EvolDir

May 1, 2013

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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Amsterdam PlantGenomeEvolution Sep8-10

Plant Genome Evolution 2013 - Amsterdam, The Netherlands

Last month to submit your abstract!

Submit your abstract before Monday, 29 April, 2013

More info: http://www.plantgenomeevolution.com/ It is our pleasure to announce the second Current Opinion Conference on Plant Genome Evolution, to be held in Amsterdam, September 8-10th, 2013. We are delighted to be holding this (now biannual) event again after a very successful first meeting in 2011 where renowned plant researchers gave inspiring talks and where many discussed their latest research in the field.

For the 2013 meeting, which will be at least half a day longer, we are even more ambitious and are trying to put together an even more exciting program focused on plant genomes, natural variation, and systems biology, of course all with a strong emphasis on evolution and evolutionary aspects.

This meeting will be the unique opportunity to meet and discuss with colleagues, get updated on the newest developments and insights in plant genome evolution, and will provide unique possibilities to network and discuss collaborations. Also, we are delighted already that Prof. Doug Soltis (University of Florida, USA) has agreed to deliver the plenary lecture on Sunday, opening the meeting.

On behalf of the Conference Committee, Yves Van de Peer, Ghent University, Belgium J. Chris Pires, University of Missouri, USA Topic List

* (Novel) Genome Projects * Genome evolution * Gene and genome duplication * Genomic views on hybridization, heterosis and speciation * Genomic variation and population genomics * Bioinformatics and Systems Biology

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"Hoogstrate, Marije (ELS-AMS)" <m.hoogstrate@elsevier.com>

Barcelona EuropeanDrosophilaRes Oct16-19

Dear Colleagues,

I'm writing to encourage you, or members of your lab to submit an abstract to the upcoming European Drosophila Research Conference (Barcelona, Oct. 16-19). As you may know, one session is dedicated to Population genetics and Evolution, and will be chaired by Christian Schlötterer, and Benjamin Prud'homme or me. We'd like this session to bring population genetics, quantitative genetics and evo-devo together, not just side by side, but somehow interacting with each other, integrated, intermingled.

In addition, I'd like to draw your attention to a satellite workshop organized by Josefa González and Thomas Flatt in the context of the EDRC. The workshop is called "Creating a European Drosophila Population Genomics Network".

Please note that the deadline for abstract submission is 2 June 2013.

Looking forward to seeing you in Barcelona in October!

Nicolas Gompel.

Nicolas Gompel Institut de Biologie du Développement de Marseille-Luminy CNRS UMR 7288, case 907, Parc scientifique de Luminy 13288 Marseille cedex 9, France Office: + 33 4 91 26 92 06 Fax + 33 4 91 26 97 26 LAB WEBSITE

Nicolas Gompel <nicolas.gompel@univ-amu.fr>

Canberra Biogeography Jan7-11

The International Biogeography Society (IBS) and the Australian National University (ANU) would like to invite you to the INTERNATIONAL BIOGEOGRAPHY SOCIETY EARLY CAREER CONFERENCE 2014.

The conference will take place in Canberra, ACT, Australia between the 7thand the 11 th of January 2014, and is jointly supported by the IBS (http://www.biogeography.org/), the ANU Centre for Macroevolution and Macroecology (http://macroevoeco.com/), and the ANU-CSIRO Centre for Biodiversity Analysis (http://cba.anu.edu.au/). The event aims to bring together early career researchers, along with more experienced scientists, working on many aspects of biogeography.

REGISTRATION AND ABSTRACT SUBMISSION WILL BEGIN IN JUNE 2013.

The schedule of the conference is as follows:

-On the 7th of January, we will offer workshops for a limited number of participants on methods of phylogenetics and modelling species distributions.

-On the following three days (8th-10th of January 2014), talks and posters will be presented by attendees across three symposia:

1.SPECIES DISTRIBUTION ACROSS TIME AND SPACE (Dan Warren - ANU)

2.BIODIVERSITY TURNOVER ACROSS SPATIAL SCALES (Dan Rosauer - ANU)

3.ADVANCES IN PHYLOGENETIC METHODS FOR BIOGEOGRAPHY (Marcel Cardillo, Haris Saslis-Lagoudakis, Peter Cowman - ANU)

-On the final day (11th of January 2014), several field trips will be offered around the region of Canberra.

The conference will be held at ANU Commons (http://commons.anu.edu.au/), on the ANU campus. Workshops will be run at the teaching facilities of the Research School of Biology, ANU, a new complex with purpose build rooms for computer centric workshops. ANU is within a few minutes walk to the main attractions and amenities of Canberra CBD, including restaurants, bars and museums (http://www.visitcanberra.com.au/). Several accommodation options are offered near the venue (http://www.visitcanberra.com.au/Accommodation.aspx). Additional budget accommodation options will be provided for students.

Canberra is the capital of Australia, and is surrounded by beautiful nature, including several nature reserves, where visitors can see many iconic Australian animals (the platypus, koalas, kangaroos, wombats, wallabies), and plants (banksias, eucalypts), as well as cave systems. The coast is only a couple of hours away and Sydney approximately a 3 hour drive.

Student participation will be supported by awards offered by the IBS. More information to follow.

We look forward to welcoming you to Canberra in January 2014!

The ANU Organising Committee

Haris Saslis-Lagoudakis

Peter Cowman

Dan Warren

Dan Rosauer

Marcel Cardillo

ibsconference2014@gmail.com

IBS Early Career Conference 2014 <ibsconference2014@gmail.com>

Cardiff Omics Sep9-11

Announcement: 1st international Environmental Omics Synthesis conference

Cardiff University, UK, 9-11th Sept. 2013

See: http://www.environmentalomics.org/ieos2013 As part of the NERC - Mathematics and Informatics for Environmental 'Omics Data Synthesis directed programme, we are pleased to announce the first in a series of annual conferences. This year the session topics will be

- Learning from the past to inform the future - Ecological 'Omics: from workflows to adaptation - Epigenetics - Evolutionary 'Omics: models and applications - Integrated and Systems 'Omics - Community ecology: from metagenomics to function and synthetic biology

Keynote speakers: - Prof. Eske Willerslev, Centre for GeoGenetics, Natural History Museum of Denmark - Prof. John Colbourne, Chair of Environmental Genomics, University of Birmingham - Prof. Jack Gilbert, Earth Microbiome Project, University of Chicago

Registration open! Abstract submission open!

on behalf of Peter Kille and the iEOS organising committee.

Daniel

– Daniel Barker http://biology.st-andrews.ac.uk/staff/-db60 The University of St Andrews is a charity registered in Scotland : No SC013532

db60@st-andrews.ac.uk

DalhousieU Endocytobiology Aug18-22 2

12th International Colloquium on Endocytobiology and Symbiosis

August 18th - 22nd, 2013 Dalhousie University, Halifax, Nova Scotia, CANADA

FOURTH CIRCULAR (22 April 2013)

DEADLINES NEXT WEEK–REGISTRATION AND ABSTRACT SUBMISSION

APRIL 30 2013: Early registration closes. APRIL 30 2013: Deadline for receipt of presentation abstracts.

Dear Colleagues,

The 12th International Colloquium on Endocytobiology and Symbiosis of the International Society of Endocytobiology (ISE) will be held August 18th to 22nd 2013 at Dalhousie University in Halifax, Nova Scotia, Canada.

There will be registration and an opening reception the evening of Sunday August 18.

Talks will begin the morning of August 19th.

CONFERENCE WEBSITE

http://ices2013.biochem.dal.ca IMPORTANT DATES

April 30 2013: Early registration closes. April 30 2013: Deadline for receipt of presentation abstracts.

The colloquium will cover the latest research on all aspects of endosymbiosis and the biology of endosymbiotically-derived organelles. We look forward to seeing you in Halifax!

Best regards, John Archibald

John Archibald <jmarchib@dal.ca>

Gordon EastonMA BiologicalMechanismsEvolution Jun2-7

Dear colleagues,

There are still places left in the first-ever meeting of this exciting new Gordon Conference! You will see from the program at the link below that this will be an extremely exciting meeting!!

Also, we will be able to offer a reduced rate for new registrations of students in double rooms of $430 ($500 less than the designated conference) until the budget for this is exhausted, so please apply right away. The reduced fee will be allocated upon acceptance of each student application to register. Please spread the word! See you in Massachusetts in June!!

Susan Rosenberg and Christine Queitsch Chair and Vice Chair

Announcing the 2013 Gordon Research Conference on:

Biological Mechanisms in Evolution In Basic Biology, Cancer, Infectious Disease and Medicine

June 2-7, 2013 Stonehill College Easton, MA, United States

Chair: Susan M. Rosenberg

Links: Web Site < http://www.grc.org/programs.aspx?year=2013&program=biomechevo > | Online Application < http://www.grc.org/application.aspx?id=15806 > | RSS Feed < http://www.grc.org/rss/0000764.xml > | Site Information < http://www.grc.org/sites.aspx?id=72 >

If you have any questions or would like further information, please contact Holly Tobin <mailto:htobin@grc.org> , the Conference Operations Associate for this meeting. Please do not reply to this email message, as this account is not monitored.

Susan M Rosenberg, PhD Ben F Love Chair in Cancer Research

Professor, Departments of Molecular and Human Genetics, Biochemistry and Molecular Biology, and Molecular Virology and Microbiology Baylor College of Medicine One Baylor Plaza Rm S809A Mail Stop BCM225 Houston, Texas 77030-3411 USA tel: +1-713-798-6924 http://www.bcm.edu/genetics/?pmid=11034 Assistance: Tammy Reid (treid@bcm.edu, +1-713-798-8730)

NEW Gordon Research Conference!! Biological Mechanisms in Evolution: In Basic Biology, Cancer, Infectious Disease and Medicine Stonehill College, Easton, MA 2-7 June 2013 - Save the date! http://www.grc.org/programs.aspx?year=2013&program=biomechevo "Rosenberg, Susan M" <smr@bcm.edu>

InstitutPasteur Paris IMMEM CallAbstracts

Dear Colleague,

We are pleased to inform you that the call for abstracts is open on the website of the IMMEM-10 conference (http://www.immem-10.org).

You can register and submit your abstract(s) by using the online form available in the "call for abstracts" page. The submission deadline is June 15th, 2013. Your abstract will be reviewed by the Scientific Committee and all presenting authors (for oral or poster presentation) will be notified via email early July 2013.

We recommend all participants to arrange their accommodation in Paris as early as possible. Automn is a high season in Paris, and there are several medical congresses and sporting events in October, in particular, so hotels should be booked early.

Travel grants and free registration can be offered to a number of young scientists (< 36 years). Please see our website.

Sylvain Brisse, Institut Pasteur, Paris, France on behalf of the Organizing Committee *http://www.immem-10.org* *IMMEM-10 topics* The ability of microbes - bacteria, viruses, fungi and parasites - to mutate rapidly, disseminate and adapt to new hosts and environments, forces us to increase our capabilities for the early recognition of novel strains of pathogens, and to understand the factors that contribute to their diversity, evolution and dissemination. IMMEM-10 will address a variety of topics related to pathogen emergence, population-level diversity, evolution of virulence and antibiotic resistance, strain tracking, typing networks, public health and surveillance, novel typing approaches, high-throughput sequencing, genomics, and molecular epidemiology of infectious diseases. The meeting will take place at Institut Pasteur, in the heart of Paris.

Confirmed speakers: Mark Achtman (Warwick Univ., UK) Andrea Ammon (ECDC, Stockholm, Sweden) Siv Andersson (Evol. Biol. Center, Uppsala, Sweden) Alessandra Carattoli (Rome, Italy) Stewart Cole (Global Health Institute, Lausanne, Switzerland) Alex Friedrich (University Medical Center Groningen, The Netherlands) Peter Gerner-Smidt (CDC, Atlanta, USA) Matthew Gilmour (Diagnostic Services Manitoba, Winnipeg, Canada) Hajo Grundmann (University Medical Center Groningen, The Netherlands) Jörg Hacker (German Academy of Sciences Leopoldina, Berlin, Germany) Dag Harmsen (Univ. Hospital Münster, Germany) René Hendriksen (DTU, Copenhaguen, Denmark) Keith Jolley (Oxford Univ., UK) Philippe Lemey (Leuven, Belgium) Martin Maiden (Oxford Univ., UK) Claudine Médigue (CEA, Evry, France) Stefan Niemann (Borstel Univ., Germany) Julian Parkhill (Wellcome Trust Sanger Center, Hinxton, UK) Tim Peto (Oxford, UK) Laurent Poirel (Univ. Paris XI, Kremlin-Bicêtre, France) Marc Struelens (ECDC, Stockholm, Sweden) Anne-Mieke Vandamme (Katholieke Universiteit Leuven, Belgium) François-Xavier Weill (Institut Pasteur, Paris, France)

Scientific Sessions Bioinformatics tools for genome-based microbial surveillance Outbreak genomics and epidemiology Population genetics, phylogenomics, emergence Molecular typing and epidemiology Novel typing methods Surveillance networks in practice Phylodynamics of viral pathogens Crossing of species barriers by viruses Virulence: diagnostic and epidemiology Resistance: diagnostic and epidemiology Diagnostic by high-throughput sequencing Social networks and transmission modelling Strain tracking from global health to One Health

Early fee registration: June 30, 2013 *Standard fee*: 400 â¬ − *Studentfee* : 300*â*¬ ∗ *Abstractsubmissiondeadline*∗ : *June*15, 2013 ∗ *Howtoregister*∗ : *www.immem* − 10.*org*∗*Contactus*∗ : *immem* − 10@*pasteur.fr*

Sylvain BRISSE <sylvain.brisse@pasteur.fr>

Ithaca AGA2013 Jul20-22 SpeciationContinuum

Registration is open for the 2013 Symposium of the American Genetic Association, to be held July 20-22 at Cornell University in beautiful Ithaca, NY – Speciation Continuum: A Discussion on the Origin of Species.

Details and registration are at http://www.certain.com/system/profile/web/index.cfm?PKwebID=0x44728099a8&varPage=home New this year! Membership in the American Genetic Association is included with registration. Already a member? An additional year of membership accompanies registration for current members. See the many perks of membership at http://www.theaga.org/

Speakers include:

Key Distinguished Lecturer: Sergey Gavrilets, University of Tennessee, Deparment of Ecology and Evolutionary Biology

Alex Buerkle, University of Wyoming, Department of Botany Bill Etges, University of Arkansas, Program in Ecology and Evolutionary Biology Rosemary Gillespie, University of California, Division of Organisms and Environment Rick Harrison, Cornell University, Deparment of Ecology and Evolutionary Biology Scott Hodges, University of California, Santa Barbara, Department of Ecology, Evoution, and Marine Biology Jim Mallet, Harvard University, Department of Organismic and Evolutionary Biology and University College London, Department of Genetics, Evolution and Environment Tami Mendelson, University of Maryland, Department of Biological Sciences Sean Mullen, Lehigh University, Deparment of Biological Sciences Mohamed Noor, Duke University, Biology Department Kevin Oh, Cornell University, Department of Neurobiology and Behavior Brett Payseur, University of Wisonsin-Madison, Laboratory of Genetics Katie Peichel, University of Washington, Molecular & Cellular Biology Trevor Price, The University of Chicago, Deparment of Ecology and Evolution Howard Rundle, University of Ottawa, Department of Biology Rebecca Safran, University of Colorado, Deparment of Ecology and Evolution Maria Servedio, University of North Carolina at Chapel Hill, Biology Department Laurie Stevison, University of California, San Francisco, Institute for Human Genetics Sara Via, University of Maryland, Department of Biology John Willis, Duke University, Biology Department

Kerry Shaw, President American Genetic Association mailto:agajoh@oregonstate.edu

agajoh@oregonstate.edu

Ithaca AGA2013 Jul20-22 SpeciationContinuum 2

Early bird registration is open for the 2013 Symposium of the American Genetic Association, to be held July 20-22 at Cornell University in beautiful Ithaca, NY – SPECIATION CONTINUUM: A Discussion on the Origin of Species.

New this year! Membership in the American Genetic Association is included with registration. Already a member? An additional year of membership accompanies registration for current members. Details and registration are at:

http://www.certain.com/system/profile/web/-index.cfm?PKwebID=0x44728099a8&varPage=home If you have problems with this link, please go to the AGA website, http://www.theaga.org/ and click on the symposium logo.

Immediately following the symposium, 23-24 July, will be the workshop, NEXT GENERATION POPULATION GENOMICS FOR NON-MODEL TAXA. AGA student awards available! See http://www.certain.com/system/profile/web/-index.cfm?PKwebID=0x4653687924&varPage=home for details.

Workshop Instructors:

Matthew Hare, Department of Natural Resources, Cornell University Nancy Chen, Department of Ecology & Evolutionary Biology, Cornell University Andy Clarke, Department of Molecular Biology & Genetics, Cornell University Alex Buerkle, Department of Botany, University of Wyoming Pierre De Wit, University of Gothenburg, Sweden

Symposium Speakers:

Key Distinguished Lecturer: Sergey Gavrilets, University of Tennessee, Department of Ecology and Evolutionary Biology Alex Buerkle, University of Wyoming Bill Etges, University of Arkansas Rosemary Gillespie, University of California Rick Harrison, Cornell University Scott Hodges, University of California Jim Mallet, Harvard University and University College London Tami Mendelson, University of Maryland Sean Mullen, Boston University Mohamed Noor, Duke University Kevin Oh, Cornell University Brett Payseur, University of Wisonsin-Madison Katie Peichel, University of Washington Trevor Price, The University of Chicago Howard Rundle, University of Ottawa Rebecca Safran, University of Colorado Maria Servedio, University of North Carolina at Chapel Hill Laurie Stevison, University of California, San Francisco, Institute for Human Genetics Sara Via, University of Maryland John Willis, Duke University

Kerry Shaw, President American Genetic Association

agajoh@oregonstate.edu

Lyon ComparativeGenomics Oct17-19

Eleventh Annual RECOMB Satellite Workshop on Comparative Genomics

October 17-19, 2013, Lyon, France

Website: rcg2013.sciencesconf.org/

Contributions to the workshop are welcomed on any theoretical and/or empirical approach to genome-wide comparison. This includes genome evolution, algorithms for genome rearrangement, comparative tools for assembly, gene identification or annotation, comparison of functional networks, genomic variation in humans and model organisms, cancer genomics, duplication patterns of genes, segments and whole genomes, and comparative epigenetics. We encourage paper submissions that offer new biological findings or otherwise highlight their relevance to biology. Refereed papers will be published as open-access manuscripts in the journal BMC Bioinformatics.

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KEY DATES

Paper submission deadline June 21, 2013

Acceptance notification July 19, 2013

Workshop October 17-19, 2013 - Lyon, France

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CONFIRMED KEYNOTE SPEAKERS

- Tal Dagan, Heinrich Heine Universität, Dusseldorf

- Ludovic Orlando, Centre for GeoGenetics, natural History Museum of Denmark

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THEME AND SCOPE

The continuing advance of DNA sequencing technology has produced an avalanche of genome sequence and genome structural information across the evolutionary spectrum. Transforming that information into biological knowledge requires creative and innovative new computational and statistical methods for comparative genomics.

The RECOMB Satellite Workshop on Comparative Genomics aims to provide the premier forum for new computational developments applied to all aspects of comparative genomics. We solicit contributions on topics including comparison of genome structure and organization, genome function, and evolution. We particularly encourage contributions that use new computational methods to acquire new insight into biological processes. Advances in computational theory are welcome, though all submissions should include genome-scale analyses informed by comparative data.

All peer-reviewed and accepted RECOMB-CG manuscripts will be published in a supplement to BMC Bioinformatics as open-access, author-subsidized, articles.

Specific topics of interest include but are not limited to:

. Gene and genome duplication . Gene family evolution . Genome structural variation . Algorithms for comparative genomics . Genome rearrangements . Ancestral genome reconstruction . Multiple genome alignment . Genome sequence comparison . Modeling genome evolution . Comparative genomics for genome annotation . Gene tree reconciliation . Species and gene tree inference . Comparative metagenomics . Comparative genomics linked to proteomics, metabolomics, and other ˜omic data . Comparative genomics and gene expression and regulation . Applications of comparative genomic methods . Paleogenomics

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CALL FOR PAPERS

Papers should be submitted via the EasyChair system: https://www.easychair.org/conferences/?conf=3Drecombcg13. Submissions must be received in electronic form by 11:59pm (Samoa time), June 21th, 2013.

Papers submitted for review should represent original, previously unpublished work. At the time the paper is submitted to the conference, and for the entire review period, the paper should not be under review by any other conference or scientific journal.

At least one author per each successful submission is required to register and present the paper at the workshop. The paper will be included in the conference proceedings, which will be published in BMC Bioinformatics as open-access author-subsidized articles.

Authors are encouraged to use the BMC document templates when preparing manuscripts. Templates are available in Microsoft and LaTeX formats. Otherwise, submissions should be typeset as double-spaced A4 pages with at least 1-inch margins all around in a minimum of 10 point font. Submissions should be limited to 16 pages, everything included (title, authors, addresses, abstract, references, figures, tables). Exceptions to this limit may be granted by consultation with the Program Committee Chairs. Submissions must include the corresponding author's email address.

When preparing your submission please follow the instructions for authors of BMC supplements: http://www.uff.br/recombcg/docs/Instructions-for-authors-BMC-Appendix-B.pdf . Submitted manuscripts must be rendered to PDF format prior to upload into EasyChair at the review stage.

Address any questions to the program committee chairs: Macha Nikolski macha (at) labri (dot) fr and Yves Van de Peer yves (dot) vandepeer (at) psb (dot) vib (dash) ugent (dot) be

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PROGRAM COMMITTEE

Chairs: Macha Nikolski (LaBRI & CBiB, Université Bordeaux, France) Yves Van de Peer (VIB / Ghent University, Belgium)

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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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Manchester MolecularGenomeEvolution2013 May17 2

Dear Colleagues -

The Fourth Annual Manchester Molecular and Genome Evolution (MaGE) Symposium is fast approaching: Friday 17 May 2013. Registration is free, but necessary, so if you would like to attend then please register at http://tinyurl.com/ManMage2013. We are still accepting abstracts for talks and posters.

This annual symposium is an informal and friendly one-day meeting for those interested in Molecular and Genome Evolution from either the computational or experimental perspective. It will be held in the Michael Smith Lecture theatre in the Faculty of Life Sciences, at the University of Manchester.

This year talks will include: Judith Mank (UCL) on “Sex-specific selection and the genomic basis of sexual dimorphism” Lisa Crossman (TGAC, Norwich) on “Crowdsourcing outbreak genomics: E.coli 2011 and

Chalara Ash Dieback". Terry Brown on "The genotype of a historic strain of Mycobacterium tuberculosis" Rok Krasovec (Knight lab) on "Social interactions determine mutation rate in Escherichia coli" Florence Gutzwiller (Bergman lab) on "Evolution of the plant green-island phenotype and Wolbachia infection in leaf-mining micro-moths" Maria Ninova (Griffiths-Jones lab) on "Lineage-specific microRNAs are expressed in the early development of Drosophila" Jordi Paps (Oxford) on "Exploring the origins and major transitions of the Animal Kingdom with 21st century tools: a comparative genomics approach"

The remaining talks on the day will be chosen from those submitted, with a preference towards student and postdoc presentations, interspersed with the selection of titles from other more senior researchers in Manchester (and beyond). There will be prizes for the best submitted talk and the best poster.

We hope to see you in May!

Many thanks,

Douda Bensasson, PhD Faculty of Life Sciences University of Manchester Michael Smith Building Oxford Road Manchester M13 9PT Tel. +44 (0)161 2755662

Douda Bensasson <douda.bensasson@manchester.ac.uk>

Marseilles 17thEvolBiol Sep17-20 2

We are pleased to inform you that the 17th Evolutionary Biology Meeting at Marseilles will take place on 17-20 September 2013, Marseilles, France.

The following subjects will be discussed:

- Evolutionary biology concepts and modelisations for biological annotation; - Biodiversity and Systematics; - Comparative genomics and post-genomics (at all taxonomic levels); - Functional phylogeny; - Environment and biological evolution; - Origin of Life and exobiology; - Non-adaptative versus adaptative evolution; - The ≪ minor ≫ phyla: their usefulness in evolutionary biology knowledge.

Registration and abstract submission

http://sites.univ-provence.fr/evol-cgr/ Best regards

Marie-Hélène Rome For the 17th EBM meeting committee

Universite EGEE <Egee@univ-provence.fr>

NHM London TropicalBiodiversityGenomics Jun3-4

SYMPOSIUM

Tropical biodiversity in the 21st century: linking taxonomy, genomics and ecological theory

Natural History Museum London, June 3 and 4, 2013

A symposium of the NHM Biodiversity Initiative, in collaboration with the Genomic Observatories Network

This conference and workshop, marking the start of the NHM's Biodiversity Initiative, asks how we can develop inter-disciplinary, genomic approaches to accelerate the study of megadiverse tropical ecosystems and their function.

For updates on the meeting see: http://www.nhm.ac.uk/research-curation/research-initiatives/tropical-biodiversity-symposium/index.html and http://genomicobservatories.blogspot.co.uk/ Contributed talks and posters are welcome.

Confirmed external speakers: Dawn Field, CEH Oxford Johnathan Coddington, Smithsonian Institution Pierre Taberlet, University of Grenoble Douglas Yu, Kunming Institute of Zoology and University of East Anglia Bernhard Misof, Museum Koenig, Bonn Scott Miller, Smithsonian Institution Graham Stone, University of Edinburgh Cristina Banks-Leite, Imperial College London David Coomes, Cambridge University Andres Baselga, University of Santiago de Compostella Rob Ewers, Imperial College London

The Symposium The high diversity of tropical ecosystems remains poorly known and stands to benefit greatly from 'big science' projects and interdisciplinary collaboration. High-throughput sequencing enables the understanding of patterns of diversity at all levels from genes to ecosystems. This will require a global effort to integrate newly generated digital data with the existing, historical information locked away in museum collections. Making full use of these data to unravel the complexity of biodiversity patterns and function will also require the development of new theoretical frameworks. The symposium will gather participants from the fields of genomics, taxonomy, (tropical) ecology and mathematics, to discuss genome-based approaches to studying tropical biodiversity. The symposium will also host a workshop of the Genomic Observatories Network.

Admission is free, but please register on the website.

For enquiries, please send an email to the symposium organizer, Dr Alfried P. Vogler, Department of Life Sciences, Natural History Museum, email: apv@nhm.ac.uk

A.Vogler@nhm.ac.uk

NMNH Washington FrontiersPhylogenetics May20-21

We are pleased to announce the 3rd Annual Spring Symposium hosted by Frontiers in Phylogenetics at NMNH:

“Genome-scale Phylogenetics”

Baird Auditorium, National Museum of Natural History Washington, DC, Monday May 20, 2013

9:30-9:35 Opening Remarks and Logistics Michael Braun, Frontiers in Phylogenetics Program, NMNH

9:35-9:45 Introduction and Welcome to the Smithsonian Eva Pell, Undersecretary for Science, Smithsonian Institution

9:45-10:30 My Students Could Do My Thesis in Five Minutes; How to Cope with the Next Generation Rob DeSalle, Sackler Institute of Comparative Genomics, AMNH

10:30-11:00 Seminar title TBA Erich Jarvis, Duke University Medical Center

11:00-11:30 Break

11:30-12:00 Molecular Phylogenies, Genomics and the Bacterial Species Concept Margaret Riley, University of Massachusetts Amherst

12:00-12:30 Phylotranscriptomics to Bring the Understudied Ostracoda into the Fold Todd Oakley, University of California Santa Barbara

12:30-14:00 Lunch Break

14:00-14:30 Seminar title TBA Jun Wen, Department of Botany, NMNH

14:30-15:00 Genome-scale Phylogenetics of Rapid Adaptive Radiation: RAD Sequence Data Illuminates the History of Lake Victoria Cichlids Catherine Wagner, Eawag, Swiss Federal Institute for Aquatic Science and Technology

15:00-15:30 Break

15:30-16:00 Shotgun in the Dark or a Rifle in the Daylight? The Case for Using Single Copy Orthologous Gene Capture in Phylogenetics Gavin Naylor, Hollings Marine Lab, College of Charleston and Medical University of South Carolina

16:00-16:30 Achieving phylogenomic nirvana: ultraconserved elements (UCEs) capture history at the species, population, and individual levels Brant Faircloth, Department of Ecology and Evolutionary Biology, UCLA

16:30-17:00 Unsolved Challenges- Panel Discussion on Future Directions

In addition, on May 21, there will be several interactive discussion groups aimed at current issues and hurdles involved with executing phylogenetic research on the genome scale.

Admission is free but registration is required.

Please register using the following link: https://docs.google.com/forms/d/-1psN38yqyZz7mpgQqC8DczlHuqstfWQisQoRQSnqvO8M/-viewform Hope to see you there,

Sarah Kingston

Postdoctoral Researcher Smithsonian Institution, NMNH kingstons@si.edu 843.324.4909

“Kingston, Sarah” <KINGSTONS@si.edu>

Portugal EcologicalSpeciation Apr29-30 Broadcast

Conference: Portugal.Ecological_Speciation.Apr29-30

ADVANCES IN ECOLOGICAL SPECIATION (AES) Conference, CIBIO/UP, Portugal, 29-30 April 2013

LIVE BROADCAST of the AES Conference!

We are happy to announce that the AES Conference can be followed Live on streaming from http:/-/tv.campusdomar.es/directo.html If you want to join us please check out the program of the AES Conference from our website (http://www.aes-cibio.org/-). The Live broadcast will be on Portugal local time (UTC/GMT+1hour).

Invited Speakers:

Dolph Schluter (Biodiversity Research Centre and Zoology Department, University of British Columbia, Vancouver, Canada) Felicity Jones (Friedich Miescher Laboratory of the Max Planck Society, Tubingen, Germany) Walter Salzburger (Zoological Institute, University of Basel, Switzerland) Sebastien Renaut (Botany Department, University of British Columbia, Vancouver, Canada) Roger Butlin (Department of Animal and Plant Sciences, University of Sheffield, UK)

You can also follow the AES Conference on:

https://www.facebook.com/-AdvancesInEcologicalSpeciation https://twitter.com/-aes_cibio Please join us!

jmeloferreira@cibio.up.pt

SanFrancisco EvolCancer Jun12-16

THE SECOND INTERNATIONAL BIENNIAL EVOLUTION AND CANCER CONFERENCE UNIVERSITY OF CALIFORNIA SAN FRANCISCO JUNE 12-16, 2013

The Second International Biannual Evolution and Cancer Conference (IBECC) hosted by the Center for Evolution and Cancer (CEC) and the Helen Diller Family Comprehensive Cancer Center at the University of California San Francisco, will take place in San Francisco at the UCSF Mission Bay Campus, June 12-16, 2013. IBECC 2013 will bring together experts in cancer biology, oncology, evolutionary theory, microbial evolution, and the evolution of multicellularity, from across the world to address the applications of evolution to cancer research and management. The theme of IBECC 2013 is “From Unicellularity to Multicellularity and Back Again.” The two foci are: 1) cancer suppression in the evolution of multicellularity and 2) applying insights from the evolution of unicellular organisms to the study of cancer. IBECC 2013 will feature a Vision Keynote Speech by former Deputy Director of the National Cancer Institute Anna Barker, Keynote Speaker Mel Greaves a public lecture by Carl Zimmer, plenary talks by Ken Pienta, Judy Campisi, Andrew Read, and David Queller, and a special performance by Baba Brinkman of “The Rap Guide to Evolution” with a new song about evolution and cancer.

EARLY REGISTRATION and ABSTRACT submissions end APRIL 20th.

Sessions include:

Insights from Experimental Evolution Cancer and the Evolution of Multicellularity Dynamics of Somatic Evolution Peto’s Paradox, Comparative Oncology and the Evolution of Tumor Suppression Somatic Mutation and Levels of Selection Applying the Tools of Evolutionary Biology to Cancer Life History Theory in Cancer The Evolutionary Medicine of Cancer

For more information - including the Conference POSTER - go to http://cancer.ucsf.edu/evolution/-conference-2013 . Aurora M. Nedelcu University of New Brunswick Department of Biology PO Box 4400 Fredericton, NB Canada E3B 5A3 phone: (506) 458-7463

anedelcu@unb.ca

SanFrancisco EvolCancer Jun12-16 DeadlineExtended

THE SECOND INTERNATIONAL BIENNIAL EVOLUTION AND CANCER CONFERENCE UNIVERSITY OF CALIFORNIA SAN FRANCISCO JUNE 12-16, 2013

EARLY REGISTRATION AND ABSTRACT SUBMISSION EXTENDED TO MAY 10TH

Please join us for the Second International Biannual Evolution and Cancer Conference, $B!H(BFrom Unicellularity to Multicellularity and Back Again$B!I(B at the University of California, San Francisco, June 12-16, 2013 (IBECC 2013). Following the success of the first IBECC in 2011, we are again bringing together leaders in cancer biology and evolutionary theory to address cancer treatment and prevention from an evolutionary perspective, including applications to patient care. This year$B!G(Bs conference features international leaders cancer biology, evolutionary theory, the evolution of multicellularity and the growing field of Evolutionary Medicine. Session topics include comparative oncology, insights from experimental evolution, and somatic evolution during cancer progression. In addition to talks from the experts in the field, IBECC 2013 has been planned with long breaks for establishing collaborations, a poster session, a public lecture by Carl Zimmer and a concert by Baba Brinkman (featuring a new song about Evolution and Cancer).

Early registration and abstract submission has been extended to May 10th. Please forward this message to collaborators and colleagues who might be interested in attending or submitting a poster. Registration includes conference attendance, Continuing Medical Education (CME) credit, lunches, refreshments and shuttle transportation to and from the conference hotel. Email IBECC2013@evolutionandcancer.org with questions or to inquire about travel awards for underrepresented minorities. Please go to the conference website to register, submit an abstract, see the tentative program, or find hotel and travel information.

IBECC2013 Conference website: http://cancer.ucsf.edu/evolution/conference-2013 Yours,

Carlo Maley Center for Evolution and Cancer Director

Athena Aktipis Human and Social Evolution Director @ CEC

Aurora Nedelcu Education and Outreach Director @ CEC

Aurora M. Nedelcu University of New Brunswick Department of Biology PO Box 4400 Fredericton, NB Canada E3B 5A3 phone: (506) 458-7463

Aurora Nedelcu <anedelcu@unb.ca>

Snowbird Utah Evol2013 Jun21-25 DeadlineExtended

Deadline is Monday! >>>Reminder: Please REGISTER if you are a presenting author on a poster or talk. Presentations with unregistered presenters will be removed from the program.

The deadline for submitting titles for presentations* at Evolution 2013 in Snowbird is April 22. http://www.evolutionmeeting.org/Register2013.html#presub *Abstracts are required only if you are applying for an award.

The early registration deadline for Evolution 2013 in Snowbird is April 22. http://www.evolutionmeeting.org/Register2013.html EVOLUTION 2013 - THE ANNUAL EVOLUTION MEETING, JOINTLY SPONSORED BY THE AMERICAN SOCIETY OF NATURALISTS (ASN), THE SOCIETY OF SYSTEMATIC BIOLOGISTS (SSB) AND THE SOCIETY FOR THE STUDY OF EVOLUTION (SSE): http://www.evolutionmeeting.org/ REGISTRATION AND TALK TITLE SUBMISSION IS NOW OPEN -The meeting schedule will follow that of recent years with a few modifications -On Monday there will be a 1/2 day recess for recreation and field trips -There will be an all-society mixer/award ceremony instead of a banquet on Tuesday evening INCLUDED with your registration fee

The meeting will be held June 21-25, 2013 at the Meeting and Conference Center Snowbird, Utah, USA. The Snowbird Conference Center and Alpine Pedestrian Village is located at 2365 m (7,760 ft) elevation, just a short distance from Salt Lake City International Airport in Little Cottonwood Canyon on the west slope of the Wasatch Range of the Rocky Mountains. Recreation opportunities abound in and near the village/conference site with easy access to hiking, biking, and skiing (conditions permitting). All lodging, meeting rooms, restaurants, shopping, and childcare facilities are just a few minutes walk from each other and all located within the village. Snowbird is surrounded by spectacular views of mountain slopes covered with alpine meadows, cottonwoods, conifers, and impressive rock formations.

RESERVATIONS FOR LODGING IN THE SNOWBIRD ALPINE VILLAGE CAN NOW BE MADE -For reservations by phone please call 800-453-3000 -Please remember to mention "EVOLUTION 2013" when you reserve by phone. -Your reservation for lodging with Snowbird helps reduce registration costs

STUDENT PARTICIPATION IS SUPPORTED BY STUDENT AWARDS OFFERED BY THE SOCIETIES (ASN, SSB, AND SSE) AND BY VOLUNTEER OPPORTUNITIES FOR STUDENTS WITH SOCIETY AFFILIATION TO HELP WITH THE MEETING IN EXCHANGE FOR FREE REGISTRATION

We look forward to welcoming you to Evolution 2013

SEE YOU IN SNOWBIRD!

The Snowbird Organizing Committee (Drs. Fenster, Dudash and Cruzan)

cruzan@pdx.edu

Snowbird Utah Evol2013 Jun21-25 Housing

If you have had any trouble obtaining suitable accommodations for the Evolution 2013 meetings in Snowbird please call the Snowbird reservations line: 800-453-3000 They now have new availability for a range of room options.

EVOLUTION 2013 - THE ANNUAL EVOLU-

TION MEETING, JOINTLY SPONSORED BY THE AMERICAN SOCIETY OF NATURALISTS (ASN), THE SOCIETY OF SYSTEMATIC BIOLOGISTS (SSB) AND THE SOCIETY FOR THE STUDY OF EVOLUTION (SSE): http://www.evolutionmeeting.org/ REGISTRATION AND TALK TITLE SUBMISSION IS NOW OPEN -The meeting schedule will follow that of recent years with a few modifications -On Monday there will be a 1/2 day recess for recreation and field trips -There will be an all-society mixer/award ceremony instead of a banquet on Tuesday evening INCLUDED with your registration fee

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cruzan@pdx.edu

Snowbird Utah Evol2013 Jun21-25 MSI Deadline

DEADLINE APPROACHING! Evolution 2013 MSI Faculty Travel Award

Are you a faculty member at a minority-serving institution (MSI)? Apply now for a travel award to attend Evolution 2013 < http://www.evolutionmeeting.org/index.html > in Snowbird, Utah.

The National Evolutionary Synthesis Center (NESCent < http://www.nescent.org/ >), with support from the Society for the Study of Evolution (SSE < http://www.evolutionsociety.org/ >), is pleased to announce travel awards for faculty from Minority Serving Institutions to attend Evolution 2013, as part of our continuing outreach efforts focusing on groups that are underrepresented in evolutionary science.

If you are a faculty member at an MSI, HBCU or other institution with significant enrollment of underrepresented minority students, you are encouraged to apply. Funds are available to cover conference registration, travel, food and lodging.

This award is intended to provide MSI faculty with an opportunity to present original research in evolution, systematic biology, evolutionary genomics/informatics, evolution education/outreach or other disciplines typically represented at the Evolution meetings. As such, your application must include a talk/poster title and abstract. In addition, you will be asked to provide a brief (1 page) statement describing how this award will contribute to your professional/scientific development, as well as provide benefit to your students and institution.

To apply, please visit www.nescent.org/Evo2013facultyapp Application Deadline THIS FRIDAY: April 5th, 2013 (Awards will be announced by April 12th, 2013)

For more information, please contact Dr. Jory Weintraub (jory@nescent.org)

Jory P. Weintraub, PhD Assistant Director, Education & Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200, Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: jory@nescent.org Skype: jory.weintraub

“Weintraub, Jory P” <lviscrst@live.unc.edu>

Snowbird Utah Evol2013 Jun21-25 PresentationDeadline

The deadline for submitting titles for presentations at Evolution 2013 in Snowbird is April 19. http://www.evolutionmeeting.org/Register2013.html#presub

The early registration deadline for Evolution 2013 in Snowbird is April 19. http://www.evolutionmeeting.org/Register2013.html EVOLUTION 2013 - THE ANNUAL EVOLUTION MEETING, JOINTLY SPONSORED BY THE AMERICAN SOCIETY OF NATURALISTS (ASN), THE SOCIETY OF SYSTEMATIC BIOLOGISTS (SSB) AND THE SOCIETY FOR THE STUDY OF EVOLUTION (SSE): http://www.evolutionmeeting.org/ REGISTRATION AND TALK TITLE SUBMISSION IS NOW OPEN -The meeting schedule will follow that of recent years with a few modifications -On Monday there will be a 1/2 day recess for recreation and field trips -There will be an all-society mixer/award ceremony instead of a banquet on Tuesday evening INCLUDED with your registration fee

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SEE YOU IN SNOWBIRD!

The Snowbird Organizing Committee (Drs. Fenster, Dudash and Cruzan)

cruzan@pdx.edu

Snowbird Utah Evol2013 Jun21-25 RegistDeadline

Deadline is Friday! The deadline for submitting titles for presentations* at Evolution 2013 in Snowbird is April 19. http://www.evolutionmeeting.org/Register2013.html#presub *Abstracts are required only if you are applying for an award.

The early registration deadline for Evolution 2013 in Snowbird is April 19. http://www.evolutionmeeting.org/Register2013.html EVOLUTION 2013 - THE ANNUAL EVOLUTION MEETING, JOINTLY SPONSORED BY THE AMERICAN SOCIETY OF NATURALISTS (ASN), THE SOCIETY OF SYSTEMATIC BIOLOGISTS (SSB) AND THE SOCIETY FOR THE STUDY OF EVOLUTION (SSE): http://www.evolutionmeeting.org/ REGISTRATION AND TALK TITLE SUBMISSION IS NOW OPEN -The meeting schedule will follow that of recent years with a few modifications -On Monday there will be a 1/2 day recess for recreation and field trips -There will be an all-society mixer/award ceremony instead of a banquet on Tuesday evening INCLUDED with your registration fee

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We look forward to welcoming you to Evolution 2013

SEE YOU IN SNOWBIRD!

The Snowbird Organizing Committee (Drs. Fenster, Dudash and Cruzan)

Snowbird Utah Evol2013 Jun21-25 UndergradDiversity

Undergraduate Diversity at Evolution 2013

We are pleased to announce an undergraduate travel award to bring talented and diverse undergraduates to the Evolution meetings this June 21-25 in Snowbird, Utah. For the 11th year in a row we will fly a cohort of undergraduates from throughout the US and Puerto Rico to present a poster at the meetings, receive mentoring from graduate students, postdocs and faculty, and participate in a career-oriented ’Undergraduate Futures in Evolutionary Biology’ panel and discussion. The program covers the costs of travel, registration, food and accommodation at the meetings.

The application deadline is THIS FRIDAY, April 5th, and decisions will be announced by Friday, April 12th. Applications are welcomed from all undergraduates, and the admissions goal is to create a diverse pool of students.

An overview of the program and student eligibility, and a link to the online application can be found at:

www.nescent.org/eog/undergraddiversity Applications consist of a short statement of interest, a letter of recommendation and the title and abstract of the poster to be presented.

In addition, we will be soliciting names of graduate students, postdocs and faculty members who would like to serve as mentors during the meetings. Mentors meet with pairs of students and attend talks with them, introduce them to colleagues, network and generally make the meetings a welcoming place for them. Although costs are not covered for mentors it is an unusually rewarding experience. Contact Richard Kliman (rmkliman@cedarcrest.edu) if you are interested in serving as a mentor.

For inquires contact one of the organizers:

Scott Edwards - sedwards@oeb.harvard.edu

Richard Kliman - rmkliman@cedarcrest.edu

Jory Weintraub - jory@nescent.org

Jory P. Weintraub, PhD Assistant Director, Education & Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200, Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: jory@nescent.org Skype: jory.weintraub

“Weintraub, Jory P” <lviscrst@live.unc.edu>

UCalifornia Irvine WesternEvolBiol May11

The WEB (Western Evolutionary Biology) 5 Meeting will take place on the University of California, Irvine, campus on Saturday, May 11, starting at 10:00am. Registration is free and on-line, and is open to anyone who wishes to attend. Registration is due April 22nd, and abstracts are due April 29th.

Individuals associated with the UCs may be able to get their travel to Irvine covered, within reason. Contact your campus NERE Associate director for more information about travel.

Also, please check out our website: http://www.lifesci.ucsb.edu/nere-web/ Thanks, Des Ramirez UCSB NERE intern

Desmond Ramirez <des.ramirez@lifesci.ucsb.edu>

UHawaii Hilo ConservationBiol May13-15

Dear Friends and Colleagues,

Mark your calendars for the 5th Annual Research Symposium sponsored by the Tropical Conservation Biology & Environmental Science (TCBES) Program at the University of Hawaii at Hilo (http://tcbes.uhh.hawaii.edu/index.html). Over two engaging days of presentations about recent scientific research carried out in Hawaii from *May 13-15, 2013 *(Monday through Wednesday). The public is also invited to join us.

Whether you are a graduate or undergraduate student, resident or visiting faculty or student, or agency personnel, we invite you to present and listen to the latest research in TCBES!

Call For Presentations

We are now accepting applications to present a talk or poster. Research presentations in ecology, evolution, environmental science, and conservation biology related to Hawaii and the Pacific region are welcome. Studies examining the relationship between human communities and cultures, and environmental issues are also encouraged. *The deadline for submitting abstracts is 3 May 2013.*

Our goal is to increase undergraduate and graduate student participation in both the oral and poster presentation sessions. To encourage widespread participation, we are offering this event free of charge, and will be awarding prizes for outstanding presentations in various categories.

See the TCBES Research Symposium Registration page (http://tcbes.uhh.hawaii.edu/registration.html) for more information.

< http://tcbes.uhh.hawaii.edu/page23.html >

Dr. Donald Price Director TCBES Graduate Program Professor of Biology University of Hawaii at Hilo Hilo, HI 96720

donaldp@hawaii.edu http://tcbes.uhh.hawaii.edu/ http://www.hawaii.edu/uhhbiology/ http://www2.hawaii.edu/~donaldp/ donaldp@hawaii.edu

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UMontreal MathematicsOfBiodiversity Sep16-20

Mathematics for an evolving biodiversity September 16-20, 2013 CRM, Montréal (Canada)

http://www.crm.umontreal.ca/2013/Biodiversity13/index_e.php Hosted by the Center for Mathematical Research in Montréal (Canada), in the context of MATH FOR PLANET EARTH YEAR 2013 < http://mpe2013.org/ >

Organizers : Jonathan Davies (McGill), Amaury Lambert (UPMC Univ Paris 6 and Collège de France), Nicolas Lartillot (Montréal)

Early-bird registration: deadline May 15, 2013.

Contributed talks and posters are welcome.

List of invited speakers

Graham Bell (McGill University) Troy Day (Queen's University) Rampal S. Etienne (University of Groningen) Régis Ferrière (Université Pierre et Marie Curie (Paris 6)) Sergey Gavrilets (University of Tennessee) Emma Goldberg (University of Illinois) Luke Harmon (University of Idaho) Stephen Hubbell (UCLA) Steven Kembel (UQAM) Mark McPeek (Dartmouth College) Arne Mooers (Simon Fraser University) Mark Pagel (University of Reading) Todd Parsons (Univ. Pierre et Marie Curie (Paris 6)) Pedro Peres-Neto (UQAM) Daniel Rabosky (University of Michigan) Richard Ree (Field Museum of Natural History) Liam Revell (University of Massachusetts Boston) Robert Ricklefs (University of Missouri at St. Louis) James Rosindell (Imperial College) Mike Steel (University of Canterbury)

Conference agenda

This workshop will provide an overview of recent theoretical and methodological developments for modeling the complex evolutionary dynamics that have shaped the structure of contemporary biodiversity. Theoretical work at the interface between ecology and evolutionary studies will be presented, as well as its applications to empirical data. This will include mathematical and probabilistic modeling, statistical methodologies, and new insights obtained from biological data. Accordingly, the workshop will gather a variety of participants within the fields of probability, statistics, ecology and evolutionary biology, and working on the following themes:

- Likelihood-based phylogenetic tests of macroevolutionary hypotheses, based on models of diversification patterns incorporating density dependence, heterogeneity among lineages and species selection effects, as well as various models of trait evolution.

- Ecophylogenetics, and theories such as the neutral theory of biodiversity, for deriving macroevolutionary models of species distribution and turnover from first principles of community ecology.

- Adaptive dynamics and other models of evolving biodiversity, for linking micro-evolution and adaptation with global ecological patterns.

- Probabilistic models of phylogeography, and their role in our understanding of biodiversity gradients.

You might also be interested in the workshop on 'Mathematics and Sequence Evolution: Biological Models and Application', organized by Mathieu Blanchette (McGill) and Hervé Philippe (Montréal), which will take place the following week, September 23-27 2013, in Montréal, also in the context of the thematic semester on biodiversity and evolution organized by the Center for Mathematical Research: <http://www.crm.umontreal.ca/act/theme/theme_2013_2_en/mathematics_sequence_ evolution13_e.php>. You may want to make the most of your time in Montréal and attend both events.

Nicolas Lartillot <nicolas.lartillot@umontreal.ca>

UNotreDame ArthropodGenomics Jun12-15 3

7th Annual Arthropod Genomics Symposium: ARTHROPOD GENOMICS 2013 ONWARD

EXTENDED DATES!! Friday, April 19, 2013: Early Bird Registration Deadline Friday, April 19, 2013: Submit Poster Abstracts Due

The 7th Annual Arthropod Genomics Symposium and VectorBase Workshop will be held from June 12 - June 15, 2013, and is hosted by the Eck Institute for Global Health at the University of Notre Dame.

The VectorBase Workshop will begin early afternoon on Wednesday, June 12, 2013, and conclude late afternoon on Thursday, June 13, 2013.

The Arthropod Genomics Symposium will begin Thursday evening, June 13, 2013, and conclude late afternoon on Saturday, June 15, 2013 (an optional dinner is scheduled for Saturday night).

To register for the Arthropod Genomics Symposium or view more information visit:

http://globalhealth.nd.edu/7th-annual-arthropod-genomics-symposium/ "Eck Institute for Global Health - (eigh)" <eigh@nd.edu>

UStAndrews InsectMatingEvolution Sep4-6

EXTENDED DEADLINE FOR TALK & POSTER ABSTRACTS: 1st JUNE 2013

Ento '13 International Symposium and Annual National Science Meeting

"Thirty years of Thornhill & Alcock: The Evolution of Insect Mating Systems"

We are pleased to invite you to come to St Andrews this September for ENTO '13. ENTO '13 will comprise both the International Symposium and the National Science Meeting of the Royal Entomological Society.

Venue: University of St Andrews, Scotland

The International Symposium will celebrate 30 years of Thornhill and Alcock's ground-breaking book "The Evolution of Insect Mating Systems". The book has had an enormous impact on multiple generations of entomologists and behavioural ecologists, and we will celebrate that achievement and explore the progress we have made in understanding insect mating systems and reproductive behaviour since 1983. The International Symposium will take the form of invited plenary sessions on the mornings of the 4th, 5th and 6th September.

Symposium speakers include: Göran Arnqvist (Uppsala), Boris Baer (Western Australia), Bruno Buzatto (Western Australia), Doug Emlem (Montana), John Hunt (Exeter), Hanna Kokko (ANU), Trish Moore (Georgia), Ben Normark (UMASS), Mike Ritchie (St Andrews), Leigh Simmons (Western Australia), Per Smiseth (Edinburgh), Rhonda Snook (Sheffield), Nina Wedell (Exeter), and Marlene Zuk (Minnesota)

The National Science Meeting will comprise a series of themed sessions as well as general entomology sessions open to talks on any entomological topic. Oral presentations and poster presentations are invited for the themed or open sessions.

The National Science Meeting will take place on the afternoons of the 4th, 5th and 6th September. Depending on the presentations offered by delegates, sessions may be combined or delegates may be asked to present a poster instead of a talk (or vice versa). Talk slots will be 20 minutes long, inclusive of time for questions.

Themed Sessions: Sexual Selection in Insects (session chair Dr Luc Bussiere, plenary speaker Prof Darryl Gwynne) Nuptial gifts in insects (session chair Prof Karim Vahed, plenary speaker Prof Sara Lewis) Beneficial Insects: Biological Control and Beyond (session chair Prof Leo Beukeboom) Entomology for the Masses: Impact and Outreach (session chair Dr Pete Smithers) Insect Genomics (session chair Dr Dan Lawson) Pollinator Behaviour, Ecology and Evolution Insect Community Ecology

For registration (including booking accommodation) and submission of abstracts for talks and posters, as well as details about national and international travel to St Andrews, please visit the ENTO '13 website: http://www.royensoc.co.uk/content/ento-13-4-6-september-2013 For further information, please email David Shuker: ento13@st-andrews.ac.uk

EXTENDED DEADLINE FOR TALK & POSTER ABSTRACTS: 1ST JUNE 2013

Dr David M Shuker School of Biology University of St Andrews Harold Mitchell Building St Andrews KY16 9TH UK

Tel: +44 1334 463376 Fax: +44 1334 464466

Email: david.shuker@st-andrews.ac.uk

Website: http://insects.st-andrews.ac.uk dms14@st-andrews.ac.uk

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Valencia EvolutionAcousticSignals Jul3-6 CallAbstracts

Preamble: Acoustic communication within and between species reflects evolutionary processes, including the effects of evolutionary constraint. This summer in Valencia, Spain, we will be hosting a symposium on the "Neuroethology and biomechanics of acoustic communication in vertebrates", where the focus will be on the mechanisms, functions, and evolution of acoustic signals in vertebrates.

CALL FOR SUBMISSION OF ABSTRACTS

"Neuroethology and biomechanics of acoustic communication in vertebrates"

Special symposium at the annual meeting of the Society for Experimental Biology July 3-6, 2013 in Valencia, Spain.

Organizers: Coen P. H. Elemans and John M. Ratcliffe, University of Southern Denmark (coen@biology.sdu.dk, jmr@biology.sdu.dk)

Abstract deadline: May 3rd, 2013 (talks and posters)

For abstract submission, registration and more info: http://www.sebiology.org/meetings/Valencia/Valencia.html Keynote speakers: Andrew H. Bass (Cornell University) W. Tecumseh Fitch (University of Vienna)

Confirmed Speakers Ana Amador (University of Buenos Aires) Marcel van der Heijden (University of Rotterdam) Christian Herbst (University of Vienna) Nicole Kime (Edgewood College) Peter T. Madsen (University of Ãrhus) David Reby (University of Sussex) Roderick A. Suthers (University of Indiana)

Summary Sound communication is fundamental to many social interactions and essential to courtship and agonistic behaviors in a great variety of vertebrates, including man. Close to 10,000 species of birds, 5,000 species of frogs, 5,000 species of mammals, and a yet unknown number of fish, produce a multitude of sounds, ranging from clicks and grunts, howls and whistles, the precise and rapid modulations of sound amplitude and frequency in echolocation signals, to complex, learned languages.

Sound production and perception involves complex interactions between sensory systems, musculoskeletal dynamics and the brain, which can result in behaviors of both dazzling complexity and simple elegance.

These sessions will include world-leading researchers presenting on the state of the art and the future of the field. Recent advances will be illustrated by some of the most successful experimental animal models used to better understand the neural basis and biomechanics of sound communication.

< http://www.sebiology.org/meetings/Valencia/Valencia.html >

< http://www.facebook.com/pages/Society-for-Experimental-Biology/166761543400758 > < https://twitter.com/#!/SEBiology >

John Morgan Ratcliffe <jmr@biology.sdu.dk>

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BangorU SalmonIntrogression

The Molecular Ecology and Fisheries Genetics Laboratory (MEFGL: http://mefgl.bangor.ac.uk/)., School of Biological Sciences, Bangor University, UK invites applications for a 3-year PhD studentship recently awarded by the EU and linked to the project "AQUATRACE".

Background to Project The studentship is linked to AQUATRACE where the primary focus is to conduct growth and survival experiments with farmed and wild Atlantic salmon. Genetic changes associated with domestication in aquaculture pose an increasing threat to the integrity of native fish gene pools. Consequently, there is a bourgeoning need for the development of molecular tools to assess and monitor the genetic impact of escaped or released farmed fish. In addition, exploration of basic links between genetic differences among farmed and wild fish and differences in important life-history traits with fitness consequences are crucial prerequisites for designing biologically informed management strategies. The project AQUATRACE will establish an overview of current knowledge on aquaculture breeding, genomic resources and previous research projects for several marine species. The project will apply cutting-edge genomic methods for the development of high-powered, cost-efficient, forensically validated and transferable DNA-based tools for identifying and tracing the impact of farmed fish in the wild.

Aim and objectives The aim of the PhD project is to elucidate the underlying genetic differences between wild and farmed fish, and the fitness consequences of introgression between them. Some biological experiments are underway at the Institute of Marine Researchs experimental fish-farm located just outside Bergen, Norway, thereby providing advanced bespoke facilities and progress. Additional experiments will be started by the student in the autumn of 2013. The PhD student will spend most time in Bangor, but will travel to Norway 2-3 times per year, to conduct practical work associated with the experiments (co-supervisor Dr K Glover). In addition to handling and sampling fish, the candidate will take tissue samples for subsequent DNA parentage testing, and ultimately reaction norm statistical analysis. For a suitable candidate, there may also be an opportunity to participate in quantitative trait loci mapping of fitness traits (e.g. survival, growth), including the analysis of single nucleotide polymorphisms (SNPs) in Bergen. The student will benefit from joining other members/students of the consortium at workshops, and will be encouraged to integrate his/her findings into the wider context of the project.

Requirements and Eligibility

The ideal candidate will have a first or upper second class degree in zoology/biological sciences and related fields or an MSc in a relevant discipline. Some experience and interests in handling fish in an experimental setting and an aptitude for quantitative and statistical analyses are ideally required.

Host details: Bangor is located in North West Wales, situated in an area of outstanding natural beauty between Snowdonia National Park and the sea. The successful applicant will join the large, thriving team in the MEFGL, one of the largest research areas within the University. Housed within the new Environment Centre Wales Building, the MEFGL benefits from fully equipped molecular labs, second and third generation sequencing capability at the Liverpool Centre for Genome Resarch and bioinformatic development capability on the HPC Wales supercomputing genomics gateway. The MEFGL at Bangor has recently hosted several "firsts" in fish and fisheries genetics, such as generating the first gene-associated markers for tackling illegal fishing and securing eco-certification of fish products (Nature Communications, and available at http://www.nature.com/ncomms/journal/v3/n5/pdf/ncomms1845.pdf) and the first direct evidence that experimental harvesting of fish populations drives genetically based shifts in body size and maturation. The paper is published in Frontiers in Ecology and the Environment (http://www.esajournals.org/toc/fron/0/0). More information can be found at: http://www.bangor.ac.uk/news/full.php.en?nid=3D12593&tnid=3D12593, including BBC coverage - http://www.bbc.co.uk/news/uk-wales-21813736, and on BBC Radio Wales at http://www.bbc.co.uk/news/uk-wales-21827080. In addition to training in population and quantitative genetics, linked to conceptual evolutionary theory, conservation genetics and fisheries biology, the student would undertake formal University training in research skills and methods.

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Bergen Norway ComparativeEvoDevo

PhD Position Comparative development of mesodermal cell types in invertebrates±

A 3-year PhD position is offered in the framework of the FP7 Marie Curie Initial Training Network (ITN) NEPTUNE Multidisciplinary training in evo-devo and neurobiology of marine animal models± (http://neptune-itn.eu). The network unites 8 leading European labs with complementary expertise in evolutionary developmental biology, bioinformatics, functional neurobiology, and palaeontology and the industrial partners Sigma-Aldrich and Carl Zeiss Microscopy, specialised in advanced genetic manipulation technology and Lightsheet Fluorescence Microscopy.

The project will be conducted at the Sars International Centre of Marine Molecular Biology (Bergen, Norway) in the group Comparative Developmental Biology of Animals± of Dr. Andreas Hejnol and through short-term visits in the partner laboratories of NEPTUNE. The Hejnol group studies a broad range of mainly marine invertebrates using genomic, embryological, and advanced microscopic and molecular methods. The successful candidate will study a diverse range of invertebrate taxa with the goal to reconstruct the evolution of mesodermal organ systems such as the circulatory system, nephridia, muscles. The project will also address the evolution of the molecular patterning underlying the specialization of mesodermal cell types. The Sars Centre is a department of Uni Research AS < http://www.uni.no/ >, affiliated with the University of Bergen < http://www.uib.no/info/english/ >, and a partner of the European Molecular Biology Laboratory (EMBL) < http://www.embl.de >. The Sars Centre is focused on basic research in marine molecular biology, developmental biology and evolution. The institute has employee insurance and pension agreements and is an equal opportunity employer. The appointee will have the opportunity to enrol in the University of Bergens Molecular and Computational Biology Research School (MCB) < http://www.uib.no/rs/mcb > PhD program.

Applicants are required to have experience in molecular biology and imaging techniques and interest in evolution. The position is available from June 2013 and is according to the Marie Curie Early Stage Researcher (ESR) mobility rules open only to individuals who have spent less than 12 months in Norway in the last three years. In addition, applicants must be in the first four years (full-time equivalent) of their research careers and not yet have been awarded a doctoral degree. This is measured from the date when they obtained the degree that would formally entitle them to embark on a PhD program, in the country in which the degree was obtained. The starting salary for this PhD position is grade 48 (code 1017/LR 20.8) in the Civil Service pay grade table, currently NOK 391,300 gross p.a.; following ordinary meriting regulations.

For further information regarding the position and scientific content of the project please contact the Group Leader, Dr. Andreas Hejnol (email andreas.hejnol@sars.uib.no, phone +47 55 58 43 05). For information about the Marie Curie ITN granting requirements see FP7 Marie Curie People site < http://ec.europa.eu/research/mariecurieactions/-about-mca/actions/itn/index_en.htm >. Written applications, in English, should include a C.V., summary of educational and work experience, a statement describing your scientific interests, expression of interest for the position and contact information for two references. Applications marked 13Sars_05. can be mailed to: Human Resource Officer, Sars Centre, Bergen High Technology Centre, Thorm©hlensgt. 55, NO-5008 Bergen, Norway. Application deadline 21 May 2013.

Applications by e-mail only will not be considered.

Carol Bruce <Carol.Bruce@sars.uib.no>

EURAC BolzanoItaly AncientDNA

PhD position in the field of ancient DNA research

Institute for Mummies and the Iceman, EURAC research, Bolzano, Italy

We are looking for a scientist with strong expertise in advanced molecular techniques and an interest in applying innovative methods to the field of ancient DNA research. This three year doctoral position at the EURAC - Institute for Mummies and the Iceman is supported by funding from the law 14 research grant of the province Bolzano, South Tyrol, Italy.

Required qualifications. We are looking for a highly motivated and independently working scientist with a strong conceptual and practical background in the application of molecular techniques on ancient human remains. Experience in one or more of the following areas/techniques will be of advantage: genomics, microbiology, bioinformatics, population genetics. The successful candidate should have an interest in applying advanced molecular methods in the field of ancient DNA research. Proficiency in spoken and written English is mandatory.

Conditions of appointment. We offer up to 3 years of appointment as a PhD student according to the salary scheme of the EURAC. The EURAC is an equal opportunity employer.

Application. To apply, please send an email (subject: PhD ancient DNA research) to mummies.iceman@eurac.edu containing a pdf-file with a short cover letter, a detailed CV (including a brief description of research interests and of the educational background). Please attach the following consent to your personal record, in accordance to the data security decree 196/2003 about personal data handling: 'I authorize EURAC to use my personal data in accordance to decree 196/2003.' We inform that we will not be allowed to consider any application without this compliancy declaration.

Job start date is August 2013 - December 2013

Maixner Frank <frank.maixner@eurac.edu>

Edinburgh HostParasite

A PhD studentship titled "Understanding host defense and parasite offense: the coevolution of circadian rhythms" is available to be jointly supervised by Sarah Reece and Nick Savill (Edinburgh; IEB and IIIR).

Background: The discovery of biological rhythms, such as circadian rhythms, in parasite behaviours [1] and host immune responses [2] suggests that timing matters for how hosts and parasites interact with each other. For example, the developmental rhythm of many malaria parasite species is coordinated; parasites invade host red blood cells, replicate, and then release their progeny in a timed, synchronized burst. However, to date, the study of parasite biological rhythms has rarely considered whether parasites are organising their own schedules or whether parasites are passive and scheduled by aspects of host physiology with circadian rhythms. Rhythms in immune defence and parasite development could provide an evolutionary advantage to hosts, parasites or both, and both parties may to some extent control each other's rhythms [3]. This project will bridge this divide to investigate the evolutionary ecology of biological rhythms in host- parasite interactions.

The project will integrate the study of circadian rhythms, behavioural, and mathematical biology to investigate the evolutionary ecology of biological rhythms in host-parasite interactions. The project offers a novel opportunity to combine experiments and theory by collecting data from the lab [e.g. 1] and then using the data to undertake statistical inference of disease processes [e.g. 4, 5]. The project will focus on an established disease model (rodent malaria [e.g. 1,4-7]) and specific topics that could form the focus of the PhD include: (A) How are rhythms in parasite development initiated and maintained? Do parasites use their own time-keeping mechanisms to organise development or do they use cues from the host's circadian rhythms? (B) How do rhythms affect the survival and transmission of parasites? Have parasites evolved time-keeping mechanisms to better exploit host resources or to evade immune killing? (C) Are rhythms in parasite development and host immune responses adaptive for parasites, hosts, or neither?

We are looking for a highly motivated and exceptional candidate excited about working at the boundary of scientific disciplines. You should have, or expect to gain, a 1st or 2i degree classification in the life sciences. The project will be co-supervised by Sarah Reece and Nick Savill (Edinburgh) and is part of a larger project involving Nicole Mideo (Penn State/Toronto) and Bert Maier (Charite, Berlin) that is funded by a Human Frontiers of Science Project grant.

Closing date May 31st. Application instructions can be found here (please note - fees are available for UK students only): http://www.findaphd.com/search/ProjectDetails.aspx?PJID=41789&LID=455 References: [1] O'Donnell A.J., Schneider P., McWatters H.G. & Reece S.E. (2011) Fitness costs of disrupting circadian rhythms in malaria parasites, Proceedings of the Royal Society of London, Series B, 278(171): 2429-2436ââ [2] Keller M., Mazuch J., Abraham U., Eom G.D., Herzog E.D., Volk H.D., Kramer A. & Maier B. (2009) âA circadian clock in macrophages controls inflammatory immune responses.âProceedings of the National Academy of Sciences, USA, 106(50):21407-12.ââ [3] Mideo, N., Reece, S.E., Smith, A. Metcalf, C.J.E. (2013) The Cinderella Syndrome: Why do malaria-infected cells burst at midnight? Trends in Parasitology, 29: 10-16. [4] Miller M.R., Raberg L., Read A.F. & Savill N.J. (2010) Quantitative analysis of immune response and erythropoiesis during rodent malaria infection, PLoS Computational Biology, 6(9):e1000946.ââ [5] Mideo N., Savill N.J., Chadwick W., Schneider P., Read A.F., Day T. & Reece S.E. (2011) Causes of variation in malaria infection dynamics: insights from theory and data. American Naturalist, 178(6): E174-E188 [6] Pollitt L.C., Mideo N., Drew D., Schneider P., Colegrave N. & Reece S.E. (2011) Competition and the evolution of reproductive restraint in malaria parasites. American Naturalist, 177(3): 358-367 [7] Schneider P., Bell A.S., Sim D.G., O'Donnell A.J., Blanford A., Paaijmans K., Read A.F. & Reece S.E. (2012) Virulence, drug sensitivity and transmission success in the rodent malaria, Plasmodium chabaudi. Proceedings of the Royal Society of London, Series B 279(1747): 4677-85.

Subject Area(s): Evolutionâ Parasitologyâ Geneticsâ Molecular Biology âZoology/Animal Science

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

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INRA France EvolutionAnadromy

Hi Evoldir, We are seeking a postgraduate student for a 3 year PhD (starting in fall 2013) in Basque Counrty, on the link between anthropic environmental change, MHC polymorphism and the evolution of anadromy in Atlantic salmon. The project, involving indivudual-based modelling and population genetics, is managed by researchers from the UMR INRA-UPPA ECOBIOP (St Pée/Nivelle, France) and the Genomics and animal health Group at University of Basque Country (Bilbao, Spain).

More information on: http://www.bordeaux-aquitaine.inra.fr/st_pee/ Candidates should be competent in population theoretical/mathematical modelling and population genetics.

Please send application (CV, letter, name of two referees) to etienne.prevost@st-pee.inra.fr[1], olivier.lepais@st-pee.inra.fr[2], cedric.tentelier@univ-pau.fr[3] and begonamarina.jugo@ehu.es[4] before the 2nd of May. The final decision on the project (subject + candidate) will be taken by the end of June

Regards,

Cédric Tentelier UMR Ecobiop Université de Pau et des Pays de l'Adour Allée du parc Montaury 64600 Anglet 0033 5 59 57 44 47 0033 5 59 51 59 55 http://www.bordeaux-aquitaine.inra.fr/st_pee/ Liens:

[1] https://www.bordeaux.inra.fr/webmail/imp/message.php?mailbox=3DINBOX%2FEnvoyes&index=8#
[2] https://www.bordeaux.inra.fr/webmail/imp/message.php?mailbox=3DINBOX%2FEnvoyes&index=8#
[3] https://www.bordeaux.inra.fr/webmail/imp/message.php?mailbox=3DINBOX%2FEnvoyes&index=8#
[4] https://www.bordeaux.inra.fr/webmail/imp/message.php?mailbox=3DINBOX%2FEnvoyes&index=8#
cedric.tentelier@univ-pau.fr

IowaStateU TurtleChromosomeEvolution

PhD Position in Chromosome Evolution and Sex Determination of Turtles.

A PhD position is available in the laboratory of Dr. Nicole Valenzuela at Iowa State University as part of an NSF-funded PhyloGenomics project to study the genome rearrangements responsible for changes in diploid number across turtles and their association with transitions in sex determination. The project involves molecular cytogenetics, transcriptomics, bioinformatics and phylogenetics.

Prospective graduate students interested in evolutionary biology, sex determination, evo-devo, or chromosome evolution are invited to apply, and are encouraged to develop an independent research project within these areas.

For more information about the research in our lab please visit our website

http://www.public.iastate.edu/~nvalenzu/

Graduate students could join the EEB < http://www.grad-college.iastate.edu/EEB/ >, IG < http://www.genetics.iastate.edu/ > or BCB < http://www.bcb.iastate.edu/ > graduate programs at ISU:

http://www.grad-college.iastate.edu/EEB/
http://www.genetics.iastate.edu/ http://www.bcb.iastate.edu/ All prospective students must take the GRE General Test. International students whose native language is not English must take the TOEFL or IELTS.

Interested candidates should contact Dr. Nicole Valenzuela at nvalenzu@iastate.edu

Iowa State University does not discriminate on the basis of race, color, age, religion, national origin, sexual orientation, gender identity, genetic information, sex, marital status, disability, or status as a U.S. veteran.

Dr. Nicole Valenzuela

Associate Professor <nvalenzu@iastate.edu> Department of Ecology, Evolution, and Organismal Biology 253 Bessey Hall Iowa State University Ames, IA 50011, USA Phone: 515-294-1285 URL: http://www.public.iastate.edu/~nvalenzu/

nvalenzu@iastate.edu

MacquarieU 2 BehaviouralEvolution

*2 PhD positions in Behavioural Ecology, Macquarie University, Sydney, Australia. *

Project 1: *Climate-related reproductive plasticity in male birds*

Project Aims

Some Australian bird species have extended reproductive seasons, and breed across a wide range of social and environmental conditions. In such species males may have to maintain the production of viable sperm for prolonged periods (relative to well-studied species from the northern hemisphere). This project will examine individual strategies in sperm production against both climatic and social variation in two species of arid zone bird on which we have been conducting long-term behavioural and ecological research (the zebra finch and the chestnut-crowned babbler). This project develops on our recent work into both these species that has illuminated complex social and environmental sources of variation into reproductive investment. The project addresses questions relating to sperm competition, cooperative breeding, sexual conflict and climate change.

This project will involve long periods of field-work at a remote field station along with microscopy and molecular work to be conducted in the laboratory of Simon Griffith (Biological Sciences) at Macquarie University (Sydney). The project will also involve collaboration with Kate Buchanan (Deakin University) and Andy Russell (Exeter University, UK).

Project 2: *The genetics of domestication in two model finches*

Project Aims

The zebra finch and Gouldian finch are important captive model systems for the study of a broad range of questions in biology and most of this research is focused on highly domesticated populations that are sourced from populations of birds sourced from amateur aviculturists. This project will use a range of molecular approaches to investigate the effect of domestication on population genetics and genomic variation in these two species. In broad terms the project will use approaches from classical population genetics and emerging genomic techniques to investigate the genetic variation in domestic populations across the world and the selection that has resulted from many generations of artificial selection over the past century. This project develops on our recent work into both these species that has illuminated consistent differences between wild and domesticated populations in the nature of selection on a variety of life history and behavioural traits.

The project is based in the laboratory of Simon Griffith (Biological Sciences) and would involve collaboration with Lee Ann Rollins (Deakin University) and Terry Burke & (Sheffield University, UK).

Application

Both of these projects are supported by ongoing ARC funding. Scholarships are available for residents from Australia or New Zealand but there will also be possibilities for international students to get scholarship funding.

The 2013 MQRES full-time stipend rate is $24,653 pa tax exempt for 3.5 years (indexed annually). In addition to external grant support for the project, up to $20,000 is available to cover direct research expenses and domestic conference travel. Additional internal funding opportunities of up to $10,000 are available to support travel to overseas laboratories or to attend international conferences.

Prospective applicants should have a first class Honours degree or equivalent, and additional relevant research experience and/or qualifications. A demonstrated ability to work in remote and harsh conditions as well as extensive experience with capturing and handling birds is desirable. A full driving licence is necessary.

Applications should include 1) your CV, 2) a brief statement of your reasons for applying (max. 500 words) and the project you are applying to work on, and 3) contact details of two academic referees. Applications should be submitted electronically as a single PDF file.

Applications for this position are required *by May 10th 2013* and should be sent electronically to: simon.griffith@mq.edu

Further information from Dr Simon Griffith, Department of Biological Sciences, Macquarie University, Sydney, NSW 2109, Australia

thanks

Simon

Simon C. Griffith Department of Biological Sciences Macquarie University Sydney, NSW 2109, Australia. phone: +61 2 9850 1301 fax: +61 2 9850 9231 http://www.bio.mq.edu.au/avianbehaviouralecology/ http://publicationslist.org/s.c.griffith Thompson ISI Researcher ID: http://www.researcherid.com/rid/A-1996-2010 Simon Griffith <simon.griffith@mq.edu.au>

ManchesterMetU GraylingConservationGenomics

We have a PhD available funded by the Faculty of Science and Engineering, Manchester Metropolitan University for a fixed period of 3 years covering fees (Home/EU only) and a tax free stipend of £12k p.a.

Applicants should hold (or expect to obtain) a minimum upper-second honours degree in a relevant subject.

Project Title: Assessing adaptive genetic variation for effective conservation and management of European Grayling (Thymallus thymallus)

Project Summary A current trend in conservation genetics lies in investigating the relationship between functional genetic diversity and neutral genetic diversity. Understanding the extent to which functional genetic variation is affected by processes known to affect neutral diversity is central to this (i.e. it is important to examine the relative roles of genetic drift and selection in maintaining variation at functional loci). It is also important in conservation science and in evolutionary biology to assess the extent to which populations are locally adapted, in part so that the influence of human movements of organisms can be measured and any associated problems avoided. Loci involved in immunity make excellent candidates for these research themes since pathogens and infectious diseases are an important selective force in animal evolution. Measuring genetic variation of immune genes in and between small populations is also important in assessing their conservation status, risk of extinction and degree of local adaptation. We have a PhD project available examining these themes in European Grayling (Thymallus thymallus). Grayling have seen significant declines due to environmental degradation and over-exploitation and have been considered as endangered in the UK in the past.

Project Aims/Objectives

We aim to use cutting-edge next-generation sequencing technology to assess immunogenetic variation and/or local adaptation in European grayling (Salmonidae: Thymallus thymallus) in conjunction with within-river bacterial diversity and other environmental characteristics and stocking history. These data will be examined in comparison with pre-existing data from neutral loci (microsatellites). Additional work in liaison with research targets of the Environment Agency regarding grayling may be included.

Project specific requirements The project will have a significant component of molecular laboratory work, and prior experience of this is essential. The successful candidate will have experience of one or more of the following techniques: DNA isolation, PCR, DNA sequencing, microsatellite genotyping or similar work. Additionally, the project may involve some fieldwork and sampling, and the applicant should be fit and prepared to conduct long-hours of outdoor working, if necessary. It is desirable (but not essential) that candidates also have experience of population genetics analysis, bioinformatics, next-generation sequencing, fish biology and sampling.

The supervisory team will include Dr Jonathan Ellis (DoS; MMU), Dr Robin Senn (MMU), Dr Martin Taylor (UEA). We will also work with Prof. R N Hughes (Bangor University), the Grayling Research Trust and the Environment Agency.

Contact Dr Jon Ellis for further details: j.ellis@mmu.ac.uk; tel: +44 (0) 161 2476209

http://www.mmu.ac.uk/research/studentships/PGR-application-form.doc or http://www2.mmu.ac.uk/research/studentships/science-and-engineering/
Return the completed application to: pgradmissions@mmu.ac.uk

PLEASE NOTE that Section 9 of the application should be used to write a personal statement outlining your suitability for the study, what you hope to achieve from the PhD and your research experience to date.

Closing date: Friday 17th May

Dr Jonathan S. Ellis Lecturer in Molecular Conservation Biology School of Science & the Environment Manchester Metropolitan University Chester Street Manchester M1 5GD +44 (0)161 2476209

Jonathan Ellis <J.Ellis@mmu.ac.uk>

QueensU SpeciationGenomics

I am looking for a PhD student to study genomics of speciation in band-rumped storm-petrels (BRSP). BRSP represent an exciting case of repeated sympatric speciation (i.e. speciation with gene flow) by allochrony (separation of populations by breeding time). Initial studies in my lab documented the pattern of divergence. We now want to investigate the mechanisms. The project will entail application of functional gene analysis and comparative genomics to an existing large sample collection. Field work on barren tropical islands may be required. Applicants must have a background in evolutionary genetics. Practical experience with genomics and bioinformatics is an asset. The successful applicant will join a dynamic group of faculty and students studying ecology and evolution at Queen's University. Please send a resume or curriculum vitae, informal transcript, and contact information for two academic references asap to Dr. Vicki Friesen. Acceptance is conditional on the applicant receiving a Trillium Scholarship: contact Dr. Friesen asap for further information. Deadline for completed application: May 6 2013. See http://post.queensu.ca/~birdpop/index.html for more information on the Friesen lab.

Dr. Vicki Friesen, Professor Department of Biology, 4443 Biosciences, 116 Barrie Street, Queen's University, Kingston, ON K7L 3N6, Canada Tel: 613-533-6156 Fax: 613-533-6617

Haida Saying: Treat the Earth well: it is not given to us by our parents, it is loaned to us by our children.

Vicki Friesen <vlf@queensu.ca>

SanDiegoStateU UCRiverside EvolBiol

The Joint Doctoral program in Evolutionary Biology between the Department of Biology at San Diego State University and the University of California Riverside is seeking applicants for 2013. Our program is 3 years old with 8 joint Ph.D. students. We provide training in evolutionary biology that includes molecular evolution, genomics, paleontology, population biology and systematics. www.bio.sdsu.edu/eb/jdeb.html Please contact Annalisa Berta, aberta@mail.sdsu.edu for more information.

Annalisa Berta, Ph.D. Professor and Coordinator of SDSU/UCR Joint Doctoral Program in Evolutionary Biology

Department of Biology San Diego State University San Diego, CA 92182-4614 Phone: (619) 594-5392 lab: (619) 594-4584 (LS 260) fax: (619) 594-5676 email: aberta@mail.sdsu.edu http://www.bio.sdsu.edu/-faculty/berta.html www.bio.sdsu.edu/eb/jdeb.html
Annalisa Berta <aberta@mail.sdsu.edu>

Scotland PlantPathogen

PhD Studentship Fighting Ramularia leaf spot disease of barley using integrated genetics and genomics

SRUC, Scotland's Rural College, delivers comprehensive skills, education and business support for Scotland's land-based industry founded on world class, sector leading research, education and consultancy. Our 1500 staff are located on 6 campuses and around 40 business units across Scotland and the North of England. In agricultural fields of monocultures, crop plants continuously face numerous threats from pathogens that can, if left unchecked, rapidly lead to severe epidemics of disease. Leaf spot diseases are of particular concern in Europe and are frequently caused by the fungus Ramularia collo-cygni, which is especially devastating on barley. It is a disease that occurs late in the season and is characterised by small necrotic spots, usually with a yellow halo which is caused by the production of rubellin toxins within the pathogen. Thus, understanding both the production and in planta action of rubellins is vital to the design of novel strategies to protect barley and other infected cereals from leaf spot disease. This PhD project will exploit a unique combination of genomic advances that have been revealed following the recent sequencing of the R. collo-cygni genome linked with the rapid generation time and detailed genetic knowledge from Arabidopsis, combined with the large genetic diversity of barley landraces to examine the genes responsible for symptom development in the plant-pathogen relationship. The successful candidate must have or expect to obtain a minimum of an upper second class degree in a scientific discipline from a UK University or equivalent. They should be familiar with Microsoft office and excel, as well as some basic knowledge of statistical software such as Genstat and/or Minitab. Oral and writing skills in English are required to a high standard. A valid UK or EU driving license is also desirable.

The studentship offers a stipend of £13,726 per annum and is funded to pay the University of Edinburgh tuition fees for UK/EU students. The expected start date is October 2013 and the studentship is 3.5 years in length. The student will be based at SRUC, King's Buildings, West Mains Road, Edinburgh, EH9 3JG.

Electronic applications can be submitted via the SRUC website www.sruc.ac.uk/jobs Application packs are also available from Audrey Johnstone (audrey.johnstone@sruc.ac.uk) quoting reference SRUC/1026687/Fountaine. To have an informal discussion about this studentship, contact Dr James Fountaine, james.fountaine@sruc.ac.uk (+44 (0) 131 535 4370) and/or Dr Steven Spoel, sspoel@staffmail.ed.ac.uk (+44 (0) 131 650 7065)

Closing date for the return of applications is noon on 6th May 2013

Number: SC103046 - Registered Office: Peter Wilson Building, King's Buildings, West Mains Road, Edinburgh EH9 3JG SAC Commercial Limited, an SRUC company Registered in Scotland, Company Number: SC148684 - Registered Office: Peter Wilson Building, King's Buildings, West Mains Road, Edinburgh EH9 3JG

Dr Peter Hoebe Crop & Soil Systems, SRUC King's Buildings Edinburgh EH9 3JG +44 (0)131 535 4208/(0)7795047692

Peter Hoebe <Peter.Hoebe@sruc.ac.uk>

StockholmU 2 BrainEvolution

Two PhD-student positions in Ethology

Two PhD-student positions in Ethology at the Department of Zoology. Reference number SU FV-0987-13. Deadline for applications: May 2, 2013.

Two PhD-student positions in Ethology at < http://-www.zoologi.su.se/en > the Department of Zoology.

Project: Multilevel analysis of the costs and benefits of evolving an advanced brain We are seeking to recruit two PhD-students to join Niclas Kolm's group for work within a multidisciplinary project on brain evolution. The project uses mainly the guppy (Poecilia reticulata) and the house mouse (Mus musculus) as models to experimentally test the possibilities and consequences of evolving a more advanced brain. More specifically, the project addresses the costs and benefits of evolving a more advanced brain in terms of brain morphology and also if strong selection on cognitive ability affects brain morphology. As such, the project spans over multiple disciplines including assays of behaviour, physiology, life histories, primary and secondary sexual traits and state of the art analyses of the genetic architecture that orchestrates brain morphology and cognitive ability. The existing selection lines of large- and small-brained guppies will form the basis of the project but additional selection experiments on various aspects of brain morphology and cognitive ability will also be undertaken. The overall aim of the project is thus to increase our understanding of the factors that have generated the enormous variation in brain morphology that exists at all taxonomic levels among the animals.

The work will mostly be lab-oriented but includes also the possibility of field work on Trinidad. The project will require hard work but at the same time provide excellent opportunities for personal initiatives and development towards a successful academic career. An important task will be to collect and analyse complex data in a way that controls for the setups of replicated artificial selection designs.

Qualification and competence To be qualified for research studies in the program, the applicant must have completed a Master degree (or equivalent) or have passed at least 120 hp (2 years) of biological studies, including an approved independent project of at least 30 hp at advanced level within Ethology, Zoology, Behavioural Ecology, Evolutionary Biology or a related subject. Applicants who have in principle acquired the corresponding competence in Sweden or in another country are also qualified.

We are looking in particular for candidates with a strong interest in brain evolution, with excellent analytical ability and experience from quantitative analyses of behaviour and other traits of interest. Experience in working with aquatic and/or terrestrial animals in the lab is especially meriting.

Criteria for selection Among qualified applicants, selection is made according to the ability to profit from the studies. The criteria to be used are properly documented competence within the described research area, capabilities with regards to speaking and writing in English, analytical thinking, creativity, initiative, independence, and team work performance. The applicant's earlier experience within the field of research can be of relevance especially when further documented by university courses, independent research work, personal references, interview and an application indicating the applicant's motivation in written form. The decision cannot be appealed.

Job details The PhD-studies, which are aimed to start in autumn 2013, include 48 months of full-time studies. During the first year an appropriate study support will be supplied (15 500 SEK/month) which will later be changed into full employment as a PhD-student (23 200 26 800 SEK/month) with full social benefits.

Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Information For further details, contact the PI on the project,: Associated Professor Niclas Kolm, telephone +46-(0)18-471 26 39, e-mail: niclas.kolm@ebc.uu.se and niclas.kolm@zoologi.su.se.

Union representatives Anqi Lindblom-Ahlm (Saco-S) and Lisbeth Häggberg (Fackförbundet ST), telephone +46-(0)8-16 2000 (switch board), and Gunnar Stenberg (SEKO), telephone +46-(0)70-316 43 41.

Application The application should contain: 1) maximum one A4-page letter including personal presentation and motivation for the project, 2) complete CV (including list of methodological skills), 3) copy of independent project thesis, 4) copies of degree certificates and transcripts of academic records (attested), and 5) reference letters and contact details from two academic referees. A research plan is not needed at this stage.

In order to apply for these positions, please use the Stockholm University web-based application form.

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StockholmU SystematicZoology

PhD-student position in Systematic Zoology at the Department of Zoology. Reference number SU FV-0989-13. Deadline for applications: May 2, 2013.

The student will be admitted to one of the following projects, and should specify interest:

Genomics of woolly mammoth extinction The woolly mammoth became extinct some 4000 years ago. The extinction was preceded by a loss of habitat across Eurasia that lead to increasing population fragmentation until only one population on Wrangel Island remained. The project proposed here aims to use state-of-the-art genomic analysis of ancient DNA from mammoth remains to investigate three key questions related to the mammoth's extinction: 1) Did the last population of woolly mammoth suffer from inbreeding problems? 2) Did the woolly mammoth evolve in response to ecological change at the end of the last Ice Age? 3) How important was gene flow between different geographical areas for the evolution of the woolly mammoth? Addressing these questions is relevant not only for understanding mammoth evolution but also for conservation of extant endangered species, since it may help to develop a better understanding of how small populations are affected by low genetic variation and inbreeding. The PhD position will involve sequencing of partial genomes from a large number of mammoth specimens, and could also involve field expeditions to Siberia. Moreover, the PhD student will have the opportunity to visit and collaborate with world-leading scientists that belong to an international research consortium on mammoth genomics. The project will be supervised by Dr. Love Dalén at the Swedish Museum of Natural History, love.dalen@nrm.se.

Systematics and evolution of cichlid fishes (Cichlidae) The Cichlidae are one of the most important vertebrate families with an estimated 2000 species distributed in freshwaters of Africa, South and Central America, Madagascar, and Asia. Cichlid phylogeny has been intensely addressed both by molecular techniques and morphological analyses. Still numerous aspects remain to be investigated. From the systematic/phylogenetic perspective, the sister group and the deeper nodes within the family remain to be resolved; many genera remain to be analyzed for species diversity and phylogeny. Cichlids are also useful for evolutionary research: Cichlids often occur with numerous closely related species in restricted areas, so-called species flocks, as found in Lakes Tanganyika, Malawi, and Victoria. Are species flocks a prominent mode of speciation and evolution in this family, or transient bursts of evolution? Hybridization has been discovered both in South America and Africa. Is hybridization a prominent means of divergence in this group? Trophic diversity, various mating and brood care systems, and miniaturization offer additional topics. The Swedish Museum of Natural History has substantial collections of cichlid fishes waiting for a student interested in both morphological and molecular analyses of systematic and evolutionary challenges. This project will be supervised by Dr. Sven Kullander at the Swedish Museum of Natural History, sven.kullander@nrm.se.

Ecological and phylogenetic characterization of modern carnivore guilds in the context of climate change This project is part of an ongoing program investigating the ecometrics of carnivores in space and time. The primary goal is to develop tools that enable discrimination between ecological and phylogenetic drivers of ecometric differentiation between modern-day carnivore guilds. Ecomorphological datasets of carnivores have been generated within the program, but need to be augmented with new characters and additional taxa. Ancillary datasets of climatic variables, including temperature and precipitation are also available. The main task of the present project is to develop and use statistical and comparative phylogenetic methods that will allow for an amalgamation of these datasets as well as statistical testing of scenarios of structural changes to guilds in the context of models of future climate change. The project will be supervised by Prof. Lars Werdelin at the Department of Palaeobiology, the Swedish Museum of Natural History, lars.werdelin@nrm.se.

Speciation and species delimitation of water beetles on Madagascar Madagascar with it's long history as an isolated island, pronounced environmental gradients and numerous endemic species radiations is an excellent model region to study species diversification. Why did some colonizations lead to endemic radiations and others not? This is a question at the core of the mechanisms and processes involved in speciation. Water beetles are the study organisms in this project as they can deliver a number of replicated clades of both endemic radiations and clades with multiple colonizations but lacking radiations. Densely sampled species-level phylogenies will be used as a window into the processes of how species arise and how they can be inferred. Main

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SwanseaU BacterialEvolution

2 x PhD studentships in bacterial genomics and evolution. Based in Swansea University and co-supervised at Imperial College London.

Project description:

The successful applicants will join a multicentre research group (Swansea University and Imperial College London) focusing on population biology and evolution of bacterial pathogens of public health importance. They will investigate the genetic factors involved in generating and maintaining genotypic and phenotypic diversity in bacteria such as Campylobacter, E. coli and Staphylococcus. Comparative genomics approaches will examine the genetic structuring within pathogenic populations and answer fundamental questions about how genetic variation and genome plasticity influence adaptation and the evolution of pathogenicity.

Candidates must normally hold a first or upper second class UK degree and must be EU residents. Good English writing and oral skills are essential.

The studentships will cover University tuition fees plus a salary commensurate with regular UK postgraduate stipends, approximately Â£13,950 (â¬17, 062)*perannum*.

Interviews will take place in June/July and the studentship will begin in September 2013.

Position 1. Statistical geneticist or computer scientist

Good knowledge of at least one mainstream programming language such as C, Java, Python or Perl is required. Some experience of statistical data analysis, and especially computer intensive techniques such as Monte Carlo methods, would be desirable. No previous knowledge of microbiology, genetics or evolution is required, but candidates should be enthused to learn about these subjects.

Position 2. Microbiologist (genetics/genomics)

Expertise or interest in molecular techniques (PCR, sequencing) and computer based genetic analysis, is necessary but training and support will be provided to strengthen these areas. Previous experience in a microbiology or molecular biology laboratory or in bioinformatics research is also strongly desirable.

Supervisors: Dr Samuel Sheppard Dr Xavier Didelot

For further information, visit our website: https://sites.google.com/site/sheppardlab/ For other informal inquiries on the position, or for applications (include CV and motivation description) please contact us (sheppardlab@gmail.com)

Dr Guillaume Méric Medical Microbiology and Infectious Diseases group Swansea University, College of Medicine Singleton Park, ILS1, Room 527 Swansea, SA2 8PP Wales, United Kingdom E-mail: g.meric@swansea.ac.uk Phone: +44(0)1792 602419 (x2419) Web: https://sites.google.com/site/sheppardlab/ Guillaume Méric <G.Meric@swansea.ac.uk>

Trentino Italy PlantPathogen

PhD Studentship Comparative analysis of grapevine genotypes with different levels of resistance to downy mildew

The Research and Innovation Centre (CRI) is part of Fondazione Edmund Mach (FEM), a public research institution established by the government of the Autonomous Province of Trento. CRI-FEM is located in Trentino (the North of Italy) and supports studies in the field of agriculture, nutrition and environment, with the aim of sharing knowledge and contributing to economic growth, social development and overall improvement of life quality.

Project description:

Downy mildew (DM) is a widespread disease of grape caused by the oomycete Plasmopara viticola, an invasive species native to North America. This pathogen can infect grapevine cultivars as well as wild Vitis species. However, while the cultivars are highly susceptible, most of the wild species are relatively resistant. The disease is currently controlled by the application of fungicides, yet the demand for organic products is increasing and concerns that these chemicals have harmful effect on the environment and human health require growers to reduce the use of pesticides in fruit production.

Natural sources of disease resistance could be found in geographic regions where populations of pathogens and host plants co-evolve. Thus, germplasm of several Vitis species native to temperate zones of North America has been investigated for the genetic base of DM resistance. It may be possible to transfer resistance to DM from these wild grape species into susceptible domesticated grapevines, but the consequences of so-called "linkage drag" of undesired traits could not be completely eliminated, even after several cycles of backcrossing.

Recently, single local grapevine varieties of Near Eastern origin have attracted attention, because of their lower susceptibility to DM. These plants, unlike most of grapevine cultivars, have leaves and fruits without symptoms of disease during the growing season. Such natural sources of resistance to non-native pathogens stimulate genetic investigations and are of great significance for developing alternative resistance-breeding strategies.

In this project, the PhD student will use different integrative approaches to characterize these important accessions of V. vinifera, as well as to identify and mine genes and alleles associated with plant resistance to DM. The long term objective of this PhD research is to ultimately enable effective transfer of natural resistance to the most severe disease affecting fruit quality into future plant material, and to reduce the need for using fungicides, which will make grapevine cultivation more environment-friendly.

The successful candidate must have or expect to obtain a minimum of a Master's degree in a scientific discipline or equivalent qualification. Oral and writing skills in English are required to a high standard.

The studentship offers a stipend of euro 20,000 per annum and is funded to pay tuition fees. The expected start date is September 2013 and the funding is provided for 3 years with the possibility of a one-year extension.

The student will be based at FEM, San Michele all'Adige (Trentino), but will spend part of the time at the JKI - Federal Research Centre for Cultivated Plants (Siebeldingen, Germany) and at the University of Milan (Italy).

Electronic applications can be submitted via the CRI-FEM website http://cri.fmach.eu/education/Applications-Forms/application-form-FIRS-T-Second-Call-2013 For further information about the project and selection procedure, please visit the website at http://cri.fmach.eu/education/selection/FIRS-T-Second-Call-2013 (select project A_1) and http://cri.fmach.eu/education/selection . Closing date for receipt of completed applications is Friday, 24 May 2013 at 18.00 CET.

ls.grzeskowiak@gmail.com

TrinityCollege Dublin PlantEvolutionaryGenetics

Teagasc PhD Walsh Fellowship Opportunity

"Genotypic and phenotypic assessment of forage quality in Lolium in the age of large-scale, inexpensive genotyping"

Background: With the rapid advances in genotyping offered by next generation sequencing (NGS) we are at a stage in forage grass breeding where the major limiting step in linkage mapping/association mapping is likely to be phenotypic (observable characteristics) and not genotypic characterization. Thus, the collection of high-quality phenotypes will be crucial for mapping studies. Forage quality and digestibility of Lolium perenne (perennial ryegrass) is related to biomass accumulation, flowering time and lignocellulosic content. This project will combine phenotypic and genotypic studies on a diverse set of Lolium accessions to specifically assess the genetic control of these traits. Forage quality traits examined will include lignocellulose content and composition, flowering time, re-heading, biomass accumulation, and tillering capacity. We will combine this with an examination of variation in candidate genes relating to these traits using DNA sequencing and association mapping using high-density single nucleotide polymorphism (SNP) data and genic SNPs. Many of these genes are well studied in cereals and hence these genome resources can be applied to Lolium.

Requirements: Applicants should have a primary degree (First or Upper Second Class Honours) or M.Sc.

in an appropriate discipline (Biology, Plant Sciences, Biotechnology, Genetics, etc.). The candidate should be highly self-motivated and be prepared for laboratory and field work with modern analytical equipment and the use of bioinformatic / genetic techniques. A willingness to travel between experimental locations and for blocks of time is expected. A full driving license is desirable.

Award: The PhD Fellowship is a joint project between Teagasc, Oak Park and the School of Natural Sciences, Trinity College Dublin, Ireland. The student will be based at the Teagasc Research Centre at Oak Park, Co. Carlow and the University of Dublin, Trinity College, working under the supervision of Dr. Trevor Hodkinson in association with Teagasc supervisors (Dr Susanne Barth & Dr Dan Milbourne). The Fellowship will start as soon as possible in September/October 2013. The Fellowship provides a stipend of euro 22,000. University fees are paid by the student from the stipend which is tenable for 4 years.

Further Information/Applications: Dr Trevor Hodkinson, Botany Building, School of Natural Sciences, Trinity College Dublin. Ireland Phone +353 1 8961128 email: Trevor.Hodkinson@tcd.ie

Application Procedure: Submit an electronic copy of Curriculum Vitae and a letter of interest simultaneously to: Dr Trevor Hodkinson (Trevor.Hodkinson@tcd.ie) and Dr Susanne Barth (Susanne.Barth@teagasc.ie)

Closing date: May 30th 2013 or until filled.

Trevor Hodkinson Associate Professor in Botany Botany Building School of Natural Sciences Trinity College Dublin Ireland Phone 00353 1 8961128 Fax 00353 1 8961147 email Trevor.Hodkinson@tcd.ie http://people.tcd.ie/hodkinst https://twitter.com/-TrevorHodkinson hodkinst@tcd.ie

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UCL SexualSelection

NERC PhD Studentship

Project Title: Sexual selection, meiotic drive and fertility in stalk-eyed flies

Department/Institution: Department of Genetics, Evolution & Environment, University College London

Primary supervisor: Professor Andrew Pomiankowski

This project integrates field and laboratory based research on sexual selection. Stalk-eyed flies are a canonical example of sexual selection. In Teleopsis dalmanni, males have exaggerated eyespan and females show strong mate preferences for males with larger eyespan. Females have low fertility despite mating at high rates and exhibiting strong mate preference for particular males. Some populations harbour an X-linked meiotic drive system that results in female biased broods due to the degeneration of Y-bearing sperm. This project will further examine the inter-relationships between sexual selection, fertility and meiotic drive. The student will determine the frequency of drive in natural populations at established sites in Malaysia, the role of ecology and demography, and the consequences for the strength of sexual selection. In the laboratory they will exploit SNP and other genomic markers in order to reliably genotype individuals and progeny for meiotic drive, and study the association of meiotic drive with male eyespan and other aspects of male reproductive performance.

The UCL stalk-eyed fly research group (www.ucl.ac.uk/stalkie/) is led by Prof. A. Pomiankowski and Prof. K. Fowler and studies multiple facets of the evolution of sexually selected traits. Given the project's reliance on data collected from natural populations, the attributes of the successful applicant will include independence, initiative and enthusiasm in order to cope with the demands of field research. Note that applicants must have a minimum 2:1 BSc (or equivalent), preferably a Masters level degree, excellent numerate skills (computational and statistical), knowledge of population genetics and bioinformatics. Appropriate training will be provided by UCL. The studentship is funded by NERC and applicants need to satisfy NERC's UK/EU eligibility requirements (see: http://www.nerc.ac.uk/funding/-available/postgrad/eligibility.asp). It may be possible to fully fund EU candidates as well.

Applications should be sent as soon as possible, with cover letter, CV & contact details of two referees, to the primary supervisor Professor A. Pomiankowski (email: ucbhpom@ucl.ac.uk, www.ucl.ac.uk/gee/staff). Closing date: 10th May 2013.

a.pomiankowski@ucl.ac.uk

UEdinburgh ParasiteEvolution

A NERC funded research assistant position is available for up to 3 years in Dr Sarah Reece's lab for a highly organised and motivated graduate with a degree in biological sciences. You will assist on a variety of projects to investigate the evolution and ecology of malaria (Plasmodium) parasite reproductive strategies.

The environments experienced by parasites inside hosts and vectors are highly changeable. For example, resources become scarce when hosts get sick, immune responses directed at parasites develop, and parasites often have to compete with other strains and species sharing their host. Understanding the strategies that parasites have evolved to cope with the challenging environments they face inside hosts and vectors is the aim of this project. Mounting evidence is revealing considerable plasticity in parasite traits that underpin parasites ability to survive during infections and to transmit to new hosts. Our recent research shows that parasites adjust their traits in response to the conditions they experience in the host. We will investigate why parasites do this. The project will determine how host and parasite factors contribute to plasticity in parasites' reproductive effort, quantify the patterns generated across environmental gradients and parasite genetic backgrounds, test whether parasite strategies are adjusted in response to the environment in ways that benefit survival and transmission, and investigate whether plasticity is costly by testing if it is lost under selection in constant environmental conditions.

The position would suit an enthusiastic recent graduate whose degree has a strong parasitology, evolution or ecology component and an interest in evolutionary medicine. Experience with molecular techniques (e.g. PCR), experimental evolution, or working with rodent models would be an advantage but are not essential. You will be able to work as part of a team to develop new techniques, carry out experiments and collect and analyse the resulting data. You will also be able to work independently, with the potential to lead work on small projects, which may involve supervising undergraduate project students.

£25,504 - £29,541 Closing date: 14th May 2013

More info and application instructions at https:/-/www.vacancies.ed.ac.uk/pls/corehrrecruit/-erq_jobspec_version_4.display_form 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

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UExeter EvolutionAntibioticResistance

PhD, BBSRC CASE Studentship (full time 4 years) - based in Cornwall in collaboration with AstraZeneca Environmental Laboratories, Brixham, Devon.

Selection for antibiotic resistance in the aquatic environment: novel assays to determine effect concentrations of micropollutants

This Studentship will be based at The European Centre for Environment and Human Health, University of Exeter Medical School, located at the Royal Cornwall Hospital in Truro and the Environment and Sustainability Institute at the Tremough Campus (near Falmouth). The project will be jointly supervised by Dr Will Gaze (Exeter) and Dr Jason Snape and Dr. Becky Brown (AstraZeneca). The University of Exeter Medical School is seeking to attract PhD candidates of outstanding ability to join their exciting and rapidly expanding programme of internationally rated research. As part of our new developments and our commitment to research excellence, applications are invited from suitably qualified graduates, 2:1 or above, for a PhD studentship. International students must also have IELTS (International English Language Testing System) score of 7 and above (or equivalent qualification). Antibiotic resistance is an increasing problem that has been compared to climate change in that it is relentless, irreversible and poses a significant risk to human health. It is well known that antibiotic usage in the clinic is responsible for evolution of resistance; however the contribution of antibiotic residues in the aquatic environment to the overall burden of resistance is less well studied. Environmental bacteria constitute a vast reservoir of genetic diversity, including novel resistance genes. Recent evidence of selection for resistance at low concentrations combined with the diverse environmental metagenome that can be accessed by horizontal gene transfer provides opportunities for recruitment of novel genes by human associated bacteria in the natural environment. This project aims to determine the minimum selective concentrations of antibiotics which will determine whether environmental concentrations of pharmaceutical residues are likely to select for resistance in situ. Gene transfer from the metagenome to marked recipients will be determined experimentally at a range of environmentally relevant antibiotic concentrations and the effects of complex mixtures of pharmaceuticals and passage through waste water digesters on evolution of resistance will be studied.

The student will receive training in classical and molecular microbiology, and will form part of a research group studying pathogen ecology, experimental evolution, horizontal gene transfer and selection for antibiotic resistance in farmed and polluted natural environments. The project gives opportunities to work and collaborate with scientists at The University of Exeter Medical School, the Royal Cornwall Hospital, the Environment and Sustainability Institute, the Centre for Evolution and Conservation and scientists at AstraZeneca's Environmental Laboratories. The European Centre for Environment and Human Health presents unique opportunities to work at the interface of medical and environmental science.

Closing date for applications: 20th April 2013 Start date: 1st October 2013

To apply online please visit: http://www.exeter.ac.uk/-postgraduate/money/studentships/application/ and upload the following: - CV - Covering letter (outlining your academic interests, prior research experience and reasons for wishing to undertake the project). - Transcript(s) giving full details of subjects studied and grades/marks obtained (this should be an interim transcript if you are still studying)

For an informal discussion, please contact: Dr. Will Gaze on 01872258166.

Funding Notes The stipend will be £13,726 (based on full time 13/14 rate) with a CASE enhancement of approximately £4,000. Tuition fees will be paid at the home rate. This studentship is available to UK/EU students only.

William Gaze <william.gaze@pcmd.ac.uk>

UGent GeneticsDemography

The Department of Biology at Ghent University is seeking to fill the following full-time PhD position vacancy in the Terrestrial Ecology Unit

Avian genetics and demography in a fragmented biodiversity hotspot

Background Biodiversity is unevenly distributed across the globe, with the vast majority of biodiversity hotspots scattered across tropical regions. Apart from exceptional biodiversity, however, these regions are often characterized by high demographic pressure too - causing rapid and drastic environmental transformations such as the fragmentation of continuous forest blocks. In the Kenyan and Tanzanian sections of the Eastern Arc Mountains biodiversity hotspot, two long-term projects coordinated by Ghent University (Dr. Luc Lens, Belgium) and the Utah Museum of Natural History (Dr. William D. Newmark, USA) have collected extensive longitudinal demographic and genetic data on birds of fragmented cloud forest. Integration of both projects offers a unique opportunity to gain insight in ecological and evolutionary responses to recent anthropogenic disturbance in organisms that experienced stable conditions over vast time intervals.

The Project In this PhD project, the student will (i) genotype selected forest bird species from various EAM sites with neutral genetic markers and apply individual-based models to study fine-grained temporal and spatial genetic patterning; and (ii) apply state-of-the-art individual mark-recapture models to study how habitat fragmentation may alter the strength and direction of natural selection. By integrating genetic and demographic data with other ecological processes (nest predation, settlement strategies, mating systems, -), the student will contribute to a better understanding of how anthropogenic stressors drive natural populations within an evolutionary perspective. While the focus of the PhD is on labwork and analysis of existing long-term datasets, there will also be opportunity to conduct fieldwork.

Further reading Lens et al. (2002) Avian persistence in fragmented rainforest. Science 298: 1236-1238

Newmark & Stanley (2011) Habitat fragmentation reduces nest survival in an Afrotropical bird community in a biodiversity hotspot. PNAS 108: 11488-11493

Callens et al. (2011). Genetic signature of population fragmentation varies with mobility in seven bird species of a fragmented Kenyan cloud forest. Molecular Ecology 20: 1829-“1844

Profile and requirements You hold a Master degree in Biology or comparable with a strong background in ecology and evolutionary biology; You can submit outstanding academic results; You have a solid training in population genetic and/or mark-recapture analysis; Experience with avian biology and habitat fragmentation is an advantage;

We offer A doctoral scholarship for a period of four years (gross wage ca. 3440/month) The scholarship is immediately open but starting date is negotiable; You will enroll in the Ghent Doctoral School training program allowing you to take part in various courses, training programs and conferences within and outside the university; You will work in an international team of PhD students, postdocs and technical staff involved in eco-evolutionary research on birds; You will be member of the Terrestrial Ecology Unit, a dynamic research group that combines field, lab and modelling approaches to study various questions in ecological and evolutionary research (http://www.ecology.ugent.be/-terec/index.php).

Interested? 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 request Applications should be submitted by email to Prof. Luc Lens at Luc.Lens@UGent.be until the closing date: 30 April 2013 For more information, contact Luc Lens at the same email address

Luc.Lens@ugent.be

UKent RADsequencing parakeets

PhD studentship: RAD-sequencing and SNP genotyping to examine adaptation in globally invasive parakeets.

Durrell Institute of Conservation and Ecology (DICE), School of Anthropology and Conservation, University of Kent, UK.

Supervisors: Main supervisor: Dr Jim Groombridge (DICE). Co-supervisors: Dr Rob Ogden (WildGenes, Royal Zoological Society of Scotland), Dr Diederik Strubbe (University of Antwerp), Dr Ben Warren (University of Reunion), Dr Robert Prys-Jones (Natural History Museum)

Duration: 3 years This PhD studentship will be based at the University of Kent and will be fully-funded by a grant from the John Spedan Lewis Foundation, with supervisory support from a research consortium of DICE, RZSS, UA, UR and NHM. Funding is available to cover Home/EU tuition fees, full stipend plus all research costs for the 3-year studentship.

The Durrell Institute of Conservation and Ecology (DICE) at the University of Kent, in collaboration with RZSS, UA, UR and NHM, is offering an exciting PhD studentship and research opportunity for a motivated graduate. This research project aims to apply RAD-Tag sequencing and SNP genotyping techniques to identify genome-wide responses to changes in climate in ringneck parakeets as they have spread from their native range of the African and Indian continents into Europe. The ringneck parakeet is one of the World's most invasive bird species. The success of their invasion is clear from the large population sizes now established in many of Europe's major cities, including those in the UK, and their conquering of a substantial temperature gradient en route suggests they have adapted to their invasive range. Consequently, invasive parakeets provide an ideal scientific framework to examine how species evolve in response to environmental change and to identify the potential genetic basis for such adaptability and invasion success. Genetic data for some of the more extensively-sampled invasive populations, such as those in the UK which occur at the northernmost edge of their invasive range, will be combined with analysis of survey data to look for patterns of population expansion and introgression. This project will be based at the DICE Conservation Genetics laboratory (led by Dr. Jim Groombridge), with extended periods at the RZSS WildGenes laboratory in Edinburgh (led by Dr. Rob Ogden) for RAD library preparation, SNP discovery and population genotyping.

Application deadline: Wednesday 1st May 2013 Start Date: October 2013

Academic requirements: Applicants should have a First or Upper Second Class UK honours degree, or equivalent, in a relevant discipline such as bioinformatics, molecular ecology or evolutionary genetics. Knowledge/experience of bioinformatics, Next Generation sequencing techniques and/or molecular laboratory techniques would be advantageous.

Funding: Available funding will cover the tuition fees (at the UK/EU rate only), full stipend and all research costs for this 3-year studentship project.

How to apply: Please send a CV (maximum 2-pages), a covering letter (maximum one page) and contact details for two references, by email to Dr Jim Groombridge (J.Groombridge@kent.ac.uk) on or before the closing date. Interviews will be held in early/mid May 2013, with a view to the successful applicant starting in October 2013. For more information about the project, please contact Dr Jim Groombridge.

Keywords: Population genetics, wildlife, conservation, ecology, disease, molecular genetics.

Dr Jim Groombridge Reader in Biodiversity Conservation Durrell Institute of Conservation and Ecology (DICE) School of Anthropology and Conservation Marlowe Building University of Kent Canterbury Kent CT2 7NR Tel: 01227 824097 Fax:

01227 827289 Email: J.Groombridge@kent.ac.uk Website: http://www.kent.ac.uk/sac/staff-profiles/-profiles/conservation-ecology/academic-staff/-groombridge_jim.html J.Groombridge@kent.ac.uk

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UMainz ParasiteEvolution

The Faculty 10 Biology, Institute of Zoology, Dept. Evolutionary Biology at the University of Mainz is searching for

a PhD Student (3 years - 65% TVL E13)

in the research area "Parasite manipulation of host behavior"

Application is possible until position is filled, for full consideration, apply by 30th of April 2013

We invite applications for a 3-years PhD position at the JG University of Mainz, Germany. The project aims at a better understanding of the consequences of cestode infection on multiple levels in the ant species Temnothorax nylanderi. It is based on our previous findings showing severe effects of infection on the individual level, but no reduction in productivity and changed investment patterns on the colony level (Scharf et al., American Naturalist 2012, for a review in Science see http://news.sciencemag.org/sciencenow/2012/09/-scienceshot-sick-ants-dont-compr.html). In the current project we will study how insect societies can buffer detrimental effects of parasite infection. In addition, we are interested in which of the parasite-induced changes in behavior, morphology, and cuticular chemistry are by-products of the infection, can be interpreted as host defenses or manipulation of the host by the parasite. The project will include field manipulations, behavioral laboratory experiments and chemical analyses using GC-MS. The position requires a Diploma or Master degree in Biology (or a related field). The successful candidate should be highly motivated and have a strong background in behavioral / chemical ecology and evolutionary biology. Good skills in biostatistics or motivation to improve statistical knowledge are important. Previous research experiences with social insects, parasites, behavioral experiments, chemical ecology (GC-MS analyses), immunity or microsatellite analyses are advantageous, but not required. The position is fully-funded by the DFG (65% TV-L E13). Students from every nationality are encouraged to apply. The working language of the laboratory is English. Our young group offers an international, dynamic and interactive scientific environment and state-of the art, newly equipped laboratories. Information on our scientific work including recent publications can be found under http://www.bio.uni-mainz.de/-zoo/evobio/318_ENG_HTML.php. For more information, please do not hesitate to contact us foitzik@uni-mainz.de or menzelf@uni-mainz.de. The University of Mainz hosts many excellent scientific institutions (http://www.uni-mainz.de/eng) and Mainz is a historic city located on the River Rhine with many students and a rich social and cultural life (http://www.mainz.de). Interested candidates should send an application as a single pdf e-mail attachment) containing a brief explanation of their research experience and interests (max. 1 page), a curriculum vitae (with the grades of their B.Sc and M.Sc), a copy of their Master or Diploma thesis, and the names and email address of 2-3 potential referees to Dr. Susanne Foitzik (foitzik@uni-mainz.de) or Dr. Florian Menzel (menzelf@uni-mainz.de). Review of applications will begin April 30th 2013 and will continue until the position is filled. The ideal starting date for the position is June 2013, but is negotiable.

Prof. Dr. Susanne Foitzik Evolutionary Biology Institute of Zoology Johannes-v.- Müller-Weg 6 55128 Mainz Germany

+49 6131 39 27 840 foitzik@uni-mainz.de

"Foitzik, Susanne" <foitzik@uni-mainz.de>

UManchester EvolutionCooperation

Agent-based modelling of cooperative behaviour in social networks of animals

Background: Darwinian evolution and cooperative behaviour Darwinian evolution is often assumed to be inherently competitive, frequently characterized by the adage the survival of the fittest. However, individuals do not always operate as adversaries and cooperation is widespread in many animals. Humans show innate predispositions to be moral and prosocial, and these tendencies give rise to complex societies organized by social and political institutions. Group living animals can also be highly prosocial, as evidenced by cooperative breeding, coalitionary support, consolation following conflict, social grooming and even policing of conflict. This constitutes an apparent paradox, as altruism and co-operative behaviour do not fit with the notion of selfish individuals, selfish genes and the survival of the fittest in a competitive world. Explaining the evolution cooperation remains one of the great problems for evolutionary biology, it has been listed as one of the top 25 questions facing science over the next quarter-century by Science Magazine in 2005.

The Project Several mechanisms have been proposed to explain the emergence of cooperation in the face of Darwinian selection, including networked interaction structures between individuals. In evolutionary game theory, for example, population structuring has been shown to have strong impacts on the stability of cooperation. However, such models have historically used stylised population structures (for example random networks) rather than network structures derived from the interaction between individuals observed in nature. We have shown that group structure in primates is highly conserved over evolutionary time, which raises the question of whether these group structures are important promoters of stable cooperation.

This PhD will build on the theoretical work of cooperative dynamics by applying it to real-world animal social networks. Specifically, you will use agent-based models to explore how variation in animal social networks impact on the stability of cooperation. Within the general framework of game theory these models will simulate individual decisions about whether to cooperate, or not, with others based both on the benefits of cooperation and patterns of interactions across different group structures. The models will also explicitly incorporate individual characteristics such as dominance, learning strategies, and enforcement behaviour (i.e. punishment and policing). The project will be largely computational, but, depending on the background of the appointed student, it may contain significant analytical components as well.

The research environment This exciting interdisciplinary project will supervised by Susanne Schultz (Faculty of Life Sciences) and carried out in collaboration with Dr. Tucker Gilman (Faculty of Life Sciences) and Dr. Tobias Galla (School of Physics and Astronomy). Shultzs research group studies the evolution of social cognition and social structure in animals. Gilmans research group uses agent-based models to study the evolution of behaviour and social interactions. Galla is based in the statistical mechanics and complex systems group in Physics and Astronomy. The group has a strong interest in interdisciplinary questions in biology, game theory, economics and the social sciences. Galla has co-organized numerous interdisciplinary meetings, and the group runs a complexity discussion club together with social scientists. The appointed student will be welcome to contribute to these activities.

The candidate We are looking for an enthusiastic student who can drive the project. They will ideally have a quantitative background in theoretical physics, applied mathematics, computer science or an adjacent field. Good programming skills are essential. Experience in agent-based simulations, the theory of complex networks or game theory will be a plus, but is not strictly required, provided the applicant can demonstrate a strong interest in these areas. A strong interest in interdisciplinary questions is required as well as the genuine ability to engage with data collected from biological field-work. The appointed student will have excellent communication skills, and they will be able to work in a team as well as independently.

For more information please contact Susanne Shultz:

susanne.shultz@manchester.ac.uk

http://www.ls.manchester.ac.uk/people/profile/-Default.aspx?PersonID=25440&view=projects#1219
Susanne Shultz Senior Research Fellow/Royal Society University Research Fellow Michael Smith Building Faculty of Life Sciences The University of Manchester Oxford Road, Manchester M13 9PT UK Tel: 44 (0)161 275 3903

Susanne Shultz <susanne.shultz@manchester.ac.uk>

UMelbourne FemaleOrnamentation

PhD opportunity - The function of female ornamentation in lovely fairy-wrens.

A PhD project is available to investigate the function of elaborate female song and plumage in a cooperatively breeding bird, the lovely fairy-wren (Malurus amabilis). The position will be based in the Evolution and Behaviour Group in the Department of Zoology at the University of Melbourne under the supervision of Assoc Prof Raoul Mulder, and co-supervised by Dr Michelle Hall.

Studies on elaborate male traits have formed the foundation of the field of sexual selection. However, ornamentation in females is only recently attracting attention, and there is controversy over whether sexual selection or alternative mechanisms drive the evolution of female ornamentation. Lovely fairy-wrens have the most colourful female plumage among the Australian fairy-wrens, but have never been studied before. The student will be able to work independently to establish a new project investigating the function of elaborate female song and plumage in lovely fairy-wrens, and test competing hypotheses for the evolution of female ornamentation in birds.

Interested students should email their CV, contact details of two academic referees, academic transcript, and a letter describing their research interests to Raoul Mulder (r.mulderATunimelb.edu.au) and Michelle Hall (hall.mATunimelb.edu.au).

The candidate will need to obtain an Australian Postgraduate Award or International Research and Fee Remission Scholarships (for details and scholarship application forms see http://services.unimelb.edu.au/-scholarships/research). The main application deadlines for these scholarships are 31 August (International) and 31 October (Domestic).

Dr Michelle L Hall Research Fellow Department of Zoology, University of Melbourne Melbourne, VIC, 3010, Australia email: hall.mATunimelb.edu.au phone: + 61 3 83446232 www: Google Scholar Profile < http://scholar.google.com.au/citations?user=-3DBcsSi-YAAAAJ&hl=en&oi=ao >

hall.m@unimelb.edu.au

UNeuchatel HostParasite

A PhD position in the evolutionary ecology of host-parasite interactions is available for up to 4 years in Prof. Jacob Koella's lab at the University of Neuchâtel.

The position would suit an enthusiastic, motivated, and independent graduate whose degree has a strong component in parasitology, evolution or ecology. The general area of research will be the evolutlonary ecology of parasites at several levels of organization, linking the host's ecological situation with the parasite's dynamics within its host and its epidemiology, and using one of the host-parasite systems used in the lab (malaria, microsporidians and mosquitoes). The details of the project (including the balance between theoretical and empirical work) will be adapted to suit your interests, and you will be given the time to, and be expected to, have considerable input in developing the project.

The position requires some teaching of undergraduate and graduate biology labs, usually in French, and you will have the opportunity to supervise undergraduate and Masters projects. An MSc (or equivalent) in Biology is required.

The position is available as of August 1, 2013, with starting date preferably by October 1, 2013. The starting salary is about 35000 Fr.

Neuchâtel is located in the French part of Switzerland and is an attractive city with a high quality of life. The city is located on the shore of Lake Neuchâtel with the Jura Mountains to the North and a view of the Bernese Alps to the South. For outdoors enthusiasts, this is an excellent area for outdoor activities such as hiking, climbing or skiing.

If you are interested in the position, please send a 1-2 page cover letter indicating research interests and background, your CV, and two letters of reference to jkoella@gmail.com before May 18, 2013. Jacob Koella

Institut de Biologie Université de Neuchâtel rue Emile-Argand 11 2000 Neuchâtel Switzerland

jkoella@gmail.com

UNorthernColorado PlantConservation

Graduate Position: U. Northern Colorado. Plant Conservation Genetics

Masters position in Plant Conservation Genetics

A MS position is available in the laboratory of Dr. Mitchell McGlaughlin at the University of Northern Colorado. This is part of Bureau of Land Management funded project to enhance our understanding of breeding system and genetic structure in a US threatened annual Phacelia (Boraginaceae). The project will have three major components: 1) designing species specific microsatellite markers for Phacelia, 2) conducting paternity analysis of two populations where maternal plants and seeds will be genotyped to determine if the species is predominantly outcrossing or selfing, and 3) examining population genetic structure across the landscape where the species occurs. Funding will cover all lab and field expenses associated with this project. The selected student will be supported through a TA at UNC, which includes a full tuition waiver.

Students interested in conservation genetics, population genetics, plant breeding systems or evolutionary biology are encouraged to apply. Applicants to UNC are required to have taken the GRE general test, and submit undergraduate transcripts, three letters of recommendation with a department specific evaluation form, and a letter of intent. Interested applicants should contact Dr. Mitchell McGlaughlin (mitchell.mcglaughlin@unco.edu) prior to submitting an application.

For more information about application procedures and the department visit:

http://www.unco.edu/nhs/biology/students/grad_programs.html or the McGlaughlin Lab visit:

http://www.unco.edu/mcglaughlinlab/Site/Home.html – Mitchell McGlaughlin, Ph.D. Assistant Professor School of Biological Sciences 501 20th Street, Ross Hall 1560 University of Northern Colorado Greeley, CO 80639 970-351-2139 Mitchell.McGlaughlin@unco.edu http://www.unco.edu/mcglaughlinlab Mitchell.McGlaughlin@unco.edu

USDA Ames Iowa InsectEvolution

GRADUATE STUDENT POSITION

I am recruiting a graduate student (M.S. or PhD if masters degree is already in hand) for a research project involving characterization of insect flight behavior using laboratory flight mill systems in the context of resistance evolution. I am a Research Entomologist with USDA-Agricultural Research Service, Corn Insects and Crop Genetics Research Unit, with a courtesy faculty appointment in the Department of Entomology at Iowa State University, Ames, Iowa (http://www.ent.iastate.edu/). My laboratory is located on the ISU campus.

Our group's mission is to study the population ecology, genetics, and behavior of corn insect pests, and my interests are mainly in the realm of dispersal, migration, and gene flow. The graduate student will work with at least two pest insects. The western corn rootworm, Diabrotica virgifera virgifera, is a chrysomelid beetle and the worst pest of corn in North America. It also is spreading in Europe as an invasive species. It recently has developed resistance in the Midwestern U.S. to a particular type of transgenic Bt corn, with many implications for farmers, industry, public-sector scientists, and government regulators. Characterization of long-distance movement of WCR adults is critical to understanding the dynamics of resistance evolution and spread of resistance in this insect. The grad student's main project would be to investigate and compare flight behaviors of resistant and wild-type WCR using laboratory flight mills. In addition, the western bean cutworm, Striacosta albicosta, is a noctuid moth pest of corn that has undergone a recent range expansion out of the Great Plains to the East Coast. The trigger for the expansion is unknown, and almost nothing is known about this species' flight capacity and behavior. Recent establishment of a laboratory colony will allow flight mill studies. It will be a demanding project requiring attention to detail, perserverance (especially in the beginning when learning to tether insects to the flight mills), and critical thinking. The information gained for both species will be of immediate interest to the scientific community and of ultimate benefit to corn growers. There will be room for additional side projects as well depending on the student's interests and talents.

Pending final approval of funding (anticipated), this will be a research assistantship (approx. $19,632/year stipend, plus paid tuition) for 2.5 - 3 years. Start date: as soon as practicable, but no later than mid-August 2013.

If interested, please send me: 1) a cover letter describing your background in science, career goals, and research interests; 2) your C.V.; 3) contact information for three references; 4) copy of transcripts; and 5) GRE scores. Please send to Tom.Sappington@ars.usda.gov .

Thomas W. Sappington, PhD USDA-ARS Corn Insects & Crop Genetics Research Unit Genetics Laboratory, ISU Ames, IA 50011 USA

Tel: 515-294-9759 Fax: 515-294-2265 Tom.Sappington@ars.usda.gov http://www.ent.iastate.edu/dept/faculty/sappington/ "Sappington, Tom" <Tom.Sappington@ARS.USDA.GOV>

UWesternOntario ModellingEvolutionBreeding

GRADUATE STUDENT POSITION (MASTER'S OR PHD)

University of Western Ontario, London, Ontario, Canada

Department of Applied Mathematics

To begin Sept 2013

Financial Support is available

DESCRIPTION

Geoff Wild's group (www.apmaths.uwo.ca/~gwild) is looking to fill at least one graduate student position at either the Master's or Doctoral Level.

Graduate student research will focus on modelling the evolution of cooperative breeding, but project specifics can certainly be negotiated.

QUALIFICATIONS

Potential Doctoral students should have a previous degree in mathematics or related discipline, as well as a strong, demonstrated interest in evolutionary biology.

Candidates interested in study at the Master's level need not have a previous degree in mathematics. However, university-level training in differential equations, linear algebra, and multivariable calculus, are required—as is mathematics training at the senior-undergraduate level.

Excellent written and oral communication skills are required!

HOW TO APPLY

Informal inquiries should be sent via email to gwild@uwo.ca prior to engaging in the university's formal application process.

Geoff Wild <gwild@uwo.ca>

UppsalaU ComputMolEvol

I have a four year PhD student position available in my group suitable for anyone with an interest in molecular evolution and a computational/biological background. Please get in touch with me (simon.whelan@ebc.uu.se) if you have any questions or wish to discuss more details about the project. For full details see URL: http://www.uu.se/jobb/phd-students/annonsvisning?tarContentId=3D239394 Title: PhD-student in computational molecular evolution Closing date: May 14th 2013

A PhD-student position in computational molecular evolution at the Evolutionary biology center, Uppsala University. Starting date as soon as possible or as agreed upon.

Project description: Computational molecular evolution provides a way of studying and analysing differences in the genome within and between species. Such studies typically involve a multi-step process whereby a set of nucleotide or amino acid sequences are selected and arranged relative to one another in a multiple sequence alignment. Evolutionary inference is then performed using statistical methodology to (e.g.) infer the evolutionary relationship between the sequences or to investigate the selective forces acting on those sequences. These approaches have found widespread use in many areas of biology, resulting in (e.g.) new insights into the tree of life, the identification of which genes adapted on the human lineage, and the revelation that chimpanzees and gorillas are the sources of human HIV infections.

This project focuses on methodology development in computational molecular evolution. The exact topics to be studied can be tuned to the successful candidate's interests, but one possible area for study is the interaction between alignment and evolutionary inference. Existing methods for alignment usually rely on using regional similarities between sequences to identify an optimal multiple sequence alignment. This approach leads to two problems. First, few alignment methods explicitly account for the evolutionary process that gave rise to the differences between the sequences. The resultant alignment may therefore not reflect the evolutionary history of the sequences and therefore be of limited use for evolutionary inference. Second, picking a single alignment neglects uncertainty in the alignment procedure. Over-confidence in a single alignment may affect evolutionary inference, but there are relatively few ways to correct for uncertainty. In this project you will aim to create new methods for performing or processing multiple sequence alignments to make them more suitable for evolutionary inference. You will then assess the new methods' performance by examining real and simulated data.

Background of applicant: Applications are welcome from candidates with a background in Biology, Computer Science, or Statistics. Candidates from any background should be able to demonstrate a strong interest and motivation to study molecular evolution. Candidates must also be able to demonstrate, or show clearly the potential to learn, skills associated with computational molecular evolution, including the use of LINUX/UNIX and the ability to work with scripting languages (e.g. Python/PERL) and/or programming languages (e.g. C/++ or JAVA).

Conditions: The PhD training comprises four years of full time research and studies. The successful candidate will receive a fellowship the first year and a PhD-student position year 2-4. The position can be combined with up to 20% of teaching assistantship, which will then prolong the position accordingly. Please contact Simon Whelan, simon.whelan@ebc.uu.se, +46 18 471 6449 for more information. Union representatives are Anders Grundström, Saco-rådet +46 18 471 5380 och Carin Söderhäll, TCO/ST +46 18 471 1996, Stefan

Djurström, SEKO + 46 18 471 3315.

— Simon Whelan | Evolutionary Biology Centre, Uppsala University | T: +46-(0)18-4716483

simon.whelan@ebc.uu.se

Vienna PopulationGenetics

PhD positions in Population Genetics

New positions are available at *The Vienna Graduate School of Population Genetics:* the application deadline is *May 30, 2013*:

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

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

Topics include:

- Analysing next generation sequencing data and understanding the sampling properties of high throughput technologies - The 1001 Genomes Project: Population genetics of *Arabidopsis thaliana* - Speciation genetics in European columbines (*Aquilegia*) - Mutagenesis in the germline with age - Population genetic inference using Pool-Seq data - Evolution of gene expression in *Drosophila* - Speciation genomics: mapping of hybrid incompatibilities - Inference of selection from time series data - Understanding the ecology and genetics of an adaptive trait in * Drosophila* embryos - Mathematical models of spatially varying selection in subdivided populations - Statistical methods for detecting selective sweeps using genome- wide data - The footprint of adaptive gene introgression after secondary contact - Probabilistic models for the population genetics of molecular evolution - Inferring selection using *Drosophila* whole genome sequence data

Only complete applications (CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by 30.05.2013 will be considered. Two letters of recommendation need to be sent directly by the referees.

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at c/o Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 A-1210 Vienna

Tel: +43 1 25077 4338 Fax: +43 1 25077 4390

julia.hosp@gmail.com

WageningenU BehaviouralEvolution

PhD position in Behavioural Ecology, Wageningen University

How is phenotypic variation in great tits (Parus major) maintained by sexual selection?

PhD position

We offer a PhD Position (1.0 FTE) to undertake research on sexual selection and reproductive investment in great tits within the newly established Behavioural Ecology chair group at the Animal Science Department of Wageningen University, the Netherlands. This position is financed by the WIAS graduate school of Wageningen University. It is linked to an EU funded project and comes with attractive equipment and consumables support. Research will be conducted in cooperation with the Animal Ecology Department of the Netherlands Institute of Ecology (NIOO-KNAW).

Project details

This project will investigate the potential of individual differences in mate choice and reproductive investment to maintain phenotypic variation in great tits. Individual birds are expected to differ in their mate preferences and reproductive allocation in relation to their own individual characters, which may help to maintain variation within the population. The project will involve performing captive mate choice trials with wild great tits, as well as extensive fieldwork to measure reproductive investment. There is also the opportunity to complement this behavioural and phenotypic work with genetic information.

We ask

- Candidates must have an MSc or equivalent experience in a behavioural ecology or related fields (e.g.

Animal Behaviour, Animal Ecology) - Be enthusiastic about field work - Strong experimental and analytical skills - Good organizational and (written and spoken) communication skills, and a proven ability to collaborate with others. - Willingness to conduct to organize and extensive ornithological fieldwork. - 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. article9 of the WoD) is desirable.

We offer

- Employment basis: temporary for specified period. Duration of the contract: 1 + 3 years, maximum hours per week: 38. Additional conditions of employment: To begin with, a PhD-appointment for a period of 12 months. Continuation of the appointment with another 36 months will be based on performance evaluation. Gross salary per month 2062 in the first year, rising to 2638 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. Wageningen University is an internationally leading research and education institution, ranked among the top 25 universities in Europe (THE World University Rankings, 2011-12). This project will be carried out in the new Behavioral Ecology Group within the Department of Animal Sciences, and will be supervised by Dr. Camilla Hinde.

For further information, please contact Dr. Camilla Hinde (camilla.hinde@wur.nl).

The application deadline is 15 May 2013.

Please apply through this website:

http://www.wageningenur.nl/en/Jobs/Vacancies/-Show/How-is-phenotypic-variation-in-great-tits-Parus-major-maintained-by-sexual-selection.htm Links

http://www.wur.nl/uk/ http://www.zod.wur.nl/-UK/ For further information about working at Wageningen UR, take a look at www.jobsat.wur.nl "Hinde, Camilla" <camilla.hinde@wur.nl>

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AMNH NewYork CuratorProfessorDirector ComparativeBiol

Senior Search: Curator, Professor, and Director of Comparative Biology Initiative American Museum of Natural History

The American Museum of Natural History (AMNH) in New York invites applications and nominations for an outstanding scholar at the Full Curator & Full Professor level with internationally-recognized research and leadership credentials, and demonstrated, ongoing high-impact research productivity and grantsmanship, to provide innovative leadership for a new museum-wide initiative in comparative biology. This initiative will incorporate the work of multiple investigators at the Museum and at collaborating institutions in genomics and phenomics (large-scale phenotypic analysis), aimed at understanding the evolution and relationships of organisms in ways that clarify and illuminate the architecture of life. The successful candidate for this position should show experience and interest in managing large'scale, interdisciplinary, collaborative, multi-institutional projects and is expected to qualify for and be appointed as a tenured full curator in either the Division of Invertebrate Zoology or Vertebrate Zoology, and as a full professor in the Richard Gilder Graduate School at the AMNH. We seek a creative, active, broad-based researcher and dynamic academic leader who interacts well with others and who will utilize the extensive resources the Museum has to offer in the way of collections, research instrumentation and laboratories, teaching and mentoring, exhibition, and public education.

We particularly seek applications from, or nominations of, candidates with a compelling vision for the future trajectory of their science, and for comparative biology in general, and whose research addresses fundamental, cross-disciplinary questions. In addition to the above-noted expectations for high productivity and grantsmanship, the successful candidate will have outstanding communication skills in engaging diverse communities and demonstrated capabilities in management of collaborative projects and decision-making. Experience in interacting with governmental and non-governmental agencies and in fundraising are highly desirable, as are collection-based, field-based and/or computational research. Other responsibilities or opportunities include advising graduate students and postdoctoral fellows, offering courses in the Comparative Biology Ph.D. Program of the Museum^{1}s Richard Gilder Graduate School, institutional service, development activities, and participating in Museum-sponsored exhibits and educational programs.

In addition to applications, we invite recommendations or nominations of potential candidates, and request that these include a resume and contact information for the nominee. Nominations or applications can be submitted to seniorcuratorsearch@amnh.org. Applicants should submit the following materials electronically, preferably as PDF files, via a single email message toseniorcuratorsearch@amnh.org (Subject line: Senior Curator IZ-VZ Search Committee: your name): 1) a cover letter in which you indicate your interest, experience, and qualifications for the position; 2) a curriculum vitae; 3) PDF files of up to five recent publications; and 4) names and contact information for five referees (to be contacted by the Museum only for the process of tenure review in the case of a pending appointment). Inquires should be directed to John Flynn, Chair of the Search Committee and Dean of the Richard Gilder Graduate School: dean-rggs@amnh.org. Applications or nominations should be received no later than May 10, 2013.

Employer Information: The American Museum of Natural History is one of the world's preeminent scientific and cultural institutions. Since its founding in 1869, the Museum has advanced its global mission to discover, interpret and disseminate information about human cultures, the natural world and the universe through a wide-ranging program of scientific research, education and exhibition. The Museum^{1}s research collections include more than 33 million natural history and cultural objects, and AMNH scientists undertake more than 100 expeditions annually. Science at the Museum includes five academic divisions, the Richard Gilder Graduate School, Sackler Institute of Comparative Genomics, 1 million specimen-capacity Ambrose Monell Cryo Collection, Center for Biodiversity and Conservation, high performance computational facilities, Microscopy and Imaging Facility, Southwest Research Station, the largest independent natural history library in the Western Hemisphere, and an array of other scientific facilities and resources.

The American Museum of Natural History is an Equal Opportunity/ Affirmative Action Employer. The Museum encourages Women, Minorities, Persons with Disabilities, Vietnam Era and Disabled Veterans to apply. The Museum does not discriminate due to age, sex, religion, race, color, national origin, disability, marital status, veteran status, sexual

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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

AarhusU EvolutionaryGenetics

Associate Professor in Evolutionary Genetics

The Department of Bioscience, Aarhus University, Denmark, invites applications for a position as Associate Professor in evolutionary genetics starting October 1, 2013.

The research in evolutionary biology and genetics at the Department of Bioscience is conducted within the framework of the research group Integrative Ecology and Evolution±. A broad range of research topics are covered, including population and conservation genetics, quantitative genetics, bioinformatics, life-history evolution, behavioral ecology , and evolutionary responses to environmental stress.

We seek a researcher with an internationally excellent academic track-record within evolutionary genetics, who has the ability to target important research topics using state-of-the-art approaches. A strong publication record, documented skills in attracting external funding and experience with international research collaboration are emphasized.

The appointee must have documented skills and experience with teaching and supervision of students at undergraduate and graduate levels.

For more information, please contact Head of Department, Professor Bo Riemann, tel: , tel. +45 40270360, bri@dmu.dk or Professor Michael M. Hansen, tel. +45 40247191, michael.m.hansen@biology.au.dk.

All applications must be made online and received by 10/05/2013

More information about the position, including a link for online application can be found here: http://www.au.dk/en/job/nat/academicpositions/ Information about the Department of Bioscience can be found here: http://bios.au.dk/en/ Information about Aarhus University can be found here: http://www.au.dk/en/ Michael M. Hansen Professor Department of Bioscience Aarhus University Ny Munkegade, Bldg. 1540 DK-8000 Aarhus C Denmark E-mail: michael.m.hansen@biology.au.dk Web page: http://person.au.dk/michael.m.hansen@biology Tel.: +45 40247191

Michael M©ller Hansen <michael.m.hansen@biology.au.dk>

EasternKentuckyU CommunityEvolution

The Department of Biological Sciences at Eastern Kentucky University is accepting applications for a Community Ecologist at the rank of Assistant Professor. This is a 9-month, tenure-track position to begin August 15 2013. Teaching responsibilities will include courses at the undergraduate and graduate (MS) levels. Primary courses to be taught include an introductory course in ecology and evolution, community ecology, and other courses within the candidate's area of expertise. The successful candidate will be expected to establish an active research program that includes mentoring undergraduate and master's level students. Requirements include a Ph.D. from a regionally accredited or internationally recognized institution. Candidates must have a strong record of research accomplishments and must provide evidence of excellent teaching and communication skills.

Review of applications will begin on 29 April 2013, and the position will remain open until filled. All interested applicants must apply at jobs.eku.edu (search requisition #0613043) or visit http://jobs.eku.edu/applicants/Central?quickFind=71921. All offers of employment are contingent on completion of a satisfactory background check. Eastern Kentucky University is an EEO/AA institution that values diversity in its faculty, staff, and student body. In keeping with this commitment, the University welcomes applications from diverse candidates and candidates who support diversity.

Please direct inquiries to:

Stephen Richter Search Committee Chair

Eastern Kentucky University Department of Biological Sciences phone: 859-622-8688 stephen.richter@eku.edu

Cheers, -Brad

– Brad Ruhfel Assistant Professor & Curator Dept. Biological Sciences Eastern Kentucky University http://people.eku.edu/ruhfelb Brad.Ruhfel@eku.edu

FreieU Berlin ComputationalMetagenomics

Junior Professorship in Computational Metagenomics (W 1)

Freie Universität Berlin, Department of Mathematics and Computer Science Institute of Computer Science

and the

Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB)

jointly invite applications for a

Junior Professorship in Computational Metagenomics (W 1)

The successful applicant will be required to conduct research and teach in the area named above. Appointment requirements are governed by article 102a of the Berlin Higher Education Act (Berliner Hochschulgesetz).

The appointee will have an outstanding track record of university teaching and research in metagenomics data analysis and bioinformatics as applied to environmental metagenomics and biodiversity research in general. Her or his work should further strengthen an innovative research program with high international visibility and focus on data analysis and algorithm development, interlinking with and complementing existing research initiatives at the IGB as well as Freie Universität Berlin. Applicants should be familiar with grant-sponsored research. The successful candidate is expected to teach at both graduate and undergraduate levels within Freie Universität Berlin's Department of Mathematics and Computer Science. She or he will also be required to assume responsibilities within the university's institutions of academic self-governance. The working language at the IGB is English. For courses taught at Freie Universität Berlin and in order to facilitate communication among our multicultural staff, proficiency in both German and English is strongly desirable.

Aside from a work area at the Department of Mathematics and Computer Science the professor's office and staff will be located at the IGB, the largest freshwater ecology institute in Germany, which offers cutting-edge laboratory and field facilities for interdisciplinary research (including a large-scale experimental infrastructure and long-term research programs). Furthermore, the successful candidate will cooperate closely with the Berlin-Brandenburg Institute of Advanced Biodiversity Research (BBIB).

Please direct further inquiries at Univ.-Prof. Dr. Klement Tockner, Director of the IGB (tockner@igb-berlin.de), or Prof. Dr. Knut Reinert, Head of Bioinformatics at Freie Universität Berlin (knut.reinert@fu-berlin.de).

The successful candidate will be appointed as a civil servant for an initial duration of three years. Provided that her or his performance is thereafter evaluated positively, employment may be extended for three more years.

Applications quoting the reference Metagenomics should include a CV, copies of all certificates of academic qualification, a list of publications (plus copies of five representative publications); evidence of educational competence (such as courses previously taught) as well as involvement in ongoing and future research endeavours, joint research projects and externally funded projects. All materials must be received no later than 8 May 2013 at

Freie Universität Berlin Fachbereich Mathematik und lnformatik Univ.-Prof. Dr. Rupert Klein, Dekan Arnimallee 14 14195 Berlin, Germany

or via email at dekan@mi.fu-berlin.de.

Application guidelines and general information on the appointment procedure as well as requirements for junior professorships at Freie Universität Berlin can be found at www.fu-berlin.de/praesidialamt. For additional details, please visit www.igb-berlin.de, www.fu-berlin.de, www.mi.fu-berlin.de, www.math-berlin.de and www.math.tu-berlin.de/MDS.

Dr. Michael T. Monaghan Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) Mueggelseedamm 301 - 12587 Berlin - Germany monaghanlab.org - monaghan@igb-berlin.de +49 (0) 30 6418 1684

Michael Monaghan <monaghan@igb-berlin.de>

HunterCollege ResearchAssist

Job ID: 7580

Location: Hunter College

Full/Part Time: Full-Time

Regular/Temporary: Regular

GENERAL DUTIES Supports research projects and activities in connection with CUNY programs - May assist faculty research groups by configuring and testing equipment, collecting and organizing data, and preparing documentation. - Performs direct research tasks under supervision. - May develop or utilize computer-based systems to collect and analyze data. - May assist in preparing reports of research findings.

CONTRACT TITLE Research Assistant

FLSA Non-exempt

CAMPUS SPECIFIC INFORMATION The Research Assistant will assist with the research needs of the physical anthropology faculty and labs at Hunter College and perform additional tasks as required. See the Department of Anthropology Website for more details on research in the Gilbert, Pontzer, Rothman, and Steiper Labs (http://www.hunter.cuny.edu/anthropology).

MINIMUM QUALIFICATIONS Bachelor's Degree or equivalent experience relevant to the research being performed.

OTHER QUALIFICATIONS Candidates should have an undergraduate degree in anthropology or a related discipline such as biology, ecology, evolution, geology, human biology, nutrition, paleontology, or zoology. Candidates should have diverse experiences within physical anthropology laboratories or those in a related discipline. Candidates should be competent in standard computer software suites (e.g. spreadsheet and word processing programs) and have knowledge of hardware and software maintenance. The successful candidate must be organized, neat, detail-oriented, safety conscious and able to effectively manage multiple priorities. Candidates should be able to balance and triage tasks with different deadlines and levels of urgency, e.g. those have a long-range time horizon, those that are immediately needed, and those that are ongoing. Candidates should be able to work with and take direction from multiple faculty members to ensure the timely completion of all tasks.

Preferred qualifications include a graduate degree in anthropology or a related discipline such as biology, ecology, evolution, geology, human biology, nutrition, paleontology, or zoology. Experience working in nutrition, genetics, paleontology, and/or biomechanics labs is a plus. We are strongly committed to achieving excellence through diversity. As such, candidates with experiences working in diverse environments are desired.

COMPENSATION $35,244 - $40,681

BENEFITS CUNY offers a comprehensive benefits package to employees and eligible dependents based on job title and classification. Employees are also offered pension and Tax-Deferred Savings Plans. Part-time employees must meet a weekly or semester work hour criteria to be eligible for health benefits. Health benefits are also extended to retirees who meet the eligibility criteria.

HOW TO APPLY You can view and apply for this job at:

https://home.cunyfirst.cuny.edu/psp/cnyepprd/-GUEST/HRMS/c/HRS_HRAM.HRS_CE.GBL?Page=HRS_CE_JOB_DTL&Action=A&JobOpeningId=-7580&SiteId=1&PostingSeq=1 Click on the "Apply Now" button and follow the application instructions. Please have (A) 1-2 page letter of interest highlighting experiences of particular relevance to this position; (B) vitae or resume; and (C) contact information for 2 individuals who will serve as a reference available to attach into the application before you begin. The required material must be uploaded as ONE document. The document must be in .doc, .docx, .pdf, .rtf, or text format.

Informal enquiries can be directed to Michael Steiper (msteiper@hunter.cuny.edu).

CLOSING DATE The committee will begin reviewing applications on March 21, 2013. ****The search will remain open until the position is filled.****

JOB SEARCH CATEGORY CUNY Job Posting: Managerial/Professional

EQUAL EMPLOYMENT OPPORTUNITY We are committed to enhancing our diverse academic community by actively encouraging people with disabilities, minorities, veterans, and women to apply. We take pride in our pluralistic community and continue to seek excellence through diversity and inclusion. EO/AA Employer.

msteiper@hunter.cuny.edu

IKIAM Ecuador Rector

On Behalf of Tannya Lozada (tannya.lozada@conocimiento.gob.ec) RECTOR FOR AMAZONIAN REGIONAL UNIVERSITY (IKIAM), ECUADOR

The Ecuadorian Ministry of Coordination of Knowledge and Human Talent is conducting an international search for highly qualified candidates for the position of Rector of the Amazonian Regional University, IKIAM (Tena, Napo,Ecuador).IKIAM, which translates as Nature in native Shuar, is called to be at the fore front of teaching and research in Earth and Life Sciences. The area of specialization of the Rector is open. We welcome applicants with work and research experience in Latin America. The future Rector may currently be a leader of a college or university. The candidate must show management,administrative and leadership skills. This position requires a proven record of distinguished teaching, research, scholarship, and service commensurate with a faculty appointment at the rank of a tenured professor. The person called to lead IKIAM will also have a deep understanding of higher education, and of the role that this sector plays in national and regional development.

Requirements - Doctoral degree required- Hold tenure as associate or full professor - Proven track record of research (publications and/or patents) - 5+ years teaching experience - 5+ years of administrative experience - Spanish fluency

Application process For information on how to apply please visit http://www.conocimiento.gob.ec http://www.conocimiento.gob.ec/convocatoria-para-la-seleccion-del-rector-de-la-universidad-regional-amazonica-ikiam/ http://goo.gl/WG2SD After a careful consideration of review of applicants' academic production,educational background, and experience, the Ministry will present a shortlist of candidates for appointment by EcuadorÂs highest authorities, in accordance to national law.For additional information, nominations or confidential inquiries, contact Dr. Tannya Lozada, IKIAM Project Manager, +593-2-3946800 Ext. 1804 ortannya.lozada@conocimiento.gob.ec

Nora Oleas <noleas@hotmail.com>

IndianaU SouthBend 1yr Teaching

VISITING LECTURER IN BIOLOGICAL SCIENCES Indiana University South Bend invites applications for a 1-year lectureship in biological sciences with an expected start date of August 2013. The successful candidate will hold a doctorate (preferred) or master^{1}s degree in biology or related discipline, will have strong oral and written communication skills, and will show evidence of excellent teaching ability. Courses to be taught may include general biology for biology majors (especially intro course in ecology, evolution, and genetics), with possibility of some human anatomy and physiology laboratory for pre-nursing and pre-dental hygiene students.

For full consideration, please apply by April 26.

Application materials consist of a cover letter, curriculum vitae, copies of undergraduate and graduate transcripts, three confidential letters of recommendation, and a statement of teaching philosophy.

Please send materials to Dr. Andrew Schnabel (aschnabe@iusb.edu), Department of Biological Sciences, Indiana University South Bend, 1700 Mishawaka Ave., P.O. Box 7111, South Bend, IN 46634.

An AA/EEO Employer. Applications from minorities, women, veterans, and people with disability are encouraged.

aschnabe@iusb.edu

LouisianaStateU Bioinformatics

PROFESSIONAL-IN-RESIDENCE (Bioinformatics Support Group Leader) Center for Computation & Technology (CCT) Louisiana State University The Center for Computation & Technology (CCT) at Louisiana State University invites applications for a position to lead a group of research scientists in Computational Bioinformatics, broadly defined. The successful candidate will build and lead a Bioinformatics Support Group (BSG) to support data-intensive and computationally demanding research activities across various academic units on LSU's main campus, at the LSU School of Veterinary Medicine, the Pennington Biomedical Research Center, and LSU's Health Sciences Centers. The successful candidate will have the opportunity to take advantage of resources at all of these sites and will be encouraged to interface as well with industry scientists across Louisiana. Research areas that would be supported by the recruited team of scientists include but are not limited to genomics, bioinformatics data analysis, biostatistics, biomolecular structure/function, systems biology modeling, and computational neuroscience.

The CCT is an innovative research environment, advancing computational sciences, technologies and the disciplines they touch. Researchers at CCT use the advanced cyberinfrastructure high-bandwidth networks, high-performance computing, advanced data storage and analysis, and hardware and software development available on campus and across the Louisiana Optical Network Initiative (LONI) to enable research in many different fields. By uniting researchers from diverse disciplines, ideas and expertise are disseminated across LSU departments to foster knowledge and invention.

The new lead of the BSG will be charged with mobilizing this infrastructure to support the interdisciplinary research activities enumerated above. S/he will participate in and lead the development of extramural grant proposals, and provide expertise and mentoring to additional BSG research scientists who are tasked with developing tools and techniques to support LSU's wide range of bioinformatics research activities. This position will also participate in and oversee the development and presentation of tutorials and workshops as needed to strengthen the community's research activities.

Required Qualifications: Ph.D. in biology, computational science, or a related area with emphasis on bioinformatics data analysis; five years of bioinformatics research experience. Additional Qualifications Desired: Experience leading bioinformatics and biostatistics projects, teams and software use and development; experience with common software development languages and tools, software design, and architecture; an understanding of and experience with scripting in PERL, GALAXY, R/Bioconductor, and/or similar platforms and genomics tools; experience with large dataset management specific to next-generation sequencing; experience in the development of web interfaces to bioinformatics tools; experience with high-performance computing, parallel programming and/or programming frameworks; experience using virtual collaborative environments.

An offer of employment is contingent on a satisfactory pre-employment background check. Application deadline is March 31, 2013 or until a candidate is selected. Apply online and view a more detailed ad at: www.lsusystemcareers.lsu.edu Position #037064

LSU IS AN EQUAL OPPORTUNITY/EQUAL ACCESS EMPLOYER Quick link at ad URL: https://lsusystemcareers.lsu.edu/applicants/-Central?quickFind=55691 Jenn

Jennifer A. Randazzo, Staffing Partner Staffing and Employment Center Office of Human Resource Management 103 Thomas Boyd Hall Louisiana State University Phone: (225) 578-8830 Fax: (225) 578-6571 jrandazzo@lsu.edu www.lsusystemcareers.lsu.edu Jennifer A Randazzo <jrandazzo@lsu.edu>

ManchesterMU EvolBiology

Dear Evoldir

There is currently a Lectureship in Ecology vacancy at Manchester Metropolitan University. The remit for the position is broad; strong applicants will have research interests in ecological, organismal biology and be prepared to take on teaching duties including leading and participating in field courses in ecology.

The successful applicant will join the faculty of Science & the Environment in the Division of Biology and Conservation Ecology with a small group of research active and enthusiastic colleagues.

Additional details and application information here: https://www.jobs.mmu.ac.uk/mmujobsite/-VacancyDetail.aspx?VacancyUID=3D000000007720 The closing date is 26 April 2013.

Please communicate the the details of the position vacancy to anyone who may be interested.

E.Harris@mmu.ac.uk

MichiganState ResTech PlantSymbiosisGenomics

The new Friesen lab at MSU is seeking a talented person for a research technician (Research Technologist I) position starting no earlier than May 1st. Duties will include lab, greenhouse and growth chamber experiments studying ecological, evolutionary, and genomic aspects of interactions between Medicago plants and their associated microbial communities. Part of the position will be to assist with daily lab operations, including working with undergraduate and graduate students. The successful applicant will be organized, detail-oriented, work well in teams, and have strong communication skills. Experience with plants and/or microbes, and an interest in genomics, ecology, and evolution would be a plus. Initial employment term is for one year; the position may be renewed pending availability of funds and ongoing performance.

Apply with your CV (include three references) and cover letter at https://jobs.msu.edu, posting number 7579. Contact Maren Friesen (mfriesen@msu.edu) with any questions. For full consideration, applications must be received by April 9, 2013.

Institutional statement: MSU is an affirmative-action, equal-opportunity employer. MSU is committed to achieving excellence through a diverse workforce and inclusive culture that encourages all people to reach their full potential. The University actively encourages applications and/or nominations of women, persons of color, veterans and persons with disabilities.

Maren L. Friesen Assistant Professor, Dept. Plant Biology Michigan State University 612 Wilson Rd, East Lansing, MI USA 48824-6481 phone: +1 (323) 454-3023 || fax: +1 (517) 353-1926 http://friesen.plantbiology.msu.edu/ maren.l.friesen@gmail.com

NMNH Smithsonian 2 GeneticsLabTech

Two more genetics lab technician positions at the Smithsonian. They are federal positions so you must be an US citizen - sorry to those who would like to apply but are not eligible.

Good luck, Karen

Begin forwarded message:

Subject: [LabAll] Lab technician positions in NMNH - announcements open on USAJOBS

2 permanent full time positions advertised at NMNH for molecular lab technicians: Please forward/post/advertise

LAB: https://www.usajobs.gov/GetJob/ViewDetails/342031100 Entomology: https://www.usajobs.gov/GetJob/ViewDetails/342035800 ~~~ Karen Osborn osbornk@si.edu<mailto:osbornk@si.edu> 202-633-3668 Research Zoologist/Curator Department of Invertebrate Zoology Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012 Washington, DC 20013-7012 USA

Courier address: Smithsonian Institution, MRC 0163, Natural History, West Loading Dock 10th and Constitution Ave., Washington, DC 20560

OsbornK@si.edu

NMNH Smithsonian ResVertZoologist

Dear Colleagues:

The Smithsonian Institution's National Museum of Natural History is advertising a Research Zoologist and Curator position in Vertebrate Zoology (the fields of herpetology, ichthyology, mammalogy, and/or ornithology):

https://www.usajobs.gov/GetJob/ViewDetails/341551700 The advertisement will be open to applicants for 6 weeks, from Monday, April 22, 2013 to Monday, June 3, 2013.

Although the advertisement in USA Jobs describes a 4-year term position, the job is intended to become permanent after tenure evaluation. Research facilities associated with the position include one of the world's largest scientific collections of vertebrates, the Laboratories of Analytical Biology (for molecular genetics and bioinformatics research), the Global Genome Initiative and associated biorepository, a stable isotope laboratory at the Smithsonian's Museum Conservation Institute, scientific imaging services, and many other resources. Smithsonian Fellowships and Internships provide opportunities to advise undergraduate through post-doctoral scholars. In addition, many research curators in the museum have adjunct appointments at local universities. The position carries with it excellent opportunities to participate in public education (for instance, the museum's public exhibits receive 7-8 million visitors per year, making it the most visited natural history museum in the world).

Some relevant links: http://vertebrates.si.edu/ http://www.mnh.si.edu/rc/lab/index.html http://www.mnh.si.edu/ggi/ http://www.si.edu/ofg/ http://www.si.edu/ofg/Units/sorsnmnh.htm Sincerely,

kmh

Kristofer M. Helgen, Ph.D. Research Zoologist and Curator-in-Charge Division of Mammals National Museum of Natural History Smithsonian Institution P.O. Box 37012, MRC 108 Washington, D.C. 20013-7012 USA (202) 633-1270 (office)

HelgenK@si.edu http://vertebrates.si.edu/mammals/-mammals_staff_pages/helgen_kris.cfm "Helgen, Kristofer" <HELGENK@si.edu>

NatlU IrelandMaynooth 5 EvolutionaryBiol

Hi folks,

We have five permanent academic positions available in my department at the National University of Ireland Maynooth.

These are NOT tenure-track, they are permanent right from the start.

Successful candidates will have their own laboratory space and will be expected to apply for grants and carry out research in addition to their teaching responsibilities.

Applications from people with a background in evolution, genomics, bioinformatics are all encouraged and welcome.

More details here:

http://humanresources.nuim.ie/documents/-JobSpec_Lecturer_Biology_SEBLB.pdf Please pass this email on to people you think might be interested.

best,

James.

– Prof. James McInerney, | Center for Communicable Disease Dynamics, Molecular Evolution & Bioinformatics Unit,| Harvard School of Public Health, Department of Biology, | 677 Huntington Avenue Boston, National University of Ireland Maynooth, | Massachusetts 02115 Co. Kildare, Ireland. | USA

Lab site: http://bioinf.nuim.ie/james-mcinerney James McInerney <jmcinern@hsph.harvard.edu>

Smithsonian ResearchTech InvertZool

Hello all,

We are currently searching for a research technician in Invertebrate Zoology here at the Smithsonian (unfortunately only US citizens are eligible). If you know anyone who may be interested in a great federal position, please forward this to them. The duties will primarily be histology, photography, and microscopy work. Experience with a wide diversity of invertebrates is desired.

The hiring process is rather odd so please contact me if you have questions about applying or would like to learn more about the position.

Thank you, Karen

https://www.usajobs.gov/GetJob/ViewDetails/-340838300 Job Title:Museum Technician (Zoology) Agency:Smithsonian Institution Job Announcement Number:13R-JW-298171-DEU-NMNH SALARY RANGE:

$42,209.00 to $54,875.00 / Per Year

OPEN PERIOD:

Monday, April 01, 2013 to Monday, April 15, 2013

SERIES & GRADE:

GS-1016-07

POSITION INFORMATION:

Full-Time, Permanent - Federal

PROMOTION POTENTIAL: 09

DUTY LOCATIONS:

1 vacancy in the following location: Washington, DC, USView Map < https://www.usajobs.gov/GetJob/-ViewDetails/340838300 >

WHO MAY APPLY:

This position is open to all U.S. Citizens or U.S. Nationals.

Karen Osborn osbornk@si.edu 202-633-3668 Research Zoologist/Curator Department of Invertebrate Zoology Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012 Washington, DC 20013-7012 USA

Courier address: Smithsonian Institution, MRC 0163, Natural History, West Loading Dock 10th and Constitution Ave., Washington, DC 20560

OsbornK@si.edu

UCopenhagen Bioinformatics

A position for a Bioinformatician, for two years with the possibility for an extension of five years, is available from June 1, 2013 or as soon as possible thereafter. The successful applicant will be associated with the Center for Macroecology, Evolution and Climate www.macroecology.ku.dk within the Natural History Museum of Denmark.

The selected candidate will work in collaboration with CMEC scientists on research lines aiming at assessing past and current population dynamics and extinction processes and how can this knowledge about the past help to better predict the future impacts of global change in biological diversity.

The successful candidate will provide bioinformatics with the main tasks of downloading, managing and analyzing phylogeographic/population genetic data from public databases (GENBANK, NCBI, EMBL), with the aim of building a phylogeographic dataset for a variety of different taxa (plants and animals) across different biomes. The bioinformatician will also work together with a PhD student and a post-doctoral researcher to implement population genetic and phylogeographic analyses, and will provide support for other bioinformatic needs as they arise. Experience in managing and maintaining clusters and/or multi-core large workstations is needed.

The successful candidate will have an MsC or a PhD title in population genetics, molecular biology or computer science. Applicants must have experience in gathering large dataset from public DNA database, including NGS datasets. Experience with bioinformatics tools like BIO++ or BIOPearl would clearly be an advantage. The successful applicant will be competent in the programming languages Perl, Java, Python, C or C++ and demonstrable experience working in UNIX/Linux environments. We will also strongly consider applicants with in bioinformatics, phylogenetic and statistical phylogeographic analyses, including likelihood-based, Bayesian coalescent modeling (such as ABC and HABC models).

The bioinformatician will be employed by the University of Copenhagen, Natural History Museum and will work at the Center for Macroecology, Evolution and Climate (CMEC), a Center of Excellence directly funded by the Danish National Research Foundation and comprising 40 researchers from 16 different countries working on multi-disciplinary research line http:/-/macroecology.ku.dk. Within CMEC, the Phylogeography and Extinction Theme is a key area of research focus over the next few years.

CMEC is part of the Natural History Museum of Denmark, a dynamic research environment containing different Centers of Excellence and a successful track record of graduating Masters and PhD students and hosting postdoctoral researchers from all over Europe, North America and Asia.

For more information on the position or the Center for Macroecology, Evolution and Climate, or to submit an application, click here: http://macroecology.ku.dk/-opportunities_new/ (When you reach the job portal, tick the research/science box.)

Applicants seeking further information are invited to contact: Associate Professor David Nogués-Bravo, phone +45 35321314 email: dnogues@bio.ku.dk

Applications should be submitted no later than 10 May 2013.

Katharine A. Marske, Ph.D.

Postdoctoral Researcher Center for Macroecology, Evolution and Climate Department of Biology University of Copenhagen DK-2100 Copenhagen Ø Denmark +45 35 32 13 34 http://macroecology.ku.dk/

KAMarske@bio.ku.dk

UGraz Austria EvolutionaryBiol

Professor Position Open:

University of Graz/Karl-Franzens-Universität Graz, Austria

The Department of Zoology at the

Faculty of Natural Sciences is seeking to appoint a Professor of Evolutionary Biology

(40 hours per week; fixed-term employment for 5 years pursuant to §99 (1) UG (Austrian Universities Act); Expected starting date 01 October 2013)

The applicant is expected to possess a dynamic research personality and a superb performance record in an organismic field with a distinctive evolutionary background. Innovative scientific approaches as well as excellent analytical skills in connection with molecular and/or genetic methodologies are required. The research focus of the successful candidate will not be limited to any particular group of animals, but must be compatible with existing infrastructure. Field-oriented approaches are also desired, as well as synergetic effects with the existing research groups. Teaching competence in basic zoology and ecology is expected. Furthermore, the involvement in the Research Core Area

"Environmental and Global Change" is desired. The teaching language is primarily German, although advanced classes are also held in English. A completed habilitation or equivalent qualification is desired. We also expect competence in the field of gender mainstreaming.

The minimum salary according to the classification scheme of the University Collective Agreement (A1) is EUR 4571.20 gross per month. Salary subject to negotiation.

Applications are to be submitted by 15 May 2013 and must quote the reference number PR/11/99 ex 2012/13. For details on application procedures and requirements, please click on jobs.uni-graz.at/en/PR/11/99

Christian Sturmbauer, Professor Department of Zoology University of Graz Universitätsplatz 2 A-8010 Graz Austria Tel. +43 316 380-5595 FAX +43 316 380-9875

<christian.sturmbauer@uni-graz.at>

UGroningen EvolutionBehaviour

The Centre for Behaviour and Neurosciences of the University of Groningen (Netherlands), is recruiting two tenure track assistant professors and one full professor.

Candidates are expected to strengthen the profile of the institute, focusing on behaviour and neurosciences within an eco-evolutionary context. The institute provides excellent facilities for both animal and human research.

Deadline for applications is April 24!

Details about the vacancies:

http://www.rug.nl/about-us/work-with-us/job-opportunities/scientific (scroll down the list)

Vacancy numbers 213065-67

Information about the biology department of the University of Groningen:

http://www.rug.nl/research/cbn/ http://www.rug.nl/research/cees/ http://www.rug.nl/research/gbb/ m.e.maan@rug.nl

ULondon Lect MolecularEcology

Lecturer in Molecular Ecology School of Biological Sciences Royal Holloway University of London

We are seeking to appoint a lecturer in Molecular Ecology to join our research centre for Ecology, Evolution and Behaviour. Royal Holloway is based in the vicinity of London, in a beautiful, leafy campus. Research in the School is of international reputation and covers the breadth of biology. In the 2008 UK Research Assessment Exercise it was ranked among the best Biological Science Departments in the UK. (http://www.rhul.ac.uk/biologicalsciences/)

The candidate will be involved in research and teaching in the broad area of molecular ecology. We seek an individual who uses molecular techniques to answer questions at the population, ecosystem or evolutionary level, in either terrestrial or aquatic systems. The individual will be expected to establish an independent research programme and to collaborate widely within RHUL and with external organisations.

You will have experience of undergraduate teaching in molecular techniques and a good publications record. Experience of working in areas of strength in the School, such as conservation biology, behaviour or evolutionary biology would be an advantage. The ideal candidate will have a BSc and PhD in a relevant subject and will be a Scholar with at least a national reputation.

Allowance This is a full time and permanent post, available from 1st August 2013 or as soon as possible thereafter, with a salary in the range £39,516 to £46,741 per annum inclusive of London. Planned Interview Date: Last week of May 2013

For an informal discussion about the post, please contact the Head of School, Professor Alan Gange on a.gange@rhul.ac.uk or (0)1784 443188.

To view further details of this post and to apply please visit https://rhul.engageats.co.uk Closing Date: Midnight,Sunday 19thMay 2013

Sent by Vincent.jansen@rhul.ac.uk

UOxford SeniorLabManager

Senior Laboratory Management and Research Support Officer

Edward Grey Institute, Department of Zoology, University of Oxford, UK

Grade 8: £37,382 to £44,607

Deadline of 12.00 midday on 15 May 2013

http://www.zoo.ox.ac.uk/jobs/list#job_107452 The Edward Grey Institute (EGI) is a centre for world-class research in ecology and evolution. Well known for its long-term population studies of birds, the institute is also home to research programmes using reptile, insect and microbial study systems. Research in the EGI addresses topics including social ecology, epidemiology, learning and phenotypic plasticity, sexual selection, life-history theory and genetics.

Work conducted in the EGI laboratory ranges from sex determination, genetic diversity, epigenetics, molecular phylogenetics and population dynamics, to transgenic analyses and protein quantification. The EGI lab is also a repository of large sample banks of long-term populations of birds and lizards. See our website at:

http://www.zoo.ox.ac.uk/egi/ The laboratory management and research support officer role will involve the day to day running of the laboratory, training of new EGI members in laboratory techniques, and organisation of currently existing and future biological sample banks. In addition the holder of this post will help facilitate fieldwork via ordering and cataloguing field equipment, and maintaining licenses and safety protocols.

Responsibilities

1 Management of laboratory, staff, and shared infrastructure: - Establishment of laboratory protocols. - Organisation of shared space and infrastructure. - Implementation of health and safety protocols. - Purchase, maintenance and record-keeping of equipment. - Management of consumables supply/disposal. - Induction and training of new staff in molecular techniques. - Formulation of curatorial protocols for sample banks. - Coordination of transition between sample collection and care in the laboratory.

2 Management of field equipment and licenses, e.g. maintenance of: - Equipment inventories and purchase of new equipment. - Fieldwork licenses, imports/exports documentation, safety protocols, DEFRA guidelines.

3 Work effectively in a team to facilitate high-calibre research.

Essential qualifications and experience: - Bachelor's degree in an appropriate discipline. - Experience of laboratory management. - Excellent organisational and communication skills. - Expertise and ability to train others in molecular techniques (e.g. DNA/RNA/protein extractions, PCR, qPCR genotyping, westerns).

Only applications made online before the closing deadline of 12.00 midday on 15 May 2013 will be considered. You will be required to upload your CV and a covering letter.

See http://www.zoo.ox.ac.uk/jobs/list#job_107452 Dr. Stuart Wigby Edward Grey Institute Department of Zoology University of Oxford www.zoo.ox.ac.uk/egi/ Twitter @StuartWigby

sites.google.com/site/stuartwigby

s.wigby@gmail.com

UYork Tech EvolutionaryMicrobiology

Research Technician in Evolutionary Microbiology

Department of Biology Based atUniversity of York - Heslington Campus Hours of work - Part-time Contract status - Fixed term Salary - £19,606 to £22,700 a year, reduced pro rata Apply by 01/05/2013

Role Description

We are seeking a motivated and enthusiastic technician to work on a project investigating the experimental evolution of bacteria-plasmid associations led by Prof. Michael Brockhurst. The post is funded by NERC and The University of York, and forms part of a wider research program in Brockhursts lab investigating the role of horizontal gene transfer in bacterial adaptive evolution.

You will work alongside two postdoctoral research associates to characterize the dynamics and fitness effects of adaptive mutations identified by whole-genome next generation sequencing that have arisen during long-term experimental evolution. You should hold a BSc in biology or a closely related discipline and have both a practical and theoretical knowledge of bacterial genetics. Candidates with experience of genetic manipulation of Pseudomonads will be particularly welcome.

This post is available from 3 June 2013 for a period of two years part-time (29.6 hours per week).

Informal enquiries can be made directly to Prof. Michael Brockhurst (michael.brockhurst@york.ac.uk).

The University of York is committed to promoting equality and diversity.

https://jobs.york.ac.uk/wd/plsql/wd_portal.show_job?p_web_site_id=3885&p_web_page_id=164492 Michael Brockhurst <michael.brockhurst@york.ac.uk>

Vienna Bioinformatics

The University of Natural Resources and Life Sciences, Vienna, invites applications for a tenured professorship in "Bioinformatics".

The research and teaching is focused on the establishment of improved quantitative experimental assays and the development of modern computational methods such as hierarchical probabilistic models or integration of heterogeneous data sources for the characterization and exploration of complex systems in living organism.

The research focus of the professorship should be in one of the following areas (in alphabetical order): Biodiversity Research of cell systems and plants, Functional Genomics and Proteomics (including Glycoproteomics), Genome Assembly and Annotation, Modeling and Analysis of datasets derived from Bioprocess Engineering, Molecular Phylogenetics, Structural Bioinformatics and Structure Prediction, Systems Biology.

more information can be obtained at: http://www.boku.ac.at/fileadmin/_/mitteilungsblatt/MB_2012_13/MB12/Bioinformatics__final_.pdf Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://i122server.vu-wien.ac.at/pop Vienna Graduate School of Population Genetics http://www.popgen-vienna.at schlotc@gmail.com

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Call proposals SMBE satellite meetings

Hi folks,

Apologies for cross-posting.

Call for 2013 SMBE Satellite Meetings

Purpose

The Society for Molecular Biology and Evolution (SMBE) exists to "provide facilities for association and conference among molecular evolutionists and to further the goals of molecular evolutionary biology and its practitioners, including the publication of two journals, *Molecular Biology and Evolution*, and *Genome Biology and Evolution" (Society By-Laws, amended November 7, 2008). In addition to supporting its annual meeting, SMBE Council will provide funds in aid of one or more workshops or small meetings per calendar year, that number depending on total cost. SMBE's first satellite meeting sponsored under this competition was "Phylomedicine" held March 2012 at Arizona State University (http://www.smbe.org/-phylomed). In spring 2013, SMBE supported three satellite symposia: "Eukaryotic Metagenomics" (http://www.smbe.org/2013/smbe-satellite-meeting-on-eukaryotic-omics/), "Mechanisms of Protein Evolution II" (http://www.smbe.org/2013/smbe-satellite-meeting-mechanisms-of-protein-evolution-ii/), "The Origin of Life" (http://www.pctp.princeton.edu/-pcts/Originoflife2013/Originoflife2013.html).

SMBE is now calling for proposals for small satellite meetings and/or workshops to be held in Fall 2013/Spring 2014. Funds will be awarded on a competitive basis to members of the molecular evolution research community to run a small meeting or workshop on an important, focused and timely topic of their choice.

Guidelines

- Funds will be awarded on a competitive basis to members of the molecular evolution research community to run a small meeting or workshop on an important, focused and timely topic. The suggested size is ˜50 participants. At least one of the meeting organizers must be a member of SMBE.

- SMBE will provide financial support for up to 80% of the cost of each meeting, up to maximum of $40,000 USD per meeting. A detailed projected budget including expected number of participants, travel/food/lodging costs, and registration fees must be submitted with the application.

- Meetings will be selected based on the scientific importance, timeliness and anticipated impact on the fields of molecular biology, genome biology, and evolution.

- Proposals will be received and reviewed by the *SMBE Satellite Workshop Committee*, which will consist of four individuals: one SMBE Council Member (who will also serve as Chair) and three other members of SMBE. The committee will make a recommendation to SMBE Council, whose decision is final. The committee or SMBE Council may decide not to support any meeting in any particular year.

- Events will be named *"SMBE Satellite Meeting on XYZ" or "SMBE Satellite Workshop on XYZ".*

- The meeting/workshop must be a standalone event. It should not form a symposium or other part of a larger meeting. It should not immediately follow or precede any other meeting.

- Organizers will be required to submit a copy of the final workshop/symposium program and a short (˜2 page) summary of the workshop/symposium highlights to SMBE Council within 3 months of the event. The summary should be sent to Harmit Malik (hsmalik@fhcrc.org). **

Instructions for proposals to organize an SMBE Satellite Meeting

Satellite meeting / workshop proposals shall be sent by email to the Chair of the SMBE Satellite Workshop Committee (Soojin Yi < soojin.yi@biology.gatech.edu>). Please refer to the workshop guidelines for more information.

The deadline for submission of proposals is 25 May, 2013.

*1.** Provide the name(s) and full contact information for all organizer(s) and institution(s) involved. Universities / organizations providing additional financial support, if involved, should also be listed.*

*2. Workshop summary.** Describe the scientific rationale for your proposed workshop. In doing so, be sure to clearly state (1) the importance and timeliness of the topic, (2) the anticipated short-term and long-term impacts of your satellite meeting on the fields of molecular biology, genome biology, and evolution, (3) the extent and nature of student / postdoctoral fellow involvement, (4) the proposed structure of your workshop (e.g., lectures only, lectures + hands-on training sessions, poster sessions, etc.), (5) an indicative list of proposed invited speakers, and (6) why a workshop/small meeting format is preferable to a symposium at the

SMBE annual meeting. (2 pages max).*

*3. Financial summary.** Please summarize your financial request, including estimated total budget, registration costs (if any), travel support for

— / —

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

Cicada emergences

Dear EVOLDIR Readers,

We are looking for biologists or friends of biologists who have had 13- or 17-year cicadas on their property. We would like protected sites where we can dig nymphs once per year. We are especially interested in people who have 13-year Brood XIX (emerged in 2011), 17-year Brood XIV (emerged in 2008), and 13-year Brood XXII (will emerge in Louisiana in 2014). But other broods are also useful. We are also looking for high schools and university campuses that have periodical cicadas. We would like to find collaborator-teachers who would like to participate in following nymphal growth annually.

Please contact chris.simon@uconn.edu

Thanks! And enjoy Brood II along the east coast of the US this spring! And if you see then, report your sightings to Magicicada.org!

Chris

Chris Simon Professor, Ecology & Evolutionary Biology 75 North Eagleville Road, University of Connecticut Storrs, CT 06269-3043

chris.simon@uconn.edu Office (860) 486-4640; Lab (860) 486-3947; Fax (860) 486-6364, Office: Biopharm 305D, Lab: Biopharm 323,325

C. Simon Home page: http://hydrodictyon.eeb.uconn.edu/projects/cicada/simon_lab/member_pages/c_simon.php Simon Lab Home: http://hydrodictyon.eeb.uconn.edu/projects/cicada/simon_lab/lab_pages/current.php Reprints: http://hydrodictyon.eeb.uconn.edu/projects/cicada/resources/reprints.html Magicicada Brood II will appear along the east coast of the US in Spring 2013, watch Magicicada.org for information.

chris.simon.uconn@gmail.com

Entomology Awards

The International Branch of the Entomological Society of America offers three awards each year: two (2) student awards and one (1) late career award. In 2013, the application deadline for all three awards is April 15,

1. The International Branch Graduate Student Award is a cash award ($250 USD) provided to a graduate student member of the International Branch of the ESA in recognition for their course work and research culminating in scholarship.

Eligibility: candidates must currently be researching an entomological problem at a recognized graduate institution and be members of the Entomological Society of America International Branch.

More information: see attached, or go to http://www.entsoc.org/PDF/International/GraduateStudentAward2013.pdf 2. The J. H. Comstock Graduate Student Award is given to one graduate student from each of the Entomological Society of America's six Branches to promote interest in the science of entomology at the graduate level and to stimulate interest in attending the ESA Annual Meeting.

Eligibility: Applicants must be enrolled as a graduate student and in graduate school at the time of (or have completed the degree within the last 12 months preceding) the presentation of the Award. Students must be pursuing a course leading to a graduate degree with a major focus in entomology and be members of the Entomological Society of America International Branch. Students may only apply for the J. H. Comstock Award in one ESA Branch on a given year.

More information: see attached, or go to http://www.entsoc.org/PDF/International/JHComstockAward2013.pdf 3. The Distinguished Scientist Award provides recognition to members of the International Branch of the Entomological Society of America who have made outstanding contributions to the science of entomology.

Eligibility: The nominee must be widely recognized in both the International Branch and in the ESA as a major contributor to the science of entomology. The nominee must be a current member of the International Branch.

More information: see attached, or go to http://www.entsoc.org/PDF/International/DistinguishedScientistAward2013.pdf MEMBERSHIP INFORMATION: regular member: $141 USD, student member: $35 USD Member benefits: http://entsoc.org/Membership/overview/benefits How to join ESA: http://entsoc.org/how-join-esa In accordance with the ESA Bylaws, members of ESA who reside in the geographical area of another Branch may elect to become a member of the International Branch by notice to the ESA Executive Director.

For more information on the International Branch of the ESA: http://entsoc.org/international-branch judgek3@macewan.ca

EvoDevoGrants EDEN Apr30Deadline

Dear Colleague,

This email is to remind you that the upcoming deadline for research exchange grants from the Evo-Devo-Eco Network (EDEN) is April 30, 2013. EDEN is a program funded by the National Science Foundation Research Coordination (http://edenrcn.com/).

One of EDEN's major goals is to enable graduate students, postdoctoral fellows, and faculty to undertake research exchanges in the field of Evo-Devo-Eco, in order to develop or share techniques, protocols and tools for use with emerging model systems.

Please note that the updated eligibility for EDEN funding is as follows:

Researchers based anywhere in the world can apply for funding to visit labs in the US.

Researchers based in the US are eligible for funding to visit labs anywhere in the world.

This spring EDEN will award approximately five research exchanges to be held in 2013-2014. Each exchange will consist of an award of up to $3,000 per researcher toward travel, lodging and subsistence costs. You can find out more about this program at http://edenrcn.com/funding/index.html. If you know of outstanding lab personnel who would be interested, please forward this announcement to them.

You can read more about EDEN's activities and opportunities at http://www.edenrcn.com, where you will be able to obtain protocols for evo-devo-eco work developed with EDEN funding.

Please also consider attending the upcoming EDEN Symposium, "The Evolution of Gene Regulatory Networks", which will take place at the Annual Evolution 2013 Meeting on June 21-25, 2013, at the Snowbird Alpine Village in Utah. Details of the speakers for this symposium will soon be confirmed and available on the EDEN website. Visit http://www.evolutionmeeting.org/ for further details of this meeting.

Please feel free to email edenrcn@fas.harvard.edu with questions about the program, and forward this email to colleagues who you think would be interested in EDEN.

Best wishes,

Cassandra Extavour

perlo@fas.harvard.edu

Experimental design EEB textbook

Dear evoldir members,

I am looking for a good book on experimental design that could be used at the early undergraduate level.

It is hard to know exactly what I am after. It would have to be descriptive, with very simple and graphical examples, cover a wide variety of topics and ideally describe both empirical and modeling approaches. I guess it would probably be something like Gotelli & Ellison's "Primer in Ecological Genetics" but focused on experimental design in ecology and evolution. Maybe "Experimental design in organismal biology for dummies" if such a thing exists...

Does anyone know of a good title?

Thanks in advance, Rafa

Rafael Rubio de Casas *Departamento de Ecología* < http://ecologia.ugr.es > Facultad de Ciencias Universidad de Granada Granada, E-18071 (+34) 958 249 861

Rafael Rubio de Casas <rubiodecasas@ugr.es>

NESCent EvolutionFilmFestival

NESCent Evolution Film Festival - Submission Deadline Approaching!

Scientists and science educators of all stripes X students, postdocs, faculty, and full- or part-time science communicators X are invited to enter the third annual Evolution Video Competition, sponsored by the National Evolutionary Synthesis Center (NESCent). To enter, please submit a video that explains a fun fact, key concept, compelling question, or exciting area of evolution research in THREE MINUTES OR LESS.

Entries may be related or unrelated to your own research, and should be suitable for use in a classroom (K-12, undergraduate, graduateKyour choice). Videos should be both informative and entertaining. (In other words, no taped lectures or narrated Powerpoint presentations!) Animations, music videos, and mini documentaries are all fair game.

The finalists will be screened at the 2013 Evolution meeting in Snowbird, Utah. (You do not need to attend the conference in order to enter a video.)

First- and second-place winners will receive up to $1,000 and $500, respectively, to cover travel expenses to the meeting of their choice, any time within a year of the festival.

The deadline to submit your video(s) is FRIDAY, MAY 31st, 2013.

For more information (and to see entries from previous years) please visit filmfestival.nescent.org

Jory P. Weintraub, PhD Assistant Director, Education & Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200, Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: jory@nescent.org Skype: jory.weintraub

“Weintraub, Jory P” <lviscrst@live.unc.edu>

NSF review process survey

Program Directors in the Division of Environmental Biology at the National Science Foundation (NSF) ask Principal Investigators (PIs) (current, past, or future) to take a survey (http://www.surveymonkey.com/s/-DEB_IOS_program_feedback) to provide feedback on our new proposal review process. This is an important opportunity to provide the NSF with feedback. Survey must be completed by Wednesday, 1 May 2013.

In brief, the Divisions of Environmental Biology (DEB) and Integrative Organismal Systems (IOS) in the Biological Sciences Directorate (BIO) at the NSF made significant changes to the core program review process that began in 2012. These changes (including the new preliminary proposal requirement, a switch to an annual deadline, and a cap on the number of proposals that PIs can submit per cycle) were made to protect the integrity of the merit review system, which was increasingly compromised by steep increases in proposal submissions, diminished participation of the community in the proposal review process, and flat budgets.

This survey is an important mechanism that the NSF is using to obtain quantitative feedback about the new review process. The target audience is investigators who have had funding from DEB or IOS or who are likely to submit a proposal to DEB and/or IOS in the next 1-2 years. The results of the survey, which will be anonymous, will be used to assess the level of satisfaction with various aspects of the new review process. All answers are confidential, and will have no bearing on future interactions with the NSF. The survey should require 10-20 minutes to complete.

edb9j@virginia.edu

PHASE scripts

Dear all

I was wondering whether anyone has scripts in R, perl or python that can convert the output phased haplotype file from PHASE2 to an input file suitable for Pardis Sabeti’s “Sweep” program or the R program “rehh”?

rehh takes fastPHASE output data, but unfortunately fastPHASE does not phase trio data, which is the data I have, so I cannot use it for phasing...

Any scripts/help would be much appreciated, I don’t want to reinvent the wheel!

Ed Hollox, PhD Lecturer in Genetics, University of Leicester

Research group pages http://tinyurl.com/hollox Departmental staff page http://www2.le.ac.uk/-departments/genetics/people/hollox Room G8a, Department of Genetics, Adrian Building University Road, Leicester LE1 7RH UK

Tel: +44 (0)116 252 3407 (office G8a) +44 (0)116 223

1366 (lab G3)

“Hollox, Ed J. (Dr.)” <ejh33@leicester.ac.uk>

Phyloseminar EdDeLong May13

Next up on http://phyloseminar.org/ “How Carl Woese transformed the field of microbial ecology” Ed DeLong (MIT)

The challenges of dissecting naturally occurring microbial assemblages, with respect to their community composition, interspecies interactions, functional attributes, and activities, are numerous and daunting. For many years, these challenges impeded our understanding of the properties and dynamics of microbial communities, and thus hindered development of the field of microbial ecology. Enter Carl Woese: the theory and application of molecular phylogenetics and genomics in studies of microbial evolution and ecology can be traced directly to Woese and one of his primary collaborators, Norman Pace. This lecture will trace the logic and roots of the application of molecular phylogenetics and genomics to the study of microbial ecology, through a historical review and examination of its past and current applications.

West Coast USA: 10:00 (10:00 AM) on Monday, May 13 East Coast USA: 13:00 (01:00 PM) on Monday, May 13 UK: 18:00 (06:00 PM) on Monday, May 13 France: 19:00 (07:00 PM) on Monday, May 13 Japan: 02:00 (02:00 AM) on Tuesday, May 14 New Zealand: 05:00 (05:00 AM) on Tuesday, May 14

– Frederick “Erick” Matsen, Assistant Member Fred Hutchinson Cancer Research Center http://matsen.fhcrc.org/ ematsen@gmail.com

Query FST vs GD

which is the best matrix to generate a phylogenetic tree. which of the following produces a more accurate phylogenetic tree, Pairwise Fst or Genetic distance.

Thank you and regards

omkar

– K.Omkar Babu S.R.F Institute of Biotechnology U.A.S Dharwad-580005 Karnataka INDIA

Omkar Babu <omkarbabu.k@gmail.com>

RAXml platform

Dear folks,

I am an user of the raxml plataform (http://phylobench.vital-it.ch/raxml-bb/index.php). I am trying to submit a datafile but it seems that the plataform is not working. Am I right? Or probably I am doing a bad job!!! I found a new reference for the Light RaxMl at San Diego Supercomputer Center. Is it nowadays the single Raxml plataform or the previous (http://phylobench.vital-it.ch/raxml-bb/index.php) is still working?

Thanks and best regards Rodrigo

“Rodrigo A. Torres” <rodrigotorres@ufpe.br>

Reprint request

Hello evoldir members, Does anyone have a (electronic?) copy of this publication:

Wen, Jun, Ickert-Bond, S., Nie, Z. -L and Li, R. 2010. Timing and modes of evolution of eastern Asian - North American biogeographic disjunctions in seed plants. In: Long, M., Gu, H. and Zhou, Z., Darwin’s Heritage Today : Proceedings of the Darwin 2010 Beijing International Conference. Beijing: Higher Education Press, pp.252-269.

I would much appreciate a copy. Many thanks already.

Heidi Schwaninger Heidi.Schwaninger@ars.usda.gov

“Schwaninger, Heidi” <Heidi.Schwaninger@ARS.USDA.GOV>

Reptile SexRatio data

EVOLDIR ANNOUNCEMENT Request for data on sex ratios in reptiles

For a comparative project with Andras Liker, Robert Freckleton and Tamas Szekely, I am looking for data on juvenile and adult sex ratios.from well-studied reptile populations. We need percentage of males out of all individuals (males plus females).

We appreciate the data in the following structure: (i) scientific name of the species (ii) juvenile sex ratios (JSR) ie proportion juvenile males out of all juveniles (iii) number of juveniles used to estimate juvenile sex ratio (iv) type of JSR estimate, eg counting, capture-recaptures, demography (v) adult sex ratios (ASR) ie proportion adult males out of all adults (vi) number of adults used to estimate juvenile sex ratio (vii) type of ASR estimate, eg counting, capture-recaptures, demography

Please also say how we should cite the data.

Best regards, Ivett Pipoly, University of Pannonia, Hungary pipoly.ivett@gmail.com

Pipoly Ivett Ornithology Research Group University of Pannonia Tel.: +36 88 624249 Fax: +36 88 624747 pipoly.ivett@gmail.com +36 20 / 9236407

Ivett Pipoly <pipoly.ivett@gmail.com>

Reptile divorceRates

Request for data on divorce rates in reptiles

For a comparative project with Andras Liker, Robert Freckleton and Tamas Szekely, I am looking for data on juvenile and adult sex ratios.from well-studied reptile populations. We need percentage of males out of all individuals (males plus females).

We appreciate the data in the following structure: (i) scientific name of the species (ii) juvenile sex ratios (JSR) ie proportion juvenile males out of all juveniles (iii) number of juveniles used to estimate juvenile sex ratio (iv) type of JSR estimate, eg counting, capture-recaptures, demography (v) adult sex ratios (ASR) ie proportion adult males out of all adults (vi) number of adults used to estimate juvenile sex ratio (vii) type of ASR estimate, eg counting, capture-recaptures, demography

Please also say how we should cite the data.

Best regards, Ivett Pipoly, Pannonia University, Hungary pipoly.ivett@gmail.com

– *Pipoly Ivett* Ornithology Research Group University of Pannonia Tel.: +36 88 624249 Fax: +36 88 624747 pipoly.ivett@gmail.com +36 20 / 9236407

Ivett Pipoly <pipoly.ivett@gmail.com>

RohlfMedal Nominations

2013 CALL FOR NOMINATIONS

The Rohlf Medal

The Rohlf Medal was established in 2006 by his family and friends to mark the 70th birthday of F. James Rohlf, Distinguished Professor of Ecology and Evolution and longtime Stony Brook University faculty member. Recipients of the Rohlf Medal will be recognized for excellence in their body of work on the development of new morphometric methods or for their applications in the biomedical sciences, including evolutionary biology, population biology, physical anthropology, and medicine. The term “morphometrics” is intended to include high-dimensional pattern analyses of biological shape, especially those that analyze shape in a comprehensive way, or of covariation of shape patterns with other variables. The award can recognize advances in the mathematical or statistical theory underlying morphometric methods, new software that implements or visualizes new methods, or specific new biological findings that rely crucially on contemporary morphometric methods and represent major advances.

Candidates for the Rohlf Medal may be self-nominated or nominated by others. They must have attained the postdoctoral level or its equivalent. Nomination packages should include (1) a description of the body of work (not to exceed two pages) on which the candidacy is based, (2) reprints of no more than three relevant papers and/or software products, (3) a curriculum vitae, and (4) the names and addresses of three referees. Nominating packages should be uploaded to the Rohlf Medal website (http://life.bio.sunysb.edu/-ee/rohlf_medal/apply.html) and received by 15 August 2013 to be assured of full consideration.

The successful candidate will receive the Rohlf Medal and a cash prize at Stony Brook University in mid-Fall 2013 (final date to be determined). She or he will deliver a lecture that is appropriate for an educated general audience concerning the morphometric research for which the Rohlf Medal was awarded.

Dean

Dr. Dean C. Adams Professor Department of Ecology, Evolution, and Organismal Biology Department of Statistics Iowa State University Ames, Iowa 50011 www.public.iastate.edu/ ˜ dcadams/ phone: 515-294-3834

dcadams@iastate.edu

SSB StudentSymposium

Student Symposium sponsored by the Society of Systematic Biologists in honor of Ernst Mayr

Each year the Society of Systematic Biologists (SSB) sponsors a symposium with invited student speakers at the joint annual meeting of American Society of Naturalists, Society of Systematic Biologists, and Society for the Study of Evolution. Of the participating speakers, the Ernst Mayr Award is given to the outstanding student talk, as judged by the quality and creativity of the research. The award consists of $1000, a certificate of distinction, and a two-year subscription to the journal Systematic Biology.

We encourage all students interested in participating in the symposium who meet the criteria below to apply.

Eligibility:

Members of the Society who are advanced PhD students or have completed their Ph.D. within the last 15 months are eligible. Applicants may be from any country, but MUST be members of SSB, and are advised to join the Society as soon as possible to be considered (to join go to:

http://systbio.org/?q=node/6). Previous Mayr award winners are not eligible.

Application Procedure to participate in the symposium:

1. To be considered as a participant in the symposium, as well as the award, you will need to either (i) submit an abstract of your talk to the Evolution 2013 meeting website (http://www.evolutionmeeting.org/) at the time of registration, or (ii) submit an abstract to Sen Brady, bradys@si.edu, with symposium application± in the subject line.

2. Abstracts should clearly indicate methods used, conclusions, and the relevance to systematics. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible.

3. Applications will be accepted only until the end of early registration (April 19, 2013).

4. At the closing of early registration, a subset of applicants will be selected by the SSB Awards Committee to present their talks in the Mayr Symposium during the meeting. Based on submitted abstracts, the Awards Committee (appointed by the Awards Chair, Sean Brady) will select a maximum of 16 applicants for inclusion in the symposium.

All applicants will be notified about selection decisions approximately May 15.

Judging talks for consideration of the Mayr Award:

The symposium will be held at a single venue as a continuous session. Talks will be judged on creativity, depth and excellence of research, and on quality of presentation. Competitive students are expected to be in the final stages of their doctoral program, presenting results of a major body of work.

Co-Authors:

The talk may be co-authored. It is understood that the ideas, data and conclusions presented are primarily and substantially the work of the student presenter, and the intention is that the student presenter will be senior author on the published version of the paper.

Notification of Winner:

The winner of the award will be announced at the SSB business meeting in Snowbird and again during the Awards Session at the conclusion of the Evolution Meetings, whereupon the winner will be given an award certificate. An announcement of the winner of the Mayr Award will be published in Systematic Biology and placed on the SSB website (see last year's winner at http://systbiol.org/).

Please see the SSB website (http://systbio.org/?q=node/10) for additional information or updates on participating in the symposium. Questions via email may be addressed to Sean Brady (bradys@si.edu)

ABSTRACT SUBMISSION DEADLINE IS APRIL 19, 2013

Sean Brady Research Entomologist Curator of Hymenoptera National Museum of Natural History Smithsonian Institution bradys@si.edu

"Brady, Sean" <BRADYS@si.edu>

Software DAMBE update

Dear All,

I have

1) published an update of DAMBE (Xia, X. 2013. DAMBE5: A comprehensive software package for data analysis in molecular biology and evolution. Molecular Biology and Evolution doi:10.1093/molbev/mst064), available at http://mbe.oxfordjournals.org/cgi/content/abstract/mst064?ijkey=ZmONZZtkrLjkpGx&keytype=ref
2) uploaded a new version of DAMBE to its release site at

http://dambe.bio.uottawa.ca/dambe.asp Please use the new version of DAMBE and cite the new MBE paper instead of the outdated book/paper. Thank you.

Best Xuhua

Xuhua Xia Professor Biology Department University of Ottawa Rm 278 Gendron 30 Marie Curie, Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 http://dambe.bio.uottawa.ca http://www.biology.uottawa.ca/details.php?lang=3Deng&id=3D31 Xuhua.Xia@uottawa.ca

Software MetaPIGA v3 1

Stable version of MetaPiga (v3.1) is available for download (with Codon models, GPU computing, and more)

Thanks to the feed back of users, we are now happy to release a stable version of MetaPIGA 3 that resolves minor (but annoying) bugs causing problems, e.g. with some Linux machines and in console mode.

MetaPIGA is a versatile and easy-to-use software that implements robust stochastic heuristics (including the Metapopulation Genetic Algorithm, metaGA) for large phylogeny inference under maximum likelihood. MetaPIGA allows analyses of binary and molecular data sets under multiple substitution models, Gamma rate heterogeneity, and data partitioning. The software is for all types of users as it can be run through an extensive and ergonomic graphical interface or by using batch ïand console interface on your local machine or on distant servers. MetaPIGA is platform independent, runs on 32- and 64-bits systems, and easily takes advantage of multiprocessor and/or multicore computers.

Version 3 of MetaPIGA includes new functionalities such as:

* Maximum likelihood models for codon evolution (Goldman-Yang 1994 and Empirical Models) with access to multiple genetic codes (universal, mitochondria, chloroplaste, etc); * Likelihood computation on CUDA-compatible Nvidia graphic cards (reducing run time by a factor of 10 to 20 for Protein/Codon data); * Ancestral-state reconstruction using empirical Bayesian inference.

Some of the other functionalities implemented in MetaPIGA are:

* Simple data quality control (testing for the presence of identical sequences as well as of excessively ambiguous or excessively- divergent sequences); * Automated trimming of poorly aligned regions using the trimAl < http://trimal.cgenomics.org/ > algorithm; * The Likelihood Ratio Test, the Akaike Information Criterion, and the Bayesian Information Criterion methods for easy selection of the substitution model that best fits your data; * Detailed monitoring of run progress; * Convergence statistics for automatically defining when an analysis is complete; * Ancestral-state reconstruction of all nodes in the tree; * Viewing and manipulation of result trees.

MetaPIGA v.3 and its manual can be downloaded from the new website at www.metapiga.org. Don't hesitate to contact us (Dorde.Grbic@unige.ch or Michel.Milinkovitch@unige.ch) for additional questions, assistance, or bug reports.

Prof. Michel C. Milinkovitch Laboratory of Artificial & Natural Evolution (LANE) Dept of Genetics & Evolution University of Geneva

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Visit www.lanevol.org

Visit www.metapiga.org and try MetaPIGA v2, a software for large phylogeny inference

Visit www.mantisdb.org and try MANTiS, linking multi-species genome comparisons & functional analysis

"Michel C. Milinkovitch"

<Michel.Milinkovitch@unige.ch>

Software MetaPIGA v3 1 AppleVersion

Mac OS X Mountain Lion (OS X 10.8.3) installation restrictions

Some Mac OS X Mountain Lion users were getting an error message (broken installer) when installing MetaPIGA 3.1. The problem is caused by the 'Security & Privacy' panel when the option "Allow applications downloaded from Mac App Store and identified developers only" was used.

Although there is an easy workaround (by choosing the option "Allow applications downloaded from Anywhere"), we now generated an 'Apple-certified' version of MetaPiga v3.1 $B!D(B such that the software is now recognised by your Mac whatever is your security option.

Sorry for the inconvenience.

Djordje Grbic & Michel Milinkovitch

Prof. Michel C. Milinkovitch Laboratory of Artificial & Natural Evolution (LANE) Dept of Genetics & Evolution University of Geneva

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Visit www.lanevol.org Visit www.metapiga.org and try MetaPIGA v2, a software for large phylogeny inference Visit www.mantisdb.org and try MANTiS, linking multi-species genome comparisons & functional analysis

"Michel C. Milinkovitch" <Michel.Milinkovitch@unige.ch>

SouthAfrica VolunteerFieldAssist EvolutionSmallMammals

2 volunteers needed from May / June 2013 onwards

2 volunteers needed from August 2013 onwards

as field assistants for the project:

Evolution and Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work relating to eco-physiology, animal behavior, evolution, and ecology before starting an MSc or PhD project.

Project: We study the evolutionary and ecological reasons as well as physiological mechanisms of group living, paternal care, communal nesting and social flexibility in the striped mouse. One focus is on the adaptation to droughts, combining physiological, behavioral, ecological and evolutionary research. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o' clock), and stops its activity with dusk (19 o' clock). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small social group.

Work of field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers will also see how blood samples are collected for physiological measurements. Volunteers are expected to help with maintenance of the research station (water pump, solar power, etc.).

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1250 (around 180 US$, 120 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 2500, approx. 360 US$ or 250 Euro/month). Including extras (going out for dinner; shopping), you should expect costs of about 600 US$, 450 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country.

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: At the moment we are looking for 2 volunteers starting in May / June and 2 in August 2013. Volunteers are expected to stay at least three months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to succulent.karooo.research.station@kabelbw.de.

More information under

http://stripedmouse.com/site1_3_5.htm http://www.youtube.com/watch?v=w6rvF5XrVn0&list=UUd12oFYqs5OobiiKMhDnFtw&ind ex=1

Contact via e-mail: succulent.karoo.research.station@kabelbw.de

Succulent Karoo Research Station

Dr. Carsten Schradin (Director)

South Africa

The research station is a South African non-profit organization

Director Succulent Karoo Research Station <succulent.karoo.research.station@kabelbw.de>

StAndrews BotanicGarden

Save St Andrews Botanic Garden...

St Andrews Botanic Garden is under threat of closure due to insufficient funding. It was established by St Andrews University in the early 1960s and for the past 25 years has been leased to the local Council who have funded its maintenance and development as an educational and community facility. The lease runs out later this year and the Council is no longer willing to cover all of the running costs.

The Garden is an absolute gem and a wonderful biodiversity resource. It contains >8,000 living plant species, i.e. ~3 times the total number of plant species occurring naturally in Britain. These are displayed in diverse open habitats (Heath, Rock, Woodland and Water) and a range of different glasshouse environments (Tropical, Temperate, Alpine and Hot Desert). It is located in the midst of St Andrews and is open daily to the public!

You can sign a petition against the closure of the Garden by going to http://www.st-andrews-botanic.org and clicking on “Sign the Save the Garden Petition”. Couldn’t be easier. The petition closes on 5 May and will be presented to the University in June together with a business plan for the Garden’s future development.

Richard Abbott Professor Richard Abbott School of Biology University of St Andrews St Andrews, Fife KY16 9TH, UK

Email. rja@st-and.ac.uk

Websites: http://bio.st-andrews.ac.uk/staff/rja.htm http://openwetware.org/wiki/User:Richard_J._Abbott rja@st-andrews.ac.uk

Subularia samples

Dear EvolDir members,

We are startinga conservation project on water awlwort- /**Subula//ria aqua//tica/ (Brassicaceae)- in the Pyrenees. This species is an endangered aquatic plantthat is mainly found in oligotrophic lakes. Ithas a palearctic and nearctic distribution. We are seeking for leaf samples from different countries. Any helpwould be more than welcome.

Many thanks

Nathalie

– Nathalie Escaravage Enseignant-Chercheur Laboratoire Evolution et Diversité Biologique Université Paul Sabatier/CNRS 5174 Bâtiment 4R1, porte 106 118 route de Narbonne 31062 TOULOUSE cedex 09 France

Tel : 33 (0)5 61 55 67 52 Interne : 66752

Escaravage Nathalie <nathalie.escaravage@univ-tlse3.fr>

Training in phylogeny answers 2

Dear evoldir members,

Since I received extra information about courses in phylogeny / highthroughput sequencing, I send this to the community in order to complete my precedent e-mail.

I'm rather surprised not to see these mentioned:

http://www.embl.de/training/events/ In particular, courses like http://www.embl.de/training/events/-2013/GMX13-01/index.html seem about right.

I know of another great phylogenetics workshop that did not

get on your list:

http://regaweb.med.kuleuven.be/veme-workshop/-2012/ http://www.bioafrica.net/news.php?ida the 2013 version of this workshop will be in Gainesville Florida

Thanks to David & Brian for their contribution !

All the best,

Gwennaël

Gwennaël Bataille <gwennael.bataille@uclouvain.be>

UCalifornia LosAngeles Volunteers AvianEvolution

I am conducting a study of geographical variation in song characteristics and I am looking for volunteers to take a survey. Participants will rate the similarity of the songs of several species.

If you are able to volunteer to take this survey, please e-mail me at nathanbwarbler@gmail.com, and I will send you an e-mail with the URL to the survey and more information.

Thank you in advance,

Nathan Burroughs Department of Ecology & Evolutionary Biology University of California, Los Angeles nathanbwarbler@gmail.com

Nathan Burroughs <nathanbwarbler@gmail.com>

UZurich FieldAssist SwedishLapland SongThrushEvol

Expenses paid field assistant positions to study life-history evolution in Song Thrushes in Swedish Lapland, University of Zurich

For the upcoming field season (May-July 2013) we are looking for a highly motivated expenses paid field volunteer to join our field project (main responsible Michael Griesser, University of Zurich, Switzerland) investigating life-history evolution in Song Thrushes. The study population is located near Arvidsjaur, Swedish Lapland.

Our current project investigates the influence of habitat quality on offspring quality. The work of the field volunteer will be to help in locating nests, field experiments, behavioural observations, , measuring nestlings, and data management. This work will give insight into exciting experimental fieldwork and will be carried out partly in managed forests and partly in scenic pristine boreal habitats.

Qualifications: (1) BSc/MSc in Biology, Ecology or similar qualification (2) Previous field experience (3) Ability to work in small teams and sociable personality (4) Knowledge in observing & handling birds (5) Driving licence (6) Fluent in English

We will cover for the accommodation, travel expenses from and to the study site (in total up to 300 Euros) as well as the living expenses.

Applications - including a CV, a letter of motivation (1 page) and the name of two referees - should be sent to Xenia Schleuning: xenia.schleuning@uzh.ch

Applications received until 15th April 2013 will be given full consideration, or until position is filled.

For further information on the project, see: http:/-/www.aim.uzh.ch/Research/birdfamilies.html xenia.schleuning@uzh.ch

VolunteerFieldAssist AvianPersonality Australia

Volunteer field assistants: We are looking for field assistants to help monitor a colour-banded population of superb fairy-wrens near Melbourne, Australia for a study on animal personalities. Time periods: August - September 2013 (2 months mist-netting and testing personalities) or October 2013 - January 2014 (4 months nest-searching and behavioural observations). Duties include regular censusing of colour-banded birds, searching for and monitoring nests, mist-netting, behavioural observations, video analysis, and data proofing. Working days are long, with early starts six days a week. Enthusiasm, self-motivation, and a strong work ethic are a must. The study is based at Serendip Sanctuary, a small reserve on the outskirts of Melbourne. Qualifications: experience monitoring colour-banded birds, nest-searching, and mist-netting. Must also be early riser, physically fit, able to work in extreme weather conditions, and enjoy basic shared living conditions. Onsite accommodation in a house with shared dorm-style room is provided, but assistants cover travel to the site and their own food costs. The project will reimburse up to AUD$500/mo towards receipted food and travel expenses. For more information contact: Michelle Hall (hall.m@unimelb.edu.au) and Raoul Mulder (r.mulder@unimelb.edu.au). To apply, please email a letter outlining previous relevant field research experience, and a resume including names and contact information for 3 referees.

Dr Michelle L Hall Research Fellow Department of Zoology, University of Melbourne Melbourne, VIC, 3010, Australia email: hall.m@unimelb.edu.au phone: + 61 3 83446232 www: Google Scholar Profile < http://scholar.google.com.au/citations?user=-3DBcsSi-YAAAAJ&hl=en&oi=ao >

hall.m@unimelb.edu.au

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BrownU PhylogeneticsGeneExpression

Postdoctoral Research Position - Phylogenetic analysis of gene expression data

A postdoctoral position is available in the Center for Computational and Molecular Biology (http://www.brown.edu/research/projects/computational-molecular-biology/) at Brown University in Providence, Rhode Island. The successful candidate will develop new statistical methods and computational tools for the phylogenetic analysis of gene expression data, and will work collaboratively with the labs of Casey Dunn (http://dunnlab.org) from the Department of Ecology and Evolutionary Biology, and Jean Wu (http://www.stat.brown.edu/zwu/) and Rossi Luo (http://sites.google.com/site/xirossiluo/) from the Department of Biostatistics.

Research will focus on extending and implementing the ideas presented in the preprint available at:

http://arxiv.org/abs/1302.2978 Funding is available for one year, with the possibility of additional funding for subsequent years. The position is available immediately.

Applicants should hold a PhD in Evolutionary Biology, Statistics, Math, Computer Science, or a related field. Prior experience with the analysis of RNA-seq data is preferred. The candidate should have a strong background in statistics, and at least basic computational experience (eg Python, R, Unix, and git skills).

Please apply be sending a cover letter, CV, and contact information for three references to Casey Dunn (casey_dunn@brown.edu). General inquiries are welcome. The position is available immediately.

– http://dunnlab.org http://creaturecast.org http://practicalcomputing.org casey_dunn@brown.edu

CityUNewYork EvolutionaryBiol

Job Title: Research Associate (Post-Doctoral Fellow) - Biology Job ID: 7746 Location: Brooklyn College, CUNY

Under the mentorship and guidance of the Associate Professor of Evolutionary Biology (Principal Investigator), the Research Associate will carry out independent and collaborative research, and train and supervise student researchers.

The Research Associate will:

- Develop plans, collect and analyze data based on projects prepared together with the Principal Investigator. - Prepare reports of completed projects for publication in scientific journals, academic presentations or for further applied or theoretical research activities. - Ensure the efficient functioning of the laboratory areas using various experimental techniques. - Provide administrative and laboratory support to the Principal Investigator including, but not limited to: managing laboratory budgets and ordering supplies. - Train and supervise undergraduate and graduate researchers.

Qualifications: - Ph. D in Evolutionary Biology, with a minimum of 3 years of laboratory experience - Experience with genomic/bioinformatics research methods, including both wet lab and computer work - Field experience in marine evolutionary ecology and/or experience with the husbandry of marine animals - Outstanding communication and writing skills - Laboratory management experience a plus - Preference will be given to candidates with record of innovative project contributions including peer-reviewed publications and grant funding.

Closing Date: April 24, 2013

For complete job description and application instructions please see our employment page at:

http://www.brooklyn.cuny.edu/adminjobs and click on Job ID 7746.

Brooklyn College is an AA/EO/IRCA/ADA Employer.

Jennifer Tsui <JTsui@brooklyn.cuny.edu>

All applications MUST be submitted online. E-mail or hard copy applications will NOT be accepted. applications will NOT be accepted.

Dartmouth MicrobialEvolution

Postdoctoral Position in Comparative Genomics and Microbial Evolution

A postdoctoral researcher position is available in the lab of Olga Zhaxybayeva at the Biological Sciences

Department of Dartmouth College in Hanover, NH. Zhaxybayeva's lab uses computational approaches to study how microbes evolve and adapt to their environments. Ongoing projects fall into the following broad areas: 1) Studying impact of horizontal gene transfer on microbial populations; 2) Characterization of microbial communities; and 3) Deciphering genomic signatures of microbial adaptations. More information about Zhaxybayeva's lab is available at http://www.dartmouth.edu/~ecglab/ . Qualified applicant must have a Ph.D. in bioinformatics, biology, microbiology, computer science, statistics or a related field with background and strong interest in molecular evolution. Some prior scripting or programming experience is required.

The successful candidate should anticipate contributing to a variety of ongoing collaborative research projects with teams across the United States and Canada. The incumbent will also have the opportunity to establish his/her own independent projects. In addition to becoming a part of a vibrant research and educational environment, the successful candidate can also take advantage of professional development programs offered by Dartmouth College's Postdoctoral Association.

Review of applications will begin immediately and continue until the position is filled. Start date is negotiable. Interested applicants should send a single PDF file containing CV, one-page statement of research interests and contact information of three referees to Olga Zhaxybayeva at ECGLabJobs@gmail.com.

Dartmouth offers competitive salary and benefits along with the opportunity to live in a picturesque rural region that offers year-round recreational activities and is located near cities of Boston, Montreal, and New York. Dartmouth College is an equal opportunity/affirmative action employer that has a strong commitment to diversity. Women, minorities, persons with disabilities, and veterans are encouraged to apply.

– Olga Zhaxybayeva, Ph.D. Assistant Professor Department of Biological Sciences Dartmouth College 026 LSC 78 College Street Hanover, NH 03755 USA

Office: (603) 646-8616 Email: olgazh@dartmouth.edu Web: http://www.dartmouth.edu/~ecglab/-http://dfd.dartmouth.edu/profiles/907 Olga.Zhaxybayeva@dartmouth.edu

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DukeU MortonArb OakPhylogenetics

Postdoctoral Research Associate in Phylogeny of Oaks at Duke University or The Morton Arboretum

Position Description: The postdoctoral research associate will work with an international team of researchers led by Andrew Hipp (The Morton Arboretum), Paul Manos (Duke University), Jeannine Cavender-Bares (University of Minnesota), Jeanne Romero-Severson (Notre Dame University), and Antonio González-Rodríguez (Universidad Nacional Autónoma de México) to study lineage and trait diversification in a diverse oak clade centered on North and Central America. The postdoc will focus on analysis of next-generation sequencing data (sequenced RAD data) and phylogenetic comparative analysis of biogeographic, morphological, and climatic niche data. Research will require the integration of morphological, ecological, and molecular phylogenetic approaches, with a focus on computational approaches. The position is funded through Duke University, but applicants have the option to work primarily at Duke or split their time between The Morton Arboretum and Duke University.

Required Qualifications: Ph.D. degree in discipline related to the research area.

Preferred Qualifications: Experience with molecular phylogenetics, genome-scale data and next-generation sequencing data, and biodiversity informatics. Evidence of strong writing and communication skills.

The successful candidate will: (1) have a strong attention to detail, (2) be an independent thinker with strong problem-solving abilities, (3) be able to take the lead authorship on manuscripts, and (4) be able to effectively work in a large collaborative framework.

Salary: $39,000 plus benefits, administered through Duke University.

To apply please submit the following to Andrew Hipp and Paul Manos:

(1) A detailed CV with publication list, successful grants, and contact information for three references. (2) A short letter explaining your interests and qualifications for this position.

Application Process: Applicants will be considered until the position is filled; however, applicants should submit by 5:00 pm EST, 1 May 2013, for full consideration. Availability for an in-person interview is preferred. The position is available starting immediately, but the start date is flexible. The appointment is for one to two years, with annual extensions dependent on satisfactory performance.

If you have any questions, please contact Paul Manos (pmanos@duke.edu) and Andrew Hipp (ahipp@mortonarb.org).

ahipp@mortonarb.org

ETHZurich Eawag HostParasitoid

The Evolutionary Ecology group based at Eawag Dubendorf and ETH Zurich in Switzerland is conducting research on host-parasite interactions. We are particularly interested in the topic of symbiont-mediated coevolution, that is in hosts adapting to their parasites by symbiosis with protective microorganisms, and in the parasites counteradapting to these protective symbionts. Our main study organisms are aphids, their bacterial endosymbionts and hymenopteran parasitoids of aphids.

To strengthen our team we are inviting applications for a

POSTDOC POSITION IN GENETICS OF HOST-PARASITE INTERACTIONS

We are seeking an enthusiastic postdoc with interest in host-parasite coevolution and experience in generating and analyzing next-generation sequencing data, ideally in transcriptome sequencing (RNA-Seq). A PhD is required for this position. The expected starting date is 1 October 2013, but can be negotiated.

This Postdoc position is funded by the Swiss National Science Foundation and is available for 2 years. The successful candidate will be working in the Evolutionary Ecology group led by Christoph Vorburger (www.evec.ethz.ch). This group is associated with the Institute of Integrative Biology at ETH Zurich, Switzerland (http://www.ibz.ethz.ch), as well as with the Department of Aquatic Ecology at Eawag, the Swiss Federal Institute of Aquatic Science and Technology (http://www.eawag.ch). These institutions offer a stimulating work environment, ample opportunities for collaboration, and excellent facilities, including the state-of-the-art Genetic Diversity Center (www.gdc.ethz.ch). Salary and benefits are competitive. Dubendorf is adjacent to Zurich, a city known for its excellent quality of life.

Applications have to be submitted online via the following link: http://internet1.refline.ch/673277/0199/-++publications++/1/index.html . Please include a cover letter explaining your motivation, research interests and relevant experience, a curriculum vitae, publication list, and the names and contact details of three academic references as a single PDF file. Deadline for applications is 31 May 2013. For enquiries about this position please contact Christoph Vorburger (+41 58 765 51 96; christoph.vorburger@eawag.ch).

We are looking forward to your application.

Gelnhausen Germany ConservationGenetics

Senckenberg Gesellschaft für Naturforschung has an international reputation in all fields of Natural History research. It runs six research institutes and two museums in Germany and is also custodian of the UNESCO World Heritage Site at Messel.

The conservation genetics section functions as National Reference Centre for Genetic Analyses of Large Carnivores in Germany. The lab performs genetic monitoring of several highly endangered wildlife species in Germany and Europe, including wolf, wildcat, beaver, saiga, and other mammals. Aside from traditional academic interests our strategy is to cooperate intensively with non-research partners, such as NGOs and conservation authorities, to ensure a tight link between genetic research and applied conservation and wildlife management. The Conservation Genetics Section at the Senckenberg Research Station in Gelnhausen seeks a postdoctoral researcher in wildlife and conservation genetics (Ref. #04-13001)

Your tasks: §co-supervision of running projects and design of new research projects §analysis of genetic datasets §manuscript drafting §communication with local and international project partners Your profile: §PhD in the field of molecular population genetics or related disciplines §experience with different molecular marker systems (microsatellites, SNPs, sequence data) §superior skills in population genetics and data analysis §excellent publishing record in high-ranked international journals §experience in student supervision and project handling is an advantage §German language skills are desirable but not mandatory §high motivation and passion for species conservation

Salary and benefits are according to a public service position in Germany (TV-H E13, 100%). The contract shall start as soon as possible and will initially run for 24 months with the possibility of extension depending on the candidate's performance. The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The type of handicap should not prevent work needed to conduct the research. The duty station will be Gelnhausen and Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft fuer Naturforschung.

Please send your application before May, 15th 2013 preferred by e-mail (attachment in a single pdf document), mentioning the reference of this position (Ref. #04-13001) and including a letter outlining your suitability for the post, a detailed CV, contact details of 2 references and, if available, publications to the Head of Personnel and Social Affairs:

Frau Britta Werner Leiterin Personal & Soziales Senckenberg Gesellschaft Senckenberganlage 25 60325 Frankfurt am Main recruiting@senckenberg.de

In addition to that, we would like you to indicate in your application the source that brought our job advertisement to your attention. For scientific enquiries please get in contact with Dr. Carsten Nowak, cnowak@senckenberg.de.

recruiting <recruiting@senckenberg.de>

IFREMER UBrest SabellariaAdaptation

LabexMer Postdoctoral Position on the

Response of *Sabellaria* reefs to environmental change across its distributional range

The honeycomb worm, *Sabellaria alveolata*, is an ecosystem engineer responsible for the construction of some of the most extensive biogenic reefs in the temperate coast of Europe. Dense aggregations of this tubeworm generate three-dimensional complexity, supporting higher biodiversity than adjacent habitats. Populations of this species are genetically divergent and span a range of contrasting environments across its distributional range. In order to understand the range of response of genetically divergent populations to environmental change, laboratory and field experiments will be conducted to observe how individuals from different locations are able to cope with thermal stress, hypoxia and acidification.

To further explore the ability of *Sabellaria* reefs to cope with environmental change, a full-time postdoctoral position is available jointly at the European Institute of Marine Sciences (IUEM) and the French Research Institute for Exploration of the Sea (IFREMER) in Brest, France, under the supervision of Dr. Flavia Nunes and Dr. Stanislas Dubois. The position is funded by the LabexMer Chair in Evolutionary Marine Ecology.

We are seeking a motivated and independent individual, who enjoys experimental and field work, and who is equally comfortable and qualified in the molecular lab. Ability to work in a team is essential and a strong publication record is desired.

The successful candidate will demonstrate proficiency in at least two of the following areas:

- Experience conducting experiments in the field and under controlled laboratory experiments

- Molecular biology, including gene expression analysis (transcriptomics, qPCR, in-situ hybridization)

- Bioinformatics for the analysis of genomic, transcriptomic and/or proteomic data

- Ecological modelling

Funding is available for up to 2 years with renewal after 1 year pending satisfactory research progress. Salary will be euro 30,000 - 32,000 plus benefits.

Brest is home to the largest oceanographic community in France. The network of academic and government institutes based here provide numerous opportunities for interactions, collaborations and sharing of resources for the exploration of the sea. The city of Brest has a rich maritime culture and is located along the charming coastline of Brittany.

To apply, please send a letter of motivation, detailed CV including publication list, and contact information for 2 references to Flavia.Nunes@univ-brest.fr

Deadline for applications: April 15, 2013

– Flávia Nunes

International Chair in Evolutionary Marine Ecology LabexMer - Institut Universitaire Européen de la Mer

IUEM Technopôle Brest-Iroise Rue Dumont d'Urville Bureau A124 29280 Plouzané FRANCE +33 2 90 91

53 76

Flavia.Nunes@univ-brest.fr

INIA Madrid AnimalBreeding

RESEARCH POST IN ANIMAL BREEDING & GENETICS AT INIA, MADRID

A research position is available at the Animal Breeding Department of INIA, Madrid (Spain) to work on the topic 'Estimation of the impact of selection and inbreeding on genetic diversity using genomic tools'.

The project is funded by the Spanish Government and is a collaboration of INIA (Beatriz Villanueva y JesÃo̱s Fernández), the 'Universidad Politécnica de Madrid' (Miguel Angel Toro) and the 'Universidad de Vigo' (Armando Caballero). In this coordinated project we will evaluate from theoretical and computational developments and analysis of empirical data, the applicability of SNP markers in the estimation of allelic diversity, purging of deleterious variants, estimation of effective population size, and footprint of selection. Tasks for this post will involve computer simulations and analysis of dairy cattle SNP data.

Candidates should have a strong background in quantitative genetics, population genetics or animal breeding and a university degree valid in Spain. Strong communication and computer skills are required. Postgraduate qualifications will be an advantage.

The post is available for 2 years. The salary will be determined according to the Spanish public research salary scale.

The deadline for applications is Friday 3rd May 2013. Unfortunately all the documentation and the application form (attached) are in Spanish.

Beatriz Villanueva Gaviña

Departamento de Mejora Genética Animal INIA (Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria) Carretera de La Coruña km 7,5 28040 Madrid, Spain

Tel.: 34 91 347 6807 Fax: 34 91 347 8743 villanueva.beatriz@inia.es

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JesÃo̱s Fernández Martín

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http://dl.dropbox.com/u/5714008/Fernandez.htm
JesÃo̱s Fernández Martín <jmj@inia.es>

INRA Nouzilly France ReproductivePhylogenetics

A postdoctoral position is available in the Reproductive and Behavior Laboratory at the INRA institute in Nouzilly, France. This lab specializes in developing phylogenetics and evolutionary methodologies to study biological functions such as reproduction and lipid metabolism. In particular, there is a need for a better understanding of how genes involved in metabolism are evolving by gene appearance, gene loss, positive selection, gene conversion.... Candidate should have PhD experience in evolutionary biology, bioinformatics, computer science, or related fields. Funding for this position is available until spring 2014 during 8 months. For informal enquiries, contact Dr. Philippe Monget via?email: pmonget@tours.inra.fr.

Best, Philippe

Philippe Monget <Philippe.Monget@tours.inra.fr>

IVIC Venezuela MycorrhizalTaxonomy

Please note the application deadline has been extended to May 10, 2013

*** Spanish version follows***

*** all replies to lfajardo@ivic.gob.ve ***

Please forward to relevant email lists:

The Ecology Center of the Instituto Venezolano de Investigaciones Científicas in Caracas, Venezuela (IVIC; http://www.ivic.gob.ve/ecologia/) announces the search for a researcher or post-doc to join our Laboratory of Soil Ecology. The ideal candidate will be available as of May, 2013, to work in the lab's arbuscular mycorrhizae group. Candidates must have a doctorate and research experience in arbuscular mycorrhizal symbiosis and taxonomy (Phylum Glomeromycota), and be willing to teach postgraduate-level classes, assume administrative responsibilities, and supervise graduate and undergraduate thesis projects. Experience with the production of inoculants and the ecophysiology of plants inoculated with arbuscular mycorrhizal fungi is particularly welcome, as this post includes coordinating the lab's ongoing production of this biofertilizer for agroecological, teaching, and research applications.

Interested applicants should send a CV and brief letter of intent to Dr. Laurie Fajardo (lfajardo@ivic.gob.ve), prior to May 10, 2013.

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Se extendio la fecha limite de postulacion al 10 de mayo de 2013

*** favor enviar respuestas únicamente a lfajardo@ivic.gob.ve ***

Favor difundir por las listas relevantes:

El Centro de Ecología del Instituto Venezolano de Investigaciones Científicas en Caracas, Venezuela (IVIC; http://www.ivic.gob.ve/ecologia/) inicia el proceso de selección para el ingreso de un investigador o posdoctorante al Laboratorio de Ecología de Suelos. El candidato ideal debe estar disponible a partir de mayo de 2013 para trabajar en el grupo de micorrizas arbusculares de dicho laboratorio. Los candidatos deben poseer un doctorado y contar con experiencia de investigación en el estudio de la asociación micorrízica arbuscular y la taxonomía de los hongos que la conforman (Phylum Glomeromycota). Además la persona seleccionada debe estar dispuesta a participar como docente en el postgrado de Ecología y en actividades administrativas, y dirigir tesis de pre y postgrado. Esta particularmente bienvenida experiencia en el estudio de la ecofisiología de plantas micorrizadas y en la producción de inoculantes micorrizicos, ya que el candidato seleccionado coordinará la producción de este biofertilizante que actualmente lleva a cabo el Lab. para aplicaciones agroecológicas, académicas y de investigación.

Los interesados deberán remitir su curriculum vitae y una breve exposición de motivos a la Dra. Laurie Fajardo (lfajardo@ivic.gob.ve), antes del 10 de mayo de 2013.

~~~~ Kathryn M. Rodriguez-Clark, Ph.D. Investigadora/Researcher Laboratorio de Ecologia y Genetica de Poblaciones, Centro de Ecologia Instituto Venezolano de Investigaciones Cientificas (IVIC) Apartado 20632 Caracas 1020-A, Venezuela

Tel: +58-212-504-1889 Fax: +58-212-504-1617

alt. email: kmrc@ivic.gob.ve ~~~~ Los acentos graficos han sido voluntariamente omitidos para evitar problemas con algunos clientes de correo electronico. Perdonen los inconvenientes que por ello puedan haberse generado. ~~~~

kmrodriguezclark@gmail.com

IowaStateU TurtleChromosomeEvolution

PostDoctoral Position in Turtle Chromosome Evolution

A postdoctoral position is available to work in the laboratory of Dr. Nicole Valenzuela at Iowa State University on an NSF-funded PhyloGenomics project to study the genome rearrangements responsible for changes in diploid number across turtles and their association with transitions in sex determination.

The project combines molecular cytogenetics, transcriptomics, bioinformatics and phylogenetic analyses.

The ideal candidate will have a PhD degree and strong background in molecular and classic cytogenetic techniques including chromosomal preparation, fluorescent in situ hybridization/chromosome painting, karyotyping, and the use of Cytovision or other chromosomal analysis platform. Other qualifications such as evolutionary biology background or experience with cell culture and bioinformatics are a plus but not required.

Funding is available for up to 3 years with annual renewal contingent upon performance. The position is available at any time starting 1 July 2013.

For inquiries or to apply please email Dr. Nicole Valenzuela at nvalenzu@iastate.edu <mailto:nvalenzu@iastate.edu>. Applicants should email a cover letter describing their research interests and experience, current CV, and copies of up to two relevant publications if available, and arrange to have two letters of recommendation be sent directly to nvalenzu@iastate.edu <mailto:nvalenzu@iastate.edu>.

Iowa State University does not discriminate on the basis of race, color, age, religion, national origin, sexual orientation, gender identity, genetic information, sex, marital status, disability, or status as a U.S. veteran.

Dr. Nicole Valenzuela Associate Professor <nvalenzu@iastate.edu> Department of Ecology,
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Evolution, and Organismal Biology 253 Bessey Hall Iowa State University Ames, IA 50011, USA

Phone: 515-294-1285

URL: http://www.public.iastate.edu/~nvalenzu/

nvalenzu@iastate.edu

Lyon MouseMolarEvolution

POST-DOCTORAL POSITION: MOUSE MOLAR EVOLUTION AND DEVELOPMENT IGFL, Lyon, France

In the Mus genus, some mice feature a "prestyle" (kind of ridge) on the anterior part of their first upper molar: this has been observed repeatedly in island populations, as well as is several laboratory strains, and correlates with a large body size. Our lab is involved in a collaborative project aiming at deciphering the processes beyond this remarkable case of parallel teeth evolution.

A post-doctoral fellow will be recruited to take charge of the evo-devo aspects of this work. In particular, she/he will look at the embryonic origin of this prestyle in lab strains selected for large body size and in strains established from wild-trapped mice. She/he will notably test a model proposed in Renaud et al. (Plos One 6(5):e18951 2011), whereby the evolution of the prestyle may involve a variation in the degree of incorporation of an abortive tooth bud found at the anterior edge of the developing first molar.

The candidate will demonstrate high motivation and the ability to independently manage aspects of the project determined to be her/his responsibility, while interacting with a collaborative group. A good general background in developmental biology/morphogenesis is essential. Good knowledge of evolutionary developmental biology and/or a previous experience with a rodent model would be an asset. Ideally, the candidate will have skills in staining and imaging methods (e.g. immunostainings, confocal microscopy) and some training with dissecting/manipulating embryos under a stereomicroscope.

A 18-months position (ANR grant funded) is on offer, and the candidate will be provided assistance to find follow funding. Expected starting date: between July 2013 and November 2013.

The Molecular Zoology group is part of the Institute for Functional Genomics of Lyon. We have been interested in rodent molar development and evolution since 2004. In September 2012, we moved to a newly built and fully equipped building in Lyon. The institute hosts international teams and largely uses English for internal communication. http://igfl.ens-lyon.fr Contact: CV and at least 2 referee contacts can be sent to: sophie.pantalacci@ens-lyon.fr Applications should be submitted before May 30th, however later applications will be considered if the position is not already filled.

sophie.pantalacci@ens-lyon.fr

MaxPlanck Cologne EvolutionaryGenomics

A postdoctoral position is available in the laboratory of Dr. Dario Riccardo Valenzano http://www.age.mpg.de/science/research-labs/valenzano/ in the Department of Evolutionary and Experimental Biology of Ageing at the Max Planck Institute for Biology of Ageing (MPI-AGE) in Cologne, Germany.

The successful candidate will join a young and dynamic research team in the study of the genetic and genomic bases of Vertebrate ageing and life history evolution, using short-lived African killifish of the genus Nothobranchius as the main model organism. The current research projects involve genetic crosses, fish transgenesis, population genetics in wild populations, and bioinformatic analysis of high throughput genomic data.

Candidates should have experience in genetics, genomics, bioinformatics, and a strong foundation in statistical and quantitative methods.

The candidate is required to hold an M.D. or a Ph.D. in biology, genetics, computer science, physics, or a related field, as well as strong written and oral communication skills. The working environment is international, and the language is English; knowledge of German is not required.

The application should include 1. cover letter 2. Curriculum Vitae 3. one page statement of research interests 4. names and contact information of 3 referees

Please submit your application as a single pdf file by May 31 to the following email address: drvalenzano(at)gmail.com

drvalenzano <drvalenzano@gmail.com>

MaxPlanck Tubingen PopGenetics

Max-Planck Institute for Developmental Biology MAX-PLANCK INSTITUT FÃR ENTWICKLUNGSBIOLOGIE

The Department for Integrative Evolutionary Biology (Director Ralf J. Sommer) invites applications for a Postdoctoral Position on Population Genetics of Phenotypic Plasticity.

The Department has an active research program in integrative evolutionary biology studying the nematode model organism Pristionchus pacificus. Our research aims for an integration of evo-devo with population genetics and ecology (Sommer, Nat Rev Gen 10:416, 2009).

P. pacificus lives in close association with scarab beetles and shows a predatory feeding behavior. Predation involves a morphological novelty building on phenotypic plasticity (Bento et al. Nature 466: 494, 2010) and nervous system rewiring (Bumbarger et al. Cell 152: 109, 2013).

The lab has a field station on La Réunion in the Indian Ocean where P. pacificus shows massive genetic diversity, ideal for population genetics (Morgan et al., Mol Ecol 21:250, 2012).

We are searching for a postdoctoral fellow interested in linking the feeding plasticity and its genetic regulation to population genetics in a well-established genomic framework. The Max-Planck Institute provides large-scale sequencing facilities, including next generation sequencing.

Experience in population genetics is mandatory. Additional experience in microscopy is a plus.

The position is for two years with a possible extension. Funding would be available from 1. October 2013. Closing date for applications: 30. April 2013.

Please submit applications to: Ralf J. Sommer Max-Planck Institute for Developmental Biology; Dept. for Evolutionary Biology 72076 Tübingen, Germany ralf.sommer@tuebingen.mpg.de http://www.eb.tuebingen.mpg.de/dept4/home.html http://www.pristionchus.org

Posted by

Doris Merrill, dmerrill@ksu.edu Kansas State University Manhattan, KS 66506

dmerrill@ksu.edu dmerrill@ksu.edu

NMNH Paris MultilocusAdaptation

Inferring adaptive processes at the multilocus scale from large-scale polymorphism data.

We propose a two-year postdoctoral position funded by the LabEx Biological and Cultural diversities (BCDiv). The postdoctoral fellow will be supervised by Frédéric Austerlitz (Laboratory “EcoAnthropology et Ethnobiology”) in collaboration with Mathieu Joron and Marianne Elias (Laboratory “Origin, Structure and Evolution of Biodiversity”) at the National Museum of Natural History (Paris, France). We seek a creative and motivated candidate, with a solid background in bioinformatics and/or computational biology. Experience in population genetics/genomics would be highly appreciated.

The aim of the postdoctoral position is to develop methods that would allow the detection of adaptive processes that would occur simultaneously on several genes, for instance when all these genes are involved in a given adaptive trait. The first step would be to develop an individual-based program that will allow simulating the evolution of populations connected by gene flow, where individuals are characterized by their phenotype for several traits, each coded by a given number of genes. Several kind of genotype/phenotype relations will be considered, for instance the genes could be involved in a gene network leading to the phenotype. Then the power of existing single-locus selection tests will be tested on these simulated data. New multi-locus test will also be developed and their power will also be assessed on the simulated data. Finally, these tests will be applied to the genome-wide polymorphism datasets available in the two laboratories (mainly on humans and tropical mimetic butterflies).

This is a two-year position, with can start as early as July 2013. Candidates should send a CV, a short letter of application and the name of three academic referees by email to Frédéric Austerlitz (austerlitz@mnhn.fr) no later than April 22th. Please feel free to contact me for any further information. Salary will depend on the candidate’s previous professional experience, with a minimum net salary of around 1900 euros/month. A few candidates will be selected for an audition (possibly by skype) that should take place at the end of April or the beginning of May.

Frédéric Austerlitz Directeur de Recherche CNRS / CNRS Research Director Laboratoire d'Eco-anthropologie et Ethnobiologie Museum National d'Histoire Naturelle, CP 139 57 rue Cuvier F-75231 Paris Cedex 05, FRANCE tel: + 33 1 40 79 54 97 / fax: +33 1 40 79 32 31 webpage: http://www.ecoanthropologie.cnrs.fr/-spip.php?article519 austerlitz@mnhn.fr

NorthCarolinaStateU PlantPopGenetics

A postdoctoral research scholar position in plant population genetics is immediately available at North Carolina State University in the Crop Science Department. The researcher will conduct research on maize genetics. Large samples of inbred and outbred maize landraces will be grown in a short day-length nursery. Each plant will be sequenced to identify parentage and inbreeding level and measured for numerous traits related to fitness. The researcher will be responsible for analysis of inbreeding depression at the gene level and testing prediction models for phenotypes.

Requirements: Ph.D. degree in plant breeding, plant population genetics, or plant genetics. Experience with collection of plant phenotype data in field experiments. Knowledge of quantitative and population genetics. Knowledge of SAS or R programming.. Significant travel will be required for experiment management and data collection.

Experience with maize genetics and bioinformatics is preferred.

Interested persons can apply directly at jobs.ncsu.edu. Search for position number 00103312.

For further information, contact:

Jim Holland

Department of Crop Science

North Carolina State University

Raleigh, NC 27695-7620

919-513-4198

james_holland@ncsu.edu

Jim Holland <james_holland@ncsu.edu>

Paris StructuralBioinformaticsEvolution

Postdoctoral position in structural bioinformatics - Université Pierre et Marie Curie - Paris

We are seeking a highly motivated postdoctoral candidate, with experience in structural bioinformatics and appropriate programming skills. The position is available for 18 months, starting between May and July 2013, in a multidisciplinary institute (IMPMC, UMR7590 CNRS - Université Pierre et Marie Curie), embedded in the highly dense research campus of Jussieu, in the center of Paris.

The research activity of the group is centered on the development of methodologies for protein sequence analyses. These are used for predicting the structure, function and evolution of proteins and are especially applied to the understanding of the molecular basis of protein dysfunctions in diseases.

In this INCA-funded project, we aim at developing original strategies for deciphering sequence-structure relationships and for identifying hidden relationships in protein sequences. These should be especially applied for large-scale investigations (at the level of genomes) and for the analysis of proteins involved in DNA damage response. The applicant will be directly involved in these developments, as well as in their applications performed in collaboration with our colleagues from the INSERM_S 768 unit (Imagine Institute of genetic diseases - Necker Hospital).

Applicants should send a curriculum vitae, a letter of motivation and the names of three references to Isabelle Callebaut (Isabelle.Callebaut@impmc.upmc.fr)

Guilhem Faure Ph.D in Structural BioInformatics LinkedIn: < http://goog_96224789 > http://www.linkedin.com/in/guilhemfaure

guilhem.faure@gmail.com

SMNH Stockholm AcoelomorphGenomicsPhylogenomics

A postdoc position is available in the research group of Ulf Jondelius at the Swedish Museum of Natural History, Stockholm.

http://www.nrm.se/ommuseet/ledigatjanster/-annonser2012/postdoctoralresearcher.18621.html
We are looking for a highly motivated postdoc with interest in animal evolution for a project using data from genome sequencing of microscopic marine worms (Acoelomorpha). Acoelomorpha are simple animals lacking many features present in other Bilateria (e.g. circulatory system, body cavity, excretory organs). Their phylogenetic position is highly contested: they have been proposed to be either the earliest extant bilaterians, part of the flatworms, or deuterostomes closely related to echinoderms and hemichordates. The conflicting hypotheses imply widely disparate interpretations of their morphological evolution as either primitively simple or secondarily reduced in complexity. We will sample genomic data to cover acoelomorph diversity aiming to reconstruct their phylogenetic position within the Metazoa and study the structure of the genomes expecting to find either a simple basal metazoan genome or higher bilaterian and deuterostome signatures. The succesful candidate will work on assembly and analysis of genomes from several acoelomorph species. The project is a collaboration with SciLife lab in Stockholm and Uppsala and colleagues at the Sars Centre in Bergen, Norway.

Requirements: The ideal candidate has a PhD in Bioinformatics, Genomics, Molecular or Evolutionary biology or related fields, experience in analyzing next-generation DNA sequence data, and a record of publishing in scientific journals. Programming experience in a scripting language (such as Python or Perl) is desirable.

Position details: The position is funded by the Swedish Research Council. The salary will be in the range of 360 000-390 000 SEK per year. Starting date is 1 September 2013 (negotiable). The appointment is for two years.

How to apply: Applicants should submit (1) a cover letter describing your research interests and background, (2) a detailed CV (including publications), and (3) the contact details of three references as a single pdf document to rekrytering@nrm.se. Mark your application as dnr x.x.x-x–2013

Closing date 10 May 2013.

Informal inquries should be directed to ulf.jondelius@nrm.se The Union representatives Bodil Kajrup, SACO-S and Yvonne Arremo, ST can be reached at telephone number + 46 8 519 540 00.

Andreas Hejnol <andreas.hejnol@sars.uib.no>

Sempach Switzerland ModellingPopulationProcesses

Modelling large-scale population processes in Swiss breeding birds

The Swiss Ornithological Institute in Sempach (Switzerland) is seeking a highly motivated post-doctoral researcher to model large-scale population processes in Swiss breeding birds. The project is funded by the Swiss National Science Foundation and aims 1) to develop methods that allow the estimation of survival and recruitment from monitoring data and 2) to model spatial and temporal variation of survival and recruitment in selected species to better understand population trends.

The main data source in the project will be the Swiss breeding bird survey (MHB), which has been producing 2-3 replicated counts per breeding season in 267 1 km2 quadrats in every breeding season since 1999. These data allow estimation of population trends in abundance while accommodating imperfect detection. However, the demographic mechanisms underlying these trends remain unknown. The model of Dail and Madsen (Biometrics 2011) enables the estimation of survival and recruitment from such data. Exploring the potential of the Dail-Madsen-model at the scale of Switzerland will be a first part of the project. A possible topic is also to develop extensions of the model, such as the inclusion of correlated spatial effects or the integration of MHB data with other data sets that are directly informative about demographic rates, such as ring-recoveries. A second part of the project is the application of the modelling framework to address relevant ecological and management questions. Candidates include the patterns of survival and recruitment along the altitudinal gradient in Switzerland or whether particular habitat types or regions are associated with higher survival or recruitment. It will be one of the duties of the selected candidate to identify relevant research topics in this field and then to expand on the identified issues using our data and the modelling framework to be developed.

The ideal candidate has solid experience in population modelling, in Bayesian statistical modelling and is a proficient programmer in the R and BUGS languages. Further, a demonstrated ability and willingness to produce high-quality publications will be an important selection criterion.

The work will be conducted in collaboration with Michael Schaub (michael.schaub@vogelwarte.ch) and Marc Kéry (marc.kery@vogelwarte.ch), which both are available for further information.

The position is initially for two years, but may be extended to a third year. The ideal starting date would be June 2013. Information on the Institute can be found at www.vogelwarte.ch/startseite-english.html Applications (preferably by e-mail) should be submitted to Michael Schaub (michael.schaub@vogelwarte.ch), Swiss Ornithological Institute, 6204 Sempach, Switzerland, before 30 April 2013 and include a letter of motivation detailing research interests and experiences, a current CV and contact information of three academic referees. Interviews will tentatively take place in May 2013.

PD Dr. Michael Schaub Leiter Ökologische Forschung Tel. ++41 41 462 97 66 michael.schaub@vogelwarte.ch www.vogelwarte.ch Schweizerische Vogelwarte | Seerose 1 | CH-6204 Sempach | Schweiz

http://www.vogelwarte.ch/michael-schaub.html
Watch out for our new book: Kéry & Schaub, Bayesian Population Analysis using WinBUGS, Academic Press. www.vogelwarte.ch/bpa Schaub Michael <michael.schaub@vogelwarte.ch>

SeoulNatlUni EvolutionBehaviorImmunogenetics

We are seeking to appoint a Post-Doctoral Fellow to work on a project on “Quantitative Assessment of Immunogenetic Similarity in Wild Amphibians”. Two years of funding is initially available, with the possibility of extension to a third year.

Allelic variation in the peptide-binding region (PBR) of major histocompatibility complex (MHC) molecules determines the pool of peptides that can be presented to trigger an immune response. These MHC peptides also facilitate vertebrate social discrimination, which should allow for quantitative assessment of genetic similarity. We will test amphibian tadpoles and adults for their abilities to discriminate among their conspecifics based on MHC-PBR amino acid sequence differences. We then will characterize the MHC-based chemical signals and sensory mechanisms by which the signals are perceived.

The Post-Doctoral Fellow will conduct genetic, behavioral, and physiological analyses on larval and adult amphibians to study how schooling behavior and mate choice are influenced by overall genetic similarity, variation in immune-system genes, and individuals’ disease infection status.

A variety of research projects are underway in our laboratory group, spanning topics such as amphibian biogeography, disease ecology, and the evolution of disease resistance. The Post-Doctoral Fellow will be encouraged to work with laboratory members on these projects as well as to develop his or her own new initiatives.

Experience in molecular biology with a strong interest in evolution is desirable. Research will be conducted in well-equipped, modern laboratory facilities. Our research group is multidisciplinary and highly interactive. The project makes use of excellent next-generation sequencing facilities and expertise available in our school.

Seoul National University is one of the leading universities in Asia and ranks internationally 37th overall and 27th in natural sciences (QS World University rankings, 2012). The campus is nestled in a mountain reserve in southern Seoul and offers excellent opportunities for outdoor activities as well as the full range of cultural activities of an exciting, dynamic city that combines traditional and modern lifestyles.

Subsidized housing and meals are available on campus. Transport is easy, inexpensive, with multilingual signage and announcements, so day-to-day living is relatively easy in Seoul.

Applications should include a curriculum vitae, names of three referees, and a brief statement of research interests and goals.

For more information, please contact Prof Bruce Waldman, email: waldman@snu.ac.kr; telephone +1 512 782 9905 (USA) or +82 10 8686 2121 (Korea); FAX +82 2 872 1993.

Bruce Waldman School of Biological Sciences Seoul National University 1 Gwanak-ro, Gwanak-gu Seoul 151-747 South Korea

Bruce Waldman <waldman@snu.ac.kr>

SmithCollege MicrobesTreeOfLife

Postdoctoral Position at Smith College: Interpreting the position and impact of microorganisms on the tree of life

Smith College invites applications for a full-time postdoctoral research position focusing on reconstructing the tree of life, with emphasis on the placement of microbial lineages. The initial appointment is for one year, with the possibility of extending for additional years. The position will be housed in Professor Laura Katz's laboratory in the Department of Biological Sciences (http://www.science.smith.edu/-departments/Biology/lkatz/Research.htm); questions should be directed to lkatz@smith.edu.

An ideal candidate will: 1) be a productive researcher with interests in phylogenetics and phylogenomics of microorganisms; 2) have experience in bioinformatics, including managing and manipulating large data sets; 3) have excellent communication and interpersonal skills; and 4) be interested in collaborating with graduate and undergraduate students in the laboratory.

The goals of the project are to synthesize data on the nature of the tree of life, with particular attention given to microorganisms. The Post-doc will participate in a large collaborative endeavor supported by the NSF AVATOL Program that is aimed at synthesizing a comprehensive tree of life from published analyses, and developing novel tools for community-driven annotation of the tree (http://opentreeoflife.org). Specific responsibilities will include: 1) assembling phylogenetic datasets from diverse microoganisms; 2) working collaboratively with other project members by contributing to method development for analyzing and integrating these datasets; and 3) outreach to the community of systematists studying microorganisms.

To apply, submit application at https://-secure.interfolio.com/apply/21574 with letter of application, C.V., a statement of research interests, representative publications, and the names and contact information of three references. Review of applications will begin May 15th, 2013.

Smith College is a member of the Five College Consortium with Amherst, Hampshire, and Mount Holyoke Colleges and the University of Massachusetts Amherst. Smith College is an equal opportunity employer encouraging excellence through diversity.

lkatz@smith.edu

Stuttgart PlantPopulationGenomics

Our research group at the University of Hohenheim (Stuttgart, Germany) invites applications for

TWO POSTDOCTORAL SCIENTISTS

to work on plant genome evolution and population genetics.

The first position involves the population genomic analysis of the two endemic plant species Arabidopsis pedemontana and Arabidopsis cebennensis to study the relationship between genetic diversity, reproductive system and natural selection in endemic plant species with small population sizes and distribution ranges. Project goals are to investigate the demographic history and the interplay of genetic drift, local adaptation and deleterious mutations to evaluate the genetic risk of extinction. We have established comprehensive collections of population samples and the next steps will include genome re-/sequencing (with project partners) and a population genetic analysis of the data. The project may involve some field work (mostly collection trips) to the Italian Alps and the French Massif Central.

The second position is part of a collaborative project to study the evolution of genes expressed in reproductive tissues of Arabidopsis thaliana and close relatives. Relevant questions are the role of gene duplication versus sequence divergence, the extent and pattern of shared ancestral vs. species polymorphisms, divergence times of species and the role of selection. For relevant publications, see Spillane et al., Nature (2007) and Gossmann and Schmid, J. Mol. Evol (2011). In addition to using data from public repositories and from project partners, we will also generate our own sequencing data with current sequencing technology.

We are looking for independent and creative scientists with a Ph. D. degree in evolutionary biology, population genetics, bioinformatics or related fields. The position requires experience with the large-scale analysis of genomic data and skills in scripting languages such as Python or R. Practical experience in working with plants and genomics-related lab work to coordinate field, greenhouse and wet lab work with technicians and students is advantageous.

Both positions are immediately available for 24 months. Salary will be according to the German government salary scale (TV-L E13) and depends on previous experience, age and marital status. Women and members of minority groups are strongly encouraged to apply.

The University of Hohenheim is located on a beautiful campus in the South German city of Stuttgart and is well integrated into national and international research networks with a critical mass of researchers working on population and quantitative genetics (mostly in the context of animal and plant breeding). Further information about our group can be obtained from www.evoplant.uni-hohenheim.de . Informal inquiries about the projects are welcome at the contact information below.

Please send your application (Cover letter, CV, publications, statement of research interests, addresses of at least two references) until 6 May 2013 as a single PDF document to Bärbel Hessenauer (baerbel.hessenauer@uni-hohenheim.de).

Dr. Karl Schmid Professor of Crop Biodiversity and Breeding Informatics Institute of Plant Breeding, Seed Science and Population Genetics (350) University of Hohenheim Fruwirthstrasse 21, D-70599 Stuttgart Tel: +49 711 459 23487 Email: karl.schmid@uni-hohenheim.de

karl.schmid@uni-hohenheim.de

Sweden PhylogeneticsMolecularDating

POST-DOC OPPORTUNITY IN EVOLUTIONARY BIOLOGY

Highly motivated and skilled applicants from all countries are invited to apply for a post-doc opportunity in the group of Alexandre Antonelli (http://antonelli-lab.net) at the University of Gothenburg, Department of Biological and Environmental Sciences, Sweden, in close collaboration with researchers in Switzerland, the Netherlands, and the USA. You will participate in a dynamic and international research environment aimed at disentangling the evolutionary processes underlying biological diversity and its future.

Work tasks

You will help selecting fossil calibration points for dating higher-level phylogenetic trees of all animals and plants. These fossils will be linked to the bioinformatic pipeline in SUPERSMART (Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages and Relationships of Taxa; see www.supersmart-project.org). You will then use time-calibrated phylogenies to test for correlations between age, species richness, range sizes and extinction threats; temperature fluctuations and changes in diversification rates; among other empirical tests and analyses.

Evaluation criteria

Requirements: Candidates are required to have a PhD and at least two scientific publications and solid experience handling phylogenetic trees. You must also be fluent in English and have excellent communication skills.

Other advantageous skills: The ideal candidate will also have experience in some or several of the following skills: molecular dating; palaeontology; biogeography; bioinformatics including programming/scripting in R, Python or Perl; statistics; GIS; ecological theory and methods.

We are seeking a candidate who is independent, self-motivated, and interested in the use or development of new methods and approaches, in short, a person willing to go beyond the state-of-the-art in the field. We will attach great importance to personal characteristics and independence in learning and working, creativity and documented productivity.

Starting date, duration and conditions

The position is available immediately or upon agreement. Please note that funding for this particular project is provided by a stipend and is therefore not associated with a formal employment at the University, which will nevertheless provide a working desk and all the working facilities given to regular employees. The grant (in total SEK 240,000) covers a 1-year full-time working duty. There is the possibility to apply for a 1-year extension. Commuting is a possibility if there are special reasons.

Application

The application should consist of a single pdf and include: 1) A short letter with the applicant's motivation for the application that describes how the applicant meets the selection criteria (max. one A4 page); 2) A list of relevant qualifications (CV; max 5 pages); 3) Complete list of publications, including submitted and accepted manuscripts.

Deadline for applications

Please submit your application, or let me know your interest in the position, as soon as possible. The evaluation process will begin on April 17th. The position will be filled as soon as an appropriate candidate is chosen.

Additional information and enquiries

Associate Professor Alexandre Antonelli. University of Gothenburg, Department of Biological and Environmental Sciences. E-mail alexandre.antonelli@bioenv.gu.se

Dr. Alexandre Antonelli Associate professor, Scientific curator http://antonelli-lab.net Gothenburg Botanical

Garden Carl Skottsbergs gata 22A, 413 19 Göteborg, Sweden & Department of Biological and Environmental Sciences University of Gothenburg Carl Skottsbergs gata 22B, 413 19 Göteborg, Sweden

Phone: + 46 (0) 31 7862557 Mobile: + 46 (0) 703 989570 E-mail: alexandre.antonelli@bioenv.gu.se

Alexandre Antonelli <alexandre.antonelli@bioenv.gu.se>

UArizona Bioinformatics

A postdoc position is available to work with Joanna Masel (http://eebweb.arizona.edu/faculty/masel) at the University of Arizona in Tucson. A popular tourist destination surrounded on all four sides by mountainous national and state parks, Tucson is a vibrant city of nearly a million people with an attractive climate.

The Masel group's main research interests are in robustness and evolvability, using a mixture of analytical theory, bioinformatic and simulation approaches. We are looking for someone to do primarily bioinformatic work, but opportunities for related, more theoretical projects (within the Masel group) and/or experimental collaborations (with structural biologist Matt Cordes) also exist. While not an intrinsic part of the primary project, the postdoc training environment will include opportunities to learn the formal methodologies of theoretical population genetics. The EEB department in Tucson was ranked in the top 10 by US News & World Report, and has many other research groups doing evolutionary biology and/or bioinformatics, e.g. those of Mike Sanderson, Ryan Gutenkunst, and Mike Barker, enriching the intellectual environment.

We are looking for someone to investigate the origin of novelty at the protein-sequence level. The conventional view is that new proteins evolve from old proteins via gene duplication and divergence. However, this poses a chicken-and-egg problem, implying an ancient "big bang" of protein creation. This project focuses instead on the ongoing de novo evolution of protein-coding genes from previously non-coding sequences. The postdoc will investigate both case studies of this phenomena, and computational predictors of biochemical properties that might facilitate such conversions over evolutionary timescales. Such predictors will be used to test concrete hypotheses that have arisen from theories of evolvability.

Excellent computer programming skills are strongly preferred, ideally with bioinformatics / genomics experience. Exceptionally strong candidates who come from a more experimental background within evolutionary biology, and who now wish to retrain as bioinformaticians, will also be considered. Experience with (or at least prior interest in) evolutionary biology, protein structure and folding, statistics and other quantitative approaches are all advantages. A start date of August 2013 is preferred but negotiable, and the position is renewable, with funding secured for at least three years.

Contact Joanna Masel at masel@u.arizona.edu for more information or to apply.

masel@email.arizona.edu

UBarcelona ChordateEvoDevoGenomics

University of BARCELONA: POST-DOC FELLOWSHIP APPLICATIONS in Chordate Fuctional Evo-Devo and Genomics

Our group on the field of Functional Evo-Devo and Genomics on Chordates is looking for candidates to apply for the recently open calls for intra-European (IEF) and international incoming (IEF) Marie- Curie and EMBO post-doc Fellowships.

Candidates need to have a highly competitive CV to successfully apply for the fellowship. Experience in Molecular Genetics, Transgenesis and Developmental Biology, and (or) Background in Bioinformatics, and Comparative Genomics will be positively considered.

Our main research interest is to understand the impact of gene losses on the evolutionary diversification of mechanisms of development in chordates at the population level. Our work focuses on comparative approaches between vertebrates (zebrafish), urochordates and cephalochordates. Our main subject of study is Oikopleura dioica, a new emergent urochordate model within our own phylum, with the smallest metazoan genome size known so far, and with an outstanding amount of gene losses (Denoeud et al., Science, 2010).

Interested candidates, please send an email to Cristian Cañestro (canestro@ub.edu), including a brief letter of interest and a CV in ONE single pdf file.

Interested candidates for future POST- or PRE-DOCTORAL applications, please feel free to contact too.

European Programs: Intra-European Fellowship IEF Marie Curie (deadline 14-8-2013) http://ec.europa.eu/research/participants/portal/page/call_FP7?callIdentifier=FP7-PEOPLE-2013-IEF&specificProgram=PEOPLE International Incoming Fellowship IIF Marie Curie (deadline 14-8-2013) http://ec.europa.eu/research/participants/portal/page/call_FP7?callIdentifier=FP7-PEOPLE-2013-IIF&specificProgram=PEOPLE EMBO (deadline 15-8-2013) http://www.embo.org/funding-awards/fellowships/long-term-fellowships

For an outline of our group's research: http://www.ub.edu/genetica/evo-devoen/canestro.htm http://www.ncbi.nlm.nih.gov/pubmed?term=3Dcanestroc[Author]&cmd=DetailsSearch&log$=details oikocris@gmail.com

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UBasel SexuallySelectedTraits

Postdoc on 'Genetics of Sexually Selected Traits' at University of Basel, Switzerland *** new deadline April 14 ***

A 2-year postdoc funded by the Swiss National Science Foundation is available in the Scharer Group (http://evolution.unibas.ch/scharer/) at the Zoological Institute, University of Basel, Switzerland. The ideal starting date is October 2013 (but both earlier and later are possible).

The research in our group focuses on the evolutionary ecology of reproduction in simultaneous hermaphrodites, using a highly suitable model, the free-living flatworm Macrostomum lignano. We integrate a broad array of approaches, including experimental lab work, molecular developmental biology, quantitative genetics, genomics and transcriptomics, field sampling, molecular phylogenetics and comparative approaches.

The current project aims at quantifying sexual selection on male and female reproductive traits along the pre- to post-copulatory axis, using a state-of-the-art approach that we recently extended to hermaphrodites (see Anthes et al. 2010, Am Nat). Using transgenic worms we can track green sperm of GFP-positive donors in their GFP-negative partners in vivo (think 'watching sperm at work') and also perform highly efficient paternity analysis. To experimentally validate the importance of identified traits we can use next-generation-sequencing approaches to identify candidate genes and then manipulate the traits using dose-dependent RNA interference (think 'phenotypic engineering of sexually selected traits')(see Sekii et al. 2013, Proc Roy Soc B).

The postdoc will likely focus on quantitative genetics, genetic architecture, and indirect genetic effects of sexually selected traits in this worm, complementing the work of a recently hired PhD student. However, the candidate's interests and backgrounds can have a considerable influence on the scope of the project, with ample room for developing own ideas and approaches.

The successful candidate will be independent, dedicated, creative, and collaborative, and have a strong background in evolutionary biology. Experience with quantitative genetics is a definite plus, and experience in molecular biology is a clear advantage, but not a prerequisite.

The Scharer Group belongs to the Zoological Institute of the University of Basel, a stimulating and international research environment with English as the predominant language (a recent count yielded ~20 nationalities). Our Institute has a strong background in experimental design, statistics, population and quantitative genetics, genomics and molecular biology. So it is a great environment for a young evolutionary biologist and the position comes with a handsome salary.

Basel is the third largest city of Switzerland and attractively situated at the foot of the Jura mountain range. It has the beautiful river Rhine, and directly borders both Germany and France, thus offering rich culinary, cultural, and outdoor possibilities.

To apply, please send a letter of motivation, a CV, a publication list, contact details of 3 referees, and a PDF of your coolest paper to lukas.scharer@unibas.ch (please send an electronic application in a single file in this order). Reviewing of applications will start on April 14, but applications will be considered until the position is filled.

For more details about our research please visit http://evolution.unibas.ch/scharer/ . Cheers,

Lukas

I am looking at these kinds of worms http://macrostomorpha.info and studying these questions http://evolution.unibas.ch/scharer PD Dr. Lukas Scharer University of Basel Zoological Institute Evolutionary Biology Vesalgasse 1 4051 Basel Switzerland

Tel: ++41 61 267 03 66 Fax: ++41 61 267 03 62 Email: lukas.scharer@unibas.ch Homepage: http://evolution.unibas.ch/scharer/index.htm lukas.scharer@unibas.ch

UCaliforniaDavis EvolutionaryGenomics

Postdoctoral researcher in evolutionary genomics

A postdoctoral position is available to work on the evolutionary genomics of maize and teosinte with Jeffrey Ross-Ibarra (www.rilab.org) in the Dept. of Plant Sciences and the Center for Population Biology at UC Davis.

The project will consist of population genetic analysis of local adaptation and inbreeding depression using whole-genome sequences of maize and its wild relative teosinte. Possibilities also exist for a successful candidate to develop new projects related to the overall goals of the research.

An ideal candidate would have prior experience with whole-genome next-generation sequencing data, strong quantitative, computational and programming skills, and a record of published work in evolutionary genetics. The position is available for one year, with the possibility of renewal. The start date is flexible, with a preference for starting in June or July 2013.

Applicants should send a single pdf including a CV, contact information for three references, and a cover letter to Jeffrey Ross-Ibarra <rossibarra@ucdavis.edu>.

For more information:

Ross-Ibarra lab: www.rilab.org Center for Population Biology: www.cpb.ucdavis.edu Dept. of Plant Sciences: http://www.plantsciences.ucdavis.edu City of Davis: daviswiki.org

Jeffrey Ross-Ibarra

Dept. of Plant Sciences 262 Robbins Hall, Mail Stop 4 University of California One Shields Ave Davis, CA 95616

www.rilab.org Tel: 530-752-1152 Fax: 530-752-4604

rossibarra@ucdavis.edu

UCalifornia LosAngeles Biomath

A two-year post-doctoral position is available (start date flexible, can start as early as June, 2013) in the group of Dr. Van Savage (http://faculty.biomath.ucla.edu/vsavage/) in the Department of Biomathematics at the David Geffen School of Medicine at UCLA. This position will be supported by a recently awarded NSF CAREER grant (http://nsf.gov/awardsearch/showAward?AWD_ID=1254159) to Savage on $B!H(BAutomated extraction of vessel data from images to construct new models for vascular networks in plants and animals$B!I(B. Savage combines mathematical models with analysis of large datasets to uncover insights into biological systems. The project has the potential to involve software development, analysis of large datasets, and construction of analytical and numerical models for the vascular system. Results from this project will help lead to a deeper understanding of resource distribution networks and allometric scaling theory, which connects to physiology and ecology. Findings will also aid in identifying differences in structure and function between plants and animals, different organs, and healthy versus diseased (e.g., tumor) tissue. The postdoctoral researcher will have the opportunity to work closely with and mentor high school, undergraduate, and graduate students. Savage will mentor the postdoc in designing and conducting research projects, writing papers, giving talks, and applying for jobs.

UCLA is a major research university with the Faculty of Arts and Sciences, Medical School, and Engineering School all on the same campus, allowing access to myriad researchers and resources that could be useful to this project. UCLA is consistently in the top 5 in terms of federally research funding awarded to universities. Los Angeles is a vibrant, diverse city with outdoor activities available nearby, including beaches and mountains. L.A. also has a wide array of arts and culture, including world-class museums, theater, music, and of course, movies.

Candidates are expected to be independent, highly motivated problem solvers who communicate well and enjoy working in a collaborative environment. The ideal candidate would have a background in mathematical modeling, knowledge of vascular systems in plants and/or animals, and experience with Matlab, R, and/or OCaml programming languages. Applicants with only a subset of these skills are encouraged to apply. Applications and any questions should be sent to vsavage@ucla.edu. The application should include a Curriculum Vitae that details education, past research, and publications. Applicants should also submit a cover letter that describes their interest in the project and should request three references to directly send letters to the email above. Review of applications will begin immediately (April 15, 2013) and continue until the position is filled.

UCLA is an AA/EOE that is strongly committed to diversity and excellence among its researchers.

Van Savage Assistant Professor Department of Biomathematics UCLA School of Medicine and Department of Ecology and Evolutionary Biology UCLA

Van Savage <vsavage@ucla.edu>

UCollegeLondon Genomics

Several postdocs in Bioinformatics and Computational Biology

We seek talented and motivated postdocs to join the Balloux Computational Genetics Group in London, UK. The group currently comprises Francois Balloux, one PhD student and four postdocs (and as many nationalities). The group is well funded thanks to its success in obtaining competitive external funding (mainly BBSRC and ERC). We run "small science" in-house projects and are also involved in a series of international "big science" collaborations. The group has an exceptional track record of former group members becoming successful scientists. Of all Masters, PhD students and postdocs who went through the lab so far (15), all except one have stayed in academia and seven have already secured permanent academic positions (Assistant Professorships or higher).

Our research

Over recent years, we have witnessed tremendous progress in genomic technologies. However, genomic data in itself does little more than clogging up computers. Our aim is to address important biological questions by developing, refining and applying the right computational tools to genomic datasets. Our work spans a large spectrum ranging from the fundamental (e.g. reconstructing the expansion of anatomically modern humans) to the applied (e.g. tracking MRSA infections in hospital wards). Indeed, we do not feel there must be a divide between fundamental and applied science, and while our research is driven by scientific curiosity, we aim at contributing with our work to the genomic revolution in medicine, public health and conservation biology.

Recent research successes include work on past epidemics of plague (Cui et al, PNAS 2012; Morelli et al., Nature Genetics 2011), human colonisation of the world by our ancestors (Eriksson et al, PNAS 2012; Rasmussen et al, Science 2011); and genomic characterisation of Bd, the fungus responsible for mass extinction in amphibian populations worldwide (Farrer et al, PNAS 2012).

Ongoing projects address the following questions.

- Can we disentangle genomic signals of genetic drift and natural selection by taking advantage of spatiotemporally explicit reconstruction demographic histories? - How does diet influence human microbiomes? - Can we predict antibiotic resistance profiles form sequence data alone? - How can we limit the spread of multiple antibiotic resistances? - What are the causes of amphibian mass extinctions?

Though our main research focus is computational population genomics, the group is open to people who wish to develop research in other related areas of genomics.

About you

We welcome applications from candidates with diverse educational backgrounds. The ideal candidates will have recently completed or be completing a PhD degree in Biology (genetics, genomics), Computational Biology (bioinformatics, systems biology), Statistics, Physics or Computer Science. Applicants must have a proven publication record.

A computing background is not strictly necessary, but you must be prepared to acquire some background in dry work. For applicants with computing experience, experience with Linux, and knowledge in one or several programming languages is required (Perl, Python, C/C++, R/BioConductor, MatLab etc).

Prior experience with handling genome-scale data is advantageous: examples include phylogenetic comparative genomics, high-throughput- sequence data analyses both for medical or evolutionary questions and analyses of RNA-seq data.

Postdocs are expected to develop and lead projects. Willingness to help supervising junior members of the group would be a plus and the ability to work in a team is essential. However, the most sought after qualities are enthusiasm, imagination, motivation and creativity.

The Environment

The group is both affiliated to the Department of Genetics, Evolution and Environment (GEE) and the UCL Genetics Institute (UGI), which offer one of the most exciting work environments in the UK. GEE is a large and collegial Department which embraces essentially all aspects of modern biology and has grown by over 25%

over the last two years. The UGI is a vibrant Institute which has been recently created as centre of excellence in medical, statistical and computational genetics. The group has a well-equipped wet lab and access to exceptional computing facility.

How to Apply

All applications should be made via http://www.ucl.ac.uk/hr/jobs/ (job references 1323870 and 1325517), where you will need to create a profile before you can submit an application. For informal applications please contact Francois Balloux (f.balloux@ucl.ac.uk)

Francois Balloux Professor of Computational Systems Biology UCL Genetics Institute Department of Genetics, Evolution and Environment University College London Gower Street London WC1E 6BT Tel: ++44 (0) 20 3108 1601 (int. 51601) Skype: francois.balloux Email: f.balloux@ucl.ac.uk

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UColorado Denver EvolutionAggression

University of Colorado Denver: Post-Doctoral Research in the Evolution of Aggression using the Stalk-Eyed Fly as a Model

A postdoctoral position is available to study the functional role and fitness consequences of pharmacologically altering brain 5-HT and OA in the modulation of aggressive behaviors across multiple behavioral contexts using stalk-eyed flies. The position is in the laboratory of Dr. John Swallow, a member of the Neuroscience Program at the University of Colorado Denver in the Department of Integrative Biology on the Downtown Campus.

Information about the Neuroscience Program can be found at: http://www.ucdenver.edu/academics/colleges/medicalschool/programs/neuroscience/Pages/Neuroscience.aspx Primary responsibilities for this position include: 1) conducting behavioral and neurochemical laboratory research, 2) analyzing data, writing manuscripts and contributing to grant proposals, and 3) helping to coordinate projects of undergraduate and graduate students involved in the project.

Successful applicants should have expertise in behavioral neuroscience and a Ph.D. in biology, animal behavior, neuroscience, or a related field. Preference will be given to candidates with experience using molecular or neurochemical approaches and behavioral analyses. Experience with invertebrate systems is not necessary but preferred. Competitive salary (tiered by years of experience) and benefits are provided; funds are available for 2 years pending satisfactory progress. The position can begin as early as June 1 2013. Review of applications will begin immediately and continue until a candidate is selected.

To apply, please send a cover letter, a statement of research interests, CV, and names and e-mail addresses of three references to John Swallow (john.swallow@ucdenver.edu), Department of Integrative Biology, University of Colorado Denver, Denver, CO 80402, USA.

UC Denver is an equal opportunity/affirmative action employer.

John G. Swallow, Ph.D. Professor and Chair Department of Integrative Biology University of Colorado Denver

Phone 303-556-6154 FAX 303-556-4352

“Swallow, John” <JOHN.SWALLOW@ucdenver.edu>

UGuelph StatMathGenomics

A postdoctoral position is available in the area of mathematical/statistical genomics. The position is jointly supervised by Drs. Cortland Griswold (Integrative Biology) and Lewis Lukens (Plant Agriculture) at the University of Guelph, in Guelph, Ontario Canada. The position is for two years with a preferred start date in July or August of 2013.

The topic of research is the application of genomic signal processing methods to improve agricultural breeding. Genomic signal processing methods involve applying basis-function transformations to genomic data, such as a Discrete Fourier Transform. While the focus of the research is in crop breeding, the principles underlying the approach are broadly applicable to animal breeding, and to the quantitative, population and evolutionary genetics of humans and other natural populations.

There is strong demand for individuals with advanced skills in this area, and the position provides significant opportunity to interact with research-intensive private sector collaborators.

The applicant should have a Ph.D. and strong quantitative skills, be it statistical or mathematical.

Please submit your application no later than May 15, 2013.

Applications should include the following: [1] Statement of qualifications and research and career goals [2] CV [3] Contact information for two references

Send applications to Cortland Griswold (cgriswol@uoguelph.ca) by email.

Research websites: C. Griswold: https://sites.google.com/site/griswoldlab/ L. Lukens: http://www.plant.uoguelph.ca/research/bioinformatics/ cgriswol@uoguelph.ca cgriswol@uoguelph.ca

UKansas GenomeInformatics

The University of Kansas is recruiting a postdoc with expertise in genomics and bioinformatics. The position is associated with the NIH-funded K-INBRE (Kansas IDeA Networks of Biomedical Research Excellence) Bioinformatics Core, which is directed by Dr. Stuart Macdonald.

A key component of this position is service-oriented, so we are seeking applications from dynamic, motivated individuals interested in helping KU researchers develop and analyze genomics projects, providing computational biology and statistical expertise to support genome biology research on campus. The postdoc would also be able to develop their own research program, advised by Dr. Macdonald, and encouraged to collaborate with other KU research faculty. The University has an Illumina HiSEQ2500 sequencer, so individuals with experience in the analysis of next-generation sequencing data are particularly encouraged to apply.

The K-INBRE Bioinformatics Core is closely associated with the Departments of Molecular Biosciences and Ecology and Evolutionary Biology, and with the NIH COBRE-funded Center for Molecular Analysis of Disease Pathways. The University has a strong group of model organism (Drosophila, C. elegans) genetics and genomics researchers, and a number of quantitative and evolutionary genetics labs. The broad range of questions in evolutionary and computational biology addressed by KU labs provides an active, collaborative environment for research.

Queries about the position can be directed to Stuart Macdonald (sjmac@ku.edu). Further details, and instructions on how to apply for the position can be found at http://employment.ku.edu/jobs/2323 . The position is open and review of applications will begin on April 15 and continue until the position is filled.

Dr. Stuart J. Macdonald Director, K-INBRE Bioinformatics Core Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321 email: sjmac@ku.edu web: http://www.molecularbiosciences.ku.edu/stuart-j-macdonald sjmac@ku.edu

UKansas Partime PhylogeneticMethods

A position for a part-time postdoctoral researcher is available in the laboratory of Dr. Mark Holder in the Department of Ecology and Evolutionary Biology at the University of Kansas (Lawrence, KS). The funding for the position allow for part-time (approximately 40% time) work for up to 3 years. The research project that funds the position focuses on developing novel methods for estimating phylogenetic relationships and dates associated with these phylogenies using data from fossil taxa. The postdoctoral researcher will be expected to devise statistical models for these processes, implement these models in open-source software, and validate the performance of the methods through a combination of simulation tests and analysis of real data. The work will also include the development of new methods for analysing rates of diversification.

The ideal candidate will be enthusiastic, motivated, have a strong background in phylogenetics, and have experience implementing Bayesian phylogenetic techniques in C++ as demonstrated by materials submitted through the application process, work experience, and/or previous publications. Demonstrated expertise in estimating divergence times is also an important qualification for the work. Application deadline 04/12/13.

For a complete job description and to apply go to http://employment.ku.edu/jobs/2352 .KU is an Equal Opportunity Employer M/F/D/V.

For more information, see the Holder web page at: http://phylo.bio.ku.edu/ sincerely, Mark

– Mark Holder

mtholder@gmail.com mtholder@ku.edu http://-phylo.bio.ku.edu/mark-holder Department of Ecology and Evolutionary Biology University of Kansas 6031 Haworth Hall 1200 Sunnyside Avenue Lawrence, Kansas 66045

lab phone: 785.864.5789 fax (shared): 785.864.5860

mtholder@gmail.com

UMichigan 2 EvolutionaryBiol

Two Postdoc Positions: one in Model-based Phylogeographic study and one in Quantitative Macroevolution and Biogeographic study

Two postdoctoral positions are available to work on quantitative evolutionary studies in the Knowles lab at the University of Michigan. Funding is available for two years for each position (contingent upon satisfactory progress), with the possibility of 1 additional year of funding.

The phylogeographic projects involve the application and development of integrative approaches to test hypotheses about the factors structuring genetic variation within species, and understand why species show similar or dissimilar patterns of variation in a given community, based on Illumina sequence data. The macroevolution projects involve the application and development of approaches to test the deterministic and stochastic components of evolutionary transitions through geographic, phenotypic, and ecological networks, by integrating phylogenetic and other data types.

For these positions we are looking for researchers with experience in using computational techniques to infer evolutionary processes.

To apply, please send your CV and a cover letter briefly explaining your background (e.g., programs that you are familiar with and your skill level with scripting and/or programming) to L. Lacey Knowles, knowlesl@umich.edu.

L. Lacey Knowles Professor and Curator Dept. of Ecology and Evolutionary Biology Museum of Zoology University of Michigan Ann Arbor MI 48109-1079

L Knowles <knowlesl@umich.edu>

UMichigan EvolutionPathogens

Postdoctoral Research Fellowship: Experimental evolution of eukaryotic pathogens

University of Michigan, Department of Ecology and Evolutionary Biology

Job Summary: A postdoctoral research position is available in the lab of Tim James at the University of Michigan. The research is for an NIH-funded project that seeks to understand the relative roles of mitotic recombination and mutation in pathogen evolution using an experimental host-pathogen system (yeast-invertebrate model). The experiment will also be used to identify candidate virulence genes using next-generation sequencing of evolved lines. Our research is motivated by the observation of rampant mitotic recombination in natural populations of diploid pathogenic fungi and protists and seeks to test how and when the genetic variation produced by mitotic recombination is adaptive and to model how it differs from meiotic recombination.

Required qualifications: Candidates should have strong molecular and bioinformatic skills, a proven record of publication, with a Ph.D. in biology, genetics, or related field. The ideal candidate will have two or more of the following skills: analysis and generation of high throughput sequence data, molecular biology, genetic manipulations such as transformation of yeast, fungi or protozoa, microbiological techniques, and mathematical modeling. The position is available immediately and will remain open until filled. Pay will be based on experience according to NIH guidelines. The initial appointment is for 1 year, with an opportunity for renewal for a second year.

To apply: Interested applicants for the postdoctoral position should send a PDF with CV, a cover letter stating research interests and qualifications, and contact information for three references to tyjames@umich.edu. Informal inquiries are welcome. We are also looking to hire a research technician to work closely with the postdoctoral fellow on the project. Contact tyjames@umich.edu for inquiries regarding this position.

The University of Michigan is a non-discriminatory/affirmative action employer. The Department of Ecology & Evolutionary Biology at the University of Michigan harbors multiple labs with a focus on evolutionary genetics (http://www.lsa.umich.edu/eeb). The campus is located in Ann Arbor, an active university town in southern Michigan 45 minutes from downtown Detroit.

Timothy Y. James Assistant Professor & Curator of Fungi Department of Ecology and Evolution University of Michigan Ann Arbor, MI 48109 734-615-7753 tyjames@umich.edu http://www.umich.edu/˜mycology/ tyjames@umich.edu

UNordland BioinformaticsGenomics

Post-doctoral research fellow in Bioinformatics and Genomics

A position as Post-doctoral research fellow in Bioinformatics and Genomics is available at the University of Nordland, Faculty of Biosciences and Aquaculture

About the University of Nordland The University of Nordland offers education at the Bachelor-, Master-, and PhD levels. Yearly, the university accepts students in over 100 study programs within both professional studies and theoretical subject disciplines, which includes PhD students in business economics, sociology, aquaculture, and professional practice. We currently have approximately 6000 students and 600 faculty and staff, divided among our Bodø campus and our study centers in Helgeland and Vesterålen.

About the Faculty of Biosciences and Aquaculture (FBA) FBA is responsible for research, teaching and dissemination within biosciences and aquaculture.

In recent years, FBA has undergone a major development both in terms of faculty and infrastructure, and today FBA stands as an internationally diverse academic environment. The current research strengths of the Faculty include aquatic animal diseases, reproductive biology, seafood quality, ecology and evolutionary biology, and genomics. The Faculty has approximately 80 employees in academic and technical/administrative support functions.

The teaching at the Faculty is research-based. FBA offers Bachelor's programmes in Biology, Export Marketing, Aquaculture Management and a unique Joint Bachelor Degree in Animal Science in collaboration with the University of Veterinary Medicine and Pharmacy in Slovakia. Moreover, we offer Master's programmes in Aquaculture and Marine Ecology, and a PhD in Aquaculture.

FBA's objective is to conduct research of high national and international quality. The Faculty's strategic research areas comprise aquaculture, marine ecology and marine genomics. The Faculty has state-of-the-art laboratory facilities and also operates Mørkvedbukta Marine Research Station, ten minutes from campus. The Research Station's primary mission is to facilitate and support seawater-related laboratory activities and research on living marine organisms.

The Faculty seeks to strengthen the relations between students, Research & Development, and industry and commerce. For more information, see The Faculty's website: http://www.uin.no/fba_english and the UiN presentation film: http://www.youtube.com/watch?v=AzOUggQtmjI&feature=player_embedded About the Position In April 2010, the Faculty of Biosciences and Aquaculture formally established an advanced genomics platform based on novel DNA sequencing technologies. The Faculty seeks to strengthen its staff associated to the genomics platform.

FBA will hire a post-doctoral research fellow for an initial period of three years, in order to strengthen the professional development of the genomics platform. Research activities at FBA reside within the marine/aquatic biosciences, specifically focusing on aquaculture and marine ecology.

Qualifications and Responsibilities The professional background of the candidate will be within genomics and bioinformatics, with experience in dealing with next-generation sequencing data. Experience in programming and database administration will be considered an asset. The Faculty encourages candidates with broadly defined research interests within the genomics field, either extending or complementing FBA's existing expertise within e.g. functional genomics, aquaculture genomics, reproductive genomics, metagenomics, population genomics, and evolutionary genomics.

The appointee will join the Marine Genomics research group and take on a lead role in developing the genomics and bioinformatics competences at the faculty. The successful candidate is expected to facilitate the analysis of NGS data and the adoption of genomics toolkits among the scientific staff, and develop active collaborations within the Faculty. Furthermore, the candidate is expected to partake in extending the Faculty's project portfolio, secure external research funding, and maintain a commendable record of high-standard publications. The appointed candidate will be involved in teaching and development of the Faculty's course portfolio within the genomics field.

Applicants should possess an academic degree (PhD or equivalent) within genomics, informatics, or related research fields. Excellent written and verbal communication skills in English are required. Candidates should also possess original scientific production related to the field(s) indicated above.

Personal Qualities The position requires a highly motivated and dynamic person with good interpersonal skills, who is a capable and confident researcher. The successful candidate should be able to work cooperatively in a team

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UOregon EcologicalGenomicsofSpeciation

POSTDOCTORAL POSITION IN ECOLOGICAL GENOMICS OF SPECIATION; INSTITUTE OF ECOLOGY AND EVOLUTION, UNIVERSITY OF OREGON

A postdoctoral position is available in the Streisfeld lab at the University of Oregon as part of a NSF-funded project to identify the ecological genomic changes that drive the early stages of species formation in Mimulus. The project will involve greenhouse, field, and laboratory components that include high-throughput SNP genotyping, next generation sequencing, QTL mapping, and field estimates of divergent selection. The postdoc will be involved in all aspects of the project, from data collection to publication, and will be actively encouraged to pursue side projects of his/her own interest.

PhD in evolutionary genetics or a related field is required. Experience with next-generation sequencing and bioinformatics analysis is preferred. The ideal candidate will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds. She/he will have an excellent understanding of experimental design and a proven publication record.

The Streisfeld Lab (www.uoregon.edu/~mstreis) in the Institute of Ecology and Evolution offers a broad and interactive environment for research in plant evolutionary biology. We share close ties with other evolutionary biology labs on campus, and benefit from shared facilities, such as the genomics core research facility. The University of Oregon is an AAU research institution located in Eugene, OR, one of the most outstanding small cities in the US. The campus is one hour from the beautiful Oregon coast and one hour from hiking and skiing in the Cascade Mountains.

To apply for this position, please send a statement of research interests, publications, CV, and letters from three references to Matt Streisfeld via ie2jobs@uoregon.edu (preferred) or c/o Postdoctoral Search # 13120, Institute of Ecology and Evolution, 5289 University of Oregon, Eugene, OR 97403-5289.

The position is available for one year with the possibility of renewal depending on research progress. Although the position is available immediately, the start date can be flexible based on the needs of the candidate. To ensure consideration, please submit application materials by May 20, 2013. The position will remain open until filled.

Women and members of groups underrepresented in science are encouraged to apply. The University of Oregon is an EO/AA/ADA institution committed to cultural diversity.

– INSTITUTE OF ECOLOGY AND EVOLUTION 5289 University of Oregon, Eugene OR 97403-5289 F (541) 346-2364 http://IE2.uoregon.edu Equal-opportunity, affirmative-action institution committed to cultural diversity and compliance with the Americans with Disabilities Act

ie2jobs@uoregon.edu

UOxford EvolutionaryGenetics

Postdoc in evolutionary genetics/genomics, University of Oxford, United Kingdom

We are seeking a highly motivated evolutionary geneticist to work on a project devoted to sex chromosome evolution in plants. The project will mainly focus on plant genus Silene that offers unparalleled opportunities to study recent evolution of separate sexes (from an ancestral hermaphroditic stage) and sex chromosomes. It will benefit from newly developed genomic resources for this genus and will build upon our previous work in this system (e.g. Filatov 2005 Genetics 170(2):975-9; Chibalina and Filatov 2011 Curr Biol 21:1475-9). Experience with evolutionary genetic/genomic analysis is required. Familiarity with handling and analysis of high-throughput sequence data will be an advantage, but bioinformatics training/support will be available, if necessary. For informal enquiries please email Dmitry.Filatov@plants.ox.ac.uk

Dmitry Filatov <dmitry.filatov@plants.ox.ac.uk>

UPennsylvania HumanEvolutionaryGenomics

The Tishkoff lab at the University of Pennsylvania is seeking candidates for postdoctoral positions. We are integrating genomic, transcriptomic, metagenomic, metabolomic, and epigenomic datasets generated from a large sample of ethnically diverse Africans. Analysis of these data includes using an evolutionary and systems biology approach towards understanding the genetic architecture of a number of adaptive traits for which we have detailed phenotype data. We are also interested in inferring the demographic history of African populations and testing models of human evolutionary history using genome-wide data. Candidates will have an opportunity to develop creative, independent projects, and novel statistical methodology. There will be opportunities to work together with an outstanding team of collaborators with expertise in statistical and population genetics theory and methodology.

Candidates with strong molecular genetics or statistical/computational genetics background are encouraged to apply. Expertise with at least three of the following is required: population genetics theory, computer programming (Ruby/PERL/Python/C++), statistical environments (R/MATLAB/ Julia), and/or quantitative analyses of complex traits. Experience with large genome-scale datasets e.g. microarray or next-generation sequencing experiments is a plus. Candidates working with non-human or model organisms who want to obtain experience working with human data are encouraged to apply. Salaries are commensurate with qualifications and experience.

The Department of Genetics is centrally located at the School of Medicine within the UPenn campus and is within short walking distance to the Children's Hospital of Pennsylvania, the Biology Department, the Translational Genomics Institute and the Anthropology Department. Outstanding core facilities are available for high throughput sequencing, genotyping, and gene expression studies and for bioinformatics and computational biology analyses. UPenn has an interactive community of researchers with interests in evolutionary biology and genomics, the genetics of complex traits, and translational medicine. Philadelphia is a vibrant city with excellent cultural events and plenty of parks and hiking/biking trails. It is also centrally located between New York City and Washington DC, with easy access via a short train or bus ride. Candidates should send curriculum vita, a statement of interest, and contact information for three references via e-mail to Dr. Sarah Tishkoff, Departments of Genetics and Biology, University of Pennsylvania, tishkoff@mail.med.upenn.edu. The starting dates of positions are flexible.

Sarah Tishkoff, Ph.D.

David and Lyn Silfen University Professor Departments of Genetics and Biology University of Pennsylvania Tel: 215-746-2670

tishkoff@mail.med.upenn.edu

http://www.med.upenn.edu/tishkoff/

USanDiego Bioinformatics

Postdoctoral fellow: Bioinformatics, Phenotypes

We are recruiting a postdoc with training in bioinformatics who is interested in studying phenotypic evolution by combining model organism genetic data with comparative anatomical data from throughout the vertebrates. One of the biggest challenges in systems biology is the inclusion of whole organism phenotypes. In the Phenoscape group, we have developed ontology-based methods for representing phenotypes of diverse species in order to integrate them with model organism developmental and genetic data. We have collected these data in a sophisticated Knowledgebase, which has an initial focus on the diversity of phenotypes in fish, including zebrafish (kb.phenoscape.org). We are currently scaling up our approach to the vertebrates as a whole, with a goal of allowing similarities to be identified between phenotypes from sources as diverse as dinosaur fossils and mouse knockout mutants.

We invite postdoctoral applicants to propose an independent project that uses the Phenoscape Knowledgebase as a research platform. In particular, we are interested in projects that will leverage functional genomic data to study the evolution of whole-organism phenotype in nonmodel organisms. Projects may range from primarily computational to primarily biological. The postdoc will work under the direction of Paula Mabee (University of South Dakota) and Todd Vision (University of North Carolina), as part of a distributed, multidisciplinary team that includes evolutionary biologists, computer scientists, model organism experts, and bioinformaticists. It will be based in South Dakota, with opportunities to travel to other sites, including the National Evolutionary Synthesis Center (NESCent), the University of Chicago, and the California Academy of Sciences.

Starting date: This two year postdoctoral position is available to be filled immediately. Required qualifications: - Ph.D. degree with strong background in bioinformatics; - Preferred previous experience in one of the following: ontologies, functional genomics, developmental biology - Demonstrated communication and writing skills, in English - Demonstrated ability to work in a team setting

How to apply: Please contact Dr. Mabee (pmabee@usd.edu) for inquiries. 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. For more information, please see https://phenoscape.org and http://kb.phenoscape.org/ . Paula.Mabee@usd.edu

USouthFlorida EvolutionaryNeuroscience

Post-doctoral opportunity in avian neuroscience at USF

Dr. Toru Shimizu and I are looking to hire a postdoc to help faciliate interdisciplinary research between our labs. Interested individuals can get more information about our research at the links below, but in brief, we're seeking candidates to aid in research in avian neuroanatomy, neuroendocrinology, and behavior, all grounded in eco-evolutionary biology.

Please send a CV, one relevant reprint, and contact info for three referees to me at the email address below. We will consider applications through 30 April 2013. Individuals with some relevant skills and background are obviously most attractive, but we are willing to consider applications from talented individuals seeking training in the above areas.

Shimizu lab: http://chuma.cas.usf.edu/ ˜ shimizu/ Martin lab: http://lbmartin.myweb.usf.edu/Martin_lab_at_USF/Welcome.html Thanks for your attention, Marty

lbmartin@usf.edu

Lynn B. Martin Associate Professor Department of Integrative Biology University of South Florida 813-974-0157

Google scholar page: http://scholar.google.com/citations?user=W7gGhjYAAAAJ "Martin, Lynn" <lbmartin@usf.edu>

UTennessee Phylogeography

Phylogeography often compares a select handful of models to answer an empirical question. We have just been funded to continue development of Phrapl, a way to examine thousands of potential phylogeographic models for fit to data. It is a bit like ModelTest, but for models of population subdivision and migration rather than substitution rates. The aim is for empiricists to be able to let their data tell them which processes are important in the phylogeographic history of a group. A postdoctoral position is available to work on improving, testing, and applying this approach. The current code is mostly in R but using other languages to speed up the computation internally is quite possible. The position is in the lab of PI Brian O'Meara at U. of Tennessee, Knoxville, but coordination with Co-PI Bryan Carstens and occasional travel to Ohio State is expected.

The O'Meara lab currently hosts five postdocs (including four co-mentored through NIMBioS) as well as a co-advised grad student. The EEB department features ten research groups whose work includes phylogenetics/phylogeography, and the presence of the National Institute for Mathematical and Biological Synthesis further creates a robust ecosystem of colleagues.

Knoxville, Tennessee, is just a half hour away from the US' most visited national park, Great Smoky Mountains NP. Cost of living is low, and the Knoxville area can cater to interests ranging from farmers' markets, local music, and handmade crafts to SEC football and NASCAR. I strive to create a lab group that is welcoming and open. We have good diversity in terms of gender (57% female), life stage (i.e., 43% with young children) but (so far) poor diversity on various other metrics. Mentoring to allow postdocs to reach their career goals is a focus. Research in the lab ranges from empirical work on plant taxonomy to quantitative trait evolution models to models of protein evolution.

Applications should include 1) A cover letter (include expected completion date of PhD, if appropriate, as well as relevant skills) 2) A CV 3) A short research statement 4) Contact information for two references 5) Link(s) to repositories with examples of code you have written or attachments including such code.

Experience in programming is strongly preferred; experience in R is desired, but not required. If in doubt, apply: please do not self-select yourself out from what might be a mutually beneficial position.

Review of applications will begin on May 1 and continue until filled (start dates are flexible). Presubmission inquiries are encouraged (I can give you a copy of the proposal, point you to the code, and answer any questions you may have).

All qualified applicants will receive equal consideration for employment and admissions without regard to race, color, national origin, religion, sex, pregnancy, marital status, sexual orientation, gender identity, age, physical or mental disability, or covered veteran status.

Eligibility and other terms and conditions of employment benefits at The University of Tennessee are governed by laws and regulations of the State of Tennessee, and this non-discrimination statement is intended to be consistent with those laws and regulations.

In accordance with the requirements of Title VI of the Civil Rights Act of 1964, Title IX of the Education Amendments of 1972, Section 504 of the Rehabilitation Act of 1973, and the Americans with Disabilities Act of 1990, The University of Tennessee affirmatively states that it does not discriminate on the basis of race, sex, or disability in its education programs and activities, and this policy extends to employment by the University.

Inquiries and charges of violation of Title VI (race, color, national origin), Title IX (sex), Section 504 (disability), ADA (disability), Age Discrimination in Employment Act (age), sexualorientation, or veteran status should be directed to the Office of Equity and Diversity (OED), 1840 Melrose Avenue, Knoxville, TN 37996-3560, telephone (865) 974-2498 (V/TTY available) or 974-2440. Requests for accommodation of a disability should be directed to the ADA Coordinator at the Office of Equity and Diversity.

Brian O'Meara Assistant Professor Dept. of Ecology & Evolutionary Biology U. of Tennessee, Knoxville http://www.brianomeara.info Students wanted: Applications due Dec. 15, annually Postdoc collaborators wanted: Check NIMBioS' website Calendar: http://www.brianomeara.info/calendars/omeara omeara.brian@gmail.com

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UTurku Bioinformatics

Research assistant or researcher in (evolutionary) bioinformatics

A position is available for a bioinformatics research assistant or researcher in Academy Professor Craig Primmer's research group (see http://users.utu.fi/primmer for more details) at the University of Turku, Finland.

The successful applicant will be expected to assist and train research group members in bioinformatics tasks related to the evolutionary genomics research being conducted in the group. This includes writing scripts for data processing and developing, maintaining and documenting analysis pipelines for various forms of molecular data from non-model organisms, including next-generation sequencing, proteomics and transcriptomics. They will also be responsible for the general maintenance of computing facilities in the group. Depending on the interests of the successful applicant, collaboration in the group's research projects, as well as carrying out their own research e.g. as a part of a PhD project, is also possible.

Applications will be considered from candidates holding either a Masters or PhD degree in bioinformatics or a bioinformatics related field. Good knowledge of relevant programming languages (Perl, python, R etc.) is essential. A demonstrated interest and/or experience in evolutionary biology is an advantage, as is being creative, exceptionally patient and a willingness to acknowledge Windows as an operating system under some circumstances.

Informal inquires and applications should be addressed to Acad. Prof. Craig Primmer (craig.primmer@utu.fi). Applications (one single pdf file) should include a full CV that includes details of formal training and practical experience in bioinformatics, a list of publications and contact details of at least two referees. Review of applications will commence on May 15 with the preferred starting date being by July. The position is initially available until the end of 2013, but an extension is likely to be possible. The salary range will be according to the university pay scale and will depend on the education level and relevant experience of the successful applicant.

–

Craig Primmer

Academy Professor Division of Genetics and Physiology Department of Biology Pharmacity 20014 University of Turku FINLAND

Office +358 2 333 5571 Mobile +358 40 1560 365 Fax. +358 2 333 6598 craig.primmer@utu.fi http://users.utu.fi/primmer pharm.shihab@gmail.com

UWarwick EvolutionAging

Postdoctoral Research Fellow Application deadline: April 10, 2013

The University of Warwick/UK is seeking to recruit

Postdoctoral Research Fellow in Evolution of Aging

to work on the evolutionary and mechanistic basis of aging. The objective is to clarify the role of developmental pathways and environment on ageing progression and lifespan. Interested candidates must have a Ph.D. and research experience in molecular biology, and in preference trained in C. elegans techniques. Salary is commensurate with experience and accomplishments.

Submit letter of interest, curriculum vitae, and at least two references to http://www.jobs.ac.uk/job/AGE515/research-fellow/. For additional information, contact Andre Pires da Silva (andre.pires@warwick.ac.uk).

The position is open and review of applications will begin on April 10 and continue until the position is filled.

"Pires da Silva, Andre" <Andre.Pires@warwick.ac.uk>

UWashington EvolutionaryGeneticsAging

The Promislow lab is moving to the University of Washington in Seattle this summer. We are seeking an enthusiastic, independent postdoctoral researcher to join our new lab to study the genetic architecture of aging in Drosophila. We study the effects of aging on genomic and metabolomic networks, and the relationship between aging and mate choice. The goal of these projects is to better understand the causes and consequences of aging in natural populations. The successful applicant may focus on empirical studies with Drosophila, on computational studies of molecular networks, or on both. Preference will be given to candidates with experience in Drosophila, population genetics, genomics, and/or systems biology & network analysis. To learn more about the lab, see http://www.promislowlab.org . The position is initially available for two years, and may be extended, but the University of Washington policy is to offer a one year appointment with subsequent renewals. Start date is flexible.

Applications should be sent by May 15, 2013 by email to Daniel Promislow (danielpromislow@gmail.com<mailto:danielpromislow@gmail.com>). Applicants are requested to send a single PDF file that includes a cover letter, a CV and one or two representative publications, and names and contact information of three references.

The University of Washington is an affirmative action, equal opportunity employer. The University is building a culturally diverse faculty and staff and strongly encourages applications from women, minorities, individuals with disabilities and covered veterans.

promislo@uga.edu

UWesternOntario TheoreticalEvolution

POST-DOCTORAL FELLOW IN THEORETICAL EVOLUTIONARY BIOLOGY

Department of Applied Mathematics The University of Western Ontario, London, Ontario, Canada Start date: September, 2013 (negotiable) Term: 1-year, with possibility of renewal. Salary: 40 000 $CAD p.a. Travel Grant: 1 500 $CAD p.a. DESCRIPTION

Research in theoretical evolutionary biology at Western tackles problems in both experimental evolution and sociobiology (see www.apmaths.uwo.ca/~lwahl and www.apmaths.uwo.ca/~gwild for details).

We are looking to hire one post-doctoral fellow interested in modeling evolution as it occurs in both laboratory experiments, and field settings. The successful candidate will be expected to carry out both independent and collaborative research, and will mentor graduate students in the group.

The successful candidate may also apply for a one-term teaching position in order to supplement his/her income, if so desired (subject to departmental approval). QUALIFICATIONS

A Ph.D in Evolutionary Biology, Mathematical Biology or a related discipline. A demonstrated interest in population genetics and theoretical evolutionary biology. Experience with differential equations, linear algebra, and/or stochastic processes. Excellent written and oral communication skills. HOW TO APPLY

Please prepare an application package that includes

(i) a one-page cover letter outlining how your qualifications match the demands of the position, (ii) current CV, (iii) a one-page statement of research interests, (iv) two relevant reprints or pre-prints, (v) names and contact information of two referees. Please email (i)-(v) **as a single pdf** to gwild@uwo.ca DEADLINE

Please submit your application **no later than June 15, 2013**

Geoff Wild <gwild@uwo.ca>

Uhull ComparativePhylogenetics

Postdoctoral Research Fellow in Comparative Phylogenetic Analysis (5 years, fixed term)

Part of a new interdisciplinary research group, you will have the freedom to work on an exciting theme for an extended period. The position forms part of a larger project entitled 'Form and function in a microbial world' supported by a Leverhulme Trust Research Leadership Award to Dr Stuart Humphries. The project's overarching aim is to understand and quantify the links between the shape, function and ecology of microbes. Working on a defined problem, you will contribute to, and benefit from, the diverse expertise in the Physical Ecology Lab at Hull (tinyurl.com/PhysEcoLab).

Using cutting edge phylogenetic methods you will disentangle the relative contributions to form or function of three major processes in bacterial evolution: evolutionary history; ecology; and lateral gene transfer. The goals are to separate on-going evolutionary processes from rapid ecologically-derived phenotypic shifts in order to explain the current diversity of bacterial cell shapes. The two major objectives for this position are (1) to use existing sequence data and phylogenies to construct a supertree of bacterial 'species' and explore the implications of lateral gene transfer for subsequent analyses; and (2) to apply and develop the phylogenetic comparative method in a Bayesian framework to understand the links between bacterial form (shape) and function.

In creating a supertree you will greatly enhance our understanding of the relationships between prokaryotic groups, while in applying and developing new comparative methods you will be able to answer a number of important questions about rates of morphological evolution, correlated evolution of form and function and the relationship between shape and pathogenicity.

A creative and motivated postdoctoral scientist, with experience in phylogenetic methods or statistics, you will be expected to contribute towards grant applications to further develop project work. If required, there is also an opportunity to gain further experience in phylogenetics and phylogenetic comparative methods in the lab of Dr Chris Venditti (University of Reading). Helping to implement the project, you will contribute to iterative exchanges with other group members and supervise both undergraduate and postgraduate students. You will also be encouraged and supported to make your own applications for funding and take advantage of our comprehensive Staff Development Programme.

This position is fixed term for five years. The preferred start date for the position is 1 August 2013.

Salary range: £25,504 - £30,424 pa

You can learn more about this position and apply online at www.hull.ac.uk/jobs (Vacancy FS00001).

Informal enquires may be made to Dr Stuart Humphries, E: s.humphries@hull.ac.uk

For information about the department visit http://www2.hull.ac.uk/science/biological_sciences_new.aspx Closing date 17 May 2013

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Dr Stuart Humphries Senior Lecturer School of Biological, Biomedical and Environmental Sciences University of Hull Kingston-upon-Hull UK HU6 7RX

+44 (0)1482 466425

tinyurl.com/PhysEcoLab

S.Humphries@hull.ac.uk

WashingtonStateU TasmanianDevilGenomics

POSTDOCTORAL RESEARCHER

Washington State University

School of Biological Sciences

We are seeking a postdoctoral researcher to work on population and landscape genomics of Tasmanian devils and Tasmanian devil facial tumor disease. This international collaboration builds on over 15 years of research tracking the spread of this unique infectious tumor across Tasmania and consequent endangerment of the iconic Tasmanian devil. Reference genomes are available for both tumor and devil. The successful applicant will have an unprecedented opportunity to analyze thousands of devil genotypes and hundreds of tumor samples taken both before and after epizootics to test for selection throughout both genomes, coevolution, patterns of resistance, etc, across Tasmania. We will then use these data to predict the course of disease in uninfected populations. The position is centered in the lab of Dr. Andrew Storfer at Washington State University, in close collaboration with Dr. Paul Hohenlohe at the nearby University of Idaho (8 miles away). Both universities have genomics core facilities, including the Institute of Bioinformatics and Evolutionary Studies (IBEST; http://www.uidaho.edu/research/ibest) with up-to-date equipment, computational facilities and staff support.

Review of applications will begin on May 15, 2013 and continue until the position is filled. A Ph.D. in Biology or a related discipline is required, and we particularly welcome applicants with experience in population genomics, infectious disease evolution, conservation, bioinformatics, and/or cancer genomics. Anticipated start date is August 16, 2013. Salary and benefits are competitive. Position is for 1-4 years, pending satisfactory progress. To apply, please send in pdf format a CV, and names, addresses and email addresses of 3 references, a research statement and up to 3 representative reprints via email to: Andrew Storfer (astorfer@wsu.edu). *WSU is an Equal Opportunity/Affirmative Action/ADA educator and employer.*

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Andrew Storfer, PhD Eastlick Distinguished Professor Associate Director for Graduate Studies School of Biological Sciences Washington State University Pullman, WA 99164 USA Phone: (509) 335-7922 Fax: (509) 335-3184 astorfer@wsu.edu www.wsu.edu/~storfer

andrew.storfer@gmail.com

YaleU EvolutionaryGenomics

Postdoc opening, Yale University:

We are searching for a candidate for a postdoctoral position on an NIH Parasitology Training Grant. The work would involve evolutionary genomics of insects (mosquitoes and/or tsetse flies) and/or the pathogens they transmit (dengue virus or trypanosomes) or some combination of vectors/pathogens. Depending on particular interests, the primary mentor would be Jeffrey R. Powell (mosquitoes and dengue) or Adalgisa Caccone (tsetse and trypanosomes) or joint mentorships. By NIH rules, candidate must be a US citizen or permanent resident of the US. The position is or 2 years.

Please send letter of interest and CV to: jeffrey.powell@yale.edu and/or adalgisa.caccone@yale.edu

"Caccone, Gisella" <adalgisa.caccone@yale.edu>

YaleU ExperimentalEvolution

Yale EEB Postdoc in Experimental Evolution and Phage Therapy

A two-year postdoctoral position is available on or after September 1, 2013 under the supervision of Dr. Paul Turner in the Department of Ecology and Evolutionary Biology at Yale University (http://www.yale.edu/turner/). The project examines experimental evolution, evolutionary genetics and recombinant engineering of bacteriophages, to improve their efficacy in phage therapy applications that target enteric bacterial pathogens. Experience with molecular microbiology, and sequence analysis is preferred but all strong candidates will be considered. Applications (CV, 1 representative publication, and contact information for 3 referees) will be reviewed starting July 1, 2013. Please direct applications and inquiries to paul.turner@yale.edu

Paul E. Turner Chair of Ecology and Evolutionary Biology Yale University New Haven, CT 06520 (203) 432-5918 http://www.yale.edu/turner/ paul.turner@yale.edu

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Barcelona PhylogeneticComparativeMethods Oct7-11

Dear Colleagues:

Registration is open for the course “Disentangling evolutionary relationships with Phylogenetic Comparative Methods - Second edition”; October 7-11, 2013.

INSTRUCTORS: Dr. Alejandro González-Voyer (EBD, Spain) and Dr. Achaz von Hardenberg (Alpine Wildlife Research Centre, Italy) .

SITE: Els Hostalets de Pierola, Barcelona, Spain.

This course will provide an introduction to phylogenetic comparative methods (PCM) focusing on Phylogenetic Generalized Least Squares (PGLS) and introducing Phylogenetic Path Analysis methods. PCMs provide a means of incorporating information about the evolutionary relationships of organisms (phylogeny) in statistical analyses. To enhance the practical approach of the course, participants are encouraged to bring their own data to conduct analyses and discuss the results.

More information: http://www.transmittingscience.org/courses/evol/pcm/

This course will be held in the facilities of the Centre de Restauració i Intepretacio Paleontologica (CRIP), and are co-organized by Transmitting Science, the CRIP and the Universidad Autónoma de Madrid. Places are limited and will be covered by strict registration order.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Soledad De Esteban-Trivigno soledad.esteban@transmittingscience.org Transmitting Science < http://www.transmittingscience.org/ >

Soledad De Esteban Trivigno <soledad.esteban@transmittingscience.org>

Coimbra Portugal Neoallopatry May22-23

The consequences of neo-allopatry

Local adaptation, reproductive isolation and beyond

*May 22-23, 2013. Centre for Functional Ecology.

Coimbra, Portugal*

Humans are eliminating dispersal barriers and dramatically expanding the global distributions of many species. The result is that some recently established populations are geographically isolated from their source populations, which has been referred to as neo-allopatry. Cross-continental introductions in particular have rapidly isolated populations of many species, and there is circumstantial evidence for divergent selection between native and non-native ranges for ecological traits such as growth, herbivore defense, and competitive ability. There is even evidence for incipient reproductive isolation between native and non-native regions or introduced species. Theory predicts that divergent selection of ecological traits can drive to speciation. Thus, exotic invasions provide exceptionally good natural experiments in which to look for the early stages of allopatric processes.

During this one-and-a-half-day workshop we will discuss the consequences of neo-allopatry at the Centre for Functional Ecology of the /Universidade de Coimbra/, Portugal. Registrations are free and mandatory, please send your CV and a one-page motivation letter to danimontesinos@gmail.com before May 3rd at 5 pm CET.

Please help us disseminate this event. Best wishes, Daniel.

*_PROGRAM_*

/ /

*_W_**_ednesday, May 22, 2013._*//

/(Anfiteatro da Galeria de Zoologia, in front of Science Museum) /

09:00 -*Presentation of the workshop*

Helena Freitas, Centre for Functional Ecology, Universidade de Coimbra, Portugal

09:30 - *A bug's life: trophic implications of plant invasions.*

Christopher Lortie, York University, Canada

10:30 - *Evolutionary changes to reproductive systems during the invasion process of the polyploid /Oxalis pes-caprae./*

Sílvia Castro, Centre for Functional Ecology, Universidade de Coimbra, Portugal

11:15 - *With a little help from their friends: the role of biotic interactions on /Acacia/ invasions*

Susana Rodríguez-Echeverría, Centre for Functional Ecology, Universidade de Coimbra, Portugal

12:00-14:00 – Lunch break

14:00 - *Non-native conditions favor non-native populations of invasive plants: demographic consequences of seed size variation?*

José Hierro, CONICET – Universidad de la Pampa, Argentina

15:00 - *Coexisting**invasive and non-invasive species show similar trait shifts between native and non-native regions.*

Daniel Montesinos, Centre for Functional Ecology, Universidade de Coimbra, Portugal

16:00 - *Does modern geographic isolation yield insight into diffuse community evolution?*

Ragan M. Callaway, The University of Montana, USA

**

*_Thursday, May 23, 2013_* (Botanical Garden Building)

Morning – *Free*

14:00-19:00 *One-to-one 30' meetings with speakers*

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Daniel Montesinos Centro de Ecologia Funcional Universidade de Coimbra Apartado 3046 3001-401 Coimbra, Portugal T: (+351) 239 855 238 (ext. 139) http://cfe.uc.pt/daniel-montesinos http://about.me/daniel.montesinos danimontesinos@gmail.com

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Cornell NonmodelGenomics Jul23-24

What: Workshop on Next Generation Population Genomics for Nonmodel Taxa When: 23-24 July (Tues-Wed) 2013 Where: Cornell University, Ithaca, NY Website: http://www.certain.com/system/profile/web/index.cfm?PKwebID=0x4653687438&varPage=home Application: 45 student capacity – applications received before May 15 will receive priority consideration.

Goal: to compare and discuss the strengths and weaknesses of different approaches to genome sequencing and bioinformatics when studying population genomics in nonmodel species. Population genomics involves sampling, financial, and bioinformatics tradeoffs, so proper experimental design requires understanding probability, sequencing technologies and evolutionary theory and how they relate to research tradeoffs. We will illustrate the computational challenges and how they interact with choices at the population and genomic sampling stages. We will not give you all the answers, but in two days we hope to help you ask the right questions to improve study design.

Travel grants are available, sponsored by the American Genetics Association. This workshop immediately follows the 2013 AGA speciation symposium (see http://www.certain.com/system/profile/web/index.cfm?PKwebID=0x44728099a8&varPage=home).

Workshop Instructors: Alex Buerkle, Department of Botany, University of Wyoming Nancy Chen, Department of Ecology & Evolutionary Biology, Cornell University Andy Clarke, Department of Molecular Biology & Genetics, Cornell University Pierre De Wit, Department of Biology and Environmental Science, University of Gothenburg, Sweden Matthew Hare, Department of Natural Resources, Cornell University

Target Audience: graduate students and postdocs

Cost: $150

Prerequisites: Students are expected to have a working knowledge of population genetics. You must bring your own laptop and some software installations should be accomplished before you arrive. Practical exercises will be on your laptop and through remote access to servers.

See the website for more information or contact Matthew Hare Associate Professor 205 Fernow Hall Department of Natural Resources Cornell University Ithaca, NY 14853 607-255-5685 mph75@cornell.edu http://www2.dnr.cornell.edu/HareLab/harelab.html mph75@cornell.edu

Cornell NonmodelGenomics July23-24 2

Workshop on Next Generation Population Genomics for Nonmodel Taxa 23-24 July, 2013 Cornell University, Ithaca, NY Website http://www.certain.com/system/profile/web/index.cfm?PKwebID=0x4653687438&varPage=home If the above URL does not work, go to http://www.theaga.org/aga2013-species-continuum/, scroll down and click on the fishy genome scan figure.

Application: 45 student capacity – applications received before May 15 will receive priority consideration.

Goal: to compare and discuss the strengths and weaknesses of different approaches to genome sequencing and bioinformatics when studying population genomics in nonmodel species. Population genomics involves sampling, financial, and bioinformatics tradeoffs, so proper experimental design requires understanding probability, sequencing technologies and evolutionary theory and how they relate to research tradeoffs. We will illustrate the computational challenges and how they interact with choices at the population and genomic sampling stages. We will not give you all the answers, but in two days we hope to help you ask the right questions to improve study design.

Travel grants are available, sponsored by the American Genetics Association. This workshop immediately follows the 2013 AGA speciation symposium (get more info at http://www.theaga.org/aga2013-species-continuum/).

Workshop Instructors: Alex Buerkle, Department of Botany, University of Wyoming Nancy Chen, Department of Ecology & Evolutionary Biology, Cornell University Andy Clark, Department of Molecular Biology & Genetics, Cornell University Pierre De Wit, Department of Biology and Environmental Science, University of Gothenburg, Sweden Matthew Hare, Department of Natural Resources, Cornell University

Target Audience: graduate students and postdocs

Cost: $150

Prerequisites: Students are expected to have a working knowledge of population genetics. You must bring your own laptop and some software installations should be accomplished before you arrive. Practical exercises will be on your laptop and through remote access to servers.

See the website for more information or contact

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Denmark Evolutionary Demography Oct11-18

I am happy to announce an intensive course in Evolutionary Demography at the University of Southern Denmark (SDU). This course is intended for biologists who wish to incorporate demographic concepts and methods into their research or increase their proficiency in this area. It is a doctoral-student level course but is also open to individuals in other life-stages.

This course will immediately follow the first meeting of the Evolutionary Demography Society. http://www.sdu.dk/en/Om_SDU/Institutter_centre/MaxO/EvoDemoS The EvoDemoS meeting runs from Oct. 6-10 and the course runs from Oct. 11-18. More details on the course are below. Questions should be sent to: levitis@biology.sdu.dk. Students wishing to take the course should also write to me at that address for information on enrollment and logistics. The course, including housing, will cost 4800 Danish Kroner (roughly euro 640 or $840) for students not enrolled at SDU.

Best wishes, Dan Levitis

Introduction to Evolutionary Demography (Fall 2013) This is an official course at SDU. Students can gain official university course credits (5ETCS) that should, in theory, be transferable to any European university.

Instructors include: Daniel Levitis Ulrich Steiner Virginia Zarulli Adam Lenart

>From the official course description: Course introduction Evolution is an inherently demographic process, and demographic traits are subject to selection and other evolutionary pressures; for both these reasons, demographic methods and concepts have proven essential for answering many questions in evolutionary biology. This two-week intensive course is designed to give biologists interested in life-histories, aging and other demographic traits an introduction to the methods and concepts of evolutionary demography. The aim is to provide graduate students with the tools they need to bring demographic thinking and quantitative tools into their research programs.

Intended learning outcome At the end of the course, the students are expected to be able to:

* Describe the connections between evolutionary biology and demography * Comment on the important recent literature in evolutionary demography * Identify major open questions in the field * Employ the more common quantitative tools of evolutionary demography * Orally present a small research project in evolutionary demography

Subject covered A) In lectures, an overview of the major concepts and topics in evolutionary demography. B) In computer-lab, introduction to the most commonly used quantitative methods in the field. C) Working in groups, students will prepare and present short projects using the methods and concepts presented.

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Gainesville ViralMolecularPhylogenetics Aug25-30

http://conferences.dce.ufl.edu/veme/ 18th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME 2013)

VEME 2013 will be organized August 25th - August 30th, 2013 at the University of Florida in Gainesville, Florida, U.S.A.

The workshop will have the following modules:

- 'Phylogenetic Inference'module offers the theoretical background and hands-on experience in phylogenetic analysis for those who have little or no prior expertise in sequence analysis.

- 'Evolutionary Hypothesis Testing' module is targeted to participants who are well familiar with alignments and phylogenetic trees, and would like to extend their expertise to likelihood and Bayesian inference in phylogenetics, coalescent and phylogeographic analyses ('phylodynamics') and molecular adaptation.

- 'Large Dataset Analysis' module will cover the more complex analysis of full genomes, huge datasets of pathogens including Next Generation Sequencing data, and combined analyses of pathogen and host. We recommend participants to buy The Phylogenetic Handbook as a guide during the workshop, and to bring their own data set.

Application Deadline is April 30, 2013

Brian Foley, PhD HIV Databases

“Foley, Brian T” <btf@lanl.gov>

Herzogenhorn Germany Bioinformatics Sep10-13

Black Forest Summer School 2013 - Bioinformatics for Molecular Biologists

DATE: September 10th - 13th, 2013 WEBSITE: http://plantco.de/BFSS2013/ WHERE: Herzogenhorn resort, Black forest, Germany REGISTRATION: open from March 11th until July 30th

KEYNOTE LECTURE: * Francis Martin, INRA Nancy, France

INSTRUCTORS: * Stefan Rensing, University of Marburg, Germany * Emily Pritchard, EBI Hinxton, UK * Klaas Vandepoele, University of Ghent, Belgium * Anne Hamm, Roche, Germany * Arnd Brandenburg, Genedata, Basel/Switzerland

The summer school is intended for PhD students and early career postdocs. Expert lectures & workshops, secluded venue and participant presentations will ensure high knowledge gain and scientific exchange. We will not teach how to program - rather, we will teach you how to use existing bioinformatics tools that are helpful for everyday lab life.

Areas to be covered include: * molecular phylogeny * animal/plant/fungal comparative genomics * NGS data * large scale multivariate data analysis

Participants are highly encouraged to present their work as a short talk or in the poster sessions.

Questions? bfss2013@data.biologie.uni-freiburg.de

Oragnized by: Plantco.de e.V. Freiburg, Germany

Kristian Ullrich <kristian.ullrich@biologie.uni-marburg.de>

Hinxton HumanGenomeAnalysis Jul24-30

Deadline THIS FRIDAY: 12 April 2013 Human Genome Analysis: Genetic Analysis of Multifactorial Diseases 24-30 July 2013 Wellcome Trust Genome Campus, Hinxton, Cambridge, UK Deadline for applications: 12 April 2013 URL: http://www.wellcome.ac.uk/Education-resources/Courses-and-conferences/Advanced-Courses-and-Scientific-Conferences/Advanced-Courses/WTX026851.htm Course summary An intensive, residential, computer-based course aimed at scientists actively involved in genetic analysis of multifactorial traits.

Programme This advanced course covers statistical methods currently used to map disease susceptibility genes, with an emphasis on (but not limited to) methods that can analyse family data or a combination of families and individuals. Discussions of the latest statistical methodology are complemented by practical hands-on computer exercises using state-of-the-art software. The statistical basics behind each method will be carefully explained so that participants with a non-statistical background can understand. With a focus on family data, we will discuss fundamental issues needed to increase success in gene mapping studies including: optimal study design, power to detect linkage and association, determining the most appropriate statistical methods and software, interpretation of statistical results and trouble shooting. We will also cover the basic principles of statistical inference, hypothesis testing, population and quantitative genetics and Mendelian inheritance. Our interactive and intensive educational program will enable one to better carry out sophisticated statistical analyses of genetic data, and will also improve one's interpretation and understanding of the results. All the software used is freely available, so that skills learned can be easily applied after the course. Teaching will take the form of lectures by invited speakers, informal tutorials, hands-on computer sessions, and analysis of disease family data sets. There will also be an opportunity to discuss participants' own data sets.

JanetS@mednet.ucla.edu

LaFouly Switzerland ExperimentalTheoEvolution Jun12-15

We still have a few open slots for the workshop "Bridging theoretical and experimental evolution" in La Fouly (Valais, Switzerland) from June 12-15 2013.

The aim of the proposed workshop is to unite experimental and theoretical evolutionary biologists, both working to resolve fundamental questions at the center of a century-old debate. For example - what is the distribution of fitness effects of new, segregating, and fixed mutations? What is the relative importance of adaptation vs. genetic drift in the evolution of natural populations? By combining expertise across wet and dry lab biology, and due to the progress of new genomic technologies, it is becoming increasing possible to gain traction on these questions which are fundamental to any basic understanding of the very mode and tempo of the evolutionary process.

The workshop will bring together top researchers in the field and students in la Fouly, a remote and beautiful location in the Swiss Alps (see www.lafouly.net), allowing for close interactions and vivid exchanges. The scientific program will consist in 2 1/2 days of a mixture of talks by invited speakers and students, and posters sessions.

The workshop will end by a hike to some nearby magnificent view points over the Mont Dolent and Mont-Blanc region.

Invited speakers:

Martin Ackermann (ETH Zurich, Switzerland) Dan Bolon (University of Massachussetts, USA) Michael Desai (Harvard University, USA) Isabel Gordo (Instituto Gulbenkian Ciência, Lisbon, Portugal) Oskar Hallatschek (Max Planck Institute for Dynamics and Self-Organization, Göttingen, Germany) Peter Keightley (University of Edinburgh, UK) Alex Wong (Carleton University, Ottawa, Canada)

Cost: 400 CHF for non-CUSO students, including conference fees, meals and accommodation (with sleeping bags).

Web site and registration (max 35 students):

http://biologie.cuso.ch/ecologie-evolution/dpee-activities/detail-activity/item/courses/bridging-theoretical-and-experimental-evolution/ Note that deadline for registration is extended to May 15th, and that a maximum of 35 students can participate. Whereas the primary target are PhD students, other people can attend, knowing that priority will be given to CUSO members and students presenting talk or poster.

The organizers:

Jeff Jensen

Laurent Excoffier

Claudia Bank

Stephan Peischl

Stephan Peischl Post-doc CMPG Institute of Ecology and Evolution University of Bern Baltzerstrasse 6 CH-3012 Bern Switzerland Phone: +41 31 631 30 36 Fax: +41 31 631 48 88 Email: stephan.peischl@iee.unibe.ch

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NESCent Durham GMODSummerSchool Jul19-23

We are now accepting applications for the 2013 GMOD Summer School, to be held at the National Evolutionary Synthesis Center (NESCent), Durham, North Carolina, on July 19th-23rd, 2013. The GMOD Summer School is the best way to learn how to install, configure, and use popular GMOD tools, including GBrowse, JBrowse, Galaxy, MAKER, Tripal, WebApollo, and Chado; courses are taught by the tool developers, and there will be evening sessions for those who want to work on their own data or troubleshoot issues with the developers.

More information and online application form:

http://gmod.org/wiki/2013_GMOD_Summer_School Applications are competitive, so we encourage you to apply well before the June 10th deadline.

If you have any questions, please contact help@gmod.org and we will be happy to answer them.

– Amelia Ireland GMOD Community Support http://gmod.org || @gmodproject

amelia.ireland@gmod.org

SummerInstStatGenetics Jul8-26 ScholarshipDeadline

SISG Scholarship Application Deadline Extended to May 10.

Some further registration-fee and travel scholarships are available for the 18th Summer Institute in Statistical Genetics in Seattle, July 8-26. Details at http://sisg.biostat.washington.edu Applications received by April 26 will be processed before May 10, others by May 17.

New modules include Introduction to R and Scripting for Biologists, Omics Data and Network Analyses, Forensic Genetics, Mixed Models in Quantitative Genetics, Metagenomics, Epidemiology of Viruses. Previously popular modules include Bayesian Statistics for Genetics, Population and Quantitative Genetic Data Analysis, QTL and Association Mapping, Gene Expression, Coalescent and MCMC Theory, Human and Animal Genetic Data Analysis, Phylogenetics, Introductory Statistics, Introductory Genomics.

Bruce Weir bsweir@uw.edu

Bruce Weir <bsweir@uw.edu>

UWashington ViralEvolutionaryDynamics Jul17-19

A 2.5 day course on Evolutionary Dynamics and Molecular Evolution of Viruses will be taught July 17-19, 2013 by Philippe Lemey and Marc Suchard at the University of Washington, Seattle, USA. This course is part of the 5th Summer Institute in Statistics and Modeling of Infectious Diseases July 8-24, 2013.

Tuition scholarships and some travel funds are available for graduate students and postdocs. Applications for scholarships are due by April 26, 2013. Please see http://depts.washington.edu/sismid for more information and the list of 13 other courses.

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Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.