib note my new address from 1.12.2011 Behavioural Ecology Group, Department of Animal

Sciences Wageningen University, De Elst 1, Building 122 6708 WD Wageningen, The Netherlands, Tel. +31 (0)317 483856 marc.naguib@wur.nl

“Naguib, Marc” <M.Naguib@nioo.knaw.nl>

WageningenU ExperimentalEvolution

PhD position:

Understanding virulence of fungi towards malaria mosquitoes using experimental evolution

We seek a PhD student for research on the mechanisms of fungal pathogenicity for the malaria mosquito Anopheles gambiae and to assess potential avenues of fungal resistance. Development of pesticide resistance shows that pesticides are not a long-term solution for the control of malaria mosquitos, leading to a pressing need for the development of alternative means of disease control that avoid resistance. The entomopathogenic fungus Beauveria bassiana has recently been successfully used in controlling populations of mosquitoes in African houses and villages, thereby significantly reducing the risk of human infection. To make this approach more effective and to anticipate the potential development of fungal resistance by the mosquito, we need to understand the components and mechanisms of fungal virulence. We will use two approaches, (i) phenotypic and genetic analysis of fungal strains from relevant geographic locations, and (ii) experimental evolution of increased virulence. We will study the differences observed within and between these approaches at the phenotypic and genetic level by using gene-expression and DNA-sequence analyses. We will identify key mechanisms of virulence and quantify to what extent they each contribute to genetic variation in natural populations.

Who we are: The project is a collaboration within Wageningen University of the Chair groups of Genetics, Entomology, and Phytopathology. The interrelationship between genetics, heredity and evolution is the focus of research of the Laboratory of Genetics. Central is the study of genetic variation that ranges from the processes that produce it, to the factors that have shaped its architecture in the past, and to the factors and processes that determine its future. The research on insect-vertebrate interactions of the Laboratory of Entomology addresses the interactions between insects and vertebrates (animals & humans) from the cellular to the community level. The research of the Laboratory of Phytopathology aims to gain fundamental knowledge about functional genomics aspects of plant pathogenic fungi and oomycetes, the interaction with their host plants and the interaction with bacteria that occur in the rhizosphere. The collaboration between these research groups reflects the different levels of organization that will be addressed and the variation in expertise that are combined in this project. From this the PhD-student is expected to greatly benefit. The student will be based at the Laboratory of Genetics, as most of the experimental work will be done here. The other Chair groups are within 5 minutes reach of the Laboratory of Genetics.

We ask: The successful candidate should have a MSc degree in Biology, Animal Sciences, Environmental Sciences, the Life Sciences and/or biotechnology, with a keen interest in linking genetic variation to functional phenotypes and fitness. The candidate will be proficient in the English language. Creativity, intelligence and enjoying to work on complex problems in a multidisciplinary team, is much more important than a specific educational background. Within Wageningen University, PhD students are encouraged to supervise MSc thesis students when such opportunities arise.

We offer: A full-time position (38 hours), initially for 1 year after which a go/no go decision will be taken on extension with another three years. Gross salary per month 2042,= in the first year rising to 2612,per month in the fourth year, for a fulltime appointment.

The candidate will be based at the Laboratory of Genetics in Wageningen.

For more information contact Prof. dr. Bas Zwaan, +31 317 484619, bas.zwaan@wur.nl, and/or Prof. dr. Willem Takken, +31 317-484652; willem.takken@wur.nl

You can apply for this job before the 31st of December 2011 at http://www.wur.nl/UK/work or send your letter of application and full CV to Bas Zwaan (bas.zwaan@wur.nl).

“Zwaan, Bas” <bas.zwaan@wur.nl>

Jobs

AMNH NewYork OrnithologyCurator

Assistant or Associate Curator of Ornithology American Museum of Natural History

The American Museum of Natural History (AMNH) in New York is inviting applications for a curatorial position at the Assistant or Associate Curator level in the Division of Vertebrate Zoology, Department of Ornithology. This is a tenure track position with the salary and duration of review for tenure being negotiable depending on the candidate's degree of professional experience and accomplishment. We seek candidates whose research addresses fundamental questions involving the systematics and evolutionary biology of living birds. The successful candidate will have an accomplished record of scholarship and publication as well as capabilities for leadership within the Division and Department. Candidates who can contribute to Museum initiatives in genomics, phenomics (large-scale phenotypic analysis), and to the global exploration of avian diversity are especially encouraged to apply. Collection and/or field-based research are highly desirable. The ability to communicate effectively within the scholarly community and to a larger public is important. AMNH curators are expected to maintain a high level of productivity in original research, to provide curatorial oversight of relevant collections, and to seek extramural funding. Other responsibilities may include serving on committees and participating in Museum sponsored exhibits and educational programs, and in the Comparative Biology Ph.D. program at the Richard Gilder Graduate School. Candidates should have postdoctoral or professional employment experience. Interested candidates should submit electronically, via a single email message, the following materials: a) complete curriculum vitae, b) a statement detailing research interests, accomplishments, future research plans, and how you envision contributing to the Department of Ornithology and to graduate and postgraduate research and education, c) up to five relevant publications (pdf files), and d) a list of dissertation advisors, committee members, co-authors and co-PIs on funded grants during the preceding five years. In addition, each applicant should have three letters of support sent to the Search Committee. All materials should be submitted electronically, preferably as pdf files, to: Ornithological Search Committee, American Museum of Natural History, Central Park West at 79th Street, New York, NY 10024-5192, to: trombone@amnh.org (Subject line: Ornithology Search Committee). Inquires should be directed to Joel Cracraft, Chair of the Search Committee: jlc@amnh.org. Applications and letters of support should be received no later than January 30, 2012.

Joel Cracraft <jlc@amnh.org>

AuburnU FunctionalGenomics

The Department of Biological Sciences at Auburn University invites applications for a tenure-track faculty appointment (9-month) at the Assistant Professor level with specialization in the area of Functional Genomics, beginning Fall 2012. Candidates are expected to possess expertise in the study of genome-to-phenotype pathways conferring functionality and adaptation in any eukaryotic system. Candidates whose research interests expand or enhance existing areas of strength within the department will be given preference. Candidates are expected to establish an extramurally funded, internationally recognized research program and to actively engage in training of graduate and undergraduate students. Instructional responsibilities will include regular participation in the department's undergraduate General Genetics offering and graduate and/or upper-division courses in the area of specialization, as well as advising graduate and undergraduate students in the major.

Applicants must have a Ph.D. in Biological Sciences or a closely related discipline, and at least 2 years of relevant postdoctoral experience. Excellent communication / interpersonal skills are required. Desired qualifications include a strong record of publication, teaching experience, potential for extramural funding, and bioinformatics experience. 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, continue working legally for the proposed term of employment, and be able to communicate effectively in English. Women and Minorities are strongly encouraged to apply.

Review of applications will begin 1 Jan 2012 and will continue until a suitable applicant is found. Applicants should submit (electronically) a cover letter emphasizing specific qualifications, a curriculum vitae, a description of research interests, a statement of teaching philosophy / experience along with the names and contact information of at least 3 references to genomeap@auburn.edu (Dr. Michael Wooten, Functional Genomics Search Committee, Department of Biological Sciences, 331 Funchess Hall, Auburn University, AL 36849-5414 - Email:wootemc@auburn.edu). More information about the department and its programs can be found at:www.auburn.edu/biology . AUBURN UNIVERSITY IS AN AFFIRMATIVE ACTION/EQUAL OPPORTUNITY EMPLOYER.

halocaridina@gmail.com

BrighamYoungU ArthropodEvolution

Arthropod Evolution

The Department of Biology at Brigham Young University seeks to fill a full time, Continuing Faculty Status-track faculty position in arthropod biology. Qualified applicants with a PhD, postdoctoral experience, and expertise in evolutionary or organismal biology (including, but not limited to, systematics, evolution, ecology, and bioinformatics) are encouraged to apply. The successful candidate is expected to maintain an externally funded research program involving both undergraduate and graduate students. Excellence in teaching is required. Teaching responsibilities will include general biology, animal diversity, and a graduate course in the candidate's area of expertise. Interested persons should apply online at https://yjobs.byu.edu by completing a faculty application, and attaching a current CV, and statements of teaching and research interests. Questions may be directed to: Dr. Michael Whiting, Arthropod Biology Search Committee Chair, 401 WIDB, Department of Biology, BYU, Provo, UT 84602 (Michael_Whiting@byu.edu).

The review process will begin February 1, 2012 for this position and continue until the position is filled. Additional department and college information is available at website: http://biology.byu.edu/home. Brigham Young University, an equal opportunity employer, does not discriminate on the basis of race, color, gender, age, national origin, veteran status, or against qualified individuals with disabilities. All faculty are required to abide by the university's honor code and dress and grooming standards. Preference is given to qualified candidates who are members in good standing of the affiliated church, The Church of Jesus Christ of Latter-day Saints. Successful candidates are expected to support and contribute to the academic and religious missions of the university within the context of the principles and doctrine of the affiliated church.

Christina George Department of Biology Brigham Young University

Christina George <christina_george@byu.edu>

Goettingen LivestockPopulationGenomics

The Faculty of Agricultural Sciences at Georg-August-Universitaet Goettingen, Germany, invites applications for a Junior Professorship (W1) for

âPopulation Genomics of Host-Pathogen-Systems in Livestockâ

The position is to be filled at the earliest possible date.

The position is a fixed-term professorship for the duration of three years. Pending a positive evaluation, the position may be extended by another period of three years.

The successful candidate shall represent the subject in research and teaching. The approaches in research will aim at a better understanding of adaptation mechanisms and interactions between host and pathogens on the genomic level. Research activities will be concentrated on selected host-pathogen-systems in livestock (including aquaculture) and may have either an experimental or a more theoretical focus.

The candidate will hold an excellent PhD in a relevant discipline (e.g., agricultural science, biology, statistics). Experience in population genomics research and interest in interdisciplinary collaboration as well as in the participation in existing collaborative projects are supposed.

Please visit www.nutztierwissenschaften.uni-goettingen.de for additional information on this position (in German)

Further requirements for employment are stated in the Niedersächsische Hochschulgesetz (NHO) from February 26th, 2007. If the applicant was employed as a research assistant either before or after obtaining the doctoral degree, the entire duration of the period of employment and of the doctoral degree should not exceed six years.

The Georg-August-University Göttingen Public Law Foundation owns the right of appointment. Further details can be given upon request.

Applications of candidates from abroad are explicitly welcome. The University of Goettingen places particular emphasis on fostering career opportunities for female scientists and scholars and therefore strongly encourage qualified women to apply. Disabled persons with equivalent qualification will be given preference.

Applications should include a full CV, a list of publications, a statement of academic achievements including teaching, as well as an own representative research paper. Please submit your electronic application until Jan. 10, 2012, to

Prof. Dr. Achim Spiller, Dean of the Faculty of Agricultural Sciences, Buesgenweg 5, D-37077 Goettingen, Germany, E-Mail: dekagrar@uni-goettingen.de

For further information please contact Prof. Henner Simianer (hsimian@gwdg.de)

Henner Simianer Professor, Animal Breeding and Genetics Department of Animal Sciences Georg-August-University Goettingen Albrecht-Thaer-Weg 3, 37075 Goettingen Tel.: +49-551-395604, Fax: +49-551-395587

Email: hsimian@gwdg.de http://www.uni-goettingen.de/tierzucht "Simianer, Henner" <hsimian@gwdg.de>

HarvardU 1year ConservationBiol

The Sarah and Daniel Hrdy Fellowship in Conservation Biology Department of Organismic and Evolutionary Biology Harvard University

The Department of Organismic and Evolutionary Biology invites applications or nominations for the Sarah and Daniel Hrdy Visiting Fellowship in Conservation Biology. The Hrdy Visiting Fellowship is available either at the senior faculty level or at the junior (i.e., postdoctoral) level for one or two semesters. Duties include teaching one course and/or giving lectures in conservation biology, as well as research and collaboration with members of the Harvard community. Recipients of this fellowship are expected to have a strong and transformative effect on the study of conservation biology at Harvard, from the undergraduate to the senior teaching level. The fellowship includes a stipend with modest additional funds for research and teaching. Applicants should contact a faculty sponsor(s), with whom they will collaborate, before applying. Applications should include a cover letter with a statement of intent, CV, and representative publications, and applicants should arrange to have three letters of reference sent.

Please submit applications online at http://-academicpositions.harvard.edu/postings/3911 Applicants should contact a faculty sponsor(s), with whom they will collaborate, before applying. Applications should include a cover letter with a statement of intent, CV, and representative publications, and applicants should arrange to have three letters of reference sent.

Further information about OEB is available at http://-www.oeb.harvard.edu. Address questions about the application/nomination process to Mr. Christopher Preheim in OEB <cpreheim@oeb.harvard.edu>.

Review of applications will begin on March 1, 2012.

Harvard University is an Affirmative Action/Equal Opportunity Employer. Applications from women and minority candidates are strongly encouraged.

Christopher Preheim

Academic Programs Coordinator Harvard University Dept. of Organismic and Evolutionary Biology 617-384-9271

"Preheim, Christopher" <cpreheim@oeb.harvard.edu>

HarvardU PlantEvolution

Harvard University Faculty Position Plant Biology

The Department of Organismic and Evolutionary Biology at Harvard University and the Arnold Arboretum of Harvard University invite applications for a tenure-track or tenured faculty position in plant biology. We seek to appoint an individual whose research on plants integrates well with the outstanding living and herbarium collections of the Arnold Arboretum and whose scholarship will complement the research and teaching missions of the Department of Organismic and Evolutionary Biology. The area of scholarship is open, and we especially encourage applications from those studying genomics, molecular genetics, developmental biology, physiology, organismic biology, phylogenetics, evolution, ecology, and community biology, whose research addresses fundamental questions regarding the origin and maintenance of plant biodiversity. Applicants will be expected to develop an innovative research program and contribute to teaching at the graduate and undergraduate levels in the Department of Organismic and Evolutionary Biology. The research laboratory will be situated in the newly opened 43,000 square foot stateofthe- art research facility in the Arnold Arboretum of Harvard University.

Applications should include a curriculum vitae, statements of research and teaching interests, and representative publications. Tenured faculty should submit these materials to the tenured faculty position in plant biology listed at https://-academicpositions.harvard.edu. Tenure-track applicants should submit these materials, along with the names and contact information of three references, to the tenure-track faculty position in plant biology listed at https://academicpositions.harvard.edu .Letters of nomination from third parties are also welcome. First review of applications will begin on December 15, 2011. Further information about OEB is available at http://www.oeb.harvard.edu; information about plant biology at Harvard can be found at http://www.pbi.fas.harvard.edu; information about the Arnold Arboretum can be found at http://arboretum.harvard.edu/. Please contact us via e-mail with any questions at aapltbio@fas.harvard.edu. Harvard University Is an Affirmative Action/Equal Opportunity Employer. Applications >From or information about female and minority candidates are encouraged.

Christopher Preheim

Academic Programs Coordinator Harvard University Dept. of Organismic and Evolutionary Biology 617-384-9271

"Preheim, Christopher" <cpreheim@oeb.harvard.edu>

MaxPlanck Seewiesen FieldAssist GreatTitBehaviour

"Temporary field assistants required April-June 2012 for behavioural project on great tit personalities and parental care at Max Planck Institute for Ornithology, Seewiesen, Germany. Specific duties will include nestbox data collection, nestbox video recording, and field experiments on parental behaviours. No salary, but expenses paid plus possible future PhD opportunities. Experience with avian fieldwork and a driving licence preferred. Contact: Prof. Jon Wright (jonathan.wright@bio.ntnu.no)."

Thank you very much.

Best wishes,

Jon.

– Prof. Jonathan Wright Department of Biology, NTNU, Trondheim, N-7491 Norway.

E-mail: jonathan.wright@bio.ntnu.no http://www.ntnu.edu/employees/jonathan.wright Tel: +47 73 596070 (office) Tel: +47 91897210 (mobile) Fax: +47 73 596100

Jonathan Wright <jonathan.wright@bio.ntnu.no>

NorthernArizonaU EvolutionaryBiol

The Department of Biological Sciences at Northern Arizona University is currently accepting applications for two tenure-track positions at the Assistant Professor level, one in the field of Genetics and one in the field of Microbiology. Complete details regarding these positions, including application instructions, can be found at the links below.

Genetics: http://hr.nau.edu/node/2796&job_req=558982 Microbiology: http://hr.nau.edu/node/2796&job_req=558959 –

Jason Wilder Assistant Professor Department of Biological Sciences Northern Arizona University 928-523-5286 (phone) Flagstaff, AZ 86011-5640 928-523-7500 (FAX)

OaklandU EvolutionaryBiology

TENURE-TRACK FACULTY POSITION ASSISTNT PROFESSOR - EVOLUTIONARY BIOLOGY

The Department of Biological Sciences invites applications for a tenure-track, Assistant Professor position in the area of Evolutionary Biology. The successful candidate is expected to develop a vigorous, externally-funded research program. Candidates with molecular, developmental, or genetic approach are particularly encouraged to apply. Laboratory space and startup package will be provided. A PhD and post-doctoral experience are required as well as a strong research track record evidenced by publications. The successful candidate will engage undergraduate and graduate students in their research program and teach evolution at the undergraduate and graduate levels.

The Department of Biological Sciences (http://www2.oakland.edu/biology/) is a modern, well equipped, and research oriented department. The department has active graduate programs at the Masters and Ph.D. level. Oakland University is a state-supported institution of 19,000 students situated on a beautiful 1,600-acre campus 25 miles north of Detroit. Oakland University is an ADVANCE institution, one of a limited number of universities in receipt of NSF funds in support of our commitment to increase diversity and the participation and advancement of women and underrepresented minorities in STEM.

Review of Applications will begin on January 15, 2012, and continue until the position is filled. Applicants should submit a cover letter, a curriculum vita, detailed statement of research plans, teaching philosophy, 3 representative publications, and a list of at least 3 references via the web at: https://academicjobs.oakland.edu/postings/97 . Inquiries should be addressed to:

Arik Dvir, Chair,

Department of Biological Sciences

(dvir@oakland.edu)

Catherine Starnes <starnes@oakland.edu>

OregonStateU GenomicsMathematician

The Department of Mathematics at Oregon State University invites applications for a full-time (1.0 FTE), 9-month, tenure-track faculty position at the Assistant Professor level in the area of genomic mathematics. Research in this area addresses shared interests of mathematicians and of scientists working in genome-enabled biology, including those of researchers affiliated with the Center for Genome Research and Biocomputing (CGRB) at Oregon State University. Areas of mathematical specialty are open for this position, but the successful candidate's research at Oregon State University might include modeling or simulation in systems biology, mathematical analysis of structures in large biological data sets, or large-scale biocomputing. A doctoral level degree in mathematics or closely related area is required. In addition to conducting research in genomic mathematics, the successful candidate will teach five quarter-based courses per academic year, ranging from entry-level undergraduate to advanced graduate courses, and will participate in advising of graduate degree candidates. A complete application includes four reference letters, curriculum vitae, teaching statement, and a research statement. The research statement must explicitly address candidate's past accomplishments and future plans for applications and interactions of mathematics to genome-enabled biology, as well as the candidate's ability to establish contact with scientists working in that area. At least two of the reference letters should address the candidate's experience and potential for applying mathematics to problems in genome-enabled biology. At least one letter should address the candidate's accomplishments and potential as a teacher. For full consideration, apply by 1/15/12. OSU is an AA/EOE and has a policy of being responsive to dual-career needs. Applications are to be completed at https://www.mathjobs.org. This is job posting number 3282.

CGRB-seminar mailing list CGRB-seminar@lists.oregonstate.edu http://-lists.oregonstate.edu/mailman/listinfo/cgrb-seminar
blouinm@science.oregonstate.edu

Portugal Bioinformatics

We are seeking a highly motivated Informatician or Bioinformatician interested in joining the research project entitled "Gamete Recognition proteins - the key for cryptic sexual selection", financed by FCT, the science funding body for Portugal (http:/-/alfa.fct.mctes.pt/).

This project aims to uncover the role played by sexual selection and reinforcement in the evolution of post-copula recognition proteins and in the ecological speciation observed in the rough periwinkle, *Littorina saxatilis*, a common intertidal gastropod distributed along the NE Atlantic coast for which several ecotypes adapted to distinct shore levels have been described as evolving repeatedly in the presence of gene flow.

This multidisciplinary project will be conducted at CIBIO, the Research Center in Biodiversity and Genetic Resources (http://cibio.up.pt/) - University of Porto, Portugal and integrates morphology, genomics, transcriptomics, proteomics and ecological modeling. The project is part of an international collaboration between labs with great experience in the evolution of sexual recognition mechanisms and the evolution of *Littorina* species.

The successful candidate will be hired for two months (which may extend up to three), starting at 7th January, and be paid 1000euro per month of work. Her/his tasks include: *i*) to compare a database of peptides obtained from tissue specific proteome with a database of putative mRNA sequences obtained from a 454 tissue specific transcriptome to identify matches between the two sources of data; *ii*) to compare the transcriptomic database with other genomic, transcriptomic and proteomic databases (such as NCBI, Ensembl, UNIprot and Littorina's database) in order to identify putative mRNAs. The candidate will be identified as an author on articles resulting from this work.

Essential qualifications are: motivation, autonomy, programming experience and previous experience in working in transcriptomic/genomic projects and ability to work with large genomic or transcriptomic databases and with BLAST tools. Candidates should send an e-mail addressed to Alexandra Sá Pinto (xanasapinto@gmail.com), with a motivation letter and CV, deadline 29 th December 2011.

For additional information send an e-mail to Alexandra Sá Pinto (xanasapinto@gmail.com).

Alexandra Sá Pinto

xanasapinto@gmail.com

SanDiegoZoo ResTech Genetics

The Research Technician will work with the Genetics Division at the San Diego Zoo Institute for Conservation Research. Applicants must have knowledge of standard laboratory procedures, safety practices, and be skilled in the use and basic maintenance of general laboratory equipment. Experience culturing and freezing somatic cells from a variety of species and karyotyping the derived cell lines is required, as is training in nucleic acid preparation and quantitation from various source materials. Proficiency with PCR, automated sequencing, and microsatellite fragment analysis is necessary. Knowledge of taxonomic nomenclature and clinical cytogenetic techniques (including FISH and CGH) is preferred. Experience in Mac and/or Windows-based computer programs is required, and familiarity with molecular data analysis programs is desired. The applicant must have the ability to take direction, work as part of a team, follow through on assignments, and be neat and well organized.

This is a permanent, full-time position with benefits. Applications close 18 December. For more information and to apply, visit https://www.hrapply.com/-sandiegozoo/AppJobList.jsp?op=3Dreset Oliver Ryder oryder@sandiegozoo.org

oryder@ucsd.edu

SouthernOregonU EvolutionaryBiology

Southern Oregon University, Department of Biology

Faculty Position in Evolutionary Biology

The department of Biology invites applications for a tenure-track *Evolutionary Biologist* position. We seek an individual committed to excellence in undergraduate teaching and research to teach an upper-division Evolution course, a core requirement of our major. Additional teaching will include an upper-division organismal course with a strong field component, participation in the introductory sequence for science majors, and development of a general education course that explores evolutionary biology with non-science majors. We are particularly interested in candidates with the demonstrated ability to integrate field studies of whole organisms with modern molecular techniques to explain evolutionary processes. Southern Oregon University is located in the heart of the Klamath-Siskiyou bioregion, one of the most ecologically diverse regions of North America. The successful candidate is expected to establish an active research program involving undergraduates that investigates questions relevant to the bioregion. For more information and to apply go to https://jobs.sou.edu. Review of applications will begin on 15 December and will continue until the position is filled. Questions regarding the position can be directed to Dr. Michael Parker, Chair, Evolutionary Biologist Search Committee, (541) 552-6749, parker@sou.edu. Southern Oregon University is an equal access AA/EOE committed to achieving a diverse work force and as such, is an inclusive campus community dedicated to student success, intellectual growth, and responsible global citizenship.

*Michael S. Parker *Chair, Department of Biology* *Professor of Biology Southern Oregon University Ashland, OR 97520 541-552-6796 phone 541-552-6415 fax

parker@sou.edu

Michael Parker <parker@sou.edu>

Syracuse InvertConservation

Assistant Professor in Invertebrate Conservation Biology

Job Description: The State University of New York College of Environmental Science and Forestry (SUNY-ESF) in Syracuse invites applications for an academic-year, tenure-track position as Assistant Professor in Conservation Biology, specializing in invertebrates.

Responsibilities: The successful candidate will be expected to build a strong, extramurally funded research program in the conservation of invertebrates. Teaching responsibilities will include two undergraduate courses (Invertebrate Zoology and Principles of Evolution), and one graduate course within area of expertise. Advising responsibilities will focus on undergraduate, M.S., M.P.S., and Ph.D. students in the Conservation Biology major and graduate area of study. Collaboration is expected with colleagues in other disciplines at the College and the broader academic community for delivering research and teaching programs. Expectations for service include to the College and Department and outreach to groups such as state and federal agencies, non- governmental organizations, professional societies and the public.

Requirements: A Ph.D. in Biology or a related discipline is required. Qualified candidates must demonstrate a primary interest in invertebrate systematics, phylogenetics, bioinformatics, and/or evolutionary ecology as a means of furthering invertebrate conservation. Preference will be given to candidates with evidence of ability to mentor undergraduate and graduate students, postdoctoral experience and a record of excellence in research, teaching and outreach, commensurate with time since degree.

Additional Information: The College and the Faculty: The College of Environmental Science and Forestry is a PhD-granting institution with one of the largest groupings of faculty dedicated to solving environmental problems through research, teaching and service. SUNY-ESF is one of the leading institutions in per-capita research funding among the 64-campus SUNY system. With a total enrollment of about 1,200 undergraduates and 600 graduate students, ESF provides an intimate small-college atmosphere with a low student/faculty ratio. Integration of research and teaching is emphasized and advanced undergraduate students regularly work with graduate students and faculty mentors. Conservation Biology is part of a larger Department of Environmental and Forest Biology (www.esf.edu/efb), a group of over 30 scientists from a variety of ecological and biological disciplines. Conservation Biology includes 150 undergraduate and 33 graduate students at the M.S. M.P.S., and PhD levels. The College is on the same campus as Syracuse University and near Upstate Medical University, giving students and faculty the added resources of a large institution of higher education, including a wide array of courses, computer and library facilities, intercollegiate and intramural sports, and health services.

ESF's field stations and properties are diverse and total over 10,000 hectares in northern and central New York (http://www.esf.edu/campuses). These facilities include the Huntington Forest and associated Adirondack Ecological Center (www.esf.edu/aec), the Cranberry Lake Biological Station (www.esf.edu/clbs) in the Adirondack Mountains, the Heiberg Forest south of Syracuse, the Thousand Islands Biological Station on the St. Lawrence River (www.esf.edu/tibs) and others. These properties provide opportunities for research and teaching for faculty and graduate students.

In accordance with the "Jeanne Clery Disclosure of Campus Security Policy and Campus Crime Statistics Act" institutions of higher education are required to prepare an annual report containing information on campus security policies and campus statistics. This report includes statistics for the previous three years concerning reported crimes that occurred on-campus; in certain off-campus buildings or property owned or controlled by SUNY-ESF; and on property within, or immediately adjacent to and accessible from the campus. The report also includes institutional policies concerning campus security, such as policies concerning sexual assault, and other matters. You can obtain a printed copy of this report by contacting SUNY-ESF University Police at 315-470-6667 or by accessing the following web site: http://www.esf.edu/univpolice/crimereports/2010Syr.pdf Application Instructions: Applications should include a letter summarizing qualifications as well as a statement of research interests and accomplishments, curriculum vitae, a statement of teaching experience and philosophy. Send three references directly to Dr. Stephen Teale at address below. To ensure

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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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TexasAMU ChairDept

Texas A&M University Professor and Head Department of Wildlife and Fisheries Sciences

Applications are invited for the position of Professor and Head for the Department of Wildlife and Fisheries Sciences. As an administrative unit of the College of Agriculture and Life Sciences, Texas AgriLife Research and Texas AgriLife Extension Service within The Texas A&M University System, the Department of Wildlife and Fisheries Sciences has a diverse and dynamic mission with 42 faculty and 19 staff members engaged in teaching, research, and extension at several locations throughout the state, nation, and world. Departmental facilities include the Texas Cooperative Wildlife Collection, Aquatic Research and Teaching Facility, Biosystematics and Biodiversity Center, Small Upland-bird Research Facility, Ecological Systems Laboratory, and the Land Information Systems Laboratory. Department personnel are based mostly in College Station but also at affiliated institutions and several research and extension centers across the state. The Department currently enrolls approximately 400 undergraduates and approximately 200 graduate students in M.S. or Ph.D. programs. The Department conducts research in five general areas: Aquatic Ecology and Fisheries Science; Conservation Biology; Ecology, Evolutionary Biology and Systematics; Marine Mammal Biology; and Wildlife Ecology, Conservation and Management. The Wildlife and Fisheries Extension Program is the largest in the nation and has been nationally recognized for its expertise in the areas of wildlife, fisheries, aquaculture, marine science, related enterprises, youth and adult education, and spatial technologies for natural resource management. More information can be obtained at http://wfsc.tamu.edu/ The successful candidate will have a Ph.D. and record of distinction in wildlife and fisheries conservation, ecology and evolutionary biology, aquaculture or related field. The candidates record should demonstrate effective leadership and management of multidisciplinary programs, and familiarity with and appreciation of basic and applied research, teaching, extension, and service missions. The candidate should possess outstanding leadership skills as well as demonstrated success in communicating effectively with diverse clientele and stakeholders. Prior experience in the Land Grant University System is desirable. Applications should be sent in electronic format (preferred) to search@biobioubunto.tamu.edu. Applications should include a letter of interest, statement of administrative philosophy, curriculum vitae, and the names and contact information for at least three references. References will be contacted only upon approval by the applicant. Review of applications will begin January 1, 2012, and continue until the position is filled.

The Texas A&M University System is an Equal Opportunity/Affirmative Action Employer. The University is committed to building a culturally diverse and pluralistic faculty and staff and strongly encourages applications from women, minorities, individuals with disabilities, and covered veterans.

– Jessica E. Light Assistant Professor and Curator of Mammals Department of Wildlife and Fisheries Sciences Texas Cooperative Wildlife Collection Texas A&M University 210 Nagle Hall, 2258 TAMUS (mailing) 320A Heep Laboratory Building (office) College Station, TX 77843 Phone: 979-458-4357 Fax: 979-845-4096 email: jlight2@tamu.edu http://people.tamu.edu/~jlight2 jlight2@tamu.edu

UCalifornia Berkeley WildlifeEvolution

Please post this ad for a lecturer in the Department of Environmental Science, Policy and Management at UC Berkeley. Although the course is Wildlife Ecology, we're certainly interested in considering evolutionary biologists as potential instructors.

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Lecturer, Wildlife Ecology Department of Environmental Science, Policy, & Management University of California, Berkeley

The Department of Environmental Science, Policy, & Management at the University of California, Berkeley seeks applications for a part-time Lecturer to teach ESPM 114, Wildlife Ecology, during the Spring 2012 semester. The course lecturer delivers two hours of lecture each week and oversees four GSIs who handle eight, one-hour discussion sections per week. The lecturer also holds weekly office hours. This position is scheduled to begin January 1, 2012 through May 31, 2012.

Course Description: This course provides an introduction to wildlife ecology and includes population, community, and ecosystem levels of organization. Specifically, the course introduces students to basic concepts and applications in physiological ecology, niche theory, population dynamics, population estimation, metapopulation and community ecology, trophic webs and a range of special topics including invasive species, wildlife disease, landscape ecology and wildlife policy. Students are evaluated on their performance on three projects, three exams and their preparedness for discussion section.

Position requirements: Candidate should have Ph.D. in ecology or related field with teaching experience and strong professional references. The primary responsibilities for this position include:

Delivering lectures Planning and preparing lessons, including: researching and developing new topics, courses and teaching materials and online resources, developing materials for the student discussion, and developing materials for discussion sections taught by GSIs Supervising four to five graduate student instructors Holding office hours Developing exams and projects, and grading them (or supervising GSIs in the marking) Maintaining accurate records and monitoring students' progress, as well as addressing any special student needs Maintaining knowledge of, and implementing, college policies Salary: Commensurate with qualifications and experience (starting annual, full-time salary is $44,636)

Applicants should submit a letter of application, curriculum vitae, statement on teaching philosophy and experience, along with the names and contact information of three references to: http://ecnr.berkeley.edu:80/sReg.php?i 2. The deadline for applications is December 19, 2011.

This is a non-tenured, temporary position: the appointments to the title of Lecturer are self-terminating (no further notice on non- reappointment will be forthcoming) and do not create an obligation on the part of the University either to extend or renew the appointment outlined above. Any reappointment will be preceded by an assessment. Employment is contingent upon proof of eligibility to work in the United States.

The University of California is an equal opportunity affirmative action employer, committed to excellence through diversity. The College seeks candidates whose research, teaching, or service has prepared them to contribute to our commitment to diversity and inclusion in higher education.

Neil D. Tsutsui Associate Professor Vice Chair for Instruction Department of Environmental Science, Policy & Management University of California, Berkeley Berkeley, CA 94720-3114

Mail:130 Mulford Hall, #3114 Office: 326 Hilgard Hall Lab: 3 & 245 Hilgard Hall Email: ntsutsui@berkeley.edu Phone: 510-642-9012 Fax: 510-643-5438

Neil Tsutsui <ntsutsui@berkeley.edu>

UCalifornia Davis EvolutionDiversity

JOB ADVERTISEMENT

EVOLUTION OF ORGANISMAL DIVERSITY, UNIVERSITY OF CALIFORNIA, DAVIS

The College of Biological Sciences, University of California, Davis invites applications and nominations for a tenure-track position in the Department of Evolution and Ecology at the ASSISTANT level, with the possibility of ASSOCIATE appointment with tenure. Candidates must have a Ph.D. (or equivalent) in the biological sciences or related fields. They should have a strong record of integrative approaches to the evolution of organismal diversity. We seek candidates with expertise in the organismal biology/natural history of a multicellular group, and whose research uses genomic data in an explicitly phylogenetic context to address questions in macroevolution, ecology, behavior and/or development. The successful candidate will be expected to teach in the department's undergraduate program and in the Population Biology Graduate Group and should be committed to departmental service. Applicants should submit materials online at: https://recruitments.ucdavis.edu/PositionDetails.aspx?PositionID=85&Title=Asst/Assoc-%20Professor-%28Tenure-Track%29 which contains additional information about the position. These should include: curriculum vitae, description of current and projected research, summary of teaching interests and experience, and up to five publications. Applicants should also provide the information requested for three referees. Once entered, referees will be prompted by email with upload instructions for their letters. Closing Date: Open until filled, but all application materials, including letters of recommendation, must be received by February 6, 2012, to assure full consideration. Administrative contact: Carla Munoz (camunoz@ucdavis.edu). Faculty contacts: Peter Wainwright, Michael Turelli, and Rick Grosberg. The University of California is an Equal Opportunity/Affirmative Action Employer with a strong institutional commitment to the development of a climate that supports equality of opportunity and respect for differences.

"Brian R. Moore" <brianmoore@ucdavis.edu>

UConnecticut PlantEvolutionaryGenomics

University of Connecticut PLANT ECOLOGICAL OR EVOLUTIONARY GENOMICS

The Department of Ecology and Evolutionary Biology at the University of Connecticut seeks applicants for a 9-month tenure-track position to begin in August 2012. Although targeted at the Assistant Professor rank, an appointment at a higher rank may be possible for a candidate who exceptionally enhances the diversity elements of our academic mission. We seek a creative individual employing genomic approaches to address key questions in the ecology and evolutionary biology of plants. Research on non-model organisms is preferred but appropriate research foci involving model organisms will also be considered. Experience in bioinformatic and statistical analyses is desirable. The successful applicant will have a Ph.D., preferably with postdoctoral experience. They will be expected to supervise an independent research program that will attract extramural funding, teach at the undergraduate and graduate levels, and provide research training for graduate and undergraduate students. Teaching duties are expected to include participation, on a rotating basis, in a) our introductory biology curriculum, b) an upper-level botany, evolution, or ecology course, and c) a graduate course in the candidate's specialty. Preferred qualifications include the ability to contribute to the diversity and excellence of the learning experience and academic community through research, teaching or service. Submit a curriculum vitae (with links to your top 3 publications), a summary of research accomplishments and future research objectives, a brief description of teaching experience and philosophy to: Husky Hire (http://jobs.uconn.edu). Please have letters from three referees sent to: (EEB.Search@uconn.edu). Review of applications will begin January 6, 2011. Questions regarding this position may be addressed to kathleen.tebo@uconn.edu

Evaluation of applicants will be made by assessment of: 1) graduate and post-doctoral experience; 2) research accomplishments, productivity and extramural funding; 3) statements of teaching and research objectives; 4) professional references; and 5) expertise in ecological or evolutionary genomics. Information about the Department of Ecology and Evolutionary Biology can be found at http://hydrodictyon.eeb.uconn.edu/-eebwww/ The University of Connecticut houses state of the art genomics instrumentation and computational facilities. The University of Connecticut encourages applications from under-represented groups, including minorities, women, and people with disabilities.

Carl Schlichting Professor Ecology & Evolutionary Biology University of Connecticut

schlicht@uconn.edu

UEdinburgh EvolutionaryBiol

Subject: University of Edinburgh: Chancellor's Fellowships

The University of Edinburgh, a global top 20 University located in one of the world's finest cities, is making a major investment in the future of its academic staff with the appointment of prestigious tenure-track Fellowships across all disciplines. These 5-year Fellowships are intended to support outstanding candidates at the start of their independent academic career. Up to 100 positions are available.

A Chancellor's Fellow will already show the ability to conduct world-leading research and exhibit clear potential to become an international leader in their discipline. The Fellow will be able to concentrate on research in the first instance, acquiring the full duties of University Lecturer across the period of the Fellowship. Subject to satisfactory review at the end of 3 years, the Fellow will move to an open contract on the University academic staff.

Appointment will normally be made on the Lecturer scale (£36,862 - £44,016), dependent on experience, and in exceptional circumstances a more senior appointment may be made. Some positions are available with immediate effect and it is expected that successful applicants will be in post from August 2012.

The School of Biological Sciences expects to appoint between five and ten Fellows across the school. The Institute of Evolutonary Biology (http://www.ed.ac.uk/-schools-departments/biology/evolutionary-biology) welcomes applicants across all relevant topics, particularly in the areas of Population Ecology and Population Genetics. Potential applicants are encouraged to contact members of IEB to discuss their research interests. Further details and the full range of priority areas within Biological Sciences may be found at http://www.ed.ac.uk/schools-departments/-biology/research/ch-fellows Applications containing a detailed CV and a 1-page outline of a proposed research programme should be made online at www.jobs.ed.ac.uk under job ref 3015150N to meet one of the closing dates 16th Jan, 29th Feb and 16th April 2012. General advice may be obtained by emailing chancellorsfellows@ed.ac.uk

Professor J.M. Pemberton Head, Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Road EH9 3JT

tel 0131 650 5505 fax 0131 650 6564 Email j.pemberton@ed.ac.uk

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

Josephine Pemberton <J.Pemberton@ed.ac.uk>

UFPE Brazil EvolutionaryGenomics

Associate Researcher at the Environmental and Evolutionary Genomics Lab - UFPE, Recife, Brazil

The Environmental and Evolutionary Genomics Lab led by Rodrigo A. Torres, D.Sc., is seeking a Brazilian (preferential) or a foreign associate researcher to integrate the research developed in the laboratory. The lab develops studies on phylogeography, population genetics, molecular systematics, landscape and conservation genetics in the Neotropical fauna. Two possible graduate courses of Animal Biology or Genetics can be the focus for hosting the associate researcher.

The program offer a 3-year fellowship of R$ 7,000.00 (at around US$ 4,400.00) monthly and R$ 20,000.00 (at around US$ 12,500.00) annually as a supporting grant for the project. An additional fellowship for a baseline scientific student is also included for each approved proposal.

The tasks of the selected researcher will include active scientific production, the supervision of undergraduate and graduate students as well as some undergraduate and graduate classes. It is expected that applicants have both expressive scientific production and significant experience with the methods permeating those mentioned areas of interest.

More detailed information can be found at the link http://www.cnpq.br/editais/ct/2011/060.htm or by emailing Dr. Rodrigo A. Torres (rodrigotorres@ufpe.br/torres_ra@yahoo.com).

rodrigotorres@ufpe.br

UGroningen ResTech MarineEvolution

Research Technician 0,6fte

The University of Groningen is one of the largest and oldest research universities in the Netherlands. It ranks among the top 200 Universities in the world (The Times World University Rankings, 2010-2011). The Centre for Ecological and Evolutionary Studies (CEES) at the Faculty of Mathematics and Natural Sciences with the University of Groningen invites applications for a position as a research technician placed at the research group Marine Evolution and Conservation (MarECON). MarECON's main research focus is the evolution and conservation of marine mammals. The group has excellent laboratory facilities for molecular analyses.

Research description

We are recruiting a Research Technician for our general research program which utilizes marine mammals, in particularly the large whales, to study the population genetics and evolution in the marine realm. The ultimate goal is to understand the mechanisms driving population genetic structuring and local adaptation of long-range migrating mammals. Many aspects of our research have conservation implications as well.

Qualifications

We are looking for an enthusiastic and self-motivated co-worker, who enjoys acquiring new skills and enjoys working with a team of researchers and students. He /she should have a Bachelor or Masters degree in Biology (HLO) or related field. The ideal candidate will have experience with (or the ability to acquire) modern molecular genetic methods and instrumentation employed in evolutionary and population genetics such as prepare libraries for next generation sequencing, Sanger sequencing, STR genotyping and cloning. Experience with database management is preferred and a good command of written and spoken English necessary.

Additional information

For more information contact Dr. Per Palsboll (p.j.palsboll@rug.nl) or Dr. Martine Berube (m.berube@rug.nl).

*Conditions of employment***

The University of Groningen offers a salary dependent on qualifications and work experience starting at EUR 1986 gross per month up to maximum of EUR 2682 (scale 7, step 10) gross per month for a 100% employment. This position is defined according to the UFO function profile 'Onderwijs-/onderzoeksmedewerker'. The part-time (60%) appointment is initially for a fixed period of 3 years and subject to an evaluation after the first year.

Application

The application should be written in English including a personal motivation, curriculum vitae, as well as the names and addresses of three referees (including telephone number and email address). The application should be emailed to: vmp@rug.nl. The reference number is 211195and the application date January 2nd, 2012.

Per J. Palsboll, Professor

Marine Evolution and Conservation Centre for Ecological and Evolutionary Studies University of Groningen Nijenborgh 7 9747 AG Groningen The Netherlands

Office phone: +31 50 363 9882 Mobile +31 64 870 3295

Mail address: PO Box 11103 9700 CC Groningen The Netherlands

p.j.palsboll@rug.nl

UGroningen ResTech MarineEvolution 2

My apologies for the second posting but it appears that I was provided incorrect instructions the first time and that application have to be submitted on-line. Please see below (at the very end).

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Research Technician 0,6fte

Organisation The University of Groningen is one of the largest and oldest research universities in the Netherlands. It ranks among the top 200 Universities in the world (The Times World University Rankings, 2010-2011). The Centre for Ecological and Evolutionary Studies (CEES) at the Faculty of Mathematics and

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Research description We are recruiting a Research Technician for our general research program which utilizes marine mammals, in particularly the large whales, to study the population genetics and evolution in the marine realm. The ultimate goal is to understand the mechanisms driving population genetic structuring and local adaptation in wide-ranging mammals. Many aspects of our research have conservation implications as well.

Qualifications We are looking for an enthusiastic and self-motivated co-worker, who enjoys acquiring new skills and enjoys working with a team of researchers and students. He /she should have a Bachelor or Masters degree in Biology (HLO) or related background. The ideal candidate will have experience with (or the ability to acquire) modern molecular genetic methods and instrumentation employed in evolutionary and population genetics such as prepare libraries for next generation sequencing, Sanger sequencing, STR genotyping and cloning. Experience with database management is preferred and a good command of written and spoken English necessary.

Additional information For more information contact Dr. Per Palsboll (p.j.palsboll@rug.nl) or Dr. Martine Berube (m.berube@rug.nl).

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Application The application should be written in English including a personal motivation, curriculum vitae, as well as the names and addresses of three referees (including telephone number and email address). The application should be submitted on-line. The link for the advertisement and on-line submission may be found at this URL http://www.rug.nl/corporate/vacatures/jobOpportunitiesRUG – Per J. Palsboll, Professor

Marine Evolution and Conservation Centre for Ecological and Evolutionary Studies University of Groningen Nijenborgh 7 9747 AG Groningen The Netherlands

Office phone: +31 50 363 9882 Mobile +31 64 870 3295

Mail address: PO Box 11103 9700 CC Groningen The Netherlands

Per J Palsboll <p.j.palsboll@rug.nl>

UHawaii Manoa ChairBotany

The Department of Botany at the University of Hawaii at Manoa will continue to accept applications for the position of Professor and Chair, with review to begin approximately January 31, 2012. The position posting is linked below:

http://www.pers.hawaii.edu/wuh/nadvert.aspx?rn=13130&si=1251124&pn=1&sn=postdate&so=desc

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Kasey E. Barton Assistant Professor Botany Department University of HawaiÊ≫i at MÄnoa 3190 Maile Way, Room 101 Honolulu, HI 96822

Website http://seedlingscience.org kbarton@hawaii.edu

UHawaii Manoa ChairBotany correctedURL

The Department of Botany at the University of Hawaii at Manoa will continue to accept applications for the position of Professor and Chair, with review to begin approximately January 31, 2012. The position posting is linked below:

http://www.pers.hawaii.edu/wuh/nadvert.aspx?rn=13130&si=1251124&pn=1&sn=postdate&so=desc

–

Kasey E. Barton Assistant Professor

Botany Department

University of HawaiÊ≫i at MÄnoa

3190 Maile Way, Room 101

Honolulu, HI 96822

Website http://seedlingscience.org Kasey Barton

<kbarton@hawaii.edu>

UIllinois ComputationalMedicine

Associate or Full Professor (Tenured) Computational and Genomic Medicine University of Illinois at Urbana-Champaign

The University of Illinois at Urbana-Champaign seeks full-time faculty for two tenured positions in areas with strong relevance to Computational and Genomic Medicine.? These positions are part of a cluster of hires supported by multiple campus units, which will make it possible to build campus expertise in Computational and Genomic Medicine with the goal of strengthening our research and educational capabilities in systems approaches to human medicine. These new positions, together with matching hires from various units, will strengthen research and teaching excellence in this field and form the core of a new theme in the Institute for Genomic Biology (see www.igb.illinois.edu). These positions will also support the strategic development of the Illinois Initiative for Health Sciences and the Mayo ? Illinois Alliance for Technology-Based Health Care. Campus units collaborating in these hires are the Institute for Genomic Biology; School of Chemical Sciences; School of Integrative Biology; School of Molecular and Cellular Biology; College of Agricultural, Consumer, and Environmental Sciences; College of Applied Health Sciences; College of Engineering; and the College of Medicine. The candidate is expected to further strengthen ties between these units and to establish interdisciplinary collaborations. The chosen candidates will be appointed in one of the following Departments: Animal Biology, Animal Sciences, Biochemistry, Bioengineering, Cell and Developmental Biology, Chemical and Biomolecular Engineering, Chemistry, Computer Science, Entomology, Food Science and Human Nutrition, Kinesiology, Mathematics, Medical Information Science, Microbiology, Molecular and Integrative Physiology, Physics, or Statistics. The applicant must specify in their cover letter the department(s) for which they would like to be considered.

The University of Illinois at Urbana-Champaign is a world-class institution that offers exceptional opportunities for innovative individuals to conduct collaborative research within the Institute for Genomic Biology, the National Center for Supercomputing Applications (NCSA), the Beckman Institute for Advanced Science and Technology, the Roy J. Carver Biotechnology Center, the Seitz Materials Research Laboratory, the Micro and Nanotechnology Laboratory, and the NSF Center for the Physics of Living Cells. These senior-level positions are part of the new multi-year Strategic Excellence Hiring Program at Illinois that focuses on: (a) Information, Technology, and Society, (b) Human Health and Wellness, (c) Energy and Sustainability, and (d) Culture, Communication, and Global Issues. Candidates with experience in computational approaches to human medicine, including genomics, systems biology, and microbial ecology are encouraged to apply.?The successful candidate will be expected to participate in developing an educational core allowing undergraduates to gain quantitative skills for their future careers in health related disciplines. Minimum qualifications include an earned doctorate in biomedical or computational research, outstanding academic credentials, and international stature. Rank and salary will be commensurate with qualifications. Starting dates for these positions are negotiable.

Applicants are asked to please create their candidate profiles at http://jobs.illinois.edu and upload letters of interest (including email address), resumes, statements of research goals, and contact information for three professional letters of reference by January 15, 2012. Applicants may be interviewed before the closing date; however, no hiring decision will be made until after that date. All requested information must be submitted for applications to be considered. For further?information regarding the application procedures, please contact Kim Johnson, kljohns@igb.illinois.edu. Salary is negotiable and commensurate with experience.

Current junior faculty positions advertised on the University of Illinois campus in Computational and Genomic Medicine can be found at http://www.igb.illinois.edu/Junior-Faculty-Positions . Illinois is an Affirmative Action/Equal Opportunity Employer and welcome individuals with diverse backgrounds, experiences, and ideas who embrace and value diversity and inclusivity (http://www.inclusiveillinois.illinois.edu).

Becky Fuller

Becky Fuller <fuller@life.illinois.edu>

UKonstanz 2 ComparativeGenomics MolecularEvolution Evodevo

UNIVERSITY OF KONSTANZ/GERMANY 2 ASSISTANT PROFESSOR/JUNIOR GROUP LEADER IN EVOLUTIONARY BIOLOGY (molecular evolution/comparative genomics or devo-evo)

Two positions as “Assistant Professor” (German government salary scale TVL or possibly Akademischer Rat) in the Chair for Evolutionary Biology (Professor Axel Meyer) at the Department of Biology of the University of Konstanz in Germany are available from March 2012 (the second at the latest from July 1st) on.

The person we are looking for should work on current research topics in the fields of either molecular evolution, comparative genomics, and/or the evolution of developmental mechanisms. The position is for a Ph.D. biologist, ideally with prior postdoc experience and a publication record in bioinformatics, molecular evolution or evolutionary developmental biology. A total of three research groups, two of which are headed by Junior Group Leaders each representing their particular subdisciplines of evolutionary biology, make up the evolutionary biology group (Lehrstuhl Evolutionsbiologie) in the Department of Biology (http://www.evolutionsbiologie.uni-konstanz.de/index.php?section=10).

The taxonomic emphasis is on fish, particularly on cichlid or zebrafish and medaka model systems. Most of the ongoing evolutionary research in Konstanz deals with comparative developmental and molecular evolutionary/genomic aspects of the origin of adaptation and speciation in cichlid fish adaptive radiations. For publications of the lab see: http://www.evolutionsbiologie.uni-konstanz.de/index.php?section=92. For a recent summary of some of our planned work see: Elmer, K.R. and A. Meyer. 2011. Adaptation in the age of ecological genomics: insights from parallelism and convergence. Trends in Ecology and Evolution 26: 298-306.

Space in a modern animal care facility is available and the exclusive help of a part-time technician will be available to this new group. Excellent opportunities are available in terms of space, equipment, departmental facilities and annual financial support for research expenses. The lab has state-of- the-art facilities for molecular and developmental biology, including Illumina and Roche FLX next-generation sequencers at the Genomics Center Konstanz (http://cms.uni-konstanz.de/en/genomics-center/).

The University of Konstanz and the Department of Biology are among the most highly ranked institutions in Germany and provide a lively and academically outstanding research environment. Konstanz is a lovely historic town located on Lake Constance on the border to Switzerland.

Appointments are initially for two to three years, and are renewable for up to six and potentially even ten years, with an annual gross salary (depending on prior experience) of about 58,000 Euros (about 73.000 US$). Habilitation is possible, and a modest amount of teaching (English or German) is required.

Additional information can be obtained from axel.meyer@uni- konstanz.de, (tel.+49 7531 884163, fax + 49 7531 883018) or from our www page. http://www.evolutionsbiologie.uni-konstanz.de . Applications including a statement of research interests, a full CV, and names and email addresses of 3 referees, should be emailed to a.meyer@uni-konstanz.de. Applications should be received before December 24, 2011. Interviews will be scheduled in January 2012. The University of Konstanz is an equal opportunity employer.

Prof. Axel Meyer, Ph.D. Chair for Evolutionary Biology Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 (0)7531 88 4163 fax + 49 (0)7531 88 3018

secretary: Ingrid.Bader@uni-konstanz.de tel. + 49 (0)7531 88 3069

www.evolutionsbiologie.uni-konstanz.de Axel Meyer <axel.meyer@uni-konstanz.de>

UOxford 3 GeneticsZoology

UNIVERSITY OF OXFORD, U.K. Department of Zoology: Search for three permanent faculty posts (Lecturer is roughly equivalent to tenured Associate Professor)

(1) Lecturer in Genetics Department of Zoology in association with Lady Margaret Hall. You will be expected to lead a research programme in experimental or analytical genetics or genomics, particularly at the interface with evolutionary biology, ecology or behaviour.

(2) Lecturer in Parasite Biology Department of Zoology in association with Christ Church. You will be expected to lead a research programme on parasites of animals or vectors of parasites, with an emphasis on their evolution, ecology, development, behaviour or transmission.

For (1) and (2), further particulars, containing details of the application procedure and of the duties, may be obtained from peter.holland@zoo.ox.ac.uk or by visiting http://www.zoo.ox.ac.uk/jobs The closing date for applications is noon on 31 January 2012.

(3) Professor of Zoology Applications are invited for the 'Professorship of Zoology' with effect from 1 October 2012 or as soon as possible thereafter. The post is one of five Established Professorships in the Department of Zoology. The appointee will be expected to engage in internationally outstanding research, provide leadership in a particular area of biological sciences, and develop a vigorous externally-funded research programme. Further particulars and details of application procedure will be posted imminently on http://www.zoo.ox.ac.uk/jobs The University is an Equal Opportunities Employer

Peter Holland <peter.holland@zoo.ox.ac.uk>

UppsalaU ComputationalBiologist

A job for a computational biologist is available at SciLifeLab with employment at the Department of Medical Biochemistry and Microbiology, IMBIM. The position is available as soon as possible for a period of 2 years, with a six months trial period.

SciLifeLab Uppsala: Science for Life Laboratory Uppsala is a center that joins together a group of prominent researchers from Uppsala University with the vision to become an internationally leading center that develops, applies, and provides access to large-scale technologies for molecular biosciences with a focus on translational medicine and on evolutionary and systems biology. The center is composed of several technology platforms in genomics, proteomics, imaging and visualization, metabolomics, and comparative genetics and two research programs in health and the environment http://www.scilifelab.uu.se Duties: The candidate will work with bioinformatics in the research environment of SciLifeLab. A main focus of this position will be to work with large novel genomes performing genome assembly, annotation and analysis in support of vertebrate genome projects in a project-based fashion. A first project involves analysis of the genome of the carrion crow (Corvus corone).

The different projects will be done in close collaboration with other groups at SciLifeLab as well as with other national and international collaborators.

The candidate will work in close collaboration with many researchers at SciLifeLab under the supervision of Manfred Grabherr. Manfred Grabherr directs a computational biology group that was just recently started. The focus of this group is to provide answers to fundamental biological questions through the application and development of complex algorithms that analyze large amounts of DNA and RNA data.

Qualifications required: To be eligible for this position, the applicant must hold a Ph.D degree. The ideal candidate will have a strong background in computational biology or bioinformatics, and have experience with the assembly, analysis and annotation of large and complex genomes and transcriptomes. The candidate should be familiar with commonly used bioinformatics tools, and be proficient in one or more scripting and/or programming languages (perl, python, C++, Java) in a UNIX environment. Experience in software development involving complex algorithms is a big plus. Excellent communication skills are required, since the candidate will collaborate with scientists of very different backgrounds. Excellent spoken and written English is required.

Salary, specify salary requirements in the application. Information about this position can be given by Manfred Grabherr, e-mail manfred.grabherr@imbim.uu.se, +4618-471 4248.

This ad including forms for online submission of applications: http://www2.personalavd.uu.se/ledigaplatser/2809researcher.html – Marc P. Hoeppner, PhD Department of Medical Biochemistry and Microbiology Uppsala University, Sweden marc.hoeppner@imbim.uu.se

"Marc P. Hoeppner" <marc.hoeppner@imbim.uu.se>

USGeologicalSurvey 2year bioinformatician

USGS is advertising for a Bioinformaticist, 2 year term position to be stationed at Leetown Science Center in Kearneysville, West Virginia Bioinformaticist: Salary Range: $62,467. - $81,204. Per year Open Period: Wednesday, December 14, 2011 ? Wednesday, January 4, 2012 Series & Grade: GS-0401-11 Position Information: Term Appointment not to exceed 2 years ? Full-time Promotion Potential: 12 Duty Locations: Leetown, WV Who may be considered: United States Citizens

To apply for this job go to: http://www.usajobs.gov/-GetJob/ViewDetails/305059100

Kay Marano Briggs, PhD Lead: Genetics & Microbiology Ecosystems Mission Area 12201 Sunrise Valley Drive MS301 Reston, VA. 20192 703-648-4046 703-648-4238 kmbriggs@usgs.gov

fikej@usgs.gov

UStirling 3 EvolutionaryBiol

Although the titles might not seem at first glance to be directly relevant to most evolutionary biologists, I am assured that the committee will try to cast as wide a net as possible to secure the best candidates.

Kind thanks,

Luc

Biological & Environmental Sciences, School of Natural Sciences, University of Stirling, Scotland Closing date for applications - 31 January 2012 Further details: http://www.stir.ac.uk/about/jobs/-details.php?nPostingId=3D57&nPostingTargetId=-85&id=QUUFK026203F3VBQB7V79V7NE&LG=UK The Posts Applications are invited for the following 3 areas: Lecturer in Conservation Biology; Lecturer / Senior Lecturer in Environmental Geography and/or Ecosystem Services; Lecturer / Senior Lecturer in Environmental/Ecological Modelling. Two posts are available and the successful candidates will be expected to undertake research, teaching, administration and other activities in Biological and Environmental Sciences, integrating with activities across the School of Natural Sciences to support and develop the School's academic profile.

The successful candidates will be expected to make a full contribution to SNSs internationally excellent research activities and contribute research-led teaching at post-graduate and under-graduate levels

Conservation Biology We seek to capitalise on our strengths in conservation and ecology. Stirling City has become a centre for conservation activity in Scotland, with a plethora of environmental organisations with offices or head offices on, or close to, the University campus (e.g. BTCV, Buglife, BTO, RSPB, Plantlife, Bat Conservation, Bumblebee Conservation Trust, Butterfly Conservation, Wildfowl and Wetland Trust, BRISC, SNH, SEPA etc.). Of these, BTO, BBCT, RSPB, WWT have offices within Biological and Environmental Sciences. This provides an unrivalled opportunity for collaboration and cooperation. The synergies to be gained from research and active conservation working hand in hand are neatly demonstrated by the success of the home-grown Bumblebee Conservation Trust, now with 8,000 members nationwide and a significant contributor to research funding at Stirling. The role of Stirling staff in establishing the trust is being used as an exemplar statement of research impact by HEFCE (Higher Education Funding Council for England). Stirling is an established leader in this field in Scotland, and is the natural partner for governmental organizations (e.g. SNH, SEPA) in providing the science base needed to inform strategic responses to issues such as: climate change and its implications; the global biodiversity crisis and the conflicting pressures on land use; provision of secure and sustainable ecosystem services; assessments and impacts of contaminated land; and aquatic conservation and restoration. This research focus also dovetails neatly with the cross-research council priority initiative “Living with Environmental Change”.

Ecosystem Services and/or Environmental Geography One of the great challenges facing Humankind is ensuring that we maintain the Ecosystem Services upon which we depend for our survival and health in the face of growing pressures on the environment. Living with Environmental Change has a significant focus on the provision of ecosystem services (e.g. pollination; carbon cycling and sequestration; clean air, soil and water; flood control and prevention, sustainable soils, resource management), and we seek a specialist in this area to enable critical mass to be attained. This is a subject area of growing interest to government and at international development level and applicants whose research has societal relevance and policy linkages are encouraged to apply. The scope encompasses the maintenance of the ecological and biogeochemical cycles upon which we depend, through provision of food, fuel and fibre, to issues concerning human health, cultural and social identity and environmental hazard mitigation.

Environmental/Ecosystem Modelling Much of BES research is empirically or process based. To evaluate fully the significance and impact of environmental change and anthropogenic disturbance on the environment and its resilience, including that of Humankind, requires the development of our modelling capabilities. The ability to explore and predict the impacts of environmental change and disturbance will complement existing expertise and provide effective tools for environmental management and conservation, and further support for science-policy and regulatory linkages. We are seeking applicants with an interest in applying modelling approaches to understanding environmental and/or ecological systems, and those with explicit focus on geographical processes/patterns, and their analysis, are strongly encouraged to apply.

These posts are full time on an open ended basis. Dependent on experience

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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

YaleU EcologyandEvolutionaryBiology

Yale University Faculty Position in Ecology and Evolutionary Biology

The Department of Ecology and Evolutionary Biology at Yale University invites applications for a tenure track faculty position at the junior level. We seek outstanding applicants working in any area of ecology and evolutionary biology and are particularly interested in applicants whose research has a strong focus in ecology. A record of outstanding achievement and a promising research program are more important than specific research area.

Application materials including a CV, three manuscripts or reprints, brief research and teaching statements and contact information for three evaluators should be submitted online at https://academicjobsonline.org/ajo/Yale/EEB. The search will remain open until the position is filled. The review of applications will begin January 13, 2012.

Yale University is an Equal Opportunity/Affirmative Action Employer. Yale values diversity among its students, staff, and faculty and strongly welcomes applications from women and underrepresented minorities.

“Suzanne H. Alonzo” <suzanne.alonzo@yale.edu>

Other

ASokoloff has passed away

Alexander Sokoloff 1920-2011

Alex Sokoloff is widely regarded as "The Father of Tribolium Genetics". Alex was of Russian ancestry, but he was born in Japan, and lived there for the first three years of his life. He lived and worked for extended periods in Mexico, and of course in America. He was a true cosmopolitan. He was a disciple of the great evolutionary biologist, Theodosius Dobzhansky, and kept up a lifelong correspondence with Dobzhansky. Many of their letters are reproduced in Sokoloff's fascinating memoir, published a few years ago. Sokoloff had the great foresight to see the potential of Tribolium as a model insect for genetic studies as early as the late 1950's, while a graduate student in the laboratory of Thomas Park. He discovered and described hundreds of genetic mutants in Tribolium, many of which are still in use and are housed in the world Tribolium Stock Center at the USDA-ARS Center for Grain and Animal Health Research, Manhattan, KS. His early work provided a spark that helped facilitate the blossoming of the arthropod genomics community in Manhattan, and that culminated in the complete genome sequencing of Tribolium castaneum, the first genome completed for any beetle and for any insect pest of agriculture. The International Tribolium Meeting is now an annual event in Europe and America. Although Alex was never able to attend, these meetings might never have come into existence if not for his pioneering work, and his inspiration of a new generation of Tribolium researchers. His four monographs, published from 1966-1977, are still regarded as the authoritative original sources for information on Tribolium genetics and biology.

Dick Beeman Research Entomologist USDA-ARS-CGAHR 1515 College Avenue Manhattan, KS 66502 TEL: 785-776-2710 FAX: 785-537-5584 richard.beeman@ars.usda.gov

"Beeman, Richard" <Richard.Beeman@ARS.USDA.GOV>

Austria summer fellowships

Summer Fellowships for Young Scientists at the International Institute for Applied Systems Analysis, Austria

Funding is available for PhD students interested in three months of collaborative research during June-August 2012 on

Evolutionary and Ecological Modeling

at the International Institute for Applied Systems Analysis (IIASA) in Laxenburg, Austria.

Young scientists from all countries are eligible for stipends provided by IIASA's Evolution and Ecology Program (EEP) that contribute to travel and accommodation costs. Students from Austria, Brazil, China, Egypt, Finland, Germany, India, Japan, Korea, Malaysia, the Netherlands, Norway, Pakistan, Russia, South Africa, Sweden, and the USA are eligible for fellowships that provide full coverage of travel, accommodation, and living expenses.

Model-based summer research projects are invited in the following indicative areas:

Evolutionary Community Ecology Food-Web Evolution VegetationDynamics Adaptive Speciation Evolutionary Conservation Biology Fisheries Management Fisheries-induced Evolution Evolution of Cooperation Governance of Common Goods Systemic Risks and Network Dynamics Eco-Evolutionary Dynamics Adaptive Dynamics Theory and Models SpatialModels in Ecology andEvolution

Applicants prepare a research proposal that corresponds to their scientific interests and to the research agenda of theirhosting IIASA Program. Accepted applicants begin work before the summer by planning their research in close collaboration with their IIASA supervisors. Previous experiences with implementing and studying evolutionary or ecological models are important assets for working in EEP. To improve chances of being selected, potential applicants are encouraged to sent informal inquiries regarding their specific research interests and plans to EEP's program leader Ulf Dieckmann (dieckmann@iiasa.ac.at).

Online applications will be accepted until Monday, January 16, 2012 (24:00 CET).

Since 1977, IIASA's annual Young Scientists Summer Program (YSSP), has attracted 1500+ students from 80+ countries. The YSSP 2012 will take place from June1 to August 31. IIASA is located in the former summer palace of Austria's royal family, ca. 15 km south of Vienna. IIASA's summer program offers exceptional opportunities for acquiring experience in an international and interdisciplinary research environment. Research training is based on regular personal interaction with advising scientists, and typically leads to a publication in an international journal, as well as to a chapter in a candidate's PhD thesis.

Some useful links:

+ www.iiasa.ac.at/Admin/YSP/reg-info/-more_about_the_program.html Details about the summer program, and online application

+ www.iiasa.ac.at/Research/EEP Information about IIASA's Evolution and Ecology Program

+ www.iiasa.ac.at/Research/EEP/Students.html Examples of successful YSSP projects

+ www.iiasa.ac.at/docs/IIASA_Info.html General information about IIASA

Ulf Dieckmann Program Leader Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

Email dieckmann@iiasa.ac.at Phone +43 2236 807 386 Phone secretary +43 2236 807 231 Fax +43 2236 807 466 or +43 2236 71313 Web http://www.iiasa.ac.at/Research/EEP Online reprints http://www.iiasa.ac.at/~dieckman FroSpects Network http://www.iiasa.ac.at/Research/EEP/FroSpects FinE Network http://www.iiasa.ac.at/Research/-EEP/FinE FishACE Network http://www.iiasa.ac.at/-Research/EEP/FishACE dieckmann@iiasa.ac.at

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ChicagoBotanicGarden undergrad experience

To the Evoldir Community,

This summer, the Chicago Botanic Garden and partner institutions will host 10 NSF-REU interns (Research Experiences for Undergraduates) conducting research under the broad theme of PLANT BIOLOGY AND CONSERVATION, from genetic to ecosystem levels of inquiry. Potential projects include work in soil ecology, systematics, reproductive biology, biogeochemistry, restoration ecology, pollinator ecology, and other fields. Students will gain laboratory and field experience, participate in professional development activities, help mentor high-school student researchers, and enjoy a fun social environment.

Participants should be U.S. citizens or permanent residents who will be enrolled as undergraduates after summer 2012. They will receive a stipend of $4,750 and room and board at a local college. Costs of travel to and from Chicago will be covered. We encourage applications from students who are members of groups underrepresented in the sciences and students who have limited research opportunities at their home institutions. The application deadline is January 31, 2012, and the 10-week program will run from June 11-August 17, 2012.

We invite interested undergraduates to find more information and apply at http://www.cbgreu.org. Questions can be directed to info@cbgreu.org.

We also ask faculty, postdocs, graduate students, and other undergraduate mentors to please help us spread the word about this exciting opportunity to exceptional undergraduates.

Apologies for cross-posting

- Evelyn Williams

Chicago Botanic Gardens REU Experience http://www.cbgreu.org/ info@cbgreu.org

ewwilli@gmail.com

DAMBE workshop Ottawa interest

Dear All,

I intend to offer a one-day workshop entitled "Phylogenetics with DAMBE" either right before or after Evolution 2012 in Ottawa (either on Jul. 5 or on Jul. 11, 2012), and wish to know how many people might be interested in attending such a workshop. The topics will include

(1) routine phylogenetic analyses and dating methods (both the conventional dating with internal node calibration or tip- dating which is used mainly for viral sequences sampled over different years)

(2) Phylogeny-based comparative methods.

(3) Evolutionary genomics

There might be a fee (but no more than $20/person) to cover room reservation, facilities, coffee and cookies. The cost would be less if all participants bring their own laptops. It would be ideal to have about 10-20 participants.

The workshop will be taught by me.

Please email me directly if you are interested in participating in the workshop. Thank you.

Best Xuhua

Xuhua Xia, Professor of Biology Biology Department University of Ottawa Rm 278 Gendron 30 Marie Curie, Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 URL: http://dambe.bio.uottawa.ca Xuhua.Xia@uottawa.ca

Evolution lab suggestions

Dear colleagues,

I am designing an upper-level undergraduate Evolutionary Biology Laboratory course, as an addition to the lecture. I am seeking suggestions on what lab activities will be good for this 2-hour 1-credit course. Ideally, I would like to have different activities for the lab, including computer simulations (on genetic drift, etc.), exercise in taxonomy and molecular phylogeny, and wet-lab experiments. I would like to hear your opinions on what computer programs are particularly good for the first two types of activities, and I will greatly appreciate your suggestions on experimental lab activities which could be run in the time of one class, across a few weeks or the whole semester and can potentially produce publishable results. If you have taught any of the above lab activities, I would like to hear from you on what works, what does not, and your suggestions for improvement. I will compile the suggestions and comments received and make them available here.

In addition, I am trying to put together a fossil collection for teaching purpose. If you have some fossils you think could be used for teaching and would like to donate, please send me a note and I will provide you the address where they can be sent to. Sorry I cannot afford to buy your fossils, but I plan to reimburse you for the shipping cost.

Thanks a lot,

Xianfa Xie

Xianfa.Xie@gmail.com

Evolution lab suggestions answers

I would like to thank all of you who have made suggestions to my question about evolutionary lab activities or offered to donate fossils for my teaching. Below, after the repeat of my original email, is a compilation of all the suggestions I have received about lab exercises, in the order of arrival. I have also attached the two files I received, which I hope will be successfully sent to the email list. Hope these suggestions and documents will be helpful to some of you. ~Xianfa

On 12/3/11 2:57 AM, “Xianfa Xie” wrote:

Dear colleagues,

I am designing an upper-level undergraduate Evolutionary Biology Laboratory course, as an addition to the lecture. I am seeking suggestions on what lab activities will be good for this 2-hour 1-credit course. Ideally, I would like to have different activities for the lab, including computer simulations (on genetic drift, etc.), exercise in taxonomy and molecular phylogeny, and wet-lab experiments. I would like to hear your opinions on what computer programs are particularly good for the first two types of activities, and I will greatly appreciate your suggestions on experimental lab activities which could be run in the time of one class, across a few weeks or the whole semester and can potentially produce publishable results. If you have taught any of the above lab activities, I would like to hear from you on what works, what does not, and your suggestions for improvement. I will compile the suggestions and comments received and make them available here.

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Thanks a lot,

Xianfa Xie

Xianfa.Xie@gmail.com

—— Forwarded Message From: Tom Gilbert <mtpgilbert@gmail.com> Date: Sat, 3 Dec 2011 09:07:31 +0100 To: <Xianfa.Xie@gmail.com> Subject: Re: Other: Evolution lab suggestions

Dear Xianfa I am not sure what range of experiments you are considering, but there is one very simple one that always goes down well that demonstrates very nicely the power/significance of drift, bottlenecks etc in genetic data. The classic 'resampling beads' experiment. If you don't know it its very simple.

You need, per group, a bag, and a selection of beads. Ideally say 100 of 3+ different colours (100 red, 100 blue, 100 yellow)

Basic idea is you start them by putting predetermined mix of 100 beads in a bag. Then to simulate bottlenecks, or drift, they just pick an appropriate number of beads randomly from the bag, which of course will vary a bit from the original ratio due to stochasticity. Then you get them to count and record the new frequency, multiply them up to 100 by adding new beads at the same ratio, and then repeat. After about 4-5 generations they can really see how the frequency is drifting away. Its a real eye opener for many students who don't initially get how drift can happen. Of course you can easily simulate bottlenecks, expansions, etc.

Very cheap. Very obvious. Very easy to modify to more or less complex situations.

There are computer programs that do this too, but frankly the hands on way is in my experience way more fruitful. As many are sceptical of computers...they think its preprogrammed to do it. But actually seeing drift first hand...

Hope this helps

Tom Gilbert

—— Forwarded Message From: Anuschka Faucci <anuschka@hawaii.edu> Date: Fri, 02 Dec 2011 22:30:26 -1000 To: <Xianfa.Xie@gmail.com> Subject: Evolution Labs

Hi, not sure you know about the attached paper (the evolution of the chocolate bar). I use a simplified version for our Intro to ecology and evolution Lab as a warm-up before the Caminalcule Lab designed by Rob Gendron. He has some great ideas on his page as well: http://nsm1.nsm.iup.edu/rgendron/Caminalcules.shtml Good luck, and I'd love to see all the responses.

Anuschka

—— Forwarded Message From: Susan Cousineau <susan.cousineau@gmail.com> Reply-To: <susan.cousineau@gmail.com> Date: Sat, 3 Dec 2011 10:00:13 +0100 To: <Xianfa.Xie@gmail.com> Subject: Evolution lab

Hi Xianfa

I'm a Masters student in the Erasmus Mundus Evolutionary Biology programme (MEME) in my second year of studies. We did some practicals in our first year that were very helpful, and I can make a few recommendations from my current 6-month projects. I don't know how familiar you are with the world of evolutionary biology so it's hard to know if these suggestions will be totally naive and unhelpful... so bear with me!

For one suggestion... A practical that involves a series of steps from getting sequences, to aligning and editing (good idea might be something

— / —

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

Fish equipment

Hi fellow evolutionary biologists!

This may be an unconventional way of getting an experimental setup together, but in the light of little funding on the one side, and potentially dust-gathering equipment that is stored away in some University basement on the other, I would like to enquire if anyone may have second-hand equipment for sale that may be used for measuring performance in small fish.

For my research in zebrafish I am currently most interested in equipment than can be used to a) measure endurance (i.e. some sort of flume) and b) velocity (either burst speed or along a track). However, I would very much appreciate additional feedback and suggestions and am going to consider any offers!

Looking forward to your reply to susanne.zajitschek@ebc.uu.se

Thanks in advance, Susi Zajitschek

Susanne Zajitschek, PhD Department of Evolutionary Biology Evolutionary Ecology Centre Uppsala University Norbyvägen 18D Uppsala, 752 36 Sweden

susanne.zajitschek@unswalumni.com susanne.zajitschek@unswalumni.com

Heredity ScienceCommunication

The Heredity Podcast is opening a competition to graduate students and undergraduates with an interest in science communication.

The task is to record an interview with an evolutionary biologist about their research, then edit it down to a

4 minutes piece including a 30 second introduction, in the style of the Heredity Podcast (examples at http://feeds.feedburner.com/ac/yKZS)

The best pieces will be broadcast, and there is a prize of membership of the Genetics Society (http://www.genetics.org.uk/) for the best undergraduate and best graduate contribution.

Instructions for how to participate are available from here (competition link): http://webspace.qmul.ac.uk/ranichols/podcast/ Richard Nichols Professor of Genetics http://webspace.qmul.ac.uk/ranichols/research.htm richard.alan.nichols@googlemail.com

HGT events

Hi all

I am currently trying to build trees to detect horizontal gene transfer among several bacterial spp. I am trying T Rex to figure it out, but also wondering what other algorithm (tree building) can be used for this purpose and what issues I should keep in mind while making bacterial gene trees for HGT. I think someone may've posted quite similar query before, but not exactly the same, so sorry if its repetition

thanks in advance cheers

– AVIK RAY Visiting Fellow National Center for Biological Sciences Tata Institute of Fundamental Research GKVK Campus Bellary Road Bangalore-560065 India Ph 91-80-23666340 Fax 91-80-2363 6662

AVIK RAY <avik.ray.kol@gmail.com>

Ideas Ecol Evol

Volume 4 (2011) of Ideas in Ecology and Evolution is now complete (http://library.queensu.ca/ojs/index.php/IEE), including year-end editorials from four Advisory Editors.

Lonnie W. Aarssen

Professor Department of Biology Queen's University Kingston, ON Canada, K7L 3N6

Editor Ideas in Ecology and Evolution http://library.queensu.ca/ojs/index.php/IEE Campus office: Room 4326, Biosciences Complex Email: aarssenl@queensu.ca Web: http://post.queensu.ca/~aarssenl/ Tel: 613-533-6133 Fax: 613-533-6617

Molecular dating software answers

Dear all,

a couple of weeks ago I posted a request (below) for a molecular dating software suitable to be used programmatically in a sort of pipeline.

Replies (shortened) follow, as some of you requested.

My feeling is that, although some methods exist that are very accurate and leave to the operator an ample flexibility in terms of analysis design and parameter tweaking, none of these seem to be really optimal to work in the context of simulations/database automated analyses, where analyses have to be fast, robust and run (as much as possible) unsupervised, even at the expense of some accuracy/flexibility. Maybe there's some space for improvement here.

..I am not really sure it can do what you want, but have you consider the ape package in R? (Miguel)

..MCMCTREE is easy and effective. http://abacus.gene.ucl.ac.uk/software/paml.html You can find a step by step manual in the end of this website. I think you can implement MCMCTREE in your pipeline. You can also implement MULTIDIVTIME in the pipeline, but MULTIDIVTIME is little bit old software. (Jun)

..Have you looked at mcmctree in PAML? (Shige)

..You may use DAMBE. The download site also has a set of tutorials. The last one (#12, I believe) is on dating. The method is in Xia and Yang (2011, MPE). You read in sequences, input a tree, right-click one or more nodes and enter the calibration time, set the options, and click Run. It is extremely fast and accurate. (Xuhua)

..do you have access to a server (or set of servers)? If so, then you could get access to condor and use it to submit and manage the execution of jobs. I suggest this because we use condor for this purpose on a cluster of computers (94 CPUs) ... As for using BEAST, I agree that is recommended. (Lars)

..if you use command line version of beast and write a good executable file to run all your files one after the other it will need no supervision at all, so maybe this would be a good solution for you. (Martyna)

..I suggest to use the software PATHd8 which is very fast, about 1 second even for very large trees (1000 terminals). The only problem is that do not estimate age confidences. http://www2.math.su.se/PATHd8/- (Joan)

Many thanks to everybody,

francesco

—–

Dear all,

I am looking for a molecular dating software that:

- works on a fixed topology and estimates dates/node-heights based on DNA sequences - produces a confidence interval for dates/node-heights - is fast (20 seq, 1kb, 1 minute)

and if possible:

- is reasonably accurate - allows partitioning of the dataset (if applicable) - is model based - can be invoked programmatically under linux

I would generally use BEAST, but this time the analysis has to be repeated many times and with little supervision, in a sort of pipeline, hence BEAST would be problematic.

Any help will be appreciated,

francesco

++ Francesco Nardi, Dr.

Dept. of Evolutionary Biology University of Siena

via Aldo Moro 2 - 53100 Siena Italy

Ph.: +39.0577.234420 (lab. 4398) Fax.: +39.0577.234476 Web: http://www.dbe.unisi.it/-index.php?option=com_content&view=article&id=-89&Itemid=113&lang=it ++

nardifra@unisi.it

Monomorphic microsatellites

Dear Evoldir members,

We have characterized and isolated nuclear microsatellite loci from enriched libaries that were sequenced on a 454 sequencer. Dinucleotide, trinucleotide and tetranucleotide repeats motif within 454 sequence data were searched using the program MSATCOMMANDER version 0.8.1 and primers designed with Primer3. However, only 3 polymorphic loci (with only two or three alleles) have been recorded, while 13 monomorphic microsatellites loci have been detected in an endangered endemic plant species of Tenerife Island (Canary Islands). There are only 4 natural populations of this endemism described, which include 170 individuals. So, our question is: Is the low genetic diversity detected a real biological phenomenon or an artifact of the technique?

Thank in advance,

Miguel Angel

Miguel Angel González Pérez Investigador Doctor en Proyecto Departamento de Biología Universidad de Las Palmas de Gran Canaria 35017 Las Palmas Islas Canarias Spain t +34 928 454 543 p +34 928 452 922 e-mail: mgonzalez@proyinves.ulpgc.es

canariensis750@hotmail.com

Optics book

Dear colleagues,

I wanted to let you know that now in print is an “optics for biologists” book written by Sonke Johnsen of Duke University. It is called “The Optics of Life”. The book is meant to be an accessible, humorous, and practical introduction to understanding and measuring light. It’s officially aimed at biologists, but I think it could be useful to anyone who wants to get started in this fascinating, but potentially confusing subject. Of course many topics in evolutionary biology hinge on the interactions of organisms and light, so I thought there could be some interest in the evoldir community.

If you’re interested, it’s available at Amazon and directly from Princeton Press (for the same price):

http://www.amazon.com/Optics-Life-Biologists-Guide-Nature/dp/0691139911/ref=sr_1_1?ie=-UTF8&qid=1323705631&sr=8-1

http://press.princeton.edu/titles/9640.html –

Todd Oakley, Professor Ecology Evolution and Marine Biology University of California, Santa Barbara Santa Barbara, CA 93106 USA

UPDATED LAB WEBSITE: http://-labs.eemb.ucsb.edu/oakley/todd/

Paper request

Dear all,

my institution doesn't sign this journal. The leading Author can't also get a copy, because the paper was published when there weren't that many pdf's around. As my last resource, can anyone help me getting a Pdf of this paper? Leonard et al 1993, Applied Animal Behaviour Science. 37(1):57-67

Many thanks Miguel

Miguel Barbosa Visiting Postdoctoral Researcher Scottish Oceans Institute School of Biology University of St Andrews KL16 8LB Scotland

"Miguel Barbosa(Gmail)" <migosas@gmail.com>

Planning PopGenet 2ndEdition

Dear Colleagues,

I am in the process of planning the second edition of my book, Population Genetics. I would be grateful for any suggestions of material or features that could be included (or excluded) in the second edition. I would especially value comments from those who have used the book in courses or workshops.

Thanks to everyone who has already contacted me with comments or to point out typographical errors.

Sincerely, Matt Hamilton hamiltm1@georgetown.edu

Matthew B. Hamilton, PhD Associate Professor Georgetown University Department of Biology, Reiss 406 37th and O Streets NW Washington, DC 20057 202-687-5924 (office) 202-687-5662 (fax) http://www9.georgetown.edu/faculty/hamiltm1/ hamiltm1@georgetown.edu

PlantBreedingGenomics Review

Evoldir community,

I am interested in finding a recent review or book chapter that summarizes the current understanding of how the 'genomics age' has influenced plant breeding. I'm most interested in how this area has or has not influenced the development of resistant plants to various plant pathogens but am also interested in other phenotypes such as water stress, salinity resistance, cold stress, etc. Given that many plants and important pathogens have had their genomes sequenced, has this actually led to any real life examples of solving any problems yet?

Thanks, Greg

Greg W. Douhan, Assistant Professor Department of Plant Pathology and Microbiology Fawcett Lab RM 238 University of California Riverside, CA 92521-0122 Office (951) 827-4130 Fax (951) 827-4132

Greg Douhan <gdouhan@ucr.edu>

Proposals K-12 education

Request for proposals in K-12 evolution education for underrepresented minorities

Deadline: January 1, 2012

As part of ongoing efforts to increase diversity in evolutionary science, the National Evolutionary Synthesis Center is sponsoring a range of targeted activities in the general area of $B!H(BK-12 Evolution Education for Underrepresented Minorities." We seek to support one or more Catalysis Meetings, Working Groups or other synergistic activities that lead to the creation of new programs, activities or initiatives designed to increase exposure and participation in evolutionary science by K-12 minority students who are historically underrepresented in the discipline.

In particular, proposals that are significantly interdisciplinary, and that demonstrate a mix of senior and emerging researchers, including graduate students, are encouraged. Competitive proposals will not only define the target audience(s) and outline strategies for developing innovative activities, but will also include detailed plans for implementation and assessment. Proposals should also indicate how activities and programs align with state and/or federal education standards.

NESCent invites researchers to submit proposals for two kinds of meetings:

Catalysis Meetings: These one-time meetings bring together ~30 scientists from diverse disciplines to focus on a major question or research area in evolutionary science. Catalysis Meetings typically last for 3-5 days.

Working Groups: Working Groups involve small groups of scientists (10-12 participants) collaborating intensively on the analysis or synthesis of data, models or both, to address a major question in evolutionary science. Working groups will typically meet 3-4 times over two years, with each meeting lasting 3-5 days.

Synergistic Activities: We also strongly encourage linkages among our science programs (see url below). We invite proposals that plan synergistic activities between two or more of the following: working groups, catalysis meetings, postdoctoral fellows, sabbatical scholars, short-term fellows, and graduate students. Proposals for each of these must be submitted separately; they should include a clear statement of linkage between proposals (including clear identifications in each of the separate proposals of which proposals are linked).

NESCent will not support collection of new data or field research, but encourages the synthesis of existing data and information resources. NESCent is committed to making data, databases, software and other products that are developed as part of NESCent activities available to the broader scientific community.

To learn more about the various types of proposals, and the proposal process, please visit https://www.nescent.org/science/proposals.php, or contact Dr. Allen Rodrigo (a.rodrigo@nescent.org) or Dr. Jory Weintraub (jory@nescent.org).

Jory Weintraub <jory@nescent.org>

Published microsat datasets for teaching

Dear all,

I am looking for microsatellite datasets of animals that I can use in a practical on conservation genetics / dispersal. I would like to let the students work with real data that has a story behind it. Thus I would be very happy to receive either an input file (Genepop, Arlequin, Structure...) or a file with raw data (in excel or something like that) preferably with alleles given as fragment-length together with a publication where the very same dataset has been used.

Interesting themes would be: sex-biased dispersal fragmented populations invasive species inbred or small populations genetic variation in endangered species

I would be very very greatful for your contributions!

Best wishes Heike Feldhaar

Prof. Dr. Heike Feldhaar Tierökologie I Universität Bayreuth 95440 Bayreuth Germany

phone: +49 921 552645 fax: +49 921 552784

e-mail: feldhaar@uni-bayreuth.de

Heike Feldhaar <feldhaar@uni-bayreuth.de>

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running ClonalFrame

Hello everybody:

I am trying to run the program ClonalFrame on my Mac workstation (system 10.6.8) and I cannot seem to get the program to run. Based on the recommendation of the program's author I have installed the gsl-1.15 library, which appears to have worked

without any problems (I got no error messages). However, when I try to run ClonalFrame

I am still getting the error:

wollenbergk$ /Applications/ClonalFrame ; exit; dyld: Library not loaded: /opt/local/lib/libgsl.0.dylib Referenced from: /Applications/ClonalFrame Reason: image not found Trace/BPT trap logout

[Process completed]

Does anyone in the community have experience running ClonalFrame on a Mac? If so, do you have any advice about how I should proceed? Time is of the essence as I am

performing this analysis to address reviewer's comments on a recent manuscript.

Cheers,

Kurt Wollenberg, Ph.D.

The most exciting phrase to hear in science, the one that heralds new discoveries, is not "Eureka!" (I found it!) but "That's funny ..." –Isaac Asimov

Kurt Wollenberg <krwollen@yahoo.com>

Software BayesRate release

BayesRate v.1.1 has been released

BayesRate is a program to estimate speciation and extinction rates from dated phylogenies in a Bayesian framework. The method is described in BMC Evolutionary Biology by Silvestro, Schnitzler, and Zizka (2011) and uses an MCMC algorithm to estimate the rate parameters while accounting for phylogenetic uncertainty.

Different models of diversification are implemented to allow rate variation through time and between clades, and to correct for incomplete taxon sampling. The program is particularly suitable to test hypotheses of diversification that the user can define as priors and constraints in the analysis.

For model selection and hypothesis testing, thermodynamic integration (Lartillot and Philippe 2006) is used to calculate the marginal likelihood of a model and perform Bayes factor tests.

BayesRate is available for Mac, Windows, and Linux. It requires Python and R, plus a few additional libraries as detailed in the manual.

More information and downloads can be found on: https://sourceforge.net/projects/bayesrate/ For queries, bug reports, suggestions: daniele.silvestro@senckenberg.de jan.schnitzler@senckenberg.de

Daniele Silvestro Biodiversity and Climate Research Centre (BiK-F) Senckenberg Research Institute Frankfurt/M, Germany

Daniele.Silvestro@senckenberg.de

Software CLUSTER DIST

Dear all,

A new software is freely available on my web page (see below). CLUSTER_DIST is intended to separate individuals in genetically homogeneous groups (i.e. clusters) following the approach presented in Rodríguez Ramilo et al. (2009 Genetics Selection Evolution 41: 49). As stated in that paper, the basic idea is grouping the individuals in such a way that the average genetic distance between a predefined number of clusters is maximised. From all the genetic distances previously published in the literature, the program calculates the Nei minimum distance, one of the most used. Therefore, no assumptions on the Hardy-Weinberg or linkage equilibrium are made for the used markers.

Jesús Fernández Martín Departamento de Mejora Genética Animal 34-91 3471487 Instituto Nacional de Investigación y 34-91 3478743 (FAX) Tecnología Agraria y Alimentaria (INIA) jmj@inia.es Crta. A Coruña Km. 7,5 28040 Madrid (SPAIN)

http://dl.dropbox.com/u/5714008/Fernandez.htm
Jesús Fernández Martín <jmj@inia.es>

Software Nemo QuantiTraitLoci v220

Nemo v2.2.0 [29 Nov 2011]

A new version of the population genetics simulation software Nemo has been released.

In this new version, up to two genetically correlated quantitative (phenotypic) traits can be modeled, based on multiple pleiotropic and additive quantitative loci.

Selection on the quantitative traits can be spatially and temporally heterogenous. Nemo2.2.0 thus allows for the simulation of different scenarios of local adaptation and adaptive divergence among populations connected by gene flow, among other things.

The code released here forms the basis of work previously published in Evolution by Guillaume & Whitlock (2007), Yeaman & Guillaume (2009), Guillaume (2011), and Yeaman & Whitlock (2011).

Check the website for more information and downloads: http://nemo2.sourceforge.net If you decide to use Nemo, please register to the mailing list, and report bugs!

Happy simulations!

Frederic Guillaume Theoretical Biology, ETH Zurich, Switzerland frederic.guillaume@env.ethz.ch

+ + +

— What is Nemo?

Nemo is a forward-time, individual-based, genetically explicit, and stochastic simulation program designed to study the evolution of life history and phenotypic traits, and population genetics in a flexible (meta-)population framework.

Nemo implements different traits with a variety of genetic architectures, from neutral markers (m-sat, SNP), to deleterious mutations and quantitative trait loci (QTL), some with sex-specific expression (e.g., dispersal genes, female-inherited Cytoplasmic-Incompatibility mutations, etc.).

All this is framed within a flexible metapopulation model that allows for patch-specific carrying capacities, dispersal rates, stochastic extinction/harvesting rates, and demographic stochasticity. Populations can be dynamically modified during a simulation, allowing for population bottlenecks, patch fusion/fission, population expansion, etc. Selection on the quantitative traits can also vary during the course of a simulation and among the demes within a population.

The life cycle is also flexible, with many different events that can be included when needed (reproduction, migration, selection, crossing, regulation, etc.). Nemo also offers the possibility to output many different statistics recorded during simulation runs.

— What is the difference with quantiNEMO?

quantiNEMO (Neuenschwander et al. 2008) also implements quantitative traits. Its implementation is however based on a different mutation model (i.e., discrete number of alleles per locus versus continuum-of-allele model) and does not allow for pleiotropic loci. quantiNEMO thus doesn't offer the possibility to model genetically correlated traits. The model however allows for epistatic interactions among loci.

quantiNEMO is based on an older version of Nemo (pre-2.1.0) from which it implements the dispersal models, neutral trait, and the metapopulation framework, while improving some aspects of those elements. It however does not implement the most recent improvements brought into Nemo.

quantiNEMO can be found here: http://-www2.unil.ch/popgen/softwares/quantinemo frederic.guillaume@env.ethz.ch

Software optiFLP1 41 available

An update of optiFLP, a software for automated optimization of AFLP scoring parameters, is now available at http://sourceforge.net/projects/optiflp/ The software s now in version 1.41.

Since the original release, we have added following new functions: * optiFLP is now able to analyze also the red dye (usually associated with PET), providing compatibility with the complete ABI G5 dyeset * Improved output: Infile number and dye were added to the peak size list * A demo data set was added * As in the meantime the MER article is available in print, the 'how to cite' info was updated

–

Dr. Wolfgang Arthofer

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http://www.uibk.ac.at/ecology/forschung/-molecular_ecology.html.en Wolfgang.Arthofer@uibk.ac.at

Speciation travel grants

Dear colleagues,

The European Research Networking Programme “Frontiers of Speciation Research”, supported by 18 National Funding Organizations in member countries of the European Science Foundation, is inviting applications for travel grants intended to foster collaborations between European researchers working on topics related to the Programme.

Support is available for short visits (up to 2 weeks) and exchange grants (up to 3 months), with preference given to junior researchers at a graduate or postdoctoral level. A typical grant covers between EUR 1500 and EUR 2000. Applicants will want to keep in mind that, reflecting the availability of funds, applications for smaller grants are more likely to succeed than applications for larger grants, and that granted amounts are typically adjusted relative to solicited amounts so as to promote equity among selected candidates.

Applications are reviewed quarterly after a submission deadline of 24:00 CET on 15 March, 15 June, 15

September, and 15 December. About 4-6 weeks after each deadline, the ESF will inform applicants about the outcome of evaluations.

Further information and instructions on how to apply are available at www.iiasa.ac.at/Research/EEP/-FroSpects/Travel_Grants.html .

For general information about the FroSpects Research Networking Programme, please see www.iiasa.ac.at/-Research/EEP/FroSpects .

With best wishes,

Ãke Brännström & Ulf Dieckmann, on behalf of the FroSpects Steering Committee

Ulf Dieckmann Program Leader Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

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dieckmann@iiasa.ac.at

Ten must read

Dear Evolution Directory readers,

What are your 10 favorites papers related to your research/study field? Best evolutionary articles, game-changers, must-have on iPad, must-read by researchers and students.

The answers to this short query will be compiled and available on a small dedicated web page. Mendeley and/or Papers Livfe group not excluded. Your personal info will remain anonymous.

If you are interested in participating in this project: 1) email your selected references (RIS and XML files welcome) to : thierrygosselin@me.com 2) Include this subject header: 10 must-read evolutionary papers 3) Describe your research/study field with 5 keywords

Sincerely,

Thierry Gosselin Biologist, PhD

thierrygosselin@me.com

Undergraduate Experience AMNH

Do you know an exceptional undergraduate student who would like to spend a fun and engaging summer in the heart of New York City working at the American Museum of Natural History?

The Research Experiences for Undergraduates (REU) program, funded by the U.S. National Science Foundation, offers paid summer internships for qualified undergraduate students to conduct research projects with AMNH scientists in evolutionary biology, linked to specific individual research projects. Included in the program are a general orientation to the Museum and a series of weekly meetings at which students discuss their research, present informal progress reports, and participate in discussions and seminars as well as graduate and research career opportunities. At the conclusion of the internships, students deliver oral presentations of their work and prepare publication quality research papers.

The program is open to all students who are U. S. citizens or permanent residents and who are currently enrolled in a four-year undergraduate degree program.

Pending the approval of federal funding, successful applicants will receive a stipend, while dormitory housing on a nearby university campus, or an equivalent housing stipend, will be provided together with a subsistence allowance. Based on need, travel costs to and from New York City are also covered.

A description of the potential projects may be found here http://rggs.amnh.org/pages/-academics_and_research/reubio Susan Perkins, Ph.D. Associate Curator & Professor Sackler Institute for Comparative Genomics and Division of Invertebrate Zoology and Richard Gilder Graduate School American Museum of Natural History Central Park West at 79th Street New York, New York 10024

Susan Perkins <perkins@amnh.org>

PostDocs

AustralianNatlU CompGenomics

The Computational Genomics Group in the John Curtin School of Medical Research, Australian National University (Canberra, Australia) have made pioneering contributions to our understanding of genetic diversity within and between mammal species in areas including: the genomic distribution of linkage disequilibrium, human molecular adaptation, the influence of sex on mutation rates, the relationship between epigenetic state and genetic variation, and the radiation of mammals. These contributions have been accompanied by significant methodology developments in the form of both novel statistical models and open source software for analyses of genomic diversity. Our recent advances in models of context-dependent substitution, for instance, represent a significant advance in robust estimation of the mode of natural selection.

We are seeking outstanding applicants for a postdoctoral fellowship. The individual will work on the development and application of improved models of sequence divergence, joining a highly productive collaboration between Associate Professors Gavin Huttley and Von Bing Yap (Department of Statistics and Applied Probability, National University of Singapore). The work will build on the PyCogent open source software toolkit for statistical modelling of molecular evolution developed in the Huttley lab.

Application deadline: 22nd January 2012 http://jobs.anu.edu.au/PositionDetail.aspx?p=3D2266
For more details, please contact Gavin Huttley (Gavin.Huttley@anu.edu.au).

Barcelona MolecularEvolution

Postdoctoral position Evolutionary Genomics Group evolutionarygenomics.imim.es Pompeu Fabra University (UPF-IMIM-PRBB) Barcelona, Spain

The grup of Evolutionary Genomics led by M.Mar Albà at Pompeu Fabra University (Barcelona) is seeking a postdoctoral candidate to apply to the Juan de la Cierva 2012 call, a program from the Spanish Government that finances 3-year contracts to postdoctoral scientists. The contract may start as early as mid 2012.

The group investigates the mechanisms of molecular evolutionary innovation using computational analysis of high-throughput sequence data. Current available projects include the identification of novel genes in humans and other mammlas using RNAseq data, and the reconstruction of the evolutionary history of recently formed gene families. See evolutionarygenomics.imim.es for the group's most recent publications.

For the post you must hold a PhD (or be near its completion) and have a minimum of two first-author publications. You should have a strong interest in evolutionary biology and experience in large-scale sequence data analysis. Programming skills are desirable but not a must.

Qualified applicants should submit an application by email, including a letter of presentation, a CV, and the names of two references, to M.Mar Albà (malba@imim.es)

–

Mar Albà, ICREA Research Professor Evolutionary Genomics Group IMIM-UPF Research Programme on Biomedical Informatics Barcelona Biomedical Research Park (PRBB) Dr. Aiguader 88, 08003 Barcelona, Spain ph. +34 93 3160516 malba[at]imim.es; http://evolutionarygenomics.imim.es http://www.researcherid.com/rid/B-4793-2009 MAlba@imim.es

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Canberra AdaptabilityGenomics

Postdoctoral Fellow - Genomics of Climate Adaptability

Position Reference: ACT01949 Location: CSIRO Ecosystem Sciences, Canberra, Australia Tenure: 3 year term

Open to International Residents Relocation assistance may be provided to the successful candidate

The Postdoc will work in a large team investigating the genomics of climate adaptability. The focus, in the first instance, will be on 20 Drosophila species, known to differ in their response to climate stresses. The sequencing budget allows for whole genome sequencing, transcriptomic analyses of the stress responses and shallow pass re-sequencing of various stressed population samples. Some extension to other species is possible. This Postdoc will have primary responsibility for much of the bioinformatic analyses, perhaps particularly focussing on the population genomics, but may also take a role in some of the empirical work as well.

How to Apply:

Please apply for this position online at www.csiro.au/careers using the above reference number. You may be asked to provide additional information (online) relevant to the selection criteria. If so, then responding will enhance your application so please take the time to provide relevant succinct answers. Applicants who do not provide the information when requested may not be considered.

If you experience difficulties applying online call 1300 301 509 and someone will be able to assist you. Outside business hours please email: csiro-careers@csiro.au.

Referees:

If you do not already have the names and contact details of two previous supervisors or academic / professional referees included in your resume/CV please add these before uploading your CV. Contact:

If after reading the selection documentation you require further information please contact John Oakeshott (John.Oakeshott@csiro.au, phone +61 2 6246 4157).

Dr Robyn Russell Senior Principal Research Scientist Research Program Leader, Environmental Biotechnology and Genomics Chair, CSIRO Ecosystem Sciences Institutional Biosafety Committee

CSIRO Ecosystem Sciences Phone: +61 2 6246 4160 | Fax: +61 2 6246 4000 Robyn.Russell@csiro.au | www.csiro.au |

Address: GPO Box 1700, Clunies Ross Street, Canberra ACT 2601

Please consider the environment before printing this email.

Robyn.Russell@csiro.au

CNRS Montpellier Speciation Genomics

Postdoctoral position in mouse population genomics and speciation at CNRS - Institut des Sciences de l^{1}Evolution, Montpellier, France.

A two-year post-doctoral position is available at CNRS Montpellier, France (Institut des Sciences de l^{1}Evolution) to work with Carole Smadja and Pierre Boursot on the genomics of adaptive speciation in the house mouse (Mus musculus).

This ANR and EU-funded project is devoted to characterise the genetic components of sexual isolation and reinforcement in the house mouse. Cutting-edge high throughput technologies including next-generation sequencing will be used to assess genome-wide and candidate gene variation and divergence between the two European subspecies of the house mouse, a model system for the study of speciation-with-gene-flow. Research areas will thus include speciation genomics, mouse population genetics and evolutionary history, method development for analysis of next-generation sequencing data sets, natural selection detection and characterisation, and population genetics theory. The successful candidate will be in charge of designing NGS experiments, analysing and interpreting data and handling manuscript preparation.

Applicants should have a PhD in a relevant area (evolutionary biology, genomics). We are seeking for someone with a vivid interest in evolution and speciation research and a strong background in population genetics/ statistical genetics. Skills in bioinformatics and/or programming are essential. Experience in handling Next-Generation-Sequencing data will be strongly appreciated. Skills in French are not required.

The Institut des Sciences de l^{1}Evolution (Université Montpellier 2) has a long lasting history of research excellence in evolutionary biology, and Montpellier, South of France, hosts one of the most vibrant communities of biodiversity research in Europe with several research centers of excellence in the field.

Starting date: early 2012. Net monthly salary will be 2100-2500 Euros depending on experience.

Applications should be sent to: carole.smadja@univ-montp2.fr by ***January 15, 2012*** and should include a 1-2-page research statement with date of availability, a detailed CV, and the names and contact details of 2-3 referees.

Dr. Carole Smadja CNRS research scientist Chargée de recherche CNRS http://www.carole-smadja.staff.shef.ac.uk/ Institut des Sciences de l^{1}Evolution cc065, Université Montpellier 2 34095 Montpellier France Phone: +33 (0)4 67 14 92 70

carole.smadja@univ-montp2.fr

ColoradaStateU DiseaseEvolution

Disease Modeling: The Webb Lab at Colorado State University was recently funded to develop data-driven models of disease spread in the US cattle population using a contact network approach involving network theory, Bayesian modeling, simulation and other modeling approaches. The goal of the project is to both predict spread during disease outbreaks for the US and to test containment and mitigation strategies. While these types of models have been successful for understanding and managing disease outbreaks in other countries, they have not previously been developed for the US due to data limitations. We have developed a new database that should allow us to overcome these previous limitations. Qualified individuals with modeling experience who are interested in working on this project should contact Colleen Webb (ctwebb@lamar.colostate.edu) for more information.

Best, Colleen

Colleen T. Webb, Ph.D. Associate Professor Department of Biology Colorado State University Campus Delivery 1878 Fort Collins, CO 80523-1878 USA phone 970-491-4289 fax 970-491-0649

Colleen.Webb@ColoState.EDU

CSIRO Canberra EvolutionHostSymbiont

Postdoc in the ecology and evolution of host-symbiont interactions at CSIRO Canberra.

We invite applications for a three-year Post-Doctoral research position to study mutualistic interactions between plants and soil symbionts.

This project will investigate the evolution of associations between plants and soil mutualists (rhizobial bacteria and mycorrhizal fungi). These interactions take place within potentially complex networks composing a diverse array of potential partners and competitors. Characterizing these complex networks and identifying the biotic and environmental factors that determine how they are assembled is an important step towards understanding how effective mutualisms between plants and soil microbe evolve and persist. This work will utilize interactions between native Australian legumes and their associated soil symbionts. These systems provide an ideal model for testing hypotheses regarding how the community composition and function of symbiotic organisms is shaped by interactions with hosts, environmental heterogeneity (e.g. soil chemistry) and spatial variation. The postdoctoral fellow will have access to a recently developed and comprehensive host phylogeny (Acacia) to use as a foundation to design a project investigating the role of evolutionary history in structuring host symbiont interactions in an ecologically important and widespread legume group.

Applicants must have, or will shortly obtain a PhD. Ideally, the candidates PhD or other past research will be in evolutionary biology or ecology. We are looking for a highly motivated candidate with deep interests in community genetics and evolutionary ecology, as opposed to someone with a specific laboratory skill set.

Interested individuals should apply for this position online at http://csiro.nga.net.au/?jati=B46448DA-19BD-FE9C-C6F2-64DE1BDAF260. The position includes generous remuneration and relocation allowances.

Informal inquiries regarding this position should be directed to Pete Thrall (Peter.Thrall@csiro.au).

Luke.Barrett@csiro.au

CSIRO Canberra EvolutionHostSymbiont 2

Postdoc in the ecology and evolution of host-symbiont interactions at CSIRO Canberra.

The link for this position is now active. Apologies for any confusion caused.

We invite applications for a three-year Post-Doctoral research position to study mutualistic interactions between plants and soil symbionts.

This project will investigate the evolution of associations between plants and soil mutualists (rhizobial bacteria and mycorrhizal fungi). These interactions take place within potentially complex networks composing a diverse array of potential partners and competitors. Characterizing these complex networks and identifying the biotic and environmental factors that determine how they are assembled is an important step towards understanding how effective mutualisms between plants and soil microbe evolve and persist. This work will utilize interactions between native Australian legumes and their associated soil symbionts. These systems provide an ideal model for testing hypotheses regarding how the community composition and function of symbiotic organisms is shaped by interactions with hosts, environmental heterogeneity (e.g. soil chemistry) and spatial variation. The postdoctoral fellow will have access to a recently developed and comprehensive host phylogeny (Acacia) to use as a foundation to design a project investigating the role of evolutionary history in structuring host symbiont interactions in an ecologically important and widespread legume group.

Applicants must have, or will shortly obtain a PhD. Ideally, the candidates PhD or other past research will be in evolutionary biology or ecology. We are looking for a highly motivated candidate with deep interests in community genetics and evolutionary ecology, as opposed to someone with a specific laboratory skill set.

Interested individuals should apply for this position online at http://csiro.nga.net.au/cp/index.cfm?event=jobs.checkJobDetailsNewApplication&returnToEvent=jobs.listJobs&jobid=29b90385-c593-ca73-09cb-6523f560aa6a&CurATC=EXT&CurBID=62AFB35D-9273-4A11-8DCC-9DB401354197&JobListID=22FC4F47-E994-46A3-B8C9-9BC901269F43&jobsListKey=c744891f-2e49-4fc4-9826-93eaf095f038&persistVariables=CurATC,CurBID,JobListID,jobsListKey,JobID&lid=24927610126 .The position includes generous remuneration and relocation allowances.

Informal inquiries regarding this position should be directed to Pete Thrall (Peter.Thrall@csiro.au).

Luke.Barrett@csiro.au

GeorgeWashingtonU Phylogenetics

Postdoctoral Fellowship in Phylogenetics/Computer Science â The George Washington University

The High Performance Computing Lab and the Weintraub Program in Systematics are seeking a highly motivated individual to develop and establish novel approaches for phylogenetic analysis of large data sets that use the full potential of multicore processors. The position is a collaboration between these two research groups to leverage available resources at GWU to advance the field of computational phylogenetics. The successful candidate must have a PhD in an appropriate discipline, strong skills in computer science and a basic understanding of phylogenetic biology. The position is for two years, available immediately.

The Post-Doctoral Scientist will develop and establish approaches for phylogenetic analysis of large data sets that use the full potential of multicore processors.ÂÂThe successful candidate must have strong skills in computer science and a basic understanding of phylogenetic biology.ÂÂThe position will be filled by someone who would interact with the Diversity of Life program by identifying problems peculiar to DNA sequence analysis and interact with the High Performance Computing program to attempt to solve some of these problems.

Application Procedure: Please send a letter of application, a complete curriculum vitae, a brief description of research interests, and the names and contact information for three references toÂgorti@gwu.edu. More information on applying is available here: https://-www.gwu.jobs/postings/6305 The George Washington University is an Equal Opportunity/Affirmative Action Employer. The University Search Committee seeks to attract an active, culturally and academically diverse faculty of the highest caliber.

R. Alexander Pyron, Ph.D. Robert F. Griggs Assistant Professor of Biology Department of Biological Sciences The George Washington University 2023 G St. NW, Lisner Hall 345 Washington, D.C. 20052 Phone: 706-489-9727 http://www.colubroid.org Alex Pyron <rpyron@colubroid.org>

LMU Munich StatisticalAlignment

The Statistical Genetics group of Prof. Dr. D. Metzler at the Ludwig-Maximilians-Universitaet Muenchen (Munich, Germany) offers a

PostDoc Position for 3 years

for a researcher with a PhD or Dr. degree in

(Bio-)Informatics, Statistics, Mathematics or a related field.

The PostDoc will work in the project “Computational and mathematical approaches for statistical sequence alignment and phylogenetic inference on emerging parallel architectures”, which is a collaboration with Prof. Dr. A. von Haeseler (University of Vienna) and Dr. A. Stamatakis (Heidelberg Institute for Theoretical Studies). The project is funded by the German Research Foundation DFG and the Austrian Science Fund FWF within the D-A-CH collaboration.

Applicants should provide expertise in some of the following areas: Hidden Markov Models (HMMs), Stochastic models of sequence evolution, Markov-Chain Monte-Carlo Methods (MCMC), evolutionary bioinformatics, and programming, preferably in C/C++.

The University of Munich is interested in increasing the number of female employees and encourages women to apply. The university is an equal opportunity employer and handicapped candidates with equal qualifications will be given preference.

Please send your application documents until December 31, 2011 to:

Prof. Dr. Dirk Metzler LMU Biocenter Department Biologie II Grosshaderner Str. 2 82152 Planegg-Martinsried

metzler@bio.lmu.de

http://evol.bio.lmu.de/_statgen metzler@biologie.uni-muenchen.de

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MasseyU ComputationalFungalGenomics

Postdoctoral Position in Computational Fungal Genomics (A425-11ZZ)

I am looking for a motivated and productive postdoctoral fellow to explore fungal genome evolution, including lateral gene transfer, using comparative genome data and novel computational analysis. The successful candidate will have scope to drive his/her own research program within the bounds of the group’s larger research agenda, but will also engage with ongoing collaborative research projects.

This computational position requires solid quantitative skills in next generation sequencing and bioinformatics, preferably including some (basic) background in scripting or programming. Training in fungal biology and genetics can be provided as needed, and candidates from non- standard research backgrounds are strongly encouraged to apply.

Funding is available for three years, with an initial probationary period of one year and subject to satisfactory performance. The salary is extremely competitive, starting at NZ $64,000 (~US $54,000) per year.

The postdoc will be based in the Computational Biology Research Group at Massey University, New Zealand. My research team has a strong high- impact publication culture, and is firmly embedded in the international scientific community, with extensive collaborative links to the United States, France, Australia and Indonesia. Nevertheless, this position also offers a rare opportunity to experience New Zealand's unique natural and cultural environment. Palmerston North, a university town with a large international community, offers a full range of social and cultural amenities. The city is located close to both mountains and the sea, and presents regular opportunities for hiking, skiing, surfing and adventure sports.

If you have any questions, please contact Dr Murray Cox (email m.p.cox@massey.ac.nz). Information about the Computational Biology Research Group (http://massey.genomicus.com/), the Institute of Molecular BioSciences (http://imbs.massey.ac.nz/) and the Bio-Protection Research Centre (http://bioprotection.org.nz/) are available online.

To apply for this position, upload the following documents (PDF format) at the official Massey University job website: http://jobs.massey.ac.nz/ 1. A brief statement of research interests, qualifications and experience. 2. A curriculum vitae, including a list of scientific publications. 3. The names and contact details of three referees willing to provide a confidential letter of recommendation upon request.

Informal enquiries are welcome. Formal applications are due by 15 January 2012.

Dr Murray P. Cox Institute of Molecular BioSciences Massey University Private Bag 11 222 Palmerston North 4442 NEW ZEALAND

http://massey.genomicus.com/
M.P.Cox@massey.ac.nz

MasseyU HumanGenomicEvolution

Postdoctoral Position in Human Genomic Evolution (A424-11ZZ)

I am looking for a motivated and productive postdoctoral fellow to study spatial patterns of human migration and admixture using genome-scale data and cutting-edge computational and statistical analysis. The successful candidate will have scope to drive his/her own research within the bounds of the group's larger research agenda.

This computational position requires solid quantitative skills, preferably including some background in statistics and programming. Training in biology and anthropology can be provided as needed, and candidates from non-standard research backgrounds are strongly encouraged to apply.

Guaranteed funding is available for three years, with an initial probationary period of one year. The salary is extremely competitive, starting at NZ $64,000 (~US $54,000) per year.

The postdoc will be based in the Computational Biology Research Group at Massey University, New Zealand. My research team has a strong high- impact publication culture, and is firmly embedded in the international scientific community, with extensive collaborative links to the United States, France, Australia and Indonesia. Nevertheless, this position also offers a rare opportunity to experience New Zealand's unique natural and cultural environment. Palmerston North, a university town with a large international community, offers a full range of social and cultural amenities. The city is located close to both mountains and the sea, and presents regular opportunities for hiking, skiing, surfing, and adventure sports.

If you have any questions, please contact Murray Cox (email m.p.cox@massey.ac.nz). Information about the Institute of Molecular BioSciences (http://imbs.massey.ac.nz/) and the Computational Biology Research Group (http://massey.genomicus.com/) is available online.

To apply for this position, upload the following documents (PDF format) at the official Massey University job website: http://jobs.massey.ac.nz/ 1. A brief statement of research interests, qualifications and experience. 2. A curriculum vitae, including a list of scientific publications. 3. The names and contact details of three referees willing to provide a confidential letter of recommendation upon request.

Informal enquiries are welcome. Formal applications are due by 15 January 2012.

Dr Murray P. Cox Institute of Molecular BioSciences Massey University Private Bag 11 222 Palmerston North 4442 NEW ZEALAND

http://massey.genomicus.com/
M.P.Cox@massey.ac.nz

McGillU PrimateCognitiveEvolution

Department of Biology, McGill University, 1205 avenue Docteur Penfield, Montréal, Québec, Canada H3A 1B1.

Postdoctoral Research Fellow, Primate Cognitive Evolution

A 3-year postdoctoral position (reference #SB1090) is available to conduct statistical analyses of primate innovation and brain evolution. This work will include structural MRI scanning of primate brains and measurement of brain anatomy (using materials from the Netherlands Institute for Neuroscience^{1}s Primate Brain Bank). The project is a collaboration between Kevin Laland (St Andrews, UK) and Simon Reader (McGill, Canada).

Note that there is the possibility to split the position into two posts: a one-year position focused on brain scanning and neuroanatomy, and a two-year position focused on comparative statistical analyses.

Further particulars are available via: http://www.jobs.ac.uk/job/ADN435/research-fellow-comparative-statistical-met hods/

The application deadline is December 12, 2011.

Simon Reader <s.m.reader@gmail.com>

MemorialU FishHybridization

Postdoctoral Fellowship (Canada)

Phenotypic plasticity in gamete interactions and inter-population hybrization in fish

Applications are sought for a postdoctoral fellow to work on phenotypic plasticity and intraspecific hybridization related questions regarding fish reproduction.

The candidate must be able to start before April 2012 in order to design and lead several experiments related to population differences in the performance of Atlantic cod sperm (spawning March - May). Subsequently there is considerable scope for the fellow to design and undertake additional studies related to the above theme.

Base funding is secure for 1 year at $42,000. The fellow will work closely with Dr. Craig Purchase and Dr. Ian Fleming of Memorial University, and be situated primarily in the evolutionary ecology research lab of Dr. Purchase (http://www.ucs.mun.ca/˜cfpurchase), and secondarily in the lab of Dr. Fleming (http://www.mun.ca/osc/ifleming/index.php). There will be close collaboration with Dr. Ed Trippel (Fisheries & Oceans Canada) and significant interaction with other scientists (including Dr. John Brattey - Fisheries & Oceans Canada), graduate and undergraduate students.

The ideal candidate will hold a PhD in evolutionary, behavioural or fisheries ecology or a related field. Previous experience with plasticity, sperm or intraspecific hybridization research would be an asset but is not essential. The fellow is expected to disseminate results through refereed publications and be an activate participant in the research groups.

Prospective candidates should email a cover letter, CV, & contact information for three people who can serve as references.

Review of applicants will begin immediately and continue until the position is filled.

Dr. Craig Purchase Dr. Ian Fleming Biology Department, Memorial University Ocean Sciences Centre, Memorial University St. John's, NL, A1B 3X9, Canada St. John's, NL, A1C 5S7, Canada T: (709)864-4452, F:(709)864-3018 T: (709)864-3586, F:(709)864-2159 craig.purchase@mun.ca ifleming@mun.ca www.ucs.mun.ca/ ˜ cfpurchase www.mun.ca/osc/ifleming/index.php This electronic communication is governed by the terms and conditions at http://www.mun.ca/cc/policies/electronic_communications_disclaimer_2011.php
cfpurchase@mun.ca

Nanaimo BC EvolutionaryGenetics

Fisheries and Oceans Canada, Pacific Biological Station, Nanaimo, British Columbia

We are seeking a post-doctoral fellow with an interest in applied evolutionary genetics (particularly phylogenetics) and marine taxonomy to lead a DNA barcoding study on marine invertebrates as part of a larger federal government project aimed at enabling early detection of invasive species that pose risks to Canadian biodiversity and trade. The successful candidate will have the opportunity to liaise and collaborate with scientists and post-docs from other genomics-enabled federal departments/agencies.

The successful candidate will develop methods to sequence the mitochondrial cytochrome c oxidase I (COI) gene and additional nuclear genes for target taxonomic groups of marine invertebrates. They will test the utility of isolated markers for species level identifications, will develop robust protocols for successful markers, and will generate molecular phylogenies where needed to resolve taxonomic uncertainties. They will work closely with a technician assigned to assist with labwork for this project but will also be responsible for conducting labwork, particularly in marker development stages.

Stipend funding is available at NSERC Visiting Fellowship rates. Applications from international candidates will be accepted. The project start date is to be no earlier than April 2012 and project duration is a minimum of 2 years. To be considered for this position please send your CV to cathryn.abbott@dfo-mpo.gc.ca.

Cathryn Abbott, Ph.D. Tom Therriault, Ph.D.

Fisheries and Oceans Canada Pacific Biological Station 3190 Hammond Bay Road Nanaimo, BC, V9T 6N7 Canada

cathryn.abbott@dfo-mpo

“Abbott, Cathryn” <Cathryn.Abbott@dfo-mpo.gc.ca>

Perth BeeQuantGenetics

3 YEAR JOHN STOCKER POST DOCTORAL FELLOWSHIP CENTER FOR INTEGRATIVE BEE RESEARCH, PERTH, AUSTRALIA

Applications are invited from a suitably qualified scientist to work in a multi-disciplinary team environment on quantitative genomics and epigenomics of honeybees and aphids. The successful applicant will initiate and drive research projects to elucidate the effects and consequences of epigenetic modifications in two insect model systems, in particular the role of DNA methylation in insect caste determination. You will use high-throughput DNA sequencing approaches to investigate the relationship between differential DNA methylation, chromatin modifications, and the mRNA and small RNA transcriptomes in the honeybee and pea aphid invertebrate models. Applicants must have a PhD in molecular biology or related discipline awarded within the last three years.

The Centre for Integrative Bee Research (CIBER) located at The University of Western Australia is dedicated to facilitate interdisciplinary research on honeybees. CIBER combines the expertise of beekeepers, sociobiologists and evolutionary ecologists studying honeybee biology with those of biochemical, genomic and molecular biologists to harness the power of the honeybee genome. CSIRO Ecosystem Sciences undertakes research on pea aphid genomics including a leadership role in the International Aphid Genomics Consortium< http://www.aphidbase.com/aphidbase/community_links/international_aphid_genomic_consortium >. The ARC Centre of Excellence in Plant Energy Biology (CPEB) at The University of Western Australia houses state-of-the-art equipment for functional genomics approaches including a deep sequencing facility based on Illumina HiSeq and miSeq platforms and associated computing.

For further information regarding the position or the project please visit www.ciber.science.uwa.edu.au or contact Associate Professor Boris Baer, email boris.baer@uwa.edu.au, or Winthrop Professor Harvey Millar, email harvey.millar@uwa.edu.au, Some assistance with relocation expenses (if applicable) may be negotiated.

A/ Prof. Boris Baer Centre for Integrative Bee Research (CIBER) Bayliss building M316 The University of Western Australia Crawley WA 6009 Australia phone: +61 8 6488 4495 fax: +61 8 6488 4401 E-mail: boris.baer@uwa.edu.au Website: www.ciber.science.uwa.edu.au Boris Baer <boris.baer@uwa.edu.au>

Perth InsectPhylogeneticDiversity

Postdoctoral Fellow - Ecology and phylogenetic diversity of insect metacommunities

Position Reference: WA02525 Location: CSIRO Ecosystem Sciences, Perth, Australia Tenure: 2 year term

Open to International Residents Relocation assistance may be provided to the successful candidate

The Postdoc will join a multidisciplinary team of researchers investigating the ecological, evolutionary and biogeographic processes that regulate the structure of invertebrate metacommunities in the Kimberley wilderness region of northwestern Australia. The project aims to pioneer the rapid assessment and interpretation of large scale invertebrate biodiversity data generated by high throughput metagenomic sequencing technologies. This approach will provide a novel opportunity to examine metacommunity dynamics within a phylogenetic context. The Postdoc will have primary responsibility for the development of a novel set of analytic and bioinformatic tools for the ecological and evolutionary interpretation of sequence metadata, which will then be used to inform conservation planning and future environmental impact assessments. The postdoc will also participate in collecting invertebrate samples from remote rainforest habitats and, through collaboration between CSIRO Ecosystem Sciences and the University of Western Australia, will have opportunities to co-supervise post-graduate students.

How to Apply:

Please apply for this position online at www.csiro.au/careers using the above reference number. You may be asked to provide additional information (online) relevant to the selection criteria. If so, then responding will enhance your application so please take the time to provide relevant succinct answers. Applicants who do not provide the information when requested may not be considered.

If you experience difficulties applying online call 1300 301 509 and someone will be able to assist you. Outside business hours please email: csiro-careers@csiro.au.

Referees:

If you do not already have the names and contact details of two previous supervisors or academic / professional referees included in your resume/CV please add these before uploading your CV. Contact:

If after reading the selection documentation you require further information please contact Owain Edwards (Owain.Edwards@csiro.au, phone +61 8 9333 6401) or Raphael Didham (Raphael.Didham@csiro.au, raphael.didham@uwa.edu.au, phone +61 8 6488 1468).

Owain.Edwards@csiro.au

SangerInstitute Bioinformatics EvolutionaryGenomics

We currently have three post-doc vacancies - for the first position, we are particularly keen to attract candidates with expertise in comparative and population genomics analysis. You can read further details, and apply, via https://jobs.sanger.ac.uk Postdoctoral Research Fellow

Salary range £28280 to £34778 dependent on experience. Closing Date: 22nd January 2012

The Wellcome Trust Sanger Institute is a world leader in the use of large-scale sequencing, informatics and the analysis of genetic variation. We use sequence data to further our understanding of infectious diseases and generate resources of lasting value to biomedical research. The Parasite Genomics group uses large-scale sequencing approaches to study parasite species associated with diseases of global importance to human and animal health, with particular emphasis on diseases of developing countries.

We are seeking to recruit enthusiastic and ambitious postdoctoral fellows in three areas:

Postdoctoral Fellow - Parasitic helminth genomics You will contribute to a range of projects involving the application of very-high-throughput sequencing technologies to understand the biology of helminths. Existing projects build on genome sequence data to address scientific questions that span from population genomics through to functional genomics and immunology, and include working on a range of nematodes, flukes and tapeworms in collaboration with external experts in particular systems. Key aspects of this role will include the analysis of -next generation sequencing' data, genome assembly and comparison, phylogenetics, population genetics, and analyzing transcriptome data, with the exact mix of projects and approaches depending on the interests and expertise of the successful candidate.

Postdoctoral Fellow - Parasite functional genomics You will develop functional genomics projects across neglected parasite species. A major focus will be the analysis of gene expression throughout the life cycle of African trypanosomes. Using whole transcriptome sequencing (RNAseq), you will explore differences across the life cycle, for instance between bloodstream and late stage (central nervous system) forms. You will need to be an excellent communicator and work effectively with collaborators. Key aspects of this role will include the analysis of -next generation sequencing' data, especially transcriptome data. The role may involve some lab work depending on the interests and expertise of the successful candidate.

Postdoctoral Fellow - Helminth genomics R&D You will develop challenging new methodology to exploit sequencing approaches to investigating genome function for parasitic helminths. Key areas will include genome sequencing from small, precious or unusual samples, and developing novel functional genomics approaches. This position will be laboratory-based, working in the context of the spectrum of the Sanger Institute's R&D activities.

James Cotton Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge. CB10 1SA UK

james.cotton@sanger.ac.uk 01223 494864

– The Wellcome Trust Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215 Euston Road, London, NW1 2BE.

james.cotton@sanger.ac.uk

Spain ForestTreeEvolution

A three year postdoctoral fellowship is available to investigate the adaptive variation, environmental gradients and demography in Mediterranean conifers. The study organisms will be Pinus pinaster, Pinus halepensis and Taxus baccata. For this project, we are combining different approaches to investigate the evolutionary response of these conifers to selection: demographic dynamics, patterns of adaption at the phenotypic and molecular levels, and modeling of the climatic niche. More specifically, the candidate will be involved in assessing the patterns of adaptation at the phenotypic and molecular levels by identifying functional genes responsible for variation in phenotypic traits and geographical-climatic clines of adaptive variation.

The successful candidate will have experience with population genetics and genomics, especially with sequences and SNPs analysis. The candidate should hold a Ph.D. in genetics or evolutionary biology, have an excellent academic and publication record, and be a fluent speaker/writer in English. We seek an individual who is enthusiastic, highly motivated, and willing to work independently as well as with a team.

This project is a collaboration between the Center of Forest Research (CIFOR) at the National Institute of Research and Agrarian and Food Technology (INIA) in Madrid (www.inia.es), and the Center for Ecological Research and Forestry Applications (CREAF) at the Autonomous University of Barcelona (www.creaf.uab.es), and the position will be jointly based within these two Spanish research centers.

Closing date for application, January 15^th , 2012.

Applications (curriculum and cover letter, including a statement of research interests and a brief overview of previous academic and research experiences) as well as request for information should be sent to: dgrivet@inia.es and Maria.Mayol@uab.es.

dgrivet@inia.es

UArizona ComputionalPopulationGenetics

A postdoctoral research associate position is available in the Gutenkunst group, in the Department of Molecular and Cellular Biology at the University of Arizona. The Gutenkunst group integrates computational population genomics and systems biology to understand evolution, with a focus on humans. For more information, see http://gutengroup.mcb.arizona.edu or contact Dr. Ryan Gutenkunst at rgutenk@email.arizona.edu.

Emerging whole-genome data offer both great opportunities and great challenges for understanding the genetic history of natural populations. We seek a quantitatively skilled researcher to develop and apply novel computational methods for inferring demographic history and natural selection from population genomic data. A particular focus will be extending the group's previous work based on diffusion equations (http://dadi.googlecode.com) and applying the results to whole-genome human data.

Candidates should have a Ph.D. in biology, a physical or computational science, or mathematics. The University of Arizona has great strength in population genetics and quantitative biology, offering potential interactions with Drs. Michael Hammer, Joe Watkins, Joanna Masel, Michael Nachman, and others. Computational resources are similarly excellent. The campus is highly interdisciplinary and very collegial. The University of Arizona is an EEO/AA - M/W/D/V Employer.

At 2,500 feet above sea level, culturally diverse Tucson, Arizona is nestled among five mountain ranges in the beautiful Sonoran Desert and is surrounded by Saguaro National Park. Housing is affordable, quality of life is high, and outdoor recreation opportunities include the southernmost ski area in the United States. The area receives over 350 days of sunshine per year and enjoys average high/low temperatures of 82/54 degrees F.

Applications should include a C.V., cover letter, and contact information for three references. Please submit applications through http://www.uacareertrack.com, job number 49057. Application review begin December 16, 2012 and will continue until the position is filled.

– Ryan Gutenkunst Assistant Professor Molecular and Cellular Biology University of Arizona phone: (520) 626-0569 http://gutengroup.mcb.arizona.edu < http://gutengroup.mcb.arizona.edu/ >

rgutenk@email.arizona.edu

UBasle EvolutionBehaviour

POSTDOCTORAL POSITION, UNIVERSITY OF BASLE: Evolution of family interactions

The question how phenotypes expressed in animal families are shaped by conflicts and parent-offspring coadaptation is at the core to better understand the evolution of traits that are affected by social interactions. We use the European earwig (Forficula auricularia; Dermaptera) as a model to study these processes experimentally, applying methods from evolutionary/behavioral ecology and quantitative genetics and, more recently, also genomic/transcriptomic technologies.

POSITION. We are seeking a highly motivated young scientist with a keen interest in understanding how conflict and coadaptation shape family interactions. Applicants should have a PhD, a strong conceptual background and interest in evolutionary ecology, evolutionary quantitative genetics and/or social evolution - with major strengths in experimental research. Depending on interest and skills, theoretical projects may also be pursued. The successful candidate will be involved in our large-scale selection experiments, and she/he will also be expected to develop own ideas for projects of key importance within the context of our main research direction. Experience with GC/MS for analyses of chemical signals and/or molecular genetic methods for paternity assignment or population structure analysis (e.g., Microsatellites, SNPs, etc.) are beneficial, but not required.

The position is funded through a Swiss National Science Foundation (SNF) professorship research grant for up to two years. Salary is according to the guidelines of the Swiss National Science Foundation. Preferred starting date is 1. May 2012, but later starting dates are negotiable.

RESEARCH GROUP AND INSTITUTE. Our research group is part of the Zoological Institute, Department of Environmental Sciences, University of Basel. The Institute hosts seven research groups that share a common interest in evolutionary questions, jointly organize the weekly seminars, and work at the forefront of diverse research topics using various study systems and methods (see www.evolution.unibas.ch for more detail).

APPLICATION: To apply, please send your application documents (integrated into a single pdf-file) including: i) a motivation letter explaining why you are keen to do a postdoc in our group, ii) your CV with publication list, and iii) contact details for two referees to: Prof. Mathias Kolliker. E-mail: mathias.koelliker@unibas.ch. For pre-application inquiries, please contact me directly under this same address.

The search will continue until the position is filled. But applications received before **20. January 2012** are given full consideration. Interviews will take place mid-February.

Prof. Mathias Kolliker.

University of Basel, Zoological Institute, Evolutionary Biology, Vesalgasse 1, 4051 Basel. Internet:www.evolution.unibas.ch/koelliker. E-mail:

mathias.koelliker@unibas.ch

UBritishColumbia EvolutionaryMorphology

Research Associate Position in Comparative Ultrastructure of Marine Heterotrophic Flagellates

A one year, part-time Research Associate position is available in the Botany Department at The University of British Columbia. This position is being created to provide high-level electron microscopy and group support for projects that examine the evolutionary morphology of marine heterotrophic flagellates.

The successful applicant must have a PhD in a relevant field and at least 4 years of postdoctoral research at the highest international standards relating to comparative protistology, molecular phylogenetics and single cell transmission electron microscopy. The successful applicant must also have a strong publication record in the comparative ultrastructure of marine heterotrophic flagellates. Research will be within the framework of the Tula Foundation Funded Centre for Microbial Diversity and Evolution. Additional responsibilities include the presentation of research findings at conferences, continued publication of research, and assistance with the day-to-day training of other research personnel.

Applicants should mail, no later than January 6, 2012, a curriculum vitae, a concise statement of research interests, the names of three referees and copies of two representative publications to:

Brian Leander

Departments of Zoology and Botany University of British Columbia

6270 University Blvd.

Vancouver, BC, V6T 1Z4

This part-time position will begin on April 1, 2012 and will initially be for one year.

UBC hires on the basis of merit and is committed to employment equity. All qualified persons are encouraged to apply. Canadians and Permanent Residents of Canada will be given priority.

bleander@mail.ubc.ca

UCalifornia SantaBarbara Phylogenetics

Postdoctoral Position at UCSB in Phylogenetics/Convergent Evolution

We seek a highly motivated and productive postdoctoral researcher to work on NSF-funded*, collaborative research on Phylogenetics and Convergent Evolution of Sexual dimorphism in sarsielloid Ostracoda. The postdoc would work at the University of California-Santa Barbara in the laboratory of Todd Oakley.

The postdoc will first lead collecting expeditions in California, Belize, and Australia/New Zealand. Next, the postdoc will obtain high-throughput sequencing data to elucidate the phylogenetic relationships of sarsielloid ostracods. We hypothesize that a radical sexual dimorphism – where only males have eyes – evolved multiple times in the group. We are developing phylogenetics tools in the Galaxy Bioinformatics Platform to analyze the data. The postdoc will also facilitate collaborative experiments with the laboratory of Ajna Rivera at University of the Pacific, to determine expression patterns of known eye development genes in convergent ostracod species.

The position requires an individual with a PhD and experience in phylogenetics, bioinformatics, invertebrate zoology or related fields. Collecting requires snorkeling, moderate free diving to collect sediment near coral reefs, and long hours at a microscope. In addition to a willingness to learn to collect and identify ostracods, outstanding molecular, computational and/or quantitative skills and a willingness to develop bioinformatics tools in Galaxy are particularly advantageous.

Funding is available for a 12-month position, for a minimum of 1 year, and will be extended pending successful completion of project goals. The successful candidate will be expected to interface with collaborators and to become an integral member of an interactive and collaborative lab group, and to supervise and/or mentor students. There will be opportunities for the candidate to pursue his or her own research program within the broad context of the grant proposal, and in collaboration with the PI, lab, and outside collaborators.

UCSB provides a rich academic and living environment. UCSB recently ranked #7 in the world for scientific impact (http://www.ksby.com/news/ucsb-ranked-7-in-new-worldwide-poll/). UCSB ranked first in the nation in research impact in the area of Ecology/Environment for the period 2001-2005 by the Institute for Scientific Information (Science Watch, November 2006). Santa Barbara has a Mediterranean climate that facilitates year-round outdoor activities, including surfing, kayaking, biking, and hiking.

The optimal start date is June 1, 2012 but there is some flexibility. For primary consideration, applicants should apply by January 15, 2012. Informal inquiries are encouraged, prior to formal application. To formally apply, please send the following:

1. A curriculum vitae 2. Names of 3 referees willing to provide a letter of recommendation upon request 3. A brief statement of how research goals of your career fit with research on convergent evolution in ostracods

E-mail applications are preferred: oakley@lifesci.ucsb.edu

*Funding and position is pending final, formal approval

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Todd Oakley, Professor Ecology Evolution and Marine Biology University of California, Santa Barbara Santa Barbara, CA 93106 USA

NEWLY UPDATED LAB WEBSITE: http://labs.eemb.ucsb.edu/oakley/todd/ todd.oakley@lifesci.ucsb.edu

UCambridge Host-Parasite Evolution Genomics

Host-Parasite Evolution and Genomics

Department of Genetics, University of Cambridge

Two ERC funded post-doctoral positions, lasting three to five years, are available to investigate genetic variation in the susceptibility of Drosophila to viral infection.

Insects vary in their susceptibility to viral infection, and this variation affects disease transmission by vector species, and the survival of beneficial insects and pests. The successful candidates will investigate the genetic basis of this variation in Drosophila using next generation sequencing, published genome sequences and the tools of Drosophila genetics. This will not only give insights into the molecular and cellular basis of how resistance to viruses evolves in nature, but population genetic approaches will also allow us to understand the factors that maintain variation in susceptibility to infection in populations. There will be scope for the successful applicant to drive the direction of their research, and they will be expected to collaborate closely with other post-docs in the lab.

We are seeking highly motivated candidates who have a deep interest in this area of research. Applicants must have, or will shortly obtain, a PhD. Ideally the candidate's past work will be in genetics or evolutionary biology. However, this is a five year project that will include several researchers, so we are seeking applicants with a range of different interests and skills. Relevant experience would include any of the following: population genetic analysis, the analysis of next-generation sequencing data, Drosophila genetics, and host-pathogen evolution and genetics.

Start Date: The position is available immediately, but the start date is negotiable.

Enquiries: f.jiggins@gen.cam.ac.uk

The Lab: www.gen.cam.ac.uk/research/Jiggins Duration: we expect to offer a three year and a five year contract

Salary: Salary scale will be included on the website below

Closing date: 16 January 2011

Applications: formal applications are through http://www.jobs.cam.ac.uk/ (the advert will be posted here in the next few days). Please include a brief statement of research interests, qualifications and experience, together with a curriculum vitae and a list of scientific publications

Department of Genetics

University of Cambridge

Downing Street

Cambridge CB2 3EH

Telephone: 01223 333175

Mobile: 07981 496922

http://www.gen.cam.ac.uk/Research/Jiggins/ http://www.gen.cam.ac.uk/Research/Jiggins/

UConnecticut ProteaEvolution

University of Connecticut University Postdoctoral Fellow

The Department of Ecology & Evolutionary Biology at the University of Connecticut invites applications for a University Postdoctoral Fellow on an NSF-funded project investigating evolutionary radiations in Protea and Pelargonium. The successful applicant will be part of a large team that is investigating functional trait evolution in these genera in the context of the characteristics of communities in which they occur and their resilience to climate change (http://tinyurl.com/-3jtz759). The successful applicant will be responsible for design, implementation, and analysis of field and greenhouse experiments that explore the link between leaf traits, leaf physiology and leaf longevity in adaptation to broad environmental gradients in the Greater Cape Floristic Region of southern Africa. Extended travel or residence in the Greater Cape Floristic Region of southern Africa will be required for fieldwork and experiments.

Qualifications:

Minimum Qualifications: Ph.D. in biology or a closely related field; and experience in plant ecophysiology (e.g., leaf longevity, interpretation of stable isotope data, photosynthesis).

Preferred Qualifications: Experience with Geographic Information Systems (GIS); statistical analysis (R); and phylogenetic comparative methods.

This is a one year, grant funded position. Continuation of this position may be possible for an additional year if performance is satisfactory and grant funding is available.

To Apply: Interested applicants should apply online using Husky Hire www.jobs.uconn.edu. Applications should include a brief statement (1-2 pages) summarizing previous scientific work and experience, a curriculum vitae, and the names and addresses of up to three individuals able to evaluate the applicant's qualifications for the position. The position can start as soon as 1 March 2012. Review of applications will begin on January 23, 2012. Inquiries may be addressed to Carl Schlichting at: schlicht@uconn.edu. The University of Connecticut is an EEO/AA employer.

Carl Schlichting Professor Ecology & Evolutionary Biology University of Connecticut

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UDelaware AvianQuantGenetics

A postdoctoral position is available immediately in the Department of Animal and Food Sciences at University of Delaware for an enthusiastic and self-motivated individual to work in the field of quantitative and molecular genetics.

Qualifications: PhD degree in animal breeding and genetics, statistical genetics/genomics, computational biology, biostatistics, molecular biology or related fields with substantial computational and statistical expertise; experience in usage of statistical and genomics software packages (e.g. JMP, JMP Genomics, ASReml and PLINK). The candidate should have working knowledge in C++, SQL and Perl programming languages. Additional skills include working knowledge in molecular genetic techniques as RAPD, AFLPs and RFLPs are desirable.

Responsibilities: Conduct research on genotyping commercial chicken populations through implementation of next-generation sequencing (NGS) and the use of high-density SNP analysis to identify genetic markers for improving the performance of broiler chickens.

The successful candidate will work under the direction of Dr. Behnam Abasht, Assistant Professor, and will utilize laboratory facilities in the Department of Animal and Food Sciences, the Delaware Biotechnology Institute, the Integrative Avian Biology Lab and also have access to the state-of-the-art high-performance computing cluster at University of Delaware. The successful candidate is expected to collaborate with the university and industry partners, draft summary reports, write journal papers and present findings at scientific meetings.

Initial appointment is for one year, renewable for one additional year dependent upon satisfactory performance. Salary is competitive and commensurate with experience and qualifications. Applicant should send a letter of interest, a CV and three letters of recommendation to Dr. Behnam Abasht (Abasht@UDel.edu). Please mention if you are attending the Plant and Animal Genome (PAG) meeting in January 2012.

The University of Delaware is an equal opportunity employer, which encourages applications from minority group members and women.

Behnam Abasht, Ph.D. Assistant Professor, Integrative Food Animal Biology Department of Animal and Food Sciences University of Delaware 035 Townsend Hall Newark, DE 19716 Phone: 302-831-8876 (office); 302-831-0218 (lab) Fax: 302-831-2822 Email: abasht@UDel.edu

http://ag.udel.edu/anfs/faculty/abasht.html

UHelsinki Bioinformatics

University of Helsinki and Jyväskylä, bioinformatics

The newly appointed Centre of Excellence in Biological Interactions funded by the Academy of Finland calls for applications for one two-year post doc position, with the possibility for a one-year extension in evolutionary genomics. The partners of the Centre of Excellence are located at the University of Jyväskylä, Finland (Prof. Johanna Mappes and Prof. Jaana Bamford), University of Helsinki, Finland (Prof. Liselotte Sundström) and Australian National University (Prof. Hanna Kokko). We offer a stimulating, creative and international working environment, modern facilities, reliable funding, excellent career prospects and nice colleagues.

The successful candidate will work mainly on two non-model systems, the Wood Tiger Moth (Parasemia plantaginis), and the Narrow-headed Ant Formica exsecta, on research questions related to the evolution of polymorphic warning colouration, and the evolution of life-history strategies and under multi-level selection. We are looking for a motivated candidate with good track record of relevant publications, experience in transcriptome and genome bioinformatics, and who enjoys problem solving and working with a team of ecologists and evolutionary biologists. The candidate should have a PhD in evolutionary biology, genetics, bioinformatics or a related relevant field. In particular we value good programming skills (python, perl etc), an ability to manage and integrate next generation sequence data with information from existing genomic databases, and a willingness to take a leading role in supervising post-doctoral and PhD students in these procedures. Excellent communication skills are essential because the post doc will collaborate with other members (PhD students and post docs) in the group who are working in the areas of molecular biology, ecology, behavioural and chemical ecology.

In addition to the main research programme, the post doc will have an opportunity to develop related research ideas together with other members of the CoE as well as collaborators at other institutes. We offer a stimulating, creative and international working environment, modern facilities, reliable funding, excellent career prospects and nice colleagues.

Candidates are encouraged to contact Prof. Liselotte Sundström (biotiede-bioint@helsinki.fi) for informal inquiries and further particulars.

- Application deadline: 20 January 2012

- Starting date: the position is available from 1 January 2012; starting date is negotiable

- Salary: 3000-3600 (gross) monthly depending on experience; health insurance and other benefits are included

- The position is based at the Universities of Jyväskylä and Helsinki.

liselotte.sundstrom@helsinki.fi
liselotte.sundstrom@helsinki.fi

UJyvaskyla ChemicalDefence

Post doc (three years): Within-species variation in chemical defence: trade-offs, noise or alternative strategies?

The newly appointed Centre of Excellence in Biological Interactions funded by the Academy of Finland calls for applications for a post doc position focusing on within-species variation in chemical defence.

Defensive toxins are widely used by animals, plants and micro-organisms to deter natural enemies. The maintenance of toxin diversity both in quality and quantity is an important ecological question that requires consideration from an evolutionary perspective. The post doc will seek alternative evolutionary explanations for the persistence of variation, and will study toxin diversity by focusing on 1) why some individuals lack defence in an otherwise toxic prey population (cheating by automimicry), 2) why the toxin content of individuals varies within a population and 3) why the chemical constituents of defence vary. Flavobacterium columnare and the wood tiger moth Parasemia plantaginis will be used as study species.

A successful candidate will have a PhD in evolutionary biology, ecology or a related discipline. She/he is motivated, enjoys problem solving, has a strong background in designing and conducting experiments, and has a record of successful publications. Experience in chemical ecology or theoretical ecology is a bonus but ability to work together with both theoreticians and empirists is essential; therefore, excellent communication skills are required.

The partners of the Centre of Excellence are located at the University of Jyväskylä, Finland (Prof. Johanna Mappes and Prof. Jaana Bamford), University of Helsinki, Finland (Prof. Liselotte Sundström) and Australian National University (Prof. Hanna Kokko). We offer a stimulating, creative and international working environment, modern facilities, reliable funding, excellent career prospects and nice colleagues.

The position is placed at the University of Jyväskylä but the post doc is required to carry out some of the work at the University of Helsinki and the Australian National University in Canberra.

Candidates are encouraged to contact Prof. Johanna Mappes johanna.mappes@jyu.fi for informal inquiries and further particulars.

Application deadline: 31 December 2011

Starting date: the position is available from 1 January 2012, starting date is negotiable

Salary: 3000EUR-3600EUR (gross) monthly depending on experience; health insurance and other benefits are included

Applications should include 1) a cover letter with a statement of research interests, 2) CV and 3) names and contact details of two references. Applications should be emailed in PDF format to Kaisa Suisto kaisa.h.suisto@jyu.fi

eira.h.ihalainen@jyu.fi

UJyvaskyla ChemicalDefence Update

Update: Please note the extended application deadline!

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Candidates are encouraged to contact Prof. Johanna Mappes johanna.mappes@jyu.fi for informal inquiries and further particulars.

Application deadline: Evaluation of the applications begins in January 2012 but applications can still be submitted until the end of January

Starting date: the position is available from January 2012; starting date is negotiable (April 2012 at the latest)

Salary: 3000EUR-3600EUR (gross) monthly depending on experience; health insurance and other benefits are included

Applications should include 1) a cover letter with a statement of research interests, 2) CV and 3) names and contact details of two references. Applications should be emailed in PDF format to Kaisa Suisto kaisa.h.suisto@jyu.fi

eira.h.ihalainen@jyu.fi

UJyvaskyla ColourPolymorphism

Post doc (three years): Role of sexual selection in maintaining colour polymorphism

The newly appointed Centre of Excellence in Biological Interactions funded by the Academy of Finland calls for applications for a post doc position focusing on the role of sexual selection in maintaining colour polymorphism.

Experimental data show that sexual selection plays a role in the evolution of genetic colour polymorphism but little is known about the adaptive value of different mate-choice strategies and how they affect the evolutionary stability of colour polymorphism. We study the warning coloured, polymorphic wood tiger moth Parasemia plantaginis.

We are looking for a motivated candidate who enjoys problem solving and working in the field as well as in the lab. A successful candidate will have a PhD in evolutionary biology, ecology or a related discipline. She/he is experienced in designing and conducting both field and lab experiments, and has a record of successful publications. Excellent communication skills are essential because the post doc will collaborate with other members (PhD students and post docs) in the group who are working in the areas of molecular biology, ecology, behavioural ecology and chemical ecology.

The partners of the Centre of Excellence are located at the University of Jyväskylä, Finland (Prof. Johanna Mappes and Prof. Jaana Bamford), University of Helsinki, Finland (Prof. Liseotte Sundström) and Australian National University (Prof. Hanna Kokko). In addition to the main research programme, the post doc will have an opportunity to develop related research ideas together with other members of the CoE as well as collaborators at other institutes. We offer a stimulating, creative and international working environment, modern facilities, reliable funding, excellent career prospects and nice colleagues.

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The position is based at the University of Jyväskylä.

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The position is based at the University of Jyväskylä.

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UKonstanz 2 PopulationComparativeGenomics

UNIVERSITY OF KONSTANZ/GERMANY

2 Postdoc positions in EVOLUTIONARY BIOLOGY (population genomics/comparative genomics)

Two postdoc positions in the lab of Axel Meyer (http://www.evolutionsbiologie.uni-konstanz.de/-index.php?section=10) in the Department of Biology at the University of Konstanz in Germany are available from March 2012 on.

The positions are for Ph.D. biologists, ideally with prior experience in bioinformatics, molecular evolution or population genomics. We have recently received funding through an ERC advanced grant for work on the comparative genomics of parallel evolution of repeated adaptive radiations of cichlid fishes in Nicaragua (see: Elmer and Meyer. 2011. Adaptation in the age of ecological genomics: insights from parallelism and convergence. Trends in Ecology and Evolution 26: 298-306).

In the crater lakes of Nicaragua a natural experiment is taking place. Several adaptive radiations of cichlid fishes formed independently within only a few thousand years after colonization from a large ancestral lake. These extremely young adaptive radiations consist of species that arose in sympatry and evolved parallel adaptations (such as limnetic and benthic body forms, hypertrophied lips and molariform dentition) repeatedly in their new habitats. We plan to establish these Nicaraguan cichlids as a new ecological model system. Through comparative and population genomic approaches we plan to investigate the role and mechanisms of natural selection at the level of the entire genome. We will ask, what is the genetic basis of species differences and ecologically relevant morphological traits that led to parallel adaptations? Through comparative genomic and population genomic analyses (including establishing a reference genome), genome resequencing, and linkage, quantitative trait and association mapping, we plan to identify genomic regions, candidate genes, and characterize the genetic differences that contribute to the adaptive phenotypic differences between extremely young species.

For publications of the lab see: http://www.evolutionsbiologie.uni-konstanz.de/-index.php?section' Excellent working conditions are available in terms of space, equipment, departmental facilities and financial support for research expenses. The lab has state-of- the-art facilities for molecular and developmental biology, including Illumina and Roche FLX next-generation sequencers at the Genomics Center Konstanz (http://cms.uni-konstanz.de/en/genomics-center/).

The University of Konstanz and the Department of Biology are among the most highly ranked institutions in Germany and provide a lively and academically outstanding research environment. Konstanz is a lovely historic town located on Lake Constance on the border to Switzerland.

Appointments are initially for two to three years, and are renewable for up to five years, with an annual gross salary (depending on prior experience) of about 58,000 Euros (about 73.000 US$). Habilitation is possible.

Additional information can be obtained from a.meyer@uni- konstanz.de, (tel.+49 7531 884163, fax + 49 7531 883018) or from our www page.http://www.evolutionsbiologie.uni-konstanz.de . Applications including a statement of research interests, a full CV, and names and email addresses of 3 referees, should be emailed to a.meyer@uni-konstanz.de. Applications should be received before December 24, 2011. Interviews will be conducted in January 2012.

The University of Konstanz is an equal opportunity employer.

Prof. Axel Meyer, Ph.D. Lehrstuhl für Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 (0)7531 88 4163 fax + 49 (0)7531 88 3018

secretary: Ingrid.Bader@uni-konstanz.de tel. + 49 (0)7531 88 3069

www.evolutionsbiologie.uni-konstanz.de Axel Meyer <Axel.Meyer@uni-konstanz.de>

UMassachusetts DarwinFellow MicrobeGenomics

Global Warming and Forest Soil Microbiomes

Rapid advances in genomic sequencing technology are expected to result in 100 gigabases of DNA sequence data in a single day from a single machine within the next five years. This is equivalent to sequencing 20,000 individual microbial genomes. The scale and complexity of this data is transforming microbiology and in particular ecological research. Genomic data provides a foundation for an exciting "reverse ecology" framework for determining underlying networks of interactions within and between microbial communities. The impact of this data on ecological and evolutionary biology research will be dependent on designing new long-term experiments and developing novel methods for analyzing genomic data in the context of microbial community interactions.

During my sabbatical last year at Harvard Forest I began to two related projects. As part of a collaborative summer REU project we began collect and archive DNA samples from long-term soil warming experiments (see Melillo et al. 2011 PNAS). We have recently been funded to sequence a subset of samples from this site. One goal of this project is to test the hypothesis that microbial community composition, and in turn function, controls the response of plants to soil warming and ultimately ecosystem carbon cycling. The second project involves developing new computational methods to integrate analyses of species diversity and microbial function using data from the warming sites, the National Ecological Observatory Network and other large scale sequencing projects at Harvard Forest. We have several related projects ongoing in the lab including the isolation and characterization of novel bacteria involved in degrading plant litter.

I am willing to sponsor a Darwin Fellow to continue and expand my research projects at Harvard Forest. If you are interested send me an email.

Jeff Blanchard blanchard@microbio.umass.edu http://www.bio.umass.edu/micro/blanchard/ *DARWINFELLOW***

The Graduate Program in Organismic and Evolutionary Biology at University of Massachusetts Amherst announces a two-year *postdoctoral FELLOWSHIP/lectureship*.OEB draws together more than 80 faculty from the Five Colleges (University of Massachusetts Amherst and Smith, Hampshire, Mount Holyoke and Amherst Colleges), offering unique training and research opportunities in the fields of ecology, organismic and evolutionary biology. Our research/lecture position provides recent PhD's with an opportunity for independent research with an OEB faculty sponsor as well as experience developing and teaching a one-semesterundergraduate biology course. Proven teaching skills are required.//Position subject to availability of funds. 1st year salary: $35,000.2nd year salary: $37,000.

To apply, send CV, 3 letters of reference, statements of research and teaching interests, and arrange for a letter of support from your proposed OEB faculty sponsor. A list of faculty and additional information is available at */www.bio.umass.edu/oeb./ *

OEB Darwin Fellowship 319 Morrill Science Center

611 N. Pleasant Street University of Massachusetts Amherst Amherst, MA01003 413-545-0928

darwin@bio.umass.edu

Application review begins: 1/1/12 Start date: 8/19/2012

/The University of Massachusetts Amherst is an Affirmative Action/Equal Opportunity Employer. Women and members of minority groups//are encouraged to apply./

Jeffrey Blanchard <blanchard@microbio.umass.edu>

UMassachusetts DarwinFellowship

*DARWINFELLOW***

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Benjamin Normark

Associate Professor Department of Plant, Soil, and Insect Sciences Fernald Hall University of Massachusetts Amherst, MA 01003 USA

office phone and voice mail: +1-413-577-3780 fax: +1-413-545-2115

bnormark@ent.umass.edu

UPennsylvania HumanPopGen

Post-Doctoral Position - University of Pennsylvania - Perelman School of Medicine

The Voight lab invites applications for computational Post-Doctoral positions at the University of Pennsylvania School of Medicine, within the Departments of Pharmacology and Genetics. A central focus of the Voight lab is aimed toward developing computational approaches that translate discoveries from human genetics data into insights about the biological basis and genetic architecture of human disease and the history of human evolution.

Objectives: The candidate will have the opportunity to work with large collections of human genetic data sets from association and sequencing studies, many of which are paired with a range of metabolic, cardiovascular, and autoimmune related traits. The applicant will focus their efforts on the analysis of these data, by contributing to gene-mapping activities, population genetics analyses, and developing new statistical and population genetic methods to extract biological insights from these data.

For medical genetics projects, the applicant also will work to develop approaches that translate these insights into actionable information in clinical and benchlab experimental settings. Further, the applicant will also contribute to informatics and computational approaches that integrate biological information sources (e.g., CHIP-Seq, RNA-seq and gene-expression data, protein-protein networks, etc.) with genetic data. Population genetic projects using genetic data from sequencing studies in humans and other species are potentially available. The applicant will also have the opportunity to engage in collaborative efforts at the national and international stage.

The starting date is flexible and can be as early as 2012. Applications will be accepted until the positions are filled. Competitive salaries commensurate with experience and skills, complete with benefits.

Qualifications: 1. The candidate will have a MD, PhD, or equivalent doctorate, a strong background in statistics, population and/or human genetics, genetic epidemiology, computational biology and/or genomics, bioinformatics, or a related discipline. 2. The ideal candidate will have a track record of scientific productivity and leadership. 3. The ideal candidate will demonstrate a working proficiency in programming, scripting, and statistical computing (i.e., C/C++, Python, PERL, R, etc.), will have experience handling large data sets in the UNIX/LINUX operating environment, experience in high-performance cluster computing, and a working knowledge of computational tools routinely utilized in contemporary human genetics applications (e.g., PLINK, PLINK/SEQ, MACH, SNPTEST, BEAGLE, DAPPLE etc.). 4. Applicants with prior experience in projects and data related to next-generation sequencing, or with prior experience studying metabolic disorder, cardiovascular disease, and/or autoimmune disease, or population genetic studies in humans will have a strong advantage.

Application Instructions: To apply, please send (1) cover letter that includes the names and contacts for three references and a short statement of research interests, and (2) a current CV to: Benjamin Voight, PhD (bvoight@upenn.edu).

Further information about the lab can be found at: http://www.broadinstitute.org/ ˜ bvoight/index.html Benjamin F. Voight, Ph.D. Assistant Professor, Department of Pharmacology The University of Pennsylvania - Perelman School of Medicine Tel: (215) 746-8083; Email: bvoight@upenn.edu http://www.broadinstitute.org/˜bvoight/ bvoight@broadinstitute.org

UppsalaU 2 EvolBiology

Postdoc: Uppsala.2.EvolBiology

The Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University invites applications for 2 Departmental postdoctoral fellows in ecology, evolutionary biology, or genetics, broadly defined. Positions are for two years and may begin as early as March 2012.

The Evolutionary Biology Centre of Uppsala University offers a vibrant research environment and bridges a broad range of disciplines in the biological sciences. Information about the Evolutionary Biology Centre and the Department of Ecology and Genetics can be found at www.ebc.uu.se

Prior to application, candidates should identify and communicate with a potential advisor. Potential advisors are faculty and researchers at the Department. Please, see list of staff in the four research programs of the Department: Animal Ecology, Evolutionary Biology, Limnology, Plant Ecology and Evolution, and Population and Conservation Biology at http://www.ebc.uu.se/forskning/IEG/?languageId=1

To apply, candidates should submit a cover letter indicating the proposed faculty advisor(s), a curriculum vitae, and a short (1-3 pages) description of past research accomplishments and future research plans. Applicants should include names and e-mail addresses of two potential referees. Applicants should also indicate the date they will be available to begin the position, and should enclose a letter from the proposed supervisor that indicates willingness to host the suggested project and that describes the added value of the proposed project in relation to ongoing research.

For further information about the position, please contact professor Jon Agren, phone +46 18 471 2860, e-mail Jon.Agren@ebc.uu.se.

You are welcome to submit your application no later than February 7, 2012. The application form can be found using the link below

http://www2.personalavd.uu.se/ledigaplatser/3215postdoceng.html

Jon Ågren Plant Ecology and Evolution/Dept of Ecology and Genetics Evolutionary Biology Centre Uppsala University Norbyvägen 18 D SE-752 36 Uppsala Sweden

Phone: +46-18 471 2860 Telefon: 018-471 2860

Jon Ågren <jon.agren@ebc.uu.se>

UppsalaU EvolutionaryGenomics

Postdoctoral research fellowship in evolutionary genomics at Uppsala University, Sweden

A postdoctoral fellowhip is available at the Department of Evolutionary Biology at Uppsala University. The postdoc is in the research-group of Dr. Hanna Johannesson, and will focus on testing general evolutionary paradigms in the filamentous ascomycete model system Neurospora. The fellowhip is for one year, with a high likelihood of extension another year.

This postdoc project can be developed after the interest of the applicant, but should fit in to the main interest of the reseach group (http://www.ebc.uu.se/Research/IEG/evbiol/research/Johannesson/publications/)

Research areas include sex chromosome evolution, mating system evolution, local adaptation, molecular evolution and speciation.

The Program in Evolutionary Biology (http://www.egs.uu.se/evbiol/index.html) is situated in the Evolutionary Biology Centre in central Uppsala. The working atmosphere is international with English as working language. The Evolutionary Biology Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, with research programs including ecology, systematics, genetics, genomics, and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 40 minutes with train from Stockholm.

Required qualifications for applicants are 1) a PhD in Biology, Genetics, Evolutionary Biology, Microbiology, or related field, 2) experience in one or several of the following areas: molecular biology, bioinformatics, comparative genomics, population genetics, experimental evolution, evolutionary biology, genetics, microbiology, mycology, and 3) demonstrated verbal and written communication skills in English.

To apply, send your CV, including contact information for two references, and a cover letter stating your research interest to: Dr Hanna Johannesson, hanna.johannesson@ebc.uu.se.

Hanna Johannesson <hanna.johannesson@ebc.uu.se>

UppsalaU SpeciationGenomics

Post-doc Position in Avian Speciation Genomics

A post-doc position in speciation genomics is available at the Department of Evolutionary Biology in Uppsala, Sweden in the research group of Dr. Jochen Wolf. Funds are guaranteed for one year, but can be extended to a two-year period, generally with good success.

Background The study of speciation mechanisms remains one of the major challenges in fundamental biological research. The hybrid zone between carrion and hooded crows (Corvus corone spec.) is a textbook example of incipient speciation that is well characterized from an ecological and behavioural perspective. In contrast, the genetic architecture of the hybrid zone is poorly understood. The crow system represents a case of a very early phase of species divergence that requires new molecular approaches for its comprehensive description.

The project The revolution in sequencing technology allows us addressing its underlying genetic architecture for the first time using a combination of several genomic approaches. Currently, these include high quality genome assembly and annotation, a common-garden based RNA-seq gene expression study and population genomic analyses. The successful candidate will primarily work with a large whole genome re-sequencing data set from individuals collected all over Europe to trace the species' demography and unravel the decisive genetic changes between the two taxa ('60 crow genomes project').

Infrastructure We are a young, growing research group with interests in molecular evolution and evolutionary genomics with a primary focus on birds and mammals. We form part of a recently launched Centre of Excellence (http://www.uceg.uu.se) and SciLifeLab Uppsala (http://www.scilifelab.uu.se/). The group is placed within the Evolutionary Biology Centre which is one of world???s leading research institutions in evolutionary biology that successfully bridges a broad variety of disciplines in the biological sciences. It is situated in the beautiful small town of Uppsala in Sweden, that offers rich opportunities in cultural and outdoor activities and is strongly influenced by the 40 000 students living here. The Department of Evolutionary Biology excels in many aspects of genetics and evolution and offers an inspiring atmosphere in an international group.

For further information visit our website: http://-www.ebc.uu.se/Research/IEG/evbiol/research/Wolf/ If you are enthusiastic about evolutionary biology, have a good understanding of population genetics, ideally a strong background in coalescence theory and demographic modelling and/or are skilled in bioinformatic programming you are most welcome to apply for the position. Feel free to email me with an informal inquiry before submitting an application. I am certainly also happy to toss around other ideas you'd like to pursue that are in line with the general research program.

Send your application including a motivation letter describing your research background and interests (~1 page), CV and two letters of recommendation to Jochen Wolf (jochen.wolf@ebc.uu.se).

Dr. Jochen Brock Wacain Wolf Department of Evolutionary Biology Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

phone: ++46 18 471 6465 fax: ++46 18 471 6310 http://www.ebc.uu.se/Research/IEG/evbiol/-research/Wolf/ Jochen Wolf <jochen.wolf@ebc.uu.se>

UppsalaU Systematic Biology

Postdoctoral position in Systematic Biology at the Evolutionary Biology Center, Uppsala University, Sweden

A two year independent research position is offered at the Program in Systematic Biology at Uppsala University. Systematic Biology is a large and diverse department of over 30 academic research staff and students. Research interests cover a wide range of topics from systematic biology of macro- and microbial eukaryotes to comparative genomics and phylogenetics.

The Department is housed in spacious modern facilities, adjacent to the museums of zoology and paleontology, herbarium and botanical garden at one of the foremost universities in Scandinavia. For further information see: http://www.ebc.uu.se/forskning/IOB/Systematisk_biologi/ . Appointment period: The position is for 2 years.

Nature of duties: This is a pure research appointment, to be conducted independently or in collaboration with more senior scientists at the department and/or elsewhere. Opportunities also exist for some teaching at the undergraduate level and/or project student supervision.

Qualifications required: To qualify for an appointment you must have received your PhD within three years of the application deadline, with allowance for special circumstances. Applicants may not have been employed at Uppsala University in the previous 12 months.

Criteria for ranking: In ranking qualified applicants the highest priority will be attached to scientific excellence, as demonstrated by quality of scientific publications. Consideration will also be given to the applicant's potential to develop or strengthen existing research in the Program and for obtaining external support for research funding.

In filling this position, the university aims to recruit the person who, in a combined evaluation of competence, skills and documented qualifications, is judged most suitable to carry out and develop the work-in-hand and to contribute to a positive development of the department and program. Personal circumstances that may be of positive relevance to the application, for example parental leave, should be mentioned in the list of qualifications (CV).

How to apply: The application must be written in English and should include the following documents: 1) curriculum vitae with a list of scientific works, employment and training record, 2) research plan not to exceed 2 pages should include background, project plan, general methods, expected outcomes and projected timeline, and 3) name, phone number and email addresses of two professional references.

For further information about the position, please contact Prof. Sandra Baldauf, phone +46 18 471 6452, e-mail: Sandra.Baldauf@ebc.uu.se. The trade union representatives are Anders Grundström, SACO (the Swedish Confederation of Professional Associations), phone +46 18 471 5380 and Carin Söderhäll, TCO/ST (the Swedish Confederation of Professional Employees), phone +46 18 471 1996, Stefan Djurström, SEKO (the Union of Service and Communication Employees), phone +46 18 471 3315.

Applications should be submitted online, no later than 5 January 2012. Please follow the link below to access and submit an application, for this position UFV-PA 2011/2962

www2.personalavd.uu.se/ledigaplatser/2962postDoc.html

derrick.he@gmail.com

URennes Bioinformatics EvolutionaryGenomics

POSTDOCTORAL POSITION IN BIOINFORMATICS AND EVOLUTIONARY GENOMICS: Next generation sequencing and analysis of complex polyploid genomes:

The research group Genome Evolution and Speciation (Team "Mechanisms Generating Biodiversity" MOB, UMR CNRS 6553 Ecobio) at University of Rennes 1 (France) invites applications for a 18 month postdoctoral position in bioinformatics to work on the analysis of genome and transcriptome sequence data (generated using 454 Roche and Illumina technologies) in the context of allopolyploid speciation. Genomic redundancy is a characteristic of major plant lineages, and requires the development of adapted analytic strategies. In the present project, these analyses aim at exploring genome and transcriptome evolution following recent interspecific hybridization and genome duplication in highly polyploid (hexaploid and dodecaploid) /Spartina/ species invading coastal saltmarshes. The host laboratory (http://ecobio.univ-rennes1.fr) has strengths in ecology, evolution, polyploid speciation, genome evolution and phylogeny. On-campus genomic and bioinformatic facilities are available at the Biogenouest plateforms (/e.g/. http://www.genouest.org/).

*Applicants must have a PhD in bioinformatics or genomics, excellent corresponding publication record, with strong proficiency in one or more programming languages, and preferably have experience with high-throughput genome and/or transcriptome data analyses. There is no citizenship requirement, and applications from abroad are encouraged (applicants should not have stayed in France for more than 6 months at the time of the application). *

Applications should be sent to malika.ainouche@univ-rennes1.fr. Please send a cover letter describing your research interests and experience, C.V. and contact information for two references.

Best regards,

Malika Ainouche,

Research group Genome Evolution and Speciation, (MOB-Team)

UMR CNRS 6553 Ecobio, Université de Rennes 1

Bât. 14A, Campus Scientifique de Beaulieu

35 042 Rennes Cedex (France)

Tel (33) 2 23 23 51 11

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

USaoPaulo 2 ReptileSystematics

Postdoctoral Position on Gymnophthalmidae systematics (Squamata: Teiioidea) at the University of SÃ£o Paulo (USP)

A 2-year post-doctoral fellowship is available starting January 1, 2012 as part of a FAPESP (www.fapesp.br) grant entitled âCOMPARATIVE PHYLOGEOGRAPHY, PHYLOGENY, PALEOCLIMATE MODELING, AND TAXONOMY OF NEOTROPICAL REPTILES AND AMPHIBIANSâ. The specific post-doctoral project will address the phylogeny of the family Gymnophthalmidae based exclusively on morphological characters. The candidate is expected to help mentor and manage an active team of graduate and undergraduate students working on a variety of grant-supported projects. The candidate will also have the opportunity to develop and lead collaborative research project(s) if directly related to the subject of the main project. Applicants should have a track record of published or submitted peer-reviewed publications in lizard systematics (preferably on gymnophthalmids) and expertise in preparation techniques for all morphological complexes involved in the postdoctoral project (osteology, pholidosis and hemipenial morphology). Qualifications: - A Ph.D. (concluded in the previous 2 years) in Zoology or related areas; - Fluency in English (knowledge of Spanish and/or Portuguese is encouraged) Fellowship: R$ 64.000,00 per year (aprox. US$ 40.700,00); FAPESP fellowships are tax free (see details at http://www.fapesp.br/en/5427 .Deadline is December 23, 2011, or until position is filled. To apply please submit curriculum vitae, statement of research interests (maximum two pages) and two letters of recommendation by email to the lead PI - Prof. Miguel Trefaut Rodrigues, Dep. of Zoology - IB - University of SÃ£o Paulo. For further information please contact Dr. Rodrigues at mturodri@usp.br

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Postdoctoral Position on Erythrolamprus systematics (Squamata: Serpentes) at the University of SÃ£o Paulo (USP)

A 2-year post-doctoral fellowship is available starting January 1, 2012 as part of a FAPESP (www.fapesp.br) grant entitled âComparative Phylogeography, Phylogeny, Paleoclimate Modeling, And Taxonomy Of Neotropical Reptiles And Amphiblansâ. The specific post-doctoral project will address the taxonomy and phylogenetic relationships among the false coral snakes of genus Erythrolamprus Boie, 1826 (Serpentes; Xenodontinae). The candidate is expected to help mentor and manage an active team of graduate and undergraduate students working on a variety of grant-supported projects. The candidate will also have the opportunity to develop and lead collaborative research project(s) if directly related to the subject of the main project. Applicants should have a track record of published or submitted peer-reviewed publications in snake taxonomy and/or systematics (preferably on xenodontines) and expertise in techniques of data collection and analysis. Qualifications: - A Ph.D. (concluded in the previous 5 years) in Zoology or related areas; - Fluency in English (knowledge of Spanish and/or Portuguese is encouraged) Fellowship: R$ 64.000,00 per year (aprox. US$ 40.700,00); FAPESP fellowships are tax free (see details at http://www.fapesp.br/en/5427 .Deadline is December 23, 2011, or until position is filled. To apply please submit curriculum vitae, statement of research interests (maximum two pages) and two letters of recommendation by email to the lead PI - Prof. Miguel Trefaut Rodrigues, Dept of Zoology - IB - University of SÃ£o Paulo. For further information please contact Dr. Rodrigues at mturodri@usp.br

Miguel Trefaut Rodrigues <mturodri@usp.br>

USouthCarolina SharkComparativeGenomics

Postdoctoral position in comparative genomics of sharks and rays using next generation sequencing data in the laboratory of Gavin Naylor at the College of Charleston and the Medical University of South Carolina in Charleston, South Carolina. The project is part of an NSF Tree of Life project to reconstruct the evolutionary history of chondrichthyan fishes based on both molecular and morphological data.

The selected candidate will have a Ph.D. in bioinformatics or a closely related field and have strong programming skills. Applicants must have experience with methods and software tools for analyzing next generation sequencing data and transcriptomes. While experience with comparative genomics, alignment and phylogenetic analysis is desired, it is not required.

The selected candidate will work as part of a team of highly interactive evolutionary biologists exploring the evolution of vertebrate animals. Applicants should submit a CV and cover letter to Gavin Naylor (gjpnaylor@gmail.com).

gjpnaylor@gmail.com

USouthDakota ComparativeVertAnatomy

Postdoctoral fellow: Vertebrate Morphology and Bioinformatics

We are seeking a scientist with training in comparative vertebrate anatomy to participate in the Phenoscapeinformatics initiative (https://phenoscape.org) to render morphological data computable and interoperable with genetic data. The successful candidate will: 1) lead data curation and ontology development for early living and extinct vertebrates (fishes) and amphibians as part of a team comprised of scientists and software developers, and 2) conduct large-scale, data driven evo-devo research on the store of phenotypic and genetic data in the knowledgebase (kb.phenoscape.org>).

Job description:

This position presents a unique opportunity to pursue bioinformatic research relating to broad questions concerning the evolution of morphology in relation to linked developmental and genetic data. The postdoc will use state of the art tools for evolutionary biology to curate morphological from the literature on early vertebrates (fishes) and living and extinct amphibians,annotating anatomical features using ontologies, to populate a database that will be integrated with the existing databases of phenotypic and genetic data from model vertebrates (ZFIN< http://zfin.org/ >, zebrafish; Xenbase< http://www.xenbase.org/ >, Xenopus; MGI< http://www.informatics.jax.org/ >, mouse).

Responsibilities center on contributing to a large and growing vertebrate phenotype knowledgebase (kb.phenoscape.org), including annotation of comparative fin/limb skeletal phenotypes and homologies from the scientific literature. The incumbent will work closely to coordinate efforts with the curators of fin-limb mutant phenotypes from the vertebrate model organism databases; participate in regular virtual meetings with a distributed project team; develop and document curation standards for comparative data and best practices for ensuring consistency across taxa; and collaborate with software developers in the design of curation workflow tools and interfaces, including tools for semi-automated extraction of comparative phenotype data from the literature. In addition, the incumbent will have ample opportunities to leverage the data in the knowledgebase, and associated tools for large-scale analysis of phenotype similarities, towards addressing his/her own research questions. The postdoc will supervise undergraduate workers in gathering/digitizing the literature and basic data entry; publish and give conference presentations on research results; and attend project meetings as required, including annual project team meetings.

Starting date: This two year postdoctoral position is available to be filled as early as January 2012.

Required qualifications: Ph.D. degree in biological sciences withexpertise in comparative vertebrate anatomy and evolution Ability to communicate well and work as part of a distributed research team Excellent English language skills Interest or experience in informatics methods

How to apply: The postdoctoral fellow will work with Paula Mabee (University of South Dakota) and David Blackburn (California Academy of Sciences). The position will be based in South Dakota, with opportunities to travel to other sites for this project including the National Evolutionary Synthesis Center (NESCent), the University of Chicago, and theCalifornia Academy of Sciences.

Please contact Dr. Mabee (pmabee@usd.edu) with any questions about this position. Applications should be directed to Dr. Mabee and include a cover letter, CV, a brief statement detailing your research interests and career goals, and three letters of reference.

Project team: This work is funded by a collaborative NSF grant to PIs Paula Mabee (University of South Dakota) andTodd Vision (University of North Carolina Chapel Hill) with co-PIs David Blackburn (California Academy of Sciences), Judith Blake (Mouse Genome Informatics, Jackson Laboratories), Hilmar Lapp (NESCent), Paul Sereno (University of Chicago), Monte Westerfield (University of Oregon, ZFIN), and Aaron Zorn (Cincinnati's Children's Hospital and Medical Center, Xenbase).

For more information about Phenoscape: Please see https://phenoscape.org and http://kb.phenoscape.org/ . The University of South Dakota (http://www.usd.edu) is an Affirmative Action/Equal Opportunity Employer committed to increasing the diversity of its faculty, staff and students.

"Mabee, Paula" <Paula.Mabee@usd.edu>

USussex DarwinianMedicine

University of Sussex - Postdoc in Darwinian Medicine

A vacancy as a postdoctoral research fellow is available as part of an ERC funded project investigating the sex-specific genetic architecture of human traits and diseases led by Dr Edward H. Morrow. The post will primarily involve the analysis of datasets from genome wide association studies (GWAS) of quantitative and/or disease traits in humans and flies, specifically with the aim of investigating sex-specific effects. Duties will include the collation and screening of suitable datasets as well as the development of statistical models and methods for examining sex-specific genetic effects. The post holder is expected to work in close collaboration with other members of the newly established group, and will be encouraged to develop their own skills.

The position would be ideal for a highly motivated and ambitious researcher with previous experience of analysing data from human disease genome-wide association studies and an interest in applying these methods within an evolutionary framework. The candidate should have good analytical, statistical and/or bioinformatics skills. A background in evolutionary biology would be advantageous but is not essential. The post-holder must have a PhD in a biological or related subject.

The School of Life Sciences at the University of Sussex set in the beautiful South Downs includes a range of experimentalists and theoreticians working on various aspects of molecular and whole organism evolutionary biology. The Brighton and Sussex Medical School is also on our doorstep. There are good transport links between the Falmer campus and the lively towns of Brighton and London.

Salary range: starting at £29,972pa and rising to £35,788pa

Closing date for applications: 2 January 2012

The flexible starting date is February 2012.

More details: http://www.sussex.ac.uk/Units/staffing/personnl/vacs/vac474.shtml HOW TO APPLY: Please visit the University of Sussex vacancies webpage (vacancy Ref 474) and follow the instructions: http://www.sussex.ac.uk/Units/staffing/personnl/vacs/vac474.shtml Informal enquiries with a CV are also welcome: ted.morrow@ebc.uu.se

Dr Edward H. Morrow

Current Address: Department of Ecology and Evolution Animal Ecology (zooekologi) Evolutionary Biology Centre Uppsala University Norbyvägen 18-D SE-752 36 Uppsala SWEDEN Email: ted.morrow@ebc.uu.se Tel: +46 18 471 2676 Fax +46 18 471 6484 Webpage: http://www.ebc.uu.se/Forskning/IEG/zooeko/Personal/Ted_Morrow/ ResearcherID: http://www.researcherid.com/rid/C-2358-2011 Address from January 2012: University of Sussex John Maynard Smith Building Falmer Brighton, BN1 9QG UNITED KINGDOM

Edward H. Morrow Department of Ecology and Evolution Animal Ecology (zooekologi) Evolutionary Biology Centre Uppsala University Norbyvägen 18-D SE-752 36 Uppsala SWEDEN

Email: ted.morrow@ebc.uu.se Tel: +46 18 471 2676 Fax +46 18 471 6484 Webpage: http://www.ebc.uu.se/Forskning/IEG/zooeko/Personal/Ted_Morrow/ ResearcherID: http://www.researcherid.com/rid/C-2358-2011 Edward Morrow <ted.morrow@ebc.uu.se>

UWesternAustralia BeeGenomics

JOHN STOCKER POSTDOCTORAL FELLOWSHIP - RESEARCH ASSOCIATE (REF: 3815)

CENTRE FOR INTEGRATIVE BEE RESEARCH (CIBER)< http://www.ciber.science.uwa.edu.au/ > and ARC CENTRE OF EXCELLENCE IN PLANT ENERGY BIOLOGY< http://www.plantenergy.uwa.edu.au/ >

* 3 year appointment available immediately * Salary: Level A $77,328 p.a. * Plus 17% superannuation * Closing date: Friday, 20 January 2012

Applications are invited from a suitably qualified scientist to work in a multi-disciplinary team environment on quantitative genomics and epigenomics of honeybees and aphids. The successful applicant will initiate and drive research projects to elucidate the effects and consequences of epigenetic modifications in two insect model systems, in particular the role of DNA methylation in insect caste determination. You will use high-throughput DNA sequencing approaches to investigate the relationship between differential DNA methylation, chromatin modifications, and the mRNA and small RNA transcriptomes in the honeybee and pea aphid invertebrate models. Applicants must have a PhD in molecular biology or related discipline awarded within the last three years.

Application Details: Written applications quoting the reference number, personal contact details, qualifications and experience, along with contact details of three referees should be sent to Director, Human Resources, The University of Western Australia, M350, 35 Stirling Highway, Crawley WA 6009 or emailed to jobs@uwa.edu.au by the closing date.

For further information regarding the position or the project please contact Associate Professor Boris Baer, email boris.baer@uwa.edu.au, or Winthrop Professor Harvey Millar, email harvey.millar@uwa.edu.au, or Winthrop Professor Ryan Lister, email ryan-lister@gmail.com, or Dr Owain Edwards< http://www.csiro.au/people/Owain.Edwards.html >, email owain.edwards@csiro.au. Some assistance with relocation expenses (if applicable) may be negotiated.

Owain.Edwards@csiro.au

WorkshopsCourses

Arolla Switzerland EvolBiol Jun23-29

Evolutionary Biology Workshop in the Alps

23-29 June 2012, Arolla, Switzerland

3 ETSC credit points

Faculty: *Trevor Price* (University of Chicago) http://home.uchicago.edu/~pricet/home.html *Anurag Agrawal* (Cornell University) http://www.eeb.cornell.edu/agrawal/index.html *John Pannell* (University of Lausanne) http://www.unil.ch/

dee/page86963.html *Tadeusz Kawecki* (University of Lausanne) http://www.unil.ch/dee/page47578.html Target participants: PhD students, advanced master students

This workshop, based on a concept developed by Steve Stearns and John Maynard Smith, takes place in a small Alpine village (Arolla), which will allow you to focus while being able to enjoy the landscape and the Alpine flora.

The main goals of this course are to develop the following skills: . developing your scientific ideas through discussions in groups; . thinking critically and expressing oneself clearly; . turning a general idea into a research project; . writing a research proposal and defending it.

It is you, the students, who will be in charge in this course. You will be divided in groups of 4-5 students. In those groups, you will work on your ideas. You, as a group, will decide what the important questions in broadly defined evolutionary biology are, you will choose one, and attempt to develop a proposal for a research project that will address it. The faculty will visit the groups during the discussions to answer your questions, provide coaching and give you feedback on your projects, but they will generally take the back seat. Additionally, the faculty will give informal talks about their research and be available for informal discussion with individual students. At the end you will present your projects to other participants, and we will party.

Costs: CHF 430.- for room and board.

More information under http://biologie.cuso.ch/ecologie-evolution/activities/detail-activity/item/courses/evolutionary-biology-workshop-in-the-alps-1/ To apply, send a single file (pdf or rtf) containing a short motivation letter, a cv, and the name of your scientific advisor to Nadia Bruyndonckx <Nadia.Bruyndonckx@unil.ch>, with a Cc to tadeusz.kawecki@unil.ch .

Deadline for application: 15 February 2012.

Greetings, Tad Kawecki

– Tadeusz J. Kawecki Associate Professor Department of Ecology and Evolution University of Lausanne Le Biophore, CH 1015 Lausanne, Switzerland

tadeusz.kawecki@unil.ch

Barcelona Biomorfodynamics Feb13-17

Dear colleagues:

This e-mail is to inform you about the course "Biomorfodynamics: limits to the biological evolution", which may be of your interest. This course will be held in the Museum of the ICP in Sabadell (Barcelona, Spain) on 13-17 February 2012. Instructor: Prof. Miquel De Renzi.

You can find more information at: http://www.icp.cat/index.php/ca/activitats/cursos/biomorfodinamica or writing to courses@icp.cat

Places are limited and will be occupied by strict inscription order. Deadline for inscription: December 15.

With best regards

Soledad De Esteban-Trivigno

– Soledad De Esteban Trivigno Area de Paleobiología Institut Català de Paleontologia Edifici ICP, Campus de la UAB 08193 Cerdanyola del Vallès Barcelona. Spain 00-34-935868334 www.icp.cat Soledad Esteban <soledad.esteban@icp.cat>

KelloggBioStation EvolBiol Summer

ANNOUNCING: Summer 2012 Field Courses and Undergraduate Programming Kellogg Biological Station http://www.kbs.msu.edu Dear Colleagues,

The Kellogg Biological Station (Michigan State University) is excited to announce its summer programming.

We offer field based undergraduate and graduate courses and NSF REU's.

Further, we are especially excited to announce our Undergraduate Research Apprenticeship program, aimed at early career students combining class work with a heavily mentored research experience.

Our courses are: Plant Systematics Ecology/Ecology Lab Grazing and Robotic Milking Field Ecology and Evolution Aquatic Entomology Biogeochemistry Social Agroecological Systems ELME (Enhancing Linkages Between Mathematics and Ecology) Eminent Ecologist Seminar Series

http://www.kbs.msu.edu/education/summer-courses More information on REU's can be found here:

http://www.kbs.msu.edu/education/internships-reu/nsf-reus-for-undergrads And more information on our Undergraduate Research Apprenticeship can be found here:

http://www.kbs.msu.edu/education/internships-reu/research-apprenticeship Please forward this information on to colleagues or students you think might be interested.

Thank you for your help!

Rachel Prunier, PhD. Assistant Director for Education and Research Associate Kellogg Biological Station 3700 East Gull Lake Drive Hickory Corners, MI 49060 prunier@msu.edu (269) 671- 2350

“An inconvenience is only an adventure wrongly considered.” G. K. Chesterton

rachel.prunier@gmail.com

Seville ConservationGenetics Feb9-10

Workshop: There are spaces available for participants on the workshop Merging Conservation Genetics and Ecological Genomics±, a scientific workshop organized within the ConGenOmics ESF Research Network Program. The workshop will be held 9-10 February 2012 in Seville, Spain

This workshop is the first scientific workshop organized within the ESF Research Networking Programme ConGenOmics. The goal of this workshop is to discuss our current understanding in the field of conservation genomics and to indentify gaps in our current knowledge regarding this research area. We will identify fields of research of high priority in conservation genomics and share and discuss the application of genomic technologies. We will also discuss how these genomic techniques will help us addressing topical questions and influence the future of conservation genomics. By bringing together European and pan-European specialists on conservation genomics we hope to develop and improve the knowledge transfer of the technical advances and challenges in conservation genomics.

The workshop addresses 3 major research topics which will be represented in 3 separate sessions. Each session is introduced by invited speakers who are experts in the respective scientific fields. The invited speakers will sketch the topical framework of each session, after which all participants are invited to provide further input by means of topical discussions. Below you will find a short overview of the three research sessions and a list the speakers who will introduce the topics.

Session 1. The experimental studies of (genomic) mechanisms behind important biological processes of relevance for conservation. In this session we will discuss the research that aims to disentangle the genomic aspects of population genetic processes, and fitness, in a conservation context, including mechanisms such as: (i) transcriptomic, proteomic and metabolomic analyses of inbreeding and outbreeding depression, (ii) genomic mechanisms of genotype-by-environment interactions, (iii) the genomic signature and mechanisms of local adaptation, (iv) genomic mechanisms behind phenotypic plasticity, (v) epigenetic mechanisms of adaptation and evolution, and (vi) the dynamics of functional gene variation in small populations, likely to be dominated by genetic drift.

Session 2. The application and development of data handling and processing strategies in conservation genomics. This session will focus on methods and techniques for data handling. New genomic technologies potentially allow deeper, higher resolution insights in important demographic and population genetic parameters and processes, and will allow disentangling the mechanisms involved in these processes. However these new techniques generate large amounts of data, challenging traditional ways to deal with the data. In this session, standard experimental protocols, the use of limited research sources in the most efficient way, sharing genomic information and results at a European and/or global scale and data handling procedures will be discussed.

Session 3. The application of community and metagenomics in conservation biological context Conservation genetics has traditionally focused on processes at the population level, but at the same time acknowledged that genetic variation at population level and processes at species and community level are intricately related. Metagenomics is the genomic analysis (most commonly by means of next-generation sequencing technologies-see above) of microbial communities. This new science provides access to organisms that form the vast majority of microorganisms on Earth. Metagenomics thereby offers a first peek at the wide variety of life that has never been studied, thus providing new insight into the structure and function of ecosystems as diverse as a polluted habitat or the gastrointestinal tract of an endangered species. This session will focus on the studies that incorporate meta-genomic monitoring in a conservation genetic assessments, studies that aim to disentangle the relationship between genetic and genomic variation at population level and biodiversity and ecosystem functioning, studies that target the influence of species interactions on genetic variation and functional genomic activity, and studies that aim to disentangle the genomic interactions between pathogens, parasites and herbivores on one side and hosts on the other.

Location: The workshop will be held on the 9th and 10th of February 2012 in Foro de la Biodiversidad in Seville in Spain and is hosted by Professor Carles Vila from Estacion Biologica de Donana (CSIC). Held in an informal but stimulating scientific atmosphere, with a limited number of participants, we hope that this meeting will provide an excellent opportunity for strong interaction and brainstorming on the field and future of conservation genomics.

Invited speakers: The following invited speakers have confirmed:

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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

ULyon ComparativeGenomics Jan16-27

European Course "Comparative Genomics"*

Organizers: Jean-Nicolas Volff (ENS Lyon), Céline Brochier (University of Lyon 1)

Credits: 6 ECTS

Large-scale comparison of whole genomes has revolutionized our way to apprehend biology and has opened new avenues of analysis of the mechanisms driving the evolution of genes, genomes, biological networks and processes, organisms, populations and species. Genome comparison also helps to better understand phylogenetic relationships between organisms and to identify genes of medical and industrial interest.

In the frame of the recent methodological revolution of genome analysis, this course aims to initiate students to Comparative Genomics, a modern and fast-evolving science with ever growing impact on science and societies. We will particularly put the emphasis on recent major discoveries, innovating concepts and original strategies in the domains of biology, ecology, medicine and biotechnologies. Internationally reputed scientists will present their work and interact with students during conferences and round tables. The main strengths of this course are:

1- Topics related to hot recent discoveries

The topics covered by the course correspond to current big questions tackled by comparative genomics. Accordingly, they can differ from one year to the next. In past editions of this course we spoke about transposable elements, origin of new genes, gene and genome duplications, sex chromosomes, phylogenomics, bacterial genome evolution, evolutionary genomics and the origin of humans, evolution of non-coding DNA, genomics of speciation, and genome architecture.

Past speakers include Michael Lynch (Indiana University), Deborah Charlesworth (University of Edinburgh), Ken Wolfe (Trinity College Dublin), Adam Eyre-Walker (University of Sussex), Henrik Kaessmann (University of Lausanne), Ed Green (University of California), Manfred Schartl (University of Würzburg), Aoife McLysaght (Trinity College Dublin), Alex Widmer (ETH Zurich), Lluis Quintana-Murci (Pasteur Institute Paris), Eduardo Rocha (Pasteur Institute Paris), Nicolas Galtier (University of Montpellier), Laurent Duret (University of Lyon), Manolo Gouy (University of Lyon), Emmanuel Douzery (University of Montpellier), Hughes Roest-Crollius (ENS Paris) and Marc Robinson-Rechavi (University of Lausanne). Traditionally the course ends with a conference discussing the future of comparative genomics and its growing impact on societies. This conference was held by Bertrand Jordan in 2009 and Bernard Dujon in 2010 and 2011.

2- A course with top scientists, organized in conferences and round tables for students

The course is organized over two weeks, with a specific topic for each day. Each topic is held by two speakers, one in the morning and one in the afternoon, on complementary aspects of the subject. Each conference will begin with a general introduction to the topic (30 min) followed by a presentation of the research performed in the speaker's laboratory (1 hour). Finally, a round table of about one hour allows discussions between the two scientists and students on the topic of the day.

3- A course favoring interactions between international speakers and students

About half of speakers originate from foreign institutions. In addition, the course is open to students from other countries (generally 30-50% of the attending students). Hence, "Comparative Genomics" is much more similar to an international scientific meeting than to a classical course. Accordingly, teaching and discussions are all in English.

Preliminary program and Inscription form are available at http://lbbe-dmz.univ-lyon1.fr/spip_cg/ – | Céline Brochier-Armanet | | Laboratoire de Biométrie et Biologie Evolutive - UMR CNRS 5558 | Université Lyon 1, 43 Bd du 11 Novembre 1918 | 69622 Villeurbanne, France | | Tel: 33 (0)4 26 23 44 76 | Mail:celine.brochier-armanet@univ-lyon1.fr | | Web page:http://www.frangun.org | LIVRE:http://www.springer.com/life+sciences/bioinformatics/book/978-2-287-99047-2 – | Céline Brochier-Armanet | | Laboratoire de Biométrie et Biologie Evolutive - UMR CNRS 5558 | Université Lyon 1, 43 Bd du 11 Novembre 1918 | 69622 Villeurbanne, France | | Tel: 33 (0)4 26 23 44 76 | Mail: celine.brochier-armanet@univ-lyon1.fr | | Web page: http://www.frangun.org | LIVRE: http://www.springer.com/life+sciences/bioinformatics/book/978-2-287-99047-2 celine.brochier-armanet@univ-lyon1.fr

Uppsala QuantGenetics Jan30-Feb10

In the beginning of 2012 (30 Jan - 10 Feb) Prof. Bruce Walsh will visit Uppsala, Sweden to teach a course on ?Evolutionary Quantitative Genetics?. This ten full-day course will take place at the EBC (Evolutionary Biology Centre) at Uppsala University. The course is open to graduate students, postdocs and other researchers who are interested evolutionary quantitative genetics.

The course will be based on Lynch & Walsh's books ?Genetics and Analysis of Quantitative Traits? (Vol. 1, http://nitro.biosci.arizona.edu/zbook/volume_1/vol1.html) and ?Evolution and Selection of Quantitative Traits? (Vol. 2, http://nitro.biosci.arizona.edu/zbook/volume_2/vol2.html). It will cover a general introduction to quantitative genetics and topics such as resemblance between relatives, detecting genes underlying complex traits, selection, multivariate selection, multivariate response and gene by environment interactions. The course will involve short exercises in both R and Excel throughout so that there will be a mix of both lectures and problem solving. Participants are expected to bring their own laptop. The number of participants is limited to 30. Participants will need to cover their own travel and accommodation costs.

Uppsala, Sweden is located with only 30 minutes to Stockholm- Arlanda international airport (http://www.arlanda.se/en/) and 40 minutes to Stockholm (http://www.visitstockholm.com/en/), the capital of Sweden. Uppsala retains the charm of a small town, population of around 190,000, while offering urban opportunities and attractions.

Please register for the course by sending an email with your name and email address to laurarh@googlemail.com. Last day for registration is 31 December 2011. Registration is processed on a first come first served basis. After successful registration (or a spot on the waiting list) participants will be informed by email within one week.

Lára R. Hallsson, Course organizer, PhD

Animal Ecology/Department of Ecology and Genetics Evolutionary Biology Centre (EBC) Uppsala University Norbyvägen 18D 75236 Uppsala, Sweden e-mail: lara.hallsson@ebc.uu.se

lara.hallsson@ebc.uu.se

USheffield R Jan16-20

There are a few spaces available for external participants on an Advanced Statistics for Biologists Course, using R, at the University of Sheffield, Department of Animal and Plant Sciences, UK. The course runs from 16th - 20th of January 2012 and covers an introduction to using R through to specialised topics for evolutionary and ecological biologists (e.g. generalised linear models, mixed models, survival models etc.).

More details about the course can be found here:

http://www.beckslab.staff.shef.ac.uk/RTP_405_2012/ If you are interested, and/or want more information, please contact me:

a.beckerman@sheffield.ac.uk

Dr. Andrew Beckerman Department of Animal and Plant Sciences, University of Sheffield, Alfred Denny Building, Western Bank, Sheffield S10 2TN, UK ph +44 (0)114 222 0026; fx +44 (0)114 222 0002 http://www.beckslab.staff.shef.ac.uk/ See our new R Book: http://www.r4all.org http://www.flickr.com/photos/apbeckerman/ http://www.warblefly.co.uk a.beckerman@sheffield.ac.uk

UVirginia EvolutionBiol Summer

ANNOUNCING: Summer 2012 Field Courses and

REU Opportunities Mountain Lake Biological Station MLBS.org< http://mlbs.org/ >

Dear Colleagues and Friends,

Mountain Lake Biological Station (University of Virginia) is pleased to announce its summer program of field-based undergraduate and graduate-level credit courses offered by nationally recruited faculty, and its NSF REU undergraduate research internship program, now in its 20th year. Work at MLBS focuses on field-based ecology, evolution, physiology, and behavior. Learn more about the programs and apply on-line:

Courses: Plant Conservation, Field Biology of Sex, Biology of Fishes, Ethnobotany, Stream Ecology, Sculpture and Drawing - http://mlbs.org/summercourses REU: http://mlbs.org/reuprogram Please forward this information to colleagues or students you think might be interested.

Thanks for your help! Best wishes, happy and safe holidays.

**** Learn all about Mountain Lake opportunities at MLBS.org< http://mlbs.org/ > ****

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Butch Brodie

Director, Mountain Lake Biological Station

Executive Vice President, Society for the Study of Evolution

Department of Biology University of Virginia P.O. Box 400328 Charlottesville, VA 22904-4328

bbrodie@virginia.edu http://mlbs.org/ http://-faculty.virginia.edu/brodie/ Yours, Melissa Ivy Wender Office Manager Mountain Lake Biological Station 223 Gilmer Hall 1-434-982-5486 www.mlbs.org miw2m@eservices.virginia.edu

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.