EvolDir

June 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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Conferences

Asilomar AmerSocNatl Jan13-15

The American Society of Naturalists is holding an independent meeting ("21st Century Naturalists: integrating pattern and process to understand biodiversity") at the Asilomar conference center on the Monterey Peninsula, California, on January 13-15 2014. Information about the meeting is now available at http://w3.biosci.utexas.edu/amnatasilomar/ .The website will be updated periodically with additional information. Registration and lodging will open in early July. To be added to the email list for further updates, email amsocnaturalists@gmail.com with a subject message "Subscribe Asilomar".

The goal of the 2014 American Society of Naturalists meeting is to bring together a diverse array of biologists, including evolutionary biologists, behaviorists, and ecologists, who might not normally encounter one another at their regular meetings. This will be a small conference to promote new conversations and ideas (attendance is limited). We wish to create a unique setting where graduate students, postdocs, and faculty can carry out discussions that define new research directions for our disciplines, and promote integration between biological disciplines including the fusion of theory, data, and new technologies for data acquisition.

Dr. Daniel I. Bolnick

Early Career Scientist Howard Hughes Medical Institute

Associate Professor Section of Integrative Biology One University Station C0990 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878 danbolnick@austin.utexas.edu https://webspace.utexas.edu/dib73/TheBolnickLab/Home.html danbolnick@austin.utexas.edu

Barcelona EuropeanDrosophilaRes Oct16-19

Deadline approaching: 2 June 2013

The upcoming European Drosophila Research Conference in Barcelona (Oct. 16-19) will have a symposium dedicated to Population Genetics and Evolution (Chaired by Benjamin Prud'homme, Nicolas Gompel and myself). http://edrc2013.org In addition Josefa Gonzalez and Thomas Flatt organize a workshop on "Creating a European Drosophila Population Genomics Network"

The deadline for submitting abstracts is 2 June 2013!

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

Barcelona EvolMulticellularity Sep30-Oct1 2

Registration is now open

ICREA Conference on the evolution of multicellularity Barcelona, Spain, September 30-October 1, 2013

we are pleased to announce the ICREA Conference on the Evolution of Multicellularity to be held September 30th - October 1st, 2013, in Barcelona (Spain). The transition to multicellular life represents one of the most important events in the history of life. Yet, despite its significance, little is known about the mechanisms involved in this transition. In recent years, emerging data from various fields are providing new insights into this major evolutionary transition. With advances in theoretical, molecular/cell biology and genomics approaches, there is a clear need for further conversation and collaborative efforts between experimentalists and theoreticians. The ICREA Conference on the Evolution of Multicellularity will bring together researchers with diverse backgrounds with the goal of stimulating and fostering inter-disciplinary discussion and collaborations. The talks will be organized around six mini-symposia encompassing the major topics and approaches related to the evolution of multicellularity. The six symposia are: 1) Origins and mechanisms; 2) Development and Gene regulation; 3) Genomics approaches and insights; 4) Theoretical approaches; 5) Social Evolution; 6) Computational and synthetic approaches. For additional information and updates (including preliminary program, registration and abstract submission deadlines) please visit the Conference page at www.multicellularity2013.com/).

Please note that registration is free but limited to 100 participants.

Invited speakers:

Douglas H. Erwin Philip Donoghue Andrew H. Knoll David C. Queller J. Mark Cock Stuart A. Newman Gregory J. Velicer Richard E. Michod Daniel Richter Pauline Schaap

Organizers:

Iñaki Ruiz-Trillo, Institut de Biologia Evolutiva (UPF-CSIC) Ricard V. Solé, Institut de Biologia Evolutiva (UPF-CSIC) Aurora Nedelcu, University of New Brunswick

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>

Barcelona Systematics Sep25-27

Dear Friends and Colleagues:

You are kindly invited to attend the II Iberian Congress of Biological Systematics - CISA 2013 that will take place in Barcelona from September 25-27, 2013.

CISA2013 aims to provide an arena for presenting leading research in biosystematics, to encourage participation of young researchers and to stir up fruitful discussion in the field.

Registration and abstract submission is now open. Please, visit our website athttp://-www.CISA2013.orgfor registration and further information on the program, invited speakers, social events, fees and deadlines.

The CISA2013 Organizing Committee

j.gomez-zurita@ibe.upf-csic.es

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

Cardiff Omics Sept9-11

FIRST INTERNATIONAL ENVIRONMENTAL 'OMICS SYNTHESIS CONFERENCE

Cardiff University, UK, 9-11 September 2013

http://www.environmentalomics.org/ieos2013 CALL FOR ABSTRACTS

We are pleased to announce the first ever conference on 'omics applications, tools and resources, focused on the environmental sciences.

The meeting is targeted both at current and future users of 'omics, and for developers of bioinformatics and 'omics technologies. This includes dedicated introductory talks and training sessions on day one, for those who are new to the field, followed by two days of world-class science presentations delivered by several international leaders in environmental 'omics. The conference will promote exchange of ideas between all of these groups.

We encourage submission of abstracts to be considered for oral and poster presentation, and in particular encourage submissions from PhD students and postdoctoral researchers.

To register - with optional submission of an abstract - see:

http://environmentalomics.org/ieos_registration ABSTRACT DEADLINE: 1 July 2013 REGISTRATION DEADLINE: 1 August 2013

KEYNOTE SPEAKERS: Professor Eske Willerslev, Natural History Museum of Denmark Professor Jack Gilbert, University of Chicago Professor John Colbourne, University of Birmingham

INVITED SPEAKERS include: Professor Terry Brown, University of Manchester Professor Robin Allaby, University of Warwick Dr Andrew Whitehead, University of California, Davis Professor Kevin Chipman, University of Birmingham Dr Joe Shaw, Indiana University

SPONSORED in part by the NERC, STFC, Thermo Fisher Scientific, and BGI.

On behalf of 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

Chicago SMBE2013 Jul7-11 OnsiteChildcare

SMBE on-site Childcare

2013 Annual Meeting of the Society for Molecular and Evolution

July 7-11, Chicago, USA

We are pleased to annouce that this year, on-site childcare services will be available to parents attending SMBE 2013 in Chicago!

Childcare will be available from 8:00AM - 6:30 PM at the conference venue (Hyatt Regency Chicago), divided into morning and afternoon sessions, on July 8-11. Licensed childcare workers will provide fun activities for kids in a safe, caring environment.

Thanks to a generous grant from the Society for Molecular Biology & Evolution, attendees will be charged a significantly reduced rate for the service.

Detailed information about rates and payments can be found on:

http://smbe2013.org/2013/Registration/Childcare-Information.aspx Additionally, we are offering an EARLY BIRD SPECIAL up to a 20% discount for parents who pre-register their children before May 30th.

Space is limited, so register you child soon!

Questions about childcare and payment can be directed to cornellacademy4kids@gmail.com (please put 'SMBE 2013' in the subject line)

We look forward to meeting you and your children.

Maria D. Vibranovski Assistant Professor Department of Genetics and Evolutionary Biology University of São Paulo Rua do Matão 27, Cidade Universitária São Paulo, SP, 05508-090 Brazil

Phone : +55 (11) 3091-0952 e-mail : mdv@ib.usp.br

mdv@ib.usp.br

Cornell AGA2013 Jul20-22

Register by Saturday for Early Bird rates for SPECIATION CONTINUUM: A Discussion on the Origin of Species, the 2013 Symposium of the American Genetic Association. July 20-22 at Cornell University in beautiful Ithaca, NY.

Early bird registration cost is $150 for students/postdocs, $200 professional. AGA student awards available! Registration includes all lunches and reception tickets, plus a 1-yr AGA membership. Already a member? You'll get an additional year at no cost.

All talks are invited (see list below), and there will be a poster session open to all participants. Submit your poster title with registration. The Carl Becker House dormitory is located near the lecture hall and reception/poster location and is an inexpensive and convenient accommodation option. Immediately following the symposium, 23-24 July, will be the workshop, NEXT GENERATION POPULATION GENOMICS FOR NONMODEL TAXA.

For details and registration, please visit the AGA website, http://www.theaga.org/ and click on the symposium logo. Or check out our Facebook page, https://www.facebook.com/AmericanGeneticAssociation 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 mailto:agajoh@oregonstate.edu http://www.theaga.org/ AGAJOH <AGAJOH@oregonstate.edu>

Cornell NonmodelGenomics July23-24 3

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.

Registration cost is $150 for students/postdocs, $200 professional through 1 June. AGA student awards available! Registration includes all lunches and reception tickets, plus a 1-yr AGA membership. Already a member? An additional year will be added to your membership.

All talks are invited (see list below), and there will be a poster session open to all participants. Submit your poster title with registration. The Carl Becker House dormitory is located near the lecture hall and reception/poster location and is an inexpensive and convenient accommodation option.

For details and registration, please visit the AGA website, http://www.theaga.org/ and click on the symposium logo. Or check out our Facebook page, https://www.facebook.com/AmericanGeneticAssociation Immediately following the symposium, 23-24 July, will be the workshop, NEXT GENERATION POPULATION GENOMICS FOR NONMODEL TAXA. Goal: to compare and discuss the strengths and weaknesses of different approaches to genome sequencing and bioinformatics when studying population genomics in nonmodel species.

Course fee: $150. Capacity is 45 students – applications received before May 15 will receive priority consideration. AGA travel awards are available. See the AGA website or Facebook page for links to workshop and application details.

Workshop Instructors:

Matthew Hare, Department of Natural Resources, Cornell University Nancy Chen, Department of Ecology & Evolutionary Biology, Cornell University Andy Clark, 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 mailto:agajoh@oregonstate.edu http://www.theaga.org/ agajoh@oregonstate.edu

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Cornell Speciation Jul20-22

Early bird registration until June 1st for SPECIATION CONTINUUM: A Discussion on the Origin of Species, the 2013 Symposium of the American Genetic Association, to be held July 20-22 at Cornell University in beautiful Ithaca, NY.

Registration cost is $150 for students/postdocs, $200 professional. AGA student awards available! Registration includes all lunches and reception tickets, plus a 1-yr AGA membership. Already a member? You'll get an additional year at no cost.

All talks are invited (see list below), and there will be a poster session open to all participants. Submit your poster title with registration. The Carl Becker House dormitory is located near the lecture hall and reception/poster location and is an inexpensive and convenient accommodation option.

Immediately following the symposium, 23-24 July, will be the workshop, NEXT GENERATION POPULATION GENOMICS FOR NONMODEL TAXA.

For details and registration, please visit the AGA website, http://www.theaga.org/ and click on the symposium logo. Or check out our Facebook page, https://www.facebook.com/AmericanGeneticAssociation

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 mailto:agajoh@oregonstate.edu http://www.theaga.org/ agajoh@oregonstate.edu

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Denmark EvoDemography Oct6-10 DeadlineExtended

Due to a large number of "I was about to submit" messages, the deadline for abstracts has been extended to May 15th.

The Evolutionary Demography Society (EvoDemoS) invites submission of abstracts for our first meeting, October 6-10 at the University of Southern Denmark in Odense, Denmark.

The overarching goal of this meeting is to establish

EvoDemoS as a cohesive community of researchers. For this purpose we will emphasize introducing the members of EvoDemoS to each other's work and providing opportunities for discussion and interaction. We therefore welcome talks and posters in all aspects of evolutionary demography, life history evolution, and evolutionary aspects of the population ecology of all taxa.

We hope you will join us.

Details, including abstract submission and registration, can be found here: http://www.sdu.dk/en/-Om_SDU/Institutter_centre/MaxO/EvoDemoS Daniel Levitis Assistant Professor Max-Plank Odense Center on the Biodemography of Aging Institute of Biology University of Southern Denmark levitis@biology.sdu.dk

Levitis@demogr.mpg.de

Edinburgh ComplexGeneticTraits May10

The Edinburgh Alliance for Complex Trait Genetics (E-ACTG) holds occasional meetings to present and discuss research in this area. The Fourth E-ACTG Meeting is being held on the afternoon of Friday 10th May at The Royal Society of Edinburgh on George Street in the centre of Edinburgh. If you are interested in this area and can make it to Edinburgh you are very welcome to attend.

We have a really interesting and varied programme including some excellent external speakers (see below). Registration is free and we'll be providing lunch and refreshments to complement the excellent science courtesy of Wellcome ISSF funding.

To register, please email: chris.haley@roslin.ed.ac.uk giving your name and affiliation. Let us know if you have any special needs and we'll do our best to accommodate them. Spaces are strictly limited, so please get in touch soon. The last date for registration (if not full already) is Monday May 6th.

Chris Haley and Josephine Pemberton

Draft Programme - E-ACTG 4th Meeting 12.30-18.00 Friday May 10th Royal Society of Edinburgh

Kenneth Baillie (The Roslin Institute and R(D)SVS) Coexpression analysis of genome-wide signals for disease association

Camillo Berenos (Institute of Evolutionary Biology) Evolutionary genomics of body size in Soay sheep

Frank Chan (Max Planck Institute for Developmental Biology, Tübingen) How do the mice get so big? - Complex trait genomics in response to selection

Sarah Harris (Centre for Cognitive Aging and Cognitive Epidemiology) Global methylation content and cognitive and physical ability in old age: the Lothian Birth Cohort 1936

David Hume (The Roslin Institute and R(D)SVS) Promoting the genome

Augustine Kong (deCODE, Iceland) Haplotype sharing and time to common ancestor: resolving various genetics problems including the studies of rare variants and disease susceptibility variants

Albert Tenesa (The Roslin Institute and MRC Institute of Genetics and Molecular Medicine) Whole-genome modelling of colorectal cancer risk

Veronique Vitart (MRC Human Genetics Unit, MRC Institute of Genetics and Molecular Medicine) Genome-wide association analysis for circulating urate levels

Chris Haley MRC Human Genetics Unit, MRC Institute of Genetics and Molecular Medicine University of Edinburgh Western General Hospital Crewe Road, Edinburgh, EH4 2XU, UK Chris.Haley@igmm.ed.ac.uk +44 131 3322471

Roslin Institute and Royal (Dick) School of Veterinary Studies University of Edinburgh Easter Bush Midlothian, EH25 9RG, UK Chris.Haley@roslin.ed.ac.uk +44 131 651 9100

Josephine Pemberton <j.pemberton@ed.ac.uk>

Fiji ONLINE BarcodingBiodiversity Jul8-12 CallAbstracts

Dear Colleagues,

We have received many expressions of interest from potential presenters and attendees but many of them lack the travel support necessary to attend a conference in Fiji. Since both barcoding and collection digitization are community-based initiatives, the organizers have decided to make this an open, distributed Webinar. People who would like to be presenters or attendees will be able to do so from anywhere. As soon as the agenda has been finalized we will issue a call for registration which will be limited to 100 web-participants.

The Consortium for the Barcode of Life (CBOL) at the Smithsonian Institution and CSIRO in Canberra, Australia, are the co-organizers of a full-day symposium/workshop at the 12th Pacific Science Association Inter-Congress, Suva, Fiji 8-12 July 2013. The session is endorsed by the Oceania GBIF Node and the Global Taxonomy Initiative of the Convention on Biological Diversity. The description of the session is presented below. You will see that the day will be divided between presentations on barcoding as a tool for digitizing collections and a training workshop on other digitization techniques.

DEADLINE: The organizers invite you to submit abstracts by 15 June. Applicants for the barcoding session should send abstracts to David Schindel (schindeld@si.edu) and for the digitization session to Beth Mantle (Beth.Mantle@csiro.au).

====CONNECTING BIODIVERSITY COLLECTIONS IN THE PACIFIC: DIGITIZATION THROUGH DNA BARCODING AND INFORMATICS

David E. Schindel, Consortium for the Barcode of Life, Smithsonian Institution, Washington, DC, USA

Beth Mantle, Australian National Insect Collection, CSIRO, Canberra, ACT, Australia

Reference collections in museums, herbaria, botanical gardens, zoos and other repositories are critical infrastructure for research, education, regulation and legislation related to biodiversity. These collections provide documentation of research results as well as long-term changes in nature. Patterns of ecological, evolutionary and anthropogenic changes often go unseen and undocumented until samples from these collections material are analyzed and re-analyzed using the latest technology. In order to be accessible and effective, reference collections need to be digitized and their data and metadata made available to the research and education community, to policy-makers, and to the general public. Digitization in the most general sense is the association of an organism and its characteristics to a unique identifier that can be indexed for later searching and retrieval. It can take several forms, ranging from digital capture of label data (date and place of collection, taxonomic identification) to digital image capture and even DNA sequencing.

This full day session will include a half-day symposium of contributed presentations on DNA barcoding and a half-day instructional workshop on biodiversity informatics. The DNA barcoding symposium will contribute toward development of a regional strategy for Oceania for construction and use of standardized barcode libraries. These libraries could serve basic research in ecology and evolution and/or applications such as the protection of endangered species and control of invasive alien species such as agricultural pests. The biodiversity informatics workshop will showcase initiatives such as the Global Biodiversity Information Facility (GBIF), the Atlas of Living Australia (ALA), New Zealand Organisms register (NZOR), and digitization initiatives such as iDigBio and Australia's Virtual Herbarium (AVH). This session will explore applications and network tools appropriate for the small and scattered countries and territories of Oceania. Participants will learn the latest approaches to the digitization of natural history collections and explore how these could be applied to their collections. The session will conclude with a round-table discussion on strategic development of, and support for, biodiversity informatics in the Oceania region.

The Secretariat of the Convention on Biological Diversity (CBD) has expressed its support for this proposed workshop as a contribution to enhancing capacity in taxonomy (a goal of CBD's Global Taxonomy Initiative, GTI) and strengthening informatics infrastructure in the Pacific region. Academic collaborations on biodiversity facilitate achievement by CBD Parties in the region of Aichi Biodiversity Target 9 (invasive alien species) and Target 19 (Biodiversity science).

"Schindel, David" <schindeld@si.edu>

Fredericton VolvoxEvolution Jul31-Aug3 DeadlineExtended

The 2nd International Volvox Conference

EARLY REGISTRATION AND ABSTRACT SUBMISSION DEADLINE EXTENDED TO JUNE 15TH

Please join us for the 2nd International Volvox Conference (focused on the green alga Volvox and its close relatives) to be held July 31 V August 3, 2013, in Fredericton (New Brunswick, Canada). This is the second of what we hope to be a long series of Volvox meetings to be held every other year, alternating with the Chlamydomonas meetings. The first meeting, in 2011, was a great success (www.unbf.ca/vip/IVC/). Volvocine algae have become an important model system for the evolution of multicellularity, development and cellular differentiation, and lately have yielded important results in fields as diverse as genomics, hydrodynamics, and social evolution. We hope that the meeting will continue to foster exchange of ideas and expertise and will initiate new collaborations. We also wish to attract new people and to build a stronger Volvox community. The meeting (through contributed papers and posters) will highlight various aspects of the biology, taxonomy, ecology, development, genetics/genomics and evolution of Volvox and its relatives. For additional information and updates please visit the Conference page at http://www.unbf.ca/vip/IVC2013).

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>

IGFL Lyon GenomeEvolution Oct7

English The Institute of Functional Genomics, Lyon (IGFL), France, is organizing an international meeting celebrating its scientific inauguration, on Monday October 7, 2013. Research in the IGFL focuses on how genomes control fundamental aspects of animal development, physiology, and evolution. We have gathered an exciting panel of speakers including a Nobel Prize laureate and international leaders in the fields of Development, Evolution, and Physiology. Details can be found on the IGFL website at http://igfl.ens-lyon.fr/accueil?set_language=en&cl=en . The objective of this meeting is to bring together scientists from these inter-connected disciplines, and ensure a good interaction with the scientific community at IGFL, local and French institutions. The list of confirmed speakers and other information can be found in our meeting poster here: http://igfl.ens-lyon.fr/accueil/dossier-images/divers/COLLOQUE_INAUGURAL_PO STER.gif. A preliminary program is also available here: http://igfl.ens-lyon.fr/accueil/igfl/documents/program_preliminary Registration is now open (and will be closed on September 1st 2013) at: http://colloquedr7.dr20.cnrs.fr/pre-inscription.php?colloque A symbolic fee of 30 Euros will be charged to participants who wish to attend the meeting.

For assistance on accommodations in Lyon or for any other information, please contact the organizing committee at inauguration-colloque.igfl@ens-lyon.fr

French L^{1}Institut de Génomique Fonctionnelle de Lyon (IGFL) organise un colloque international pour célébrer son inauguration scientifique le Lundi 7 Octobre 2013. Les thèmes de recherche au sein de l^{1}IGFL ont pour objectif de comprendre comment le génome contrôle les aspects fondamentaux du Développement, de la Physiologie, et de l^{1}Evolution chez les animaux. Nous avons rassemblé un panel d^{1}intervenants de haut niveau, comprenant un lauréat Prix Nobel et des leaders internationaux en Développement, Physiologie et Evolution. Plus de détails sont disponibles sur le site web de l^{1}IGFL ≪ http://igfl.ens-lyon.fr/ ≫.

L^{1}objectif de ce colloque est de réunir des scientifiques dans ces domaines interconnectés afin de permettre une interaction fructueuse avec la communauté scientifique au sein de l^{1}IGFL, la communauté locale et nationale. La liste des intervenants confirmés peut être consultée sur l^{1}affiche du colloque ≪ http://igfl.ens-lyon.fr/accueil/dossier-images/divers/COLLOQUE_INAUGURAL_PO STER.gif ≫. Le programme préliminaire peut aussi être consulté sur le site ≪ http://igfl.ens-lyon.fr/accueil/igfl/documents/program_preliminary ≫.

Pour vous inscrire, connectez-vous sur le site http://colloquedr7.dr20.cnrs.fr/pre-inscription.php?colloque=83 .Le coût de l^{1}inscription est de 30 Euros, et la date limite est le 1er Septembre, 2013.

Pour obtenir des informations sur l^{1}hébergement à Lyon, ou pour toute autre information, veuillez contacter le comité d^{1}organisation ≪ inauguration-colloque.igfl@ens-lyon.fr ≫.

Abderrahman Khila <abderrahman.khila@ens-lyon.fr>

Kunming 5thBarcodeOfLife Oct27-31

Fifth International Barcode of Life Conference

27-31 October 2013, Kunming, Yunnan, China

Dear Colleagues and Friends

The Kunming Institute of Botany (KIB) and Kunming Institute of Zoology (KIZ), research institutes of the Chinese Academy of Sciences (CAS), invite you to join us in Kunming, China from 27-31 October 2013 for the Fifth International Barcode of Life Conference. The conference is co-hosted by the International Barcode of Life Project (iBOL) and the iBOL China National Committee, in consultation with the Consortium for the Barcode of Life (CBOL). DNA barcoding has come a long way since December 2011 when we met in Adelaide for the Fourth International Barcode of Life Conference. The 2013 conference will provide an opportunity for delegates from around the globe to showcase and discuss scientific advancements in DNA barcoding and the wide-ranging socio-economic applications developed since the Adelaide Conference, and to review the progress in this field over the past decade. The Kunming conference will bring barcode researchers together to exchange ideas and plan new activities, and to learn about barcoding activities in China and the region. The theme of the conference is ÂÂGlobal Change and the Barcode of Life: Challenges and OpportunitiesÂÂ±. The conference will be held at the Lian Yun Hotel near Green Lake with a stunning view of Kunming. There will be two days of pre-conference workshops, including full-day short courses that will introduce participants to the lab protocols of DNA barcoding and to the management and analysis of barcode data. The week of events will culminate in a barcoding event for the public in the Kunming Botanic Garden of KIB. Registration will be limited by the capacity of the conference venue, so please register soon to ensure your participation. Please also continue to check this website (http://dnabarcodes2013.org or http://dnabarcodes2013.csp.escience.cn) as we add information (see Important Dates). To receive future notices, online registration is needed.

We look forward to meeting you in Kunming in October!

For more details on the conference program, exhibition, abstract submission, and registration and accommodation kindly visit:http://dnabarcodes2013.orgor http://dnabarcodes2013.csp.escience.cn

Best wishes

DNAbarcodes 2013 Secretariat

DNAbarcodes <dnabarcodes2013@mail.kib.ac.cn>

Lausanne QuestForOrthologs3 Jul24-26

Dear colleagues,

We invite applications to the third Quest for Orthologs meeting, in Lausanne, Switzerland, July 24-26.

The QfO is an international scientific meeting that covers all aspects of orthology prediction, benchmarking, and application.

Further details at http://edu.isb-sib.ch/course/-view.php?id=3D144 Marc

Marc Robinson-Rechavi Department of Ecology and Evolution Biophore 3219, University of Lausanne, 1015 Lausanne, Switzerland tel: +41 21 692 4220 fax: +41 21 692 4165 http://bioinfo.unil.ch/ Twitter: @marc_rr

Swiss Institute of Bioinformatics http://www.isb-sib.ch/groups/lausanne/eb-robinson-rechavi.html La liberte ne s'use que quand on ne s'en sert pas

Marc.Robinson-Rechavi@unil.ch

London EvolutionBehaviouralMechanisms Dec5-6

We are pleased to announce that this year's ASAB Winter Conference will be held on 5-6 December, at the usual location of London Zoo (ZSL Meeting Rooms). The topic is 'The Evolution of Behavioural Mechanisms' and the keynote speakers will be Melissa Bateson, Reuven Dukas, Simon Laughlin and Marlene Zuk.

For more information, to submit an abstract (deadline: 16 August) or to register your interest, please visit http://tinyurl.com/winterasab2013 or contact us at madorganiser@gmail.com.

We look forward to seeing you in London!

Tim Fawcett, Andy Higginson & Pete Trimmer Modelling Animal Decisions (MAD) group, University of Bristol

–

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London Evolution Infectious Disease May17

British Ecological Society Centenary Symposium on Evolutionary Ecology of Infectious Disease

Friday, 17 May 2013 from 09:15 to 19:00

London, United Kingdom

Register at: http://-besevolutionsymposium.eventbrite.co.uk Ecologists have played a central role in developing the hugely successful theory of the epidemiology of infectious disease and this theory in turn has stimulated a great interest in the role of disease in natural communities. British Ecological Society (BES) members have influenced the development and advancement of the field, with many of the key papers published in BES journals. In recognition of this the BES is holding a meeting in its centenary year on the evolutionary ecology of infectious disease. The aim of the meeting is to highlight a number of ways in which ecology impacts on the evolution of and evolutionary implications of infectious disease, and how evolution may further impact on ecological dynamics. Talks will range from examining the role of ecology in determining host-parasite coevolutionary dynamics and to the parasite mediated evolution of sex, to how ecology drives plastic immune responses in hosts and determines the abundance of species, through to implications for the control of tropical disease. The day will finish with a discussion of future directions and how a better understanding of the evolutionary ecology of parasites will allow us to manage disease effectively in human, agricultural and natural populations.

Programme

9.15 Registration with tea, coffee & pastries

10.00 Professor Angus Buckling, University of Exeter Ecological determinants of host-parasite coevolution

10.40 Professor Andrea Graham, Princeton University St. Kilda's Soay sheep, from environmental to immune dynamics and back again

11.20 Coffee break

11.50 Professor Joanne Webster, Imperial College London Do schistosomes maximize fitness over changing environments?

12.30 Professor Curt Lively, Indiana University Infectious disease and the evolutionary ecology of sex

13.10 Lunch

14.10 Dr Heather Fergusson, University of Glasgow Evolution of vector behavior in response to control

14.50 Professor Janis Antonovics, University of Virginia Disease and the abundance and distribution of species

15.30 Reactors session

16.30 Drinks reception

B.L.Koskella@exeter.ac.uk

London InsectImmunityEvol May31

Dear all

There are still some slots available for talks at the Royal Entomology Society Infection and Immunity special interest group meeting 2013, which will be held on the 31st May 2013 in the Fogg Building at Queen Mary, University of London. The meeting is an informal one-day conference with a series of twenty minute talks. We particularly encourage PhD students and PostDocs to speak, although more senior researchers are of course also welcome. If anyone would like to attend or to speak, please get in touch by the end of this week so that we can finalise numbers. Just email me (r.knell@qmul.ac.uk) or Petros Ligoxygakis (petros.ligoxygakis@bioch.ox.ac.uk).

The total cost for the meeting is not yet finalised but is likely to be in the region of £10 or less, which will include lunch and coffee. Following the meeting there will be an opportunity to enjoy the scenic ambience and exciting flavours available in the East End of London.

Please pass this on to anyone who might be interested who isn't listed above, such as other people in your lab or department who we might have missed off accidentally.

regards

Rob Knell

Rob Knell r.knell@qmul.ac.uk School of Biological and Chemical Sciences, QMUL.

+44 (0)20 7882 7720

Research http://webspace.qmul.ac.uk/rknell/ Book now out: Introductory R, A Beginner's Guide to Data Visualisation and Analysis using

R www.introductoryr.co.uk r.knell@qmul.ac.uk

Marseilles 17thEvolBiol Sep17-20 Deadline

Dear all

the dead line for the abstract submissions for the 17th EBM is june 30 more info including the list of the first accepted abstract is available : http://sites.univ-provence.fr/evol-cgr/ all the best Pierre

Pierre PONTAROTTI <Pierre.Pontarotti@univ-provence.fr>

Montreal BiodiversityMathematics Sep16-20

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

EARLY REGISTRATION AND ABSTRACT SUBMISSION DEADLINE EXTENDED TO JUNE 15TH

Contributed talks and posters are welcome

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)

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) James Rosindell (Imperial College) Mike Steel (University of Canterbury) Chi Tran (Université des Sciences et Technologies de Lille) John Wiens (University of Arizona)

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@umontreal.ca

NMNH Washington Phylogenetics May20-21

The Third Annual Spring Symposium Hosted by NMNH's Frontiers in Phylogenetics Program is approaching:

Please register for one or both days using this link (admission is free):

https://docs.google.com/forms/d/-1psN38yqyZz7mpgQqC8DczlHuqstfWQisQoRQSnqvO8M/viewform Registration will close at the end of the day on Wednesday, May 15, 2013

"Genome-scale Phylogenetics"

Frontiers in Phylogenetics 3rd Annual Spring Symposium Baird Auditorium, National Museum of Natural History Washington, DC, May 20 & 21, 2013

Day 1 (Monday May 20) - Symposium Day 2 (Tuesday May 21) - Discussion Topics (schedule below)

DAY 1 - Symposium 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 Using Whole Genomes to Resolve the Avian Tree of Life 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 Evolution via the Grape Vine - Insights from Transcriptome Sequence Data 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, University of California, Los Angeles

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

DAY 2 - Discussion

Baird Auditorium, National Museum of Natural History Washington, DC, Tuesday May 21, 2013

9:00 - 9:30 workflow for phylo-transcriptomics; RNA from very small samples; Ostracoda Todd Oakley University of California Santa Barbara

9:30 - 10:00 informatics workflow for phylo-transcriptomics; insects Adam Bazinet University of Maryland

10:00 - 10:30 transcriptome assembly, preparation for downstream analysis; corals Shaadi Pooayei-Mehr American Museum of Natural History

11:30 - 11:00 BREAK

11:00 - 11:30 laboratory and informatic methods for exon capture; elasmobranchs Gavin Naylor College of Charleston

11:30 - 12:00 "Exon capture and assembly for bony fish phylogenetics: is paralogy a problem?" Guillermo Orti George Washington University

12:00 -13:30 LUNCH

13:30 - 14:00 generation and analysis of RAD-seq data; cichlid fish Catherine Wagner Swiss Federal Institute for Aquatic Science and Technology

14:00 - 14:30 UCEs, RAD-seq, amplicon-seq on MiSeq/HiSeq Brant Faircloth University of California Los Angeles

14:30 - 15:00 informatics workflow for bacterial phylogenomics Marc Allard U.S. Food and Drug Administration

15:00 - 15:30 BREAK

15:30 - 16:00 “Whole genome phylogeny of Archaea as an example of how to tackle the extremes: ancient divergences, long branches, and missing data” Rebecca Dikow National Museum of Natural History

16:00 - 16:30 “New approaches to species tree estimation in the presence of Incomplete Lineage Sorting” Tandy Warnow University of Texas

16:30 - 17:00 broad issues in phylogenomic analysis: gene selection; assignment of orthology; matrix assembly (impact of missing data); data quality in general Sabrina Simon American Museum of Natural History

KINGSTONS@si.edu

Paris MicrobialEvolution Oct2-5 CallAbstracts

Dear Colleague,

We are pleased to inform you that the scientific programme of IMMEM-10, the 10th edition of the International Meeting on Microbial Epidemiological Markers, has been updated. The novel version is available through the conference web site at http://www.immem-10.org . Novel sessions have been added: Novel typing methods for pathogen surveillance, Practical use of typing methods in epidemiology, Molecular epidemiology of viral zoonoses, and a Round table on the Global Microbial Identifier initiative.

We remind you that the call for abstracts is open. Please 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.

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.

Scientific Sessions Bioinformatics tools for genome-based microbial surveillance Outbreak genomics and epidemiology Population genetics, phylogenomics, emergence Molecular typing and epidemiology Novel typing methods for pathogen surveillance Practical use of typing methods in epidemiology Typing and surveillance networks in practice Round table: the Global Microbial Identifier initiative Phylodynamics of viral pathogens Molecular epidemiology of viral zoonoses Virulence: diagnostic and epidemiology Resistance: diagnostic and epidemiology Diagnostic by high-throughput sequencing Social networks and transmission modelling Molecular Epidemiology from Global Health to One Health

Confirmed speakers: Mark Achtman (Warwick University, UK) Andrea Ammon, European Center for Disease Control, Stockholm, Sweden Siv Andersson, Uppsala University, Sweden John Besser, CDC, Atlanta, USA Hervé Bourhy, Institut Pasteur, Paris, France Alessandra Carattoli, Institute of Public Health, Rome, Italy Stewart Cole, Global Health Institute, Lausanne, Switzerland Christian Drosten, Bonn University, Germany Pierre Formenty , World Health Organization, Genève, Switzerland Alex Friedrich, University Medical Center Groningen, The Netherlands Peter Gerner-Smidt, Center for Disease Control, Atlanta, USA Matthew Gilmour, Public Health Agency of Canada, Winnipeg, Canada Hajo Grundmann, National Institute for Public Health (RIVM), Bilthoven, The Netherlands Jörg Hacker, Leopoldina Academia, Berlin, Germany Dag Harmsen, Universitätsklinikum Münster, Münster, Germany Alan Hay, MRC National Inst. for Medical Research, UK René Hendriksen, DTU, Denmark Keith Jolley, Oxford University, UK Philippe Lemey, Leuven, Belgium Martin Maiden, Oxford University, Oxford, UK Claudine Médigue, CEA-Genoscope, Evry, France Stephan Niemann, Borstel, Germany Julian Parkhill, Wellcome Trust Sanger Institute, Hinxton, UK Tim Peto, University of Oxford, UK Laurent Poirel, Univ. Paris Sud, Kremlin-Bicêtre, France Marc Struelens, European Center for Disease Control, Stockholm Anne-Mieke Vandamme, Katholieke Universiteit Leuven, Leuven, Belgium François-Xavier Weill, Institut Pasteur, Paris, France

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

Sylvain BRISSE <sylvain.brisse@pasteur.fr>

Snowbird Utah Evol2013 Jun21-25 UndergradMentors

Mentors Needed for Undergraduate Diversity at Evolution 2013

The Undergraduate Diversity at Evolution program will be bringing 20 talented and diverse undergraduates to the Evolution meetings this June 21-25 in Snowbird, Utah. The undergrads will present a poster, participate in professional development activities and receive career-oriented mentoring.

An overview of the program can be found at: www.nescent.org/eog/undergraddiversity We are 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.

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 Evolution2013 Jun21-25 Housing 2

Housing and Childcare Updates:

1. Housing for the conference is available at Crystal Inn, which is at the base of Little Cottonwood Canyon.Crystal Inn offers free airport shuttles. In the AM Crystal Inn will transport to a nearby bus stop for public transportation to Snowbirdand there will be complementary shuttle service from the meeting site back to the hotel late in the evening (10 PM).Rooms are still available at Snowbird from June 23ˆrd onwards.Call Snowbird accommodations for more information (1-800-232-9542).

2. Cabin rental (sleeps up to 14 with two bathrooms and kitchen) is available at Snowbird for the duration of the meeting.Call Snowbird accommodations for more information (1-800-232-9542).

3. Priority childcare registration ends June 3ˆrd .Contact Camp Snowbird for more information By email: campsnowbird@snowbird.com (please put ’Evolution 2013’ in the subject line) By phone: (801) 933-2256

Evolution 2013 is the joint annual meeting of the Society for the Study of Evolution < http://www.evolutionsociety.org/ > (SSE), the Society of Systematic Biologists < http://systbiol.org/ > (SSB), and the American Society of Naturalists < http://www.amnat.org/ > (ASN), on June 21-25, 2013, at the Snowbird Alpine Village < http://www.snowbirdmeetings.com/?portfolio=snowbird-restaurants >.

This meeting is the premier annual opportunity for sharing scientific research related to evolution. Symposia presentations, concurrent contributed papers, and poster sessions will be presented by the 1,400 expected participants. Product and service providers will contribute to the meeting through their exhibits. Social activities will include an opening reception, mixers with each evening poster session, and a super-social/award ceremony - *all of these mixers and receptions are included with registration.*

Evolution 2013 meets jointly with the *iEvoBio < http://ievobio.org/ >* conference, which brings together biologists interested in evolution, systematics, biodiversity, software, and mathematics.

You can still register for the conference - for more information visit the conference web site: http://www.evolutionmeeting.org/index.html
cruzan@pdx.edu

UCambridge HumanOrigins Jul5

CALL FOR PAPERS - RELOCATING HUMAN ORIGINS - WHAT IF ADAM LIVED IN THE FOREST?

LOCATION: University of Cambridge ORGANIZERS: Doctoral Students, Division of Biological Anthropology DATE: July 5, 2013

NOW ACCEPTING ABSTRACTS FOR: “ 15 Minute Oral Presentations Live at Conference Remotely Webcast Pre-Recorded and Archived on Conference Website ” Posters

THEME: Conventional scientific wisdom holds that modern humans evolved in the East African savannah. But what if the cradle of human evolution was actually the Central African forest, as hinted by new Y-chromosome results? How might this change our understanding of human evolution? This conference explores the implications of a forest origin for human population genetics, disease ecology, social systems, and cultural evolution.

KEYNOTE SPEAKERS: Prof Mark Thomas, University College London: Genetics of Forest Ancestry Dr Corey Fincher, University of Glasgow: Origins of cultural and biological diversity Dr Tom Currie, University College London: Habitat Productivity & Ethnolinguistic Diversity Dr Peter Walsh, University of Cambridge: Disease, Social Complexity & Innovation

Can’t make it to Cambridge? The entire conference will be webcast.

PLEASE SEND YOUR ABSTRACTS TILL 07/06/2013 TO:

bioanth-conference2013-abstracts@lists.cam.ac.uk

Alexander Moerseburg

Alexander Mörseburg <am2037@cam.ac.uk>

UGroningen IndividualDifferences Nov1-3

International Conference on Individual Differences (20th KNDV Congress of Zoology) 1-3 November 2013 Groningen, The Netherlands

www.rug.nl/fwn/indiv This meeting aims to bring together different perspectives on the importance, mechanisms, function and evolution of consistent individual differences at different levels of biological organisation. Jointly organised by the Groningen Centres for Behaviour and Neurosciences (http://www.rug.nl/research/cbn/) and Ecological and Evolutionary Studies (http://www.rug.nl/research/cees/), under the auspices of the Royal Dutch Zoological Society (http://kndv.science.ru.nl/index.html).

Plenary speakers include: Stephen Suomi (National Institute of Child Health & Human Development, Bethesda, Maryland) Renee Duckworth (University of Arizona) Jonathan Seckl (University of Edinburgh)

Distinguished Zoologist Lecture: Judy Stamps (University of California at Davis)

We welcome contributions to the following seven symposia: . Individuality and neurobiology . Individuality and chronobiology . Individuality and energetics . Individuality and behaviour . Individuality and ecology, evolution and biodiversity . Individuality: applications and implications (welfare, biomedicine and conservation) . Individuality and aging

In addition, it will be possible to submit contributions to a general symposium. Registration and Abstract submission for oral and poster contributions is now open. Check the conference website: www.rug.nl/fwn/indiv Dr. Martine E. Maan

University of Groningen Department of Behavioural Biology room 5171-1.42 +31 (0)50 363 2196 visiting address: Nijenborgh 7 - 9747 AG Groningen mailing address: PO Box 11103 - 9700 CC Groningen packages: Nijenborgh 4 - 9747 AG Groningen

www.rug.nl/staff/m.e.maan www.martinemaan.nl M.E.Maan@rug.nl M.E.Maan@rug.nl

UNewEngland Genomics Jul14-19

Please join us as we convene 10 years after the first GRC on Ecological & Evolutionary Genomics!

July 14-19, 2013 University of New England Biddeford, Maine

Speakers and Discussion Leaders will present cutting-edge genome-enabled approaches that are being used to further our understanding of how organisms adapt to changing environments. Specific topics to be addressed include critical research challenges in population genetics, the study of genome evolution, the evolution of complex phenotypes, and environmental and global change biology. We have made explicit emphasis on “ecogenomics”, population genomics, and the bioinformatics required to understand the transition of genotype to phenotype.

We would like to invite you to attend this conference and join our community in discussing the frontiers and future challenges in this research area. Gordon Research Conferences are an ideal venue for informal and interactive discussions in beautiful locations in New England.

Speakers and Discussion Leaders: Julien Ayroles, Cornell University Rowan Barrett, Harvard University Holly Bik, UC Davis Mark Blaxter, The University of Edinburgh Justin Borevitz, The Australian National University Monica C. Muñoz-Torres, LBNL Sinead Collins, The University of Edinburgh Graham Coop, UC Davis Karel De Schamphelaere, Ghent University Maren Friesen, Michigan State University Omer Gokcumen, Harvard University Michael Hansen, Aarhus University Paul Hebert, University of Guelph Jessica Hellmann, University of Notre Dame Paul Hohenlohe, University of Idaho Chris Jiggins, University of Cambridge Felicity Jones, Max Planck Institute Ellen Ketterson, Indiana University Mikhail Matz, University of Texas, Austin Gos Micklem, University of Cambridge Stephen Palumbi, Stanford University Michael Pfrender, University of Notre Dame David Plachetzki, UC Davis John Quackenbush, Harvard University Christina Richards, University of South Florida Loren Rieseberg, University of British Columbia Emilie Snell-Rood, University of Minnesota Victoria Sork, UC Los Angeles Denis Tagu, INRA-RENNES Diethard Tautz, Max-Planck Institute Anne Todgham, San Francisco State University Thomas Turner, UC Santa Barbara Andrew Whitehead, UC Davis

For registration information and the speaker program, visit the GRC website: http://www.grc.org/programs.aspx?year=2013&program=ecolevol Best wishes, Gretchen E. Hofmann & John Colbourne, Mike Herman & Jack Werren

Michael Herman <mherman@ksu.edu>

UNotreDame ArthropodGenomics Jun13-15 ExtDeadline

** EXTENDED DEADLINES!! **

Arthropod Genomics 2013 Onward Seventh Annual Arthropod Genomics Symposium and VectorBase Workshop, June 12 V June 15, 2013, University of Notre Dame

** EXTENDED DEADLINE for abstract submission and registration V FRIDAY, MAY 31, 2013

For more information, visit the website at: http://globalhealth.nd.edu/7th-annual-arthropod-genomics-symposium/ “Eck Institute for Global Health - (eigh)” <eigh@nd.edu>

UWisconsin Madison SoberFest May24-25

Program

All sessions will be held at the Pyle Center (location info)

An interactive map of all workshop events can be found here.

Friday - 5/24

9:00am - Welcome to Soberfest; introductory remarks by Larry Shapiro

9:15am - 10:30am - Paradoxes of Consistency and (Revising) the Logic of Belief

Branden Fitelson (Rutgers)

Chair: John Basl (Bowling Green)

10:45am - 12:00pm - Recalibrating Morgan’s Canon

Eric Saidel (George Washington)

Chair: John Koolage (Eastern Michigan)

1:45pm - 3:00pm - Embodied Cognition and Emotion

Fred Adams (Delaware)

Chair: Melinda Hogan (Kwantlen Polytechnic)

3:15pm - 4:30pm - Non-Causal Features of Causal Explanation

Angela Potochnik (Cincinnati)

Chair: Matt Kopec (Colorado)

4:45pm - 6:00pm - KEYNOTE - Golden Gettier: What We (Should Have) Learned

Fred Dretske (Duke)

Chair: Zac Ernst (Missouri)

6:30 - 9:00 Dinner at Steenbock’s on Orchard http://steenbocksonorchard.com/ - be sure to let me (joel@joelvelasco.net) know if you prefer chicken or a vegetarian entree. There will also be a cash bar.

Saturday - 5/25

9:00am - 10:15am - Is it Prudent to be an Evidentialist?

Chris Stephens (University of British Columbia)

Chair: Shannon Spaulding (Oklahoma State)

10:30am - 11:45am - Deconstructing the Future: Causation, Interventionist Thinking, and the non-Identity Problem

Tom Bontly (Connecticut)

Chair: Matt Barker (Concordia)

1:45pm - 3:00pm - Does the philosophy of biology have any use?

Steven Orzack (The Fresh Pond Research Institute)

Chair: Paul Anders (Mount Marty)

3:15pm - 4:30pm - What is Science? Popper and Evolutionary Theory

Mehmet Elgin (MuÄla University, Turkey)

Chair: Deborah Mower (Youngstown)

4:45pm - 6:00pm - KEYNOTE - Which of the many things that are causes of a sensory impression is the one being perceived?

Denny Stampe (University of Wisconsin) Chair: Greg Novack (Wayne State)

6:30 - 9:00 Dinner at Porta Bella restaurant http://www.portabellarestaurant. biz/ - This will be appetizers and a cash bar.

After dinner: Malcolm Forster has invited everyone to come to his apartment for an after dinner party Saturday night. The address is 620 N Carroll St, Apt 713. This is about a 10 minute walk from Porta Bella (about about the same back to the Lowell Center).

program selection committee: Marc Ereshefsky, University of Calgary Larry Shapiro, University of Wisconsin Joel Velasco, California Institute of Technology

organizing committee: Joel Velasco Marc Ereshefsky Denis Walsh André Ariew Branden Fitelson Larry Shapiro Daniel Hausman Malcolm Forster

orzack <orzack@freshpond.org>

WageningenU EvolutionaryAgriculture May13

Symposium: Genetics of social life: Agriculture meets evolutionary biology

On the 13th of May 2013, the Animal Breeding and Genomics Centre of Wageningen University organizes a symposium on social genetic effects.

Program

08:30 Welcome and coffee

09:00 Welcome by Prof. Johan van Arendonk

09:10 Dr. Piter Bijma - The quantitative genetics of socially affected traits: consequences for evolution of trait values and response to artificial selection

10:00 Dr. Jason B. Wolf - A mapping approach to study social effects

10:50 Coffee Break

11:20 Dr. Hannah Dugdale - Social genetic effects in parental care behaviour

12:10 Katrijn Peeters - Social interactions in laying hens

12:25 Eric Bastiaans - Laboratory evolution of genotypes that cheat on multicellularity in fungi

12:40 Lunch

13:40 Dr. Alastair Wilson - Does competition constrain life history evolution in the wild?

14:30 Dr. Lyanne Brouwer - Social genetic effects of parental care in wild populations

14:45 Naomi Duijvestein - A Genome Wide Association study for social genetic effects of androstenone in boars

15:00 Coffee break

15:30 Prof. Laurent Keller - Genetic and social effects on ant social organization

16:20 Dr. Andrea Wilson - Social genetic effects and infectious diseases

16:50 Discussion & conclusion by Prof. Johan van Arendonk

17:00 Drinks

Location: Hotel de Nieuwe Wereld, Marijkeweg 5, 6709 PE Wageningen, The Netherlands

Date: May 13 2013

Fee: Free

Registration: Send an email to fleur.bartels@wur.nl. At registration, provide your name, department, company, and if you have diet restrictions. Deadline for registration is May 8 2013.

Information about the symposium can be found here (http://www.wias.nl/courses/view_course.php?ID=-

227).

Course: Social genetic effects: Theory and genetic analysis

>From May 14 until May 16 2013, the Animal Breeding and Genomics Centre of Wageningen University organizes a course on social genetic effects.

Aim: The course focusses on the theory and genetic analysis of social effects (Indirect Genetic Effects). Throughout the course the aim will be to learn useful approaches and strategies for analysing your own data. Data analysis exercises will be carried out by participants using ASReml. You can bring your own data.

Teacher:

- Piter Bijma, Animal Breeding and Genomics Centre, Wageningen University, the Netherlands.

Outline:

Day 1

- Trait-models with Indirect Genetic Effects (IGE; also known as associative effects, social effects or competition effects)

Day 2

- Consequences of IGEs for heritable variation and response to selection. Specific attention will be given to kin and group selection, and an overview of empirical results obtained with different selection methods will be given. Models with IGEs on fitness will also be covered briefly

- Dinner

Day 3

- The estimation of genetic parameters and breeding values for direct and indirect genetic effects will be covered, using mixed model methods. Approximately half of the time will be spent on lectures and half of the time on computer practical using exercises and/or your own data. Please bring your own laptop with ASReml. Please let us know if you have no ASReml licence.

Course Fee1 : A. WIAS PhD's2 £á 300.00 B. Other PhD's, post-docs, academia and WU staff £á 400.00 C. Industry £á 500.00

1Fee include course materials, daily coffee, tea and lunch, and a course dinner. Hotel accommodation and traveling is not included. 2For Wias PhD students with an approved TSP WIAS pays the fee.

Location: Hof van Wageningen, Lawickse Allee 9, 6701 AN Wageningen, the Netherlands.

Registration: Send an email to Esther.Ellen@wur.nl

Dates: May 14 V 16, 2013 The course will start on Tuesday May 14 at 9:00 am. The course will end at 5.00 pm on Thursday 16th of May.

Information about the course and hotel accommodation can be found here (http://www.wias.nl/courses/-view_course.php?ID=226).

Symposium and Course Organisation: Esther Ellen (Esther.Ellen@wur.nl) and Fleur Bartels (Fleur.Bartels@wur.nl)

Dr. Esther D. Ellen Postdoc

Animal Breeding and Genomics Centre, Wageningen UR (University & Research Centre) P.O. box 338, 6700 AH Wageningen, The Netherlands De Elst 1, 6708 WD Wageningen, The Netherlands

Email: esther.ellen@wur.nl Website: http://-www.wageningenur.nl/abg/ www.disclaimer-nl.wur.nl "Ellen, Esther" <esther.ellen@wur.nl>

GradStudentPositions

CanterburyChristChurchU CelegansLifespan

Natural variation in lifespan and the response to dietary restriction in Caenorhabditis elegans.

Lifespan is regulated by both genetic and environmental factors. Some environmental effects on lifespan, particularly those that result in dietary restriction (DR), are widely conserved across species. For instance, DR prolongs life in flies, worms and primates, and evidence is mounting that it also does so in humans. The nematode worm Caenorhabditis elegans is one of the most important model species in developmental biology and genetics.

Recent work undertaken at Canterbury Christ Church University (CCCU), in collaboration with Dr Jan Kammenga at Wageningen University, has identified a genomic region that affects lifespan and the response to DR in C. elegans. This work also indicates that the lines used to construct the mapping panel used in this work are sufficiently diverged that regions of their genome are incompatible. This is a feature associated with the early stages of speciation. Critically, many of these incompatibilities affect lifespan and block the effects of DR on lifespan. Understanding this link and identifying the underlying genes is therefore important for understanding the control of lifespan and DR, and also for understanding speciation. This work also demonstrate that to understand variation in lifespan and in the effects of DR, more advanced mapping panels must be used and combined analyses of lifespan, DR and incompatibilities undertaken.

Supervised by Dr Simon Harvey and Dr Lee Byrne at CCCU, this project aims to:

(1) Identify the specific gene(s) underlying the lifespan and DR effects we have already discovered. (2) Screen a newly created panel for incompatibilities, lifespan and the effects of dietary restriction on lifespan.

(3) Determine the basis of the linkage between the incompatibilities and lifespan.

This position will start 1st October 2013 and the student will be based at Canterbury Christ Church University, Kent, UK, but may be required to visit collaborators in Wageningen. The position is funded by CCCU, which provides a stipend of £11,700 pa and covers the cost of tuition. Applicants should be familiar with, and ideally experienced in, both microbiological and molecular techniques.

The closing date for this position is 31st May and the application form for this position is available here http://tinyurl.com/c6hqxcm, on the Times Higher Education jobs listings and on CCCU's jobs page (http://www.canterbury.ac.uk/AboutUs/-Workhere/Workhere.aspx).

If you wish to discuss this position, then please contact Simon Harvey (simon.harvey@canterbury.ac.uk).

simon.harvey@canterbury.ac.uk

GLIER UWindsor PopGenetics

M.Sc. or Ph.D. Examining the Population Genetics of Aquatic Invasive Species (Sept 2013)

The Conservation Genetics Lab at the Great Lakes Institute for Environmental Research (GLIER) has two paid assistantships available for new graduate students to explore the population genetics of Aquatic Invasive Species (AIS). The successful candidate will be a motivated and outstanding student with a background in Biology (B.Sc. or M.Sc.) and an interest in population genetics; experience with molecular biology techniques and analysis is preferred.

As a member of NSERC's Canadian Aquatic Species Invasion Network (CAISN), you will join affiliates from academia, government and industry across Canada in developing our knowledge of and tools to deal with AIS – widely recognized as one of the greatest threats to global biodiversity. As a student in GLIER's Environmental Science graduate program, you will benefit from world-class facilities, researcher expertise, focus on real world problems, and opportunities for working with GLIER's extensive collaborators and networks while making a difference in science, policy and innovation. The opportunity to train on cutting edge equipment within a collaborative atmosphere of world-class researchers will foster independence and advanced technical skills, increasing and diversifying your future employment possibilities.

The successful graduate student(s) will be supported on a combination of Research Assistantships and Teaching Assistantships totaling over $20,000/year.

We are currently accepting applications to begin study in September 2013. To apply, please send a letter of intent, curriculum vitae, and the names and email addresses of three references. For more information about the positions, please feel free to contact Dr. Daniel Heath (heath@uwindsor.ca). For more information about GLIER or CAISN, please see www.uwindsor.ca/glier and www.caisn.ca . saraj@uwindsor.ca

GLIER UWindsor PopulationGenetics AquaticInvasives

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For more information about GLIER or CAISN, please see www.uwindsor.ca/glier and www.caisn.ca . saraj@uwindsor.ca

IndianaStateU 2 EvolutionaryGenomics

Two PhD opportunities in Ecological Genomics

We are looking for two motivated students interested in behavioral, evolutionary, and ecological genomics to join our laboratory at Indiana State University (ISU). These graduate positions are part of an exciting new interdisciplinary initiative at ISU, The Center for Genomic Advocacy (TCGA), which is focused on the application of genomic technology to the betterment of society. TCGA is developing a state-of-the-art next generation sequencing facility, which will be used to provide hands-on experiences for students as well as strong infrastructure for modern genomic studies.

Graduate research will be expected to combine traditional behavioral ecology studies with next-generation sequencing technology to examine the evolution of polymorphism in the white-throated sparrow (www.whitethroatedsparrow.org). Students will conduct extensive laboratory work as well as participate in field based data collection during the breeding season in the Adirondack Mountains of NY. This species exhibits a clear link between phenotype and genotype, making it an ideal system in which to pinpoint the determinants of complex sexual and parental behavior. We have amassed 25 years of detailed data on this species making it possible to identify the genetic, epigenetic, and environmental bases of behavior. Morphs of the white-throated sparrow provide a unique opportunity to study intraspecific genomic differences, which have resulted from two separate, yet linked evolutionary trajectories - such results can transform our understanding of the evolution of genomes.

To apply, please send a letter of intent, curriculum vitae, and the names and email addresses of 3 references. Applications will be accepted until June 15, 2013.

For more information about the positions, please feel free to contact Dr. Elaina M. Tuttle (Elaina.Tuttle@indstate.edu) or Dr. Rusty A. Gonser (Rusty.Gonser@indstate.edu), at The Center for Genomic Advocacy (TCGA), Indiana State University, Terre Haute, IN 47809.

For more information about the lab, the department, and the university, see: www.whitethroatedsparrow.org
http://www.indstate.edu/biology/-
http://www.indstate.edu/home.php
http://www.indstate.edu/sogs/
Michael.Romanov@indstate.edu

IowaStateU MorphologicalEvolution

A PhD position is available in the laboratory of Dr. Dean Adams at Iowa State University as part of several NSF funded projects examining rates of morphological evolution of complex traits in salamanders and scallops. The broad goals of these projects are to investigate the tempo and mode of macroevolution of complex traits, to develop analytical approaches to identify patterns of evolution of shape in a phylogenetic context, and to empirically evaluate such patterns in several groups of animals (salamanders and scallops).

Prospective graduate students interested in geometric morphometrics, macroevolution, and evolutionary theory are encouraged to apply. Successful applicants may develop an independent research project within these areas, or one that complements or extends other research in the lab. For more information about the research in our lab please visit our website: http://www.public.iastate.edu/~dcadams/ Interested candidates should contact Dr. Dean Adams at dcadams@iastate.edu.

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

Dean Adams <dcadams@iastate.edu>

PennState EvolutionaryGeneticsMimicry

A PhD Graduate Student Research Assistantship is currently available in the Hines Lab at Pennsylvania State University to study the evolutionary genetics and developmental mechanisms underlying mimetic color variation in bumble bees. This project is highly integrative, including training in the areas of genetics, genomics, developmental biology, pigment chemistry, systematics, and entomology, and will likely involve bee rearing and field research. Additional research opportunities may be available for students interested in studying related topics, including butterfly mimicry, ecological field research, bioinformatic approaches to evolutionary questions, and/or projects intersecting evolutionary genetics with systematics. Enrollment for this position is through the Entomology graduate program (http://ento.psu.edu/), although options may be available in one of several other PSU graduate programs (Biology, Genetics, Bioinformatics and Genomics, or Ecology). Enrollment for Fall 2013 or Spring 2014 preferred.

For more information on this project and other research directions in the lab visit http://www.personal.psu.edu/hmh19/. Interested students should email Dr. Heather Hines (hmh19@psu.edu) with a statement of interest and curriculum vitae.

hmh19@psu.edu

StonyBrookU AppliedEvolution

The Department of Ecology and Evolution at Stony Brook seeks MA students for their Applied Ecology and Applied Evolution Programs

Deadline: June 1, 2013.

The masters program in Applied Ecology is intended to address the need for professionals in environmental sciences at federal, state, county, and other levels of government, environmental departments of large industrial companies and smaller environmental consulting firms, and non-governmental conservation and environmental protection organizations. The Applied Evolution concentration will also prepare students for work in these sectors, specifically for technical positions that require genetic, evolutionary and population based analytical skills. Career paths in biotechnology, forensics and biomedicine will also be available to graduates of this program. Both concentrations are useful for further specialized degree programs or careers in education. Both programs are particularly strong in quantitative skills, providing enhanced career opportunities for those with mastery in this area.

http://life.bio.sunysb.edu/ee/masters.htm – Liliana M. Davalos

Assistant Professor Consortium for Inter-Disciplinary Environmental Research (CIDER), and Ecology and Evolution, SUNY Stony Brook

Office phone: 631 632 1554

http://life.bio.sunysb.edu/ee/davaloslab/The_Lab.html Associate Editor, Molecular Phylogenetics and Evolution http://www.sciencedirect.com/science/journal/10557903 "Liliana M. Davalos" <lmdavalos@gmail.com>

UAberdeen DamselflyEvolution

UAberdeen.NicheEvolution

Body:

PhD POSITION IN NICHE EVOLUTION IN ISCHNURA DAMSELFLIES AT THE UNIVERSITY OF ABERDEEN

Under changing climates, many organisms are facing dramatic range shifts and expansions. The evolutionary constraints and consequences accompanying these geographic shifts are little understood, but are critical for understanding the processes of adaptation, niche evolution, and generation and maintenance of genetic diversity.

This project will investigate the evolutionary constraints on and consequences of niche evolution in the blue-tailed damselfly, Ishnura elegans, which has expanded its range northward in Great Britain by over 150 km in the past 50 years. The project involves fieldwork across the UK, and potentially also in Sweden.

Field and genetic (genome-wide SNP) data will be used to test alternative hypotheses about niche evolution and adaptation to novel ecological conditions under range expansion. The ideal student shows initiative and independent thought, but will be provided with full training and support to ensure a strong basis in evolutionary and population genetic theory, and proficiency in analytical techniques, (e.g.,) genomic, landscape genetic, and species distribution models.

This position is based within the Ecology research group the University of Aberdeen, a cutting-edge research community with many opportunities for collaboration. The student will work primarily under Dr. Lesley Lancaster, and further information about her research interests can be found here:http://www.nceas.ucsb.edu/~lancaster . Funding Notes:

Applicants for a studentship must have obtained, or be about to obtain, an upper second class UK honours degree, or the equivalent qualifications gained outside the UK.

Funding is available to UK nationals or those EU nationals who can demonstrate that they have been resident in the UK for three years.

You should apply for Degree of Doctor of Philosophy in Biological Sciences, to ensure that your application is passed to the correct College for processing.

More information about how to apply can be found here: http://www.findaphd.com/search/ProjectDetails.aspx?PJID=45283 Enquiries should be made to sbspgadmin@abdn.ac.uk.

Lesley Lancaster <Lesley.Lancaster@biol.lu.se>

UBielefeld SalamanderGenomics

UBielefeld_Germany.EcologicalGenomicsSalamanders

PhD position in ecological genomics of salamanders

University of Bielefeld, Department of Animal Behaviour, Unit Molecular Ecology and Behaviour, Germany

PhD Position in ecological genomics exploring parallel habitat adaptation in salamanders Application deadline: July 12th 2013

In a continuously changing world, the adaptation to new or altering environmental conditions is one of the most elementary and crucial biological processes. Although we have much data on how habitat adaptation can affect phenotypes and population structure of individuals, we need also to gain deeper insights into the genetic architecture of habitat-dependent adaptation. In this context, the study of parallel adaptive evolution is very promising to illuminate underlying processes and mechanisms. Unlike any other vertebrate group, amphibian species display a fascinating breadth of habitat-specific adaptations to aquatic and terrestrial habitats. The fire salamander, a terrestrial salamander species that give birth to fully developed larvae represents a nice natural system to study the genomics of parallel habitat adaptation. As larvae are deposited in quite different aquatic habitats, ranging from first order streams to completely stagnant periodic ponds, they have adapted to quite different ecological conditions. We have intensively studied the ecology and population genetics of two distinct species of fire salamanders V Salamandra salamandra in Germany and Salamandra infraimmaculata in Israel, with a special focus on how larvae can adapt to these different environmental conditions. We are now exploring in the frame of an international cooperative research program the genomics of parallel habitat adaptation in the fire salamander by transcriptome and gene expression analyses. By characterizing the ecological conditions of parallel habitat adaptation in these two species and by simultaneously screening a large number of genes for patterns of evolutionary divergence, we aim to link the ecology of habitat adaptation and gene expression patterns to a very detailed extent.

We are looking for a highly motivated PhD candidate who is willing to perform intensive fieldwork in salamander habitat sites, both in Germany and Israel, and to perform common environment experiments with subsequent gene expression analysis. The main objective of the PhD study will be to identify existing selection pressures (e.g. desiccation, presence of predators, drift, etc.) in the various habitat types and to test how larvae from different habitats can cope with specific selection pressures in common environment experiments. These larvae will then be also analysed for gene expression patterns and thus the identification of selection dependent genes or group of genes will be possible.

The research will be carried out in the framework of the German-Israeli Project Cooperation (DIP) financed by the German Research Foundation (DFG) genomics: analysis of gene expression underlying parallel habitat adaptation in distinct salamander species. The candidate will join an international team of leading scientists in the field of Ecology (Prof. Dr. Leon Blaustein, University of Haifa), Molecular Ecology (Dr. Sebastian Steinfartz, University of Bielefeld), Evolutionary Genomics (Dr. Arne Nolte, Max-Planck Institute of Evolutionary Biology), Evolution and Bioinformatics (Prof. Dr. Alan Templeton, University of Haifa) and River Ecology (Prof. Dr. Markus Weitere, Helmholtz-Centre for Environmental Research - UFZ). Moreover she/he will strongly interact with other PhD and postdoc researchers in genomics and bioinformatics, as well as with scientists in Germany and in Israel. The position (65% TV-L E13) will start at the beginning of October 2013 and is funded for three years.

Please send your application until July 12th 2013, including a curriculum vitae, a letter of motivation why you are interested in the project and addresses for references (e-mail addresses and telephone numbers) of two referees as a merged PDF to:

Dr. Sebastian Steinfartz Assistant Professor in Molecular Ecology and Behaviour

Department of Animal Behaviour University of Bielefeld Germany Telephone: +49 521 106 2653 Email: sebastian.steinfartz@uni-bielefeld.de

We expect to interview candidates in the course of August 2013.

Dr. Sebastian Steinfartz Assistant Professor of Molecular Ecology University of Bielefeld Department of Animal Behaviour Morgenbreede 45 D-33615 Bielefeld

Telephone: +49 521 106 2653 Fax: +49 521 106 2998 E-mail: sebastian.steinfartz@uni-bielefeld.de webpage: http://www.uni-bielefeld.de/biologie/vhf/SF/index.html Co-Editor of Amphibia-Reptilia http://www.brill.nl/amphibia-reptilia

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UEdinburgh EvolutionaryBiol

NERC-funded PhD studentship available at the Institute of Evolutionary Biology, University of Edinburgh, UK.

http://www.ed.ac.uk/schools-departments/biology/-evolutionary-biology/home The studentship will start in October 2013, and will cover full fees and provide a stipend to cover living costs (for UK students). The stipend is determined by NERC and is standard (see http://www.nerc.ac.uk/funding/available/postgrad/). The period is three years in the first instance, with possible extension depending on training needs.

Applicants are encouraged to contact (including their CV) potential supervisors, at the Institute of Evolutionary Biology (http://www.ed.ac.uk/-schools-departments/biology/evolutionary-biology/-staff-profiles), who will provide further information on the application procedure. Applicants should decide a priori the area and laboratory that is of most interest to them, and then contact the appropriate potential supervisor.

Applicants should contact supervisors ASAP, as we plan to move quickly on recruitment.

Further information at http://www.ed.ac.uk/schools-departments/biology/evolutionary-biology/research-opportunities

Professor Tom Little Chair of Evolutionary Biology Institute of Evolutionary Biology Kings Buildings University of Edinburgh EH9 3JT UK

+44 131 650 7781

tom.little@ed.ac.uk

http://www.biology.ed.ac.uk/research/groups/tlittle/
Tom Little <tom.little@ed.ac.uk>

UEdinburgh StatisticalGenomics

Warning: base64 decoder saw premature EOF! PhD project title: Statistical inference from genomic data

Department/Institution: Department of Genetics & Genomics, The Roslin Institute, University of Edinburgh

Primary supervisor: Pam Wiener

Project description: Genomics is currently revolutionizing many areas of biology. One application is the search for regions of the genome that show evidence of selection, while another is to make inferences about population history. However, selection and demographic events can produce similar genomic signals, making it difficult to distinguish the two forces. Regions showing clear evidence of selection may be investigated further for their association with traits favoured by humans (in the case of artificial selection) or corresponding to environmental adaptation (natural selection). The aims of this PhD project are (1) to evaluate available statistical methods for detection of selection and demographic events in terms of their applicability to genomic datasets with different features, (2) to improve and further develop methods, including distinguishing between the roles of selection and demography, and (3) to apply these methods to data from livestock and other species to make inferences about their histories.

Relevant references: S. Wilkinson, et al. 2013. Signatures of diversifying selection in European pig breeds. PLoS Genetics 9(4):e1003453. http://www.plosgenetics.org/article/info:doi/10.1371/-journal.pgen.1003453 Wiener, P. and R. Pong-Wong. 2011. A regression-based approach to selection mapping. Journal of Heredity 102: 294-305.

Wiener, P. and S. Wilkinson. 2011. Deciphering the genetic basis of animal domestication. Proceedings of the Royal Society B. 278: 3161-3170. http://rspb.royalsocietypublishing.org/content/-278/1722/3161.full?sid=bca8a388-2f03-485c-89ee-a042e135c933 Wiener, P., et al. 2011. Information content in genome-wide scans: concordance between patterns of genetic differentiation and linkage mapping associations. BMC Genomics 12: article 65. http://www.biomedcentral.com/1471-2164/12/65 Specifications: Candidates must normally hold a first or upper second class degree in a related subject area. Good quantitative skills, as well as English writing and oral skills, are essential and programming skills are desirable; additional training in genetics and genome analysis is available at the University. To qualify for funding, students must be UK or EU citizens with home tuition fee status. http://www.ed.ac.uk/-studying/postgraduate/fees-finance/fee-status The studentship will cover University tuition fees plus a salary commensurate with regular UK postgraduate stipends, approximately £13,726 (16,166) per annum. The expected start date is October 2013 and the studentship is 4 years in length.

Applications, including a cover letter and full CV with names and addresses (including email addresses) of two academic referees, should be sent to:

Pam Wiener, The Roslin Institute, The University of Edinburgh, Easter Bush, Midlothian EH25 9RG, UK Email: pam.wiener@roslin.ed.ac.uk

Informal queries requesting further information are welcome.

Closing date: 31 May 2013

Pam Wiener The Roslin Institute and Royal (Dick) School of Veterinary Studies University of Edinburgh Easter Bush, Midlothian EH25 9RG, UK

phone: 44 (0) 131 651 9209 email: pam.wiener@roslin.ed.ac.uk

pam.wiener@roslin.ed.ac.uk

UFlorida AntEvolution

Call for applications: Masters Position in Ant Biology at the University of Florida

Research Focus: ant diversity, population genetics and citizen science.

Qualifications: Bachelor's degree in entomology or closely related biological science. Applicants who have an intellectual interest in ants, evolution, ecology and outreach are especially encouraged to apply. Demonstrated ability to complete projects. Excellent written and oral communication abilities. Minimum GPA of 3.5 and competitive GRE scores are desired. Experience with the following will be an asset, but is not required: insect classification, collections management, systematics, DNA extraction and amplification (PCR), fieldwork, outreach/teaching.

Apply: Interested candidates should send a letter by email addressed to Dr. Andrea Lucky at alucky@ufl.edu with the subject header ms position in ant biology. Please include CV, statement of purpose and names and contact information of three references. Application deadline is May 31, 2013, with the ideal start date in Fall 2013.

Andrea Lucky, PhD Entomology/Nematology University of Florida 970 Natural Area Drive Gainesville, FL 32611-0620 Phone: (352) 273-3952 Email: alucky@ufl.edu www.andrealucky.com www.schoolofants.org alucky@ufl.edu

UGrenoble StatGen

PhD position in statistical genetics at the University of Grenoble (France)

Title: Genomic imputation and haplotype phasing using large-scale statistical machine learning.

The candidate will be in a diverse research environment working with both a lab of statistics for population genetics (http://membres-timc.imag.fr/Michael.Blum/) and a lab of machine learning (http://lear.inrialpes.fr/people/mairal/). Grenoble is a university town located in a beautiful alpine environment.

Subject: The amount of generated biological data grows at an unprecedented pace. Statistical and machine-learning research efforts are increasingly needed to analyse the large-scale biological data. As part of this research effort, the objective of the PhD candidate will be to develop statistical algorithms that can scale with the massive dimension of genomic data. One major use of genomic data is to make associations between genomic features and disease traits. Key technical steps in making associations between genes and diseases consists of identifying the genetic variants that are co-located on the same chromosome (phasing) and imputing missing genetic variants based on reference panels (genotype imputation). These two steps are performed with statistical algorithms that may hit a computational wall soon because of the massive dimension of the genomic data. The objective of the PhD will be to develop statistical models and algorithms for handling massive data. A first direction will be to adapt matrix completion techniques, which are are popular for web recommender systems and which can also provide accurate and fast results for genotype imputation. The proposed models and algorithms will be implemented in an open-source software during the course of the PhD project.

Profile: The typical background of the candidate will be in statistics or machine learning. Students from related disciplines, such as physics, computer sciences or mathematics are also welcome to apply. Applicants with a genuine interest for interdisciplinary PhD education will be preferred.

The Phd candidate will be co-supervised by Julien Mairal, INRIA researcher in machine learning and Michael Blum, CNRS researcher in Bayesian statistical genetics.

Deadline: Applicants should send by email a CV and a recommendation letter from an academic reference before the 31st of May.

Contacts: Michael Blum http://membres-timc.imag.fr/Michael.Blum/ Michael.blum@imag.fr

Julien Mairal http://lear.inrialpes.fr/people/mairal/- julien.mairal@inria.fr

Blum michael <michael.blum@imag.fr>

UGroningen TheoreticalEvolution

We are looking for a candidate to fill a PhD position in theoretical ecology, with some evolutionary aspects..

The project is titled “Competition theory with a dominance/tolerance trade-off: a mathematical approach to predict species abundances and distributions. Model development, analysis, and application to data on salt marsh.” The supervisors areClaire de Mazancourt and Bart Haegeman, Station d’Ecologie Expérimentale de Moulis, and Rampal S. Etienne, Centre for Ecological and Evolutionary Studies, University of Groningen, The Netherlands. The student will be based at the Centre for Biodiversity Theory and Modelling, Station d’Ecologie Expérimentale de Moulis, Ariège, France, with visits to the University of Groningen, The Netherlands.

For more information see http://www.sevab.ups-tlse.fr/fr/popup/detailsSujet.php?id=758(in French) or contact Claire de Mazancourt (claire.demazancourt@ecoex-moulis.cnrs.fr) or Rampal Etienne (r.s.etienne@rug.nl).

We are looking for a candidate with - good communication skills in English - experience in theoretical ecology or a background in mathematics/physics or similar and affinity for biology

Interested candidates should apply before *31 MAY 2013* by sending a CV and the names of three references to Claire de Mazancourt (claire.demazancourt@ecoex-moulis.cnrs.fr) or Rampal Etienne (r.s.etienne@rug.nl).

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Rampal S. Etienne Associate Professor, Community and Conservation Ecology Group University of Groningen The Netherlands +31 50 363 2230 http://www.rug.nl/staff/r.s.etienne/research Visiting address: Centre for Life Sciences Nijenborgh 7 9747 AG Groningen The Netherlands

Mail address: Box 11103 9700 CC Groningen The Netherlands

“R.S. Etienne” <R.S.Etienne@rug.nl>

UHelsinki EvolutionButterflyImmunity

PHD STUDENT POSITION IN ECOLOGY AND EVOLUTION OF IMMUNE DEFENCE IN A BUTTERFLY METAPOPULATION AT THE UNIVERSITY OF HELSINKI

Applications are invited for a PhD fellowship to study the interplay between ecology and genetics in shaping immune defence in natural butterfly (meta)population. The project is funded by the Kone Foundation (http://www.koneensaatio.fi/fi/-tiivistelmaet/#Saastamoinen: in Finnish only) Motivated students with a MSc degree in ecology, evolutionary biology or molecular biology (or other related fields) are encouraged to apply. Prior expertise in experimental design, statistical analysis or laboratory work are a bonus but your most important assets are enthusiasm for research, motivation to learn new things, and ability to work independently while being an active member of a research team.

The project is centered within a larger study of the ecological processes and the underlying genetic mechanisms that allow the Glanville fritillary butterfly (Melitaea cinxia) to cope with environmental challenges in the wild. This particular project will focus on the immune defence. In your project you will ask what are the significance of encapsulation response in terms of disease and parasitism resistance, how does it relate to other immunological assays, and if between individual variation influenced by population dynamics? In practice, you will carry out field work in the Ãland Islands archipelago (SW Finland) and conduct experimental work in the laboratory and under semi natural field conditions. There is also potential to use recently developed genomic tools to identify genes involved in immune defence. You are expected to present your findings in scientific meetings and workshops, as well as prepare publications for international scientific journals.

The research group of Dr Marjo Saastamoinen is part of the Metapopulation Research Group, Centre of Excellence appointed by the Academy of Finland, where you’ll find a wide range of expertise in ecological and evolutionary questions within a spatial framework.

Please send your application to

marjo.saastamoinen@helsinki.fi by 7 June 2013. Attach a CV (with publications included), a copy of your transcript records (= printout of the courses you've completed during your MSc), contact details of two references (e.g. MSc thesis supervisor), and a letter (MAX 1 page) with a description of your researcher interests and why you would be a suitable candidate for the project.

The work is scheduled to start in August 2013. The Phd student will receive a personal researcher grant (2100 per month, 25200 annually). The Kone Foundation grants funding one year at the time, so funding for the successive years need to be applied.

For more information, please contact Dr Marjo Saastamoinen (marjo.saastamoinen@helsinki.fi) and visit the website at (https://tuhat.halvi.helsinki.fi/-portal/en/persons/marjo-anna-kaarina-%280d792de9-7077-4683-8e2b-4e15b5e9620d%29.htm). For information on the University of Helsinki, please visit: http://www.helsinki.fi/university/index.html Marjo Saastamoinen, PhD Metapopulation Research Group Department of Biological Sciences PO Box 65 (Viikinkaari 1) FI-00014 University of Helsinki FINLAND

Phone +358 9 191 57741

marjo.saastamoinen@helsinki.fi

ULausanne EvolutionSocialInsects

PhD position: communication and decision-making in social insects, University of Lausanne (Switzerland)

We invite applications for a 3-year SNSF (Swiss National Science Foundation) funded PhD position at the University of Lausanne, Switzerland. We are looking for a highly motivated student to study communication, learning and decision-making in ants and bees. In many social insect species, workers communicate about profitable food sources or nest-sites. Honeybees, for example, use the waggle dance to direct nest-mates to profitable resources. Many ants and tropical bees use pheromone trails. However, not all species communicate about foraging sites and even in species with communication foragers often search for food independently. The project investigates the circumstances that favour different information-use strategies and explores the relationship between flexible individual foraging strategies and colony fitness. The research will include experimental work in and around Lausanne, with a possibility to perform field work in Brazil and/or develop simulation models. The main study animals are honeybees, ants and stingless bees.

We are looking for a candidate with a Masters degree (or equivalent) in Biology and a strong background in behaviour, ecology or evolution. Good English skills and an ability to work independently are important. Experience with social insects, statistical or modelling methods and a basic knowledge of French are helpful but not a requirement.

Supervisors and laboratory: Dr. Christoph Grüter (principal supervisor) & Prof. Laurent Keller, Laboratory of Evolutionary Genetics and Ecology of Social Life, University of Lausanne, Switzerland.

Web Sites: www.socialinsect-research.com, www.unil.ch/dee/page6763.html How to apply: applications include (1) a one-page cover letter describing your motivation, previous research activities and current research interests, (2) a CV, (3) two reference letters and (4) publications (if existing; e.g. MSc thesis). Send all documents except the publications in a single pdf file. Applications must be written in English and should be sent to christophgrueter77@gmail.com before the 15th July 2013. Earliest possible start date is the 1st of September 2013.

Informal enquiries: christophgrueter77@gmail.com

Dr. Christoph Grueter University of São Paulo Faculdade de Filosofia Ciências e Letras de Ribeirão Preto Departamento de Biologia Av. Bandeirantes, 3900 14040-901 - Ribeirao Preto, SP, Brazil Tel: 0055 16 3602 3815 Website: www.socialinsect-research.com Christoph Grueter <C.Grueter@sussex.ac.uk>

ULaval GenomicsBehaviouralManipulation

PHD POSITION: GENOMIC AND PROTEOMIC MECHANISMS OF BEHAVIOURAL TAKE-OVER OF STICKLEBACKS BY A PARASITIC FLATWORM

We are looking for a motivated student to join our team to work on the ecological genomics of host-parasite interactions at UNIVERSITÉ LAVAL, Quebec City, Canada. Our labs are part of the Biology Department and are located in the INSTITUTE OF INTEGRATIVE AND SYSTEMS BIOLOGY. The PhD position offered is part of a FRQNT-Équipe project (Quebec, Canada) to study the interaction between the genomes of the threespine stickleback (Gasterosteus aculeatus) and of its flatworm parasite (Schistocephalus solidus). The project leaders are Dr. Nadia AUBIN-HORTH (behavioural genomics and neuroendocrinology) & Dr. Christian LANDRY (bioinformatics, evolutionary genomics and proteomics). We work in collaboration with Dr. Iain BARBER (evolution of host-parasite interactions and their consequences) from University of Leicester.

PROJECT: Sticklebacks parasitized by the cestod flatworm do not show the normal behavioural response to predation risk and, as a consequence, are more frequently captured by their bird predator. These behaviour modifications are often presented as adaptations of the parasite to enhance transmission rates to its final bird host in order to complete its life cycle, as the changes in stickleback behaviour occur specifically when the flatworm is ready to mature in its final host, suggesting a stage-specific active manipulation by the parasite. However, we know very little about the molecular mechanisms that underlie this host-parasite interaction. Our team aims to answer questions about the molecular changes happening in the host and the parasite and how their genomes interact.

Motivated students with a MSc degree in life sciences (ecology, evolution, molecular biology or other related fields) are encouraged to apply. A strong interest for an INTEGRATIVE APPROACH, combining novel tools in GENOMICS, PROTEOMICS and BIOINFORMATICS with BEHAVIOURAL ASSAYS and pharmacological manipulation and working actively in a team is a must. Prior experience in animal behaviour, endocrinology, molecular biology, genomics, proteomics, bioinformatics or statistical analysis is an advantage. A PhD fellowship is available for 3 years for the chosen candidate.

To apply, please send an email including a CV, a letter describing your research experience in link with the project and your research interest, your diplomas and transcripts, and the names and email addresses of 3 references (including your M.Sc. Advisor). Applications will be accepted until July 15, 2013 or until a candidate is selected. The position will start in September 2013. For more information about the position, please feel free to contact the head of the team, Dr. Nadia Aubin-Horth (Nadia.Aubin-Horth@bio.ulaval.ca). For more information about the labs, see: http://wikiaubinhorth.ibis.ulaval.ca/Main_Page http://www.bio.ulaval.ca/landrylab/en/pmwiki.php Nadia Aubin-Horth Associate professor Biology Department Institute of Integrative and Systems Biology Laval University Quebec City (QC) G1V 0A6 Canada

Aubin-Horth Nadia <Nadia.Aubin-Horth@bio.ulaval.ca>

URennes PolyploidGenomeEvolution

Three-year funded PhD fellowship available at University of Rennes 1 (UMR CNRS 6553 Ecobio), France:

***Evolution of polyploid genomes and functional innovation: *

The history of plants is punctuated by recurrent events of genome duplications (polyploidy) which led to the emergence of most existing angiosperm lineages and to increased complexity of functions that played a critical role in species adaptation. This functional evolution has important ecological consequences (such as the expansion of invasive species) and is also widely exploited in agriculture (domestication of polyploid species). Understanding of the molecular mechanisms associated with genome duplication (especially in hybrid /i.e./ allopolyploid contexts) is currently the subject of active research in the scientific community. The goal of the thesis is to understand how ecologically important functions may take place during evolution following genome duplication, using genus /Spartina/ (Poaceae, Chloridoideae) as a model system. /Spartina/ species are perennial grasses colonizing salt-marshes. Polyploidy and interspecific hybridization are recurrent in this genus where various ploidy levels are encountered from tetraploid (2n@) to dodecaploid (2n0-122). The planned studies will focus on the hexaploid species /Spartina alterniflora/ and /Spartina maritima/ and their recent hybrid and invasive allopolyploid (/Spartina anglica/) derivatives. The recent technological and methodological developments resulting from high-throughput sequencing now offer new opportunities for integrated approaches in evolutionary and ecological genomics.Various molecular approaches (genomic, transcriptomic and proteomic) will be combined to biochemical, physiological phenotyping and phylogenetic analyses. Handling of high-throughput data and bioinformatic processing are planned.

The project is developed in the research group “Mechanisms and Origins of Biodiversity (MOB)” under supervision of Prof. Malika Ainouche in the framework of an International Associated Laboratory “ECOGEN: Ecological Genomics of Polyploidy” with the support of the

Partner University Funds through a collaborative programme with Prof. JF Wendel (Iowa State University, USA).

Applicants must have a Master (or equivalent) degree and must apply at the Ecole Doctorale Vie Agro Santé (VAS) of University of Rennes 1 (http://www.vas.univ-rennes1.fr/) *_BEFORE 9 JUNE 2013_* to participate to the Annual Competitive Admission Process which includes 2 steps: 1) Pre-selection based on application 2) Interview with the selection committee (26-27 june 2013); interviews in English or French. The results will be available before July 6th.

Detailed information on the application process is provided on the VAS website (http://www.vas.univ-rennes1.fr/). The applicants will have to specify their choice regarding this PhD thesis, /i.e/. reference 102 in the list provided on the VAS website. Interested applicants are invited to contact (with CV) Malika Ainouche (malika.ainouche@univ-rennes1.fr) BEFORE submitting their application

Prof. University of Rennes 1 UMR CNRS 6553 Ecobio Bat. 14A Campus de Beaualieu 35 042 Rennes Cedex tel +33 (0)2 23 23 51 11

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

UUppsala EvolutionaryGenetics

PhD position in evolutionary genetics, Uppsala

A PhD-student position in evolutionary genetics is available at the Department of Evolutionary Biology, Uppsala University. Starting date 15th of August 2013, or as agreed upon.

Project description: Non-genetically inherited or epigenetic factors are now known to have a major impact on most biological processes, including evolutionary processes and heredity. In your PhD project, you will focus on the causes and consequences of paternal non-genetic effects transferred from the father to the offspring. You will use the zebrafish as a model system to investigate such sperm-mediated epigenetic effects by combining experimental work with next generation sequencing methods to elucidate the possible mechanisms.

See the Immler lab web-page for more information and recent publications (http://www.ebc.uu.se/Research/IEG/evbiol/research/Immler/) or contact Simone Immler directly (Simone.Immler@ebc.uu.se).

Qualifications: An MSc degree (or equivalent) in a relevant field is required. The ideal candidate is highly motivated with thorough education and strong interest in evolutionary biology and potentially developmental biology. Previous experience with experimental setups, the wet-lab and some basic bioinformatics are beneficial. Candidates must be fluent in English.

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 Simone Immler (Simone.Immler@ebc.uu.se, +46 18 471 6465) 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.

How to apply: The application should include 1) a letter describing your research interests and motivation for PhD studies, 2) a short description of your education, 3) a CV, 4) an authorized copy of your MSc degree, 5) the names and contact information (address, email address, and phone number) of at least two reference persons, 6) relevant publications (including MSc thesis). The application must be written in English.

You are welcome to submit your application no later than 21st of June 2013, UFV-PA 2012/1600. Use the link below to access the application form: http://www2.personalavd.uu.se/jobb/appform.php?lang=en&case=UFV-PA%202013/1600 Dr Simone Immler Evolutionary Biology Centre Evolutionary Biology University of Uppsala Norbyvägen 18d SE - 752 36 Uppsala Sweden

Email: simone.immler@ebc.uu.se Phone: +46 (0)18 471 6465 Homepage: http://www.ebc.uu.se/forskning/IEG/evbiol/forskning/Immler/ Simone Immler <simone.immler@ebc.uu.se>

UValencia EvolutionaryBiol

mBEI_Mster en Biologa Evolutiva Integrativa_ Universitat de Valncia_Curso2013-2014

What: Masters Degree in Integrative Evolutionary Biology

When: 2013-2014

Where: Cavanilles Institut on Biodiversity and Evolutionary Biology - University of Valncia

Places available for new students: 24

Languages used in class: Spanish and English

More information:

http://www.uv.es/biodiver/c/docencia/index.htm
Contact:

manuel.serra@uv.es

Guillem Prez i de Lanuza <guillem.perez-lanuza@uv.es>

UWesternOntario 2 EvolutionaryPhysiology

Evolutionary Physiology in the cold: 2 PhD studentships

Several PhD positions available in the Sinclair lab, Department of Biology, University of Western Ontario.

1.Evolutionary physiology of insect freeze tolerance.This project will use a combination of transcriptomics and physiology to determine the common factors that allow some insects to withstand internal ice formation.

2.Overwintering adaptations associated with the northward spread of the invasive land snail /Cepaea nemoralis/.This project will use a combination of physiology and population genetics to examine evolutionary change in cold tolerance of an invasive snail whose geographic range is expanding beyond that predicted from its native distribution in Europe.In collaboration with Dr. Annegret Nicolai.

The Sinclair lab is a vibrant, social and diverse group of individuals dedicated to understanding how winter drives natural processes.We are question-driven, and use a wide range of techniques, and interact with a broad range of collaborators in Canada and abroad.The Sinclair lab provides an exceptional training environment, and members have enjoyed success, winning scholarships, awards... and occasionally even jobs!

The Department of Biology has a large graduate programme that provides competitive stipends, flexible start dates, excellent training and sensible times-to-completion.The University of Western Ontario is located in London, Ontario, Canada, and has over 5000 graduate students on a beautiful urban campus.London, situated mid-way between Detroit and Toronto, has a population of 450,000, a thriving arts scene, and all amenities expected for a city its size.

Exceptional students from any nationality are encouraged to apply, however, applications from Canadian citizens and permanent residents are especially encouraged.For more information, visit publish.uwo.ca~bsincla7, or contact Dr. Brent Sinclair, bsincla7@uwo.ca. Applications should include a cover letter, CV and unofficial copy of an academic transcript (a scanned version is fine) and should be received by August 31, 2013.

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Dr Brent Sinclair Associate Professor, Department of Biology Biological & Geological Sciences Room 2078 (Lab: Room 2056) University of Western Ontario, 1151 Richmond St N, London, Ontario N6A 5B7

bsincla7@uwo.ca tel: 519-661-2111 ext 83138; Fax 519-661-3935 http://publish.uwo.ca/~bsincla7/ Come to ISEPEP5! 12-16 August, 2013, London, ONtario, Canada http://www.uwo.ca/biology/ISEPEP5/ Brent Sinclair <bsincla7@uwo.ca>

UZurich 2 Biodemography

Subject: Two Biodemography PhD Positions at University of Zurich

There are two biodemography PhD positions available in my research group at the University of Zurich. The details of these position can be found here: http://popecol.org/temp/PhD_UZH.pdf The prospective candidates are welcome to contact me with any questions.

All the best, Arpat Ozgul

Assistant Professor of Population Ecology

Institute of Evolutionary Biology and Environmental Studies | University of Zurich Office: 34-J-24 | Tel: +41 (0)44 63 *54746* | arpat.ozgul@ieu.uzh.ch | popecol.org

Arpat Ozgul <arpat.ozgul@ieu.uzh.ch>

UppsalaU PopulationGenetics

PhD position in population genomics

2013-05-15

at the department of Plant Ecology and Evolution, EBC, Uppsala University, SwedenâApplication no later than 2013-06-15. UFV-PA 2013/1479.

Project description: Polyploidy, or whole genome duplication (WGD), occurs in virtually all vascular plants and has played a major role in evolution. In your PhD project you will take advantage of the recent developments in sequencing technology and previous studies in the Capsella genus to characterize genomic and phenotypic changes associated to WGD in the shepherd's purse (C. bursa-pastoris), a recently formed tetraploid weed. You will first conduct whole-genome resequencing and gene expression studies of accessions from Europe and from China. In a second step, the association between genomic variation and putative adaptive traits will be assessed through association and linkage mapping. These data, together with data in its diploid relatives, will be used to address questions about the genomic consequences of WGD between species and between groups of accessions within species and questions on the consequences of WGD for putative adaptive traits. Part of this work will be done in close cooperation with research groups in Canada and China.âAn important part of your work will include statistical and genome analyses of large DNA sequence data sets from a number of Capsella genomes. In addition, molecular and experimental studies of specific pathways and phenotypic traits may be included. The exact workplan of the thesis will be settled together with the doctoral student. The PhD student will be based in the group of Martin Lascoux at the Evolutionary Biology Center. (http://www.ebc.uu.se/forskning/IEG/-Plant/Research_groups/Lascoux_group/)ââ

Qualifications: An MSc degree or equivalent in a relevant field is required. We seek a highly motivated student with thorough education and strong interest in evolutionary genetics/genomics, and population genetics. Previous experience with bioinformatical and statistical analysis of modern sequence data is required and a working knowledge of Perl and Python or related programming languages is highly recommended. We are looking for individuals who can work independently but also as part of a team. Candidates must be fluent in English (orally and written). The successful candidate will receive her/his postgraduate training within the postgraduate school at the Evolutionary Biology Centre (http://www.ebc.uu.se/?languageId=1) that is one of world's leading research institutions in evolutionary biology.â

Conditions: The postgraduate training comprises four years of full time studies. The successful candidate will receive a postgraduate fellowship the first year (15500SEK/month) and a postgraduate position year 2-4 (23100-27500 SEK/month). The position can be combined with up to 20% of teaching assistantship, which will then prolong the position accordingly. Please feel free to contact Martin Lascoux (Martin.Lascoux@ebc.uu.se, +46 18 471 6416) for more information. Union representatives are Anders Grundström, Saco-rÃdet, tel. +46 18 471 53 80 och Carin Söderhäll, TCO/ST, tel. +46 18 471 19 96, Stefan Djurström, Seko, tel. +46 18 471 33 15.ââ

How to apply: Please prepare a letter of intent including descriptions of 1) your motivation for PhD studies in general and for this position in particular, 2) your education, especially in evolutionary biology, genetics/genomics/bioinformatics, molecular biology, and statistics. The application should further include a CV, an authorized copy of your MSc degree, and the names and contact information (address, email address, and phone number) of at least two reference persons. Relevant publications (including BSc/MSc thesis) should be enclosed. The application must be written in English.â

You are welcome to submit your application no later than June 15, 2013, UFV-PA 2013/1479. Use the link below to access the application form.

http://www2.personalavd.uu.se/jobb/-appform.php?lang=en&case=UFV-PA%202013/1479

Martin Lascoux Department of Ecology and Genetics EBC, Uppsala University Norbyvägen 18D 75236 Uppsala Sweden Tel +46 (0) 18 471 64 16 Fax +46 (0) 18 471 64 57

martin Lascoux <Martin.Lascoux@ebc.uu.se>

Vienna PopulationGenetics

Reminder: Call deadline for PhD positions at The Vienna Graduate School of Population Genetics:

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 BehaviouralManipulation

A PhD position is available at the Laboratory of Virology, Wageningen University, to study the mechanism of viral manipulation of insect behaviour.

Job description:

We are looking for a talented and highly motivated PhD student to study the mechanism of viral manipulation of insect behaviour. More and more examples accumulate of viruses that manipulate the behaviour of their hosts to increase transmission probability. The goal of this study is to unravel the molecular mechanisms behind behavioural manipulation by viruses in insects, for which caterpillars infected with baculoviruses will be used as a model. As a first step in this research, a viral gene that induces hyperactivity in baculovirus-infected caterpillars was identified. In this project you will apply transcriptomic and proteomic approaches to reveal differences in expression patterns and protein content between hyperactive insects as a consequence of infection with the wild type virus and insects infected with mutant viruses that do not induce this behaviour. These data will provide information about signal transduction pathways and insect effector genes that lead to altered host behaviour. A number of differentially regulated genes and proteins will be selected for follow-up studies (including both molecular and behavioural analyses) to confirm and specify their role in parasitic manipulation.

Requirements:

We ask: the candidate will have an MSc degree in Biology, Molecular Life Sciences or Biotechnology. Experience with bioinformatics is highly recommended. Knowledge on molecular biology and virology is advantageous, as is affection with behavioural studies. The candidate should have experience with working with complex data sets in a biological setting and will be proficient in the English language. Excellent interpersonal and communication skills are essential, as well as the ability to work in a multidisciplinary team in a collaborative spirit. The candidate should also be prepared to assist in the education of BSc and MSc students.

Conditions of employment:

We offer a full-time position (38 hours), initially for 1 year after which a go/no go decision will be taken on extension with another three years. Gross salary per month 2062 in the first year, rising to 2664 per month in the fourth year, for a fulltime appointment. The candidate will be based at the Laboratory of Virology in Wageningen. Occasional visits to collaborating institutes in Europe are expected. The PhD candidate will be offered a course program via the graduate school Production Ecology and Resource Conservation, which can be tailored to the desires of the candidate and the research team. Information on the research: Dr. Vera Ros, +31(0)317 484461 (vera.ros@wur.nl) and Prof. Dr. Monique van Oers +31(0)317 485082 (monique.vanoers@wur.nl). Information on the selection procedure: Mrs. Eva Siebelink (eva.siebelink@wur.nl).

Don't send your application directly to the people mentioned above but use the website to apply www.wageningenur.nl/en/jobs/vacancies .Contract type: Temporary, Tijdelijk dienstverband.

Organisation:

Wageningen UR (University & Research centre) The Laboratory of Virology is part of the Plant Science Group of Wageningen University. We are situated at the recently established Wageningen Campus. Currently, over 30 researchers, including technicians, PhD students and Postdocs work in the Laboratory of Virology. We offer a lively, research-driven work environment. Research in the Laboratory of Virology focuses on plant viruses, arboviruses and insect viruses. Plant viruses form a major threat for crops and ornamentals and are often transmitted by insect vectors. Arboviruses are transmitted by insects as well and cause disease in humans and animals. Insect-infecting viruses on the other hand are pathogenic to insects and are used to control pest insects. Insect viruses are also in use biotechnologically to produce recombinant proteins in insect cells for instance for vaccines. Our research concentrates on virus-host and virus-vector interactions viruses, with special attention for defence mechanisms, viral evasion strategies and host manipulation mechanisms.

Wageningen University & Research centre Delivering a substantial contribution to the quality of life. That's our focus each and every day. Within our domain, healthy food and living environment, we search for answers to issues affecting society such as sustainable food production, climate change and alternative energy. Of course, we don't do this alone. Every day, 6,500 people work on the quality of life, turning ideas into reality, on a global scale. Could you be one of these people? We give you the space you need.

For further information about working at Wageningen UR, take a look at www.wageningenur.nl/en/Jobs.htm . Additional information:

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iDiv Leipzig PlantBiodiversity

The German Centre for Integrative Biodiversity Research (iDiv) is one of the seven National Research Centres funded by the German Research Foundation (DFG). It is located in the city of Leipzig and jointly hosted by the Martin Luther University Halle-Wittenberg (MLU), the Friedrich Schiller University Jena (FSU), the University of Leipzig (UL) and the Helmholtz Centre for Environmental Research (UFZ). It is supported by the Max Planck Society, the Leibniz Association, the Klaus Tschira Foundation and the Free State of Saxony. Its central mission is to promote theory-driven synthesis and data-driven theory in this emerging field. The concept of iDiv encompasses the detection of biodiversity, understanding its emergence, exploring its consequences for ecosystem functions and services, and developing strategies to safeguard biodiversity under global change.

Embedded in the active research environment of iDiv, the Young BioDiversity Research Training Group (yDiv) will be established. Its goal is to educate a new generation of scientists in transdisciplinary biodiversity research, who will have gained expertise both in experimental as well as theoretical fields of research.

The University of Leipzig offers the following position:

Doctoral fellowship (initially limited to 3 years, 65 percent of a full-time employment) Salary: Entgeltgruppe 13 TV-L on Plant Physiology/Biospectroscopy

Topic/job description: - development of measuring protocols for IR spectroscopy - development of mathematical algorigthms for spectral analysis (chemometrics) - biochemical quantification of selected components of material from different plants - integration of IR results into a theoretical background of species specific C-allocation pattern

Requirements / expected profile: - an excellent master's degree in a relevant field of research - experience in biochemical analysis of plant material - experience in in-vivo spectroscopy of plants - experience of multivariate statistical analyses - good use of spoken and written English and ambition to publish in international journals - creativity, enthusiasm and endurance

We offer you a PhD position, affiliated with the University of Leipzig and supervised by Prof. Christian Wilhelm, department of Plant Physiology, Institute of Biology/University of Leipzig (http://www.uni-leipzig.de/~pflaphys).

Applications are accepted until May 20, 2013.

All applications should include:

- filled application form (download under http://www.idiv-biodiversity.de/ydiv/positionsjobs - cover letter describing research interests & relevant experience - curriculum vitae - one letter of recommendation - MA/BA/Diploma certificates

Applications should be directed to the yDiv coordinator Dr. Jula Zimmermann (ydiv@idiv-biodiversity.de) in a single PDF file with reference file number (54/2013) in the subject line.

We prefer applications in electronic form (hard copy applications can be sent to Dr. J. Zimmermann; German Centre for Integrative Biodiversity Research - iDiv; Deutscher Platz 5e; 04103 Leipzig)

For queries on the application process please contact ydiv@idiv-biodiversity.de

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*Dr. Jula Zimmermann *

/Scientific Coordinator of the Graduate School - yDiv / Wissenschaftliche Koordinatorin der Graduiertenschule - yDiv German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig/

//iDiv_Logo

Phone +49(0)341-97-33125 Fax +49(0)341-97-31264 Email jula.zimmermann@idiv-biodiversity.de<mailto:friederike.heinze@idiv-biodiversity.de>

German Centre for Integrative Biodiversity Research(iDiv) Halle-Jena-Leipzig Deutscher Platz 5d 04103 Leipzig Germany

iDiv ist ein Forschungszentrum der Deutschen Forschungsgemeinschaft (DFG). Es ist eine zentrale Einrichtung der Universität Leipzig im Sinne des §92 Abs. 1 SächsHSFG und wird zusammen mit der Martin-Luther-Universität Halle-Wittenberg, der Friedrich-Schiller-Universität Jena sowie dem Helmholtz-Zentrum für Umweltforschung (UFZ) betrieben. Sieben außeruniversitäre Einrichtungen unterstützen iDiv finanziell sowie durch ihre Expertise: das Max-Planck-Institut für Biogeochemie (MPI BGC), das Max-Planck-Institut für chemische Ökologie (MPI CE), das Max-Planck-Institut für evolutionäre Anthropologie (MPI EVA), das Leibniz-Institut Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), das Leibniz-Institut für Pflanzenbiochemie (IPB), das Leibnitz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) und das Leibniz-Institut Senckenberg Museum für Naturkunde Görlitz (SMNG). USt-IdNr. DE 141510383

Jula Zimmermann <jula.zimmermann@idiv-biodiversity.de> Jula Zimmermann <jula.zimmermann@idiv-biodiversity.de>

Jobs

ArizStateUniv TechSupport

Technology Support Position

A staff position is available in the Center for Evolutionary Medicine at Arizona State University (cemi.asu.edu). We invite applicants with expertise in system administration and desktop support. Knowledge of evolution and/or bioinformatics is a plus.

You can see a detailed job description at the following tiny URL:

http://goo.gl/fgbbt

You must submit a complete application at the above URL. Applications will be reviewed immediately.

If you have any questions, please contact Sudhir Kumar (s.kumar@asu.edu).

s.kumar@asu.edu

FloridaStateU REU Summer2013

Summer Research Experience for Undergraduates

Undergraduates interested in gaining research experience in evolutionary biology are invited to apply for a summer National Science Foundation Research Experience for Undergraduates (REU) position available this summer in the lab of Emily Moriarty Lemmon at Florida State University. The summer REU student will help conduct genetic analyses of population structure in chorus frogs (Pseudacris) to test whether behavioral changes in phenotype correlate with population and landscape level genetic changes. The REU student will learn molecular techniques for working with DNA (traditional genotyping and high-throughput sequencing) and bioinformatic techniques for analyzing sequence data. Candidates should have an interest in evolutionary genetics and learning statistical methods for analyzing genetic data. Compensation will be $480 per week (corresponding to $12.00/hr; for approximately 8 hours/day; 5 days/week) for a total of 8 weeks and will also include a $1,200 stipend for housing and $1,208 for subsistence during the 8 week period. For students planning on graduate school, this experience would look great on your resume.

To apply for this position, please contact Dr. John Malone at jmalone@bio.fsu.edu and include a CV along with contact information for three references.

jmalone@bio.fsu.edu

FloridaStateU Tech Phylogenomics

Research Scientist / Postdoctoral Researcher Organization: Florida State University Job Location: Tallahassee, FL Job Description: To join our integrative laboratory team, which is generating data for phylogenomics, phylogeography, and population genetics on a massive scale using enrichment procedures and high-throughput sequencing (i.e., Illumina). Researcher will serve as the project coordinator, organizing collaborative research projects, managing the laboratory, developing novel applications for hybridization-based enrichment, providing training to laboratory members, and performing bench-level molecular work (e.g., library preparation, hybrid enrichment). Researcher will have opportunities for authorship and co-authorship on relevant papers. Qualifications: Candidate must have demonstrated organizational skills, excellent laboratory experience and troubleshooting skills, a strong background in molecular biology, good experience in protocol development, solid leadership skills, and a record of high productivity. Candidate must have the strong interpersonal skills necessary for interacting with a wide range of collaborators. Candidates with a background in genomic data collection and/or several years of experience in molecular laboratory management will be given precedence during application review. Start Date: June-Sept 2013 (earlier end of this range preferred) Characteristic Duties: - Organize and manage collaborative projects - Assist in development and troubleshooting of new genomic protocols - Conduct various bench level experiments - Oversee assistant laboratory technicians - Maintain laboratory (order reagents, etc. or delegate these duties) - Provide advice and/or training in molecular techniques to fellow lab members - Assist in mentoring undergraduate lab projects - Attend weekly meeting for planning experiments Essential requirements: (1) BS, MS, or PhD degree with either graduate experience or a minimum of two years of professional molecular laboratory experience (2) Strong background in molecular biology techniques (3) Excellent organizational, time management, and communication skills required; must be able to work independently, solve problems, and interact with lab members. Contact Information: chorusfrog@bio.fsu.edu Please insert “Lemmon Lab Research Scientist” in subject header and attach a CV. Letters will be requested as needed. About Our Organization: The researcher selected will become part of the integrative laboratory groups of Alan Lemmon and Emily Moriarty Lemmon in the Department of Biological Science at Florida State University (in state capital Tallahassee, Florida). Our research interests and active research areas include theoretical and empirical phylogenetics, genomics, bioinformatics, speciation, behavioral evolution, phylogeography, population genetics, and development of new methods for data collection and data analysis for high-throughput phylogenomics.

For information about Florida State University: www.bio.fsu.edu/ For information about Tallahassee, Florida: www.visittallahassee.com/ For information about research in the Lemmon Laboratories: www.evotutor.org/LemmonLab/ www.bio.fsu.edu/chorusfrog/index.html www.bio.fsu.edu/faculty-moriarty-lemmon.php Emily Moriarty Lemmon Department of Biological Science Florida State University 319 Stadium Drive, P.O. Box 3064295 Tallahassee, FL 32306-4295 Phone: 850-645-9170 http://www.bio.fsu.edu/chorusfrog/index.html http://www.bio.fsu.edu/faculty-moriarty-lemmon.php chorusfrog@bio.fsu.edu

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GeorgeWashingtonU ResTech SpermEvol

Research Technician working on Drosophila sperm evolution, genetics and development

A Research Technician position is available in the lab of Mollie Manier (http://mkmanier.expressions.syr.edu/home), a beginning assistant professor in the Department of Biological Sciences at the George Washington University (http://departments.columbian.gwu.edu/biology/) in Washington, D.C. My research program investigates the evolutionary, molecular and developmental mechanisms of rapid diversification of reproductive traits. The goals of the current project are (1) to understand the molecular genetics behind the extraordinarily long sperm of Drosophila (up to 5.8 cm in length), (2) to describe the molecular evolution of sperm length genes across the Drosophila lineage, and (3) to investigate their roles during spermatogenesis.

The technician will provide technical support for research on the molecular and evolutionary genetics and developmental biology of sperm length in * Drosophila*. Responsibilities of the position include, but are not limited to, ordering materials and supplies; preparing media, reagents and materials; procuring and maintaining laboratory *Drosophila* stocks and other lab organisms; hiring and managing undergraduate work study students and researchers; assisting the PI and postdoc in designing and executing experiments; and R&D of protocols.

The successful candidate must be familiar with or able to be trained in all methods employed in the lab, including Drosophila culture and handling, DNA and RNA extraction and amplification, qPCR, sequencing, Drosophila testis dissection, Drosophila RNAi knockdown, RNA in situ hybridization, protein immunohistolocalization, tissue culture, fluorescence microscopy, and data management and analysis. The position requires neatness, attention to detail, good organizational skills, independence, and the ability to work well with and manage others. Evening and weekend hours will sometimes be necessary for time-sensitive collecting and experiments.

The minimum degree required for this position is BA/BS in biology or related field, with specialization in developmental biology, molecular and cell biology, evo-devo or evolutionary biology priortized. Previous research experience and/or a graduate degree will also be prioritized. The position is available August 1, 2013, but the exact start date is somewhat negotiable. Funding is available for three years, with continuation after the first year commensurate upon mutual agreement. Starting salary is $30,000 with benefits, commensurate upon experience.

To apply, e-mail Dr. Mollie Manier at maniermk@gmail.com with (1) your CV, (2) a statement of interest including a summary of your research experience and goals for the next five years, (3) unofficial transcripts from your undergraduate institution, and (3) contact information for 3 references. Application deadline is May 15.

maniermk@gmail.com

HongKong EvolutionaryBotanist

Kadoorie Farm & Botanic Garden Corporation

Notice of Vacant Post: Senior Botanist/Senior Ecologist

JOB SUMMARY The general remit of the post is to implement KFBG's plant and forest conservation and restoration strategy through planning and implementing plant conservation, plant biodiversity assessment and forest restoration projects in Hong Kong. The work will be underpinned by analysing ecological, molecular and environmental data, developing regional to international-level policy recommendations for biodiversity conservation, communicating findings to stakeholders in biodiversity conservation and writing scientific publications and reports relevant to nature conservation. Major projects of the team include permanent forest dynamic plots, forest restoration projects and conservation projects for rare and endangered plants of the region. The job holder will manage a team of three scientific and five to seven ground staff to implement the above duties and to maintain the routine operations of KFBG's native tree nursery and herbarium.

Applicants should have a PhD and Postdoctoral experience in the field of botany or ecology (preferably restoration ecology), a minimum of 10 years working experience, strong leadership skills with experience of supervising a team and managing large internally/externally funded projects. Strong communication skills in English, advanced knowledge of statistics, strong computational skills are required. Experience in supervising MSc and PhD students would be a plus.

The job holder will primarily be based in Hong Kong, but she/he may also need to work outside Hong Kong to implement projects.

Interested parties should send a detailed CV, expected salary, and a short essay (describing relevant work experience and reasons for interest in the post) to:

Dr. Gunter Fischer, Head of Flora Conservation Department, Kadoorie Farm & Botanic Garden Corporation Lam Kam Road, Tai Po, N.T., Hong Kong Email: gfischer@kfbg.org

gfischer@kfbg.org

LausanneU EntomologyEvolution

The Faculty of Biology and Medicine of the University of Lausanne, Switzerland invites applications for the position of a tenure-track Assistant Professor in Entomology. The position is at the Department of Ecology and Evolution, but is also linked to the Museum of Zoology and Botanical Garden.

The Department of Ecology and Evolution (http://www.unil.ch/dee) has a long track record of excellence in research.

A start-up package, a state-of-the-art research infrastructure as well as an annual research allowance for positions and consumables will be available within an environment favoring collaborations. The successful candidate is expected to develop an internationally recognized research program funded by external sources and take a leading role in a new initiative aimed at developing interactions between the University of Lausanne and the Museum of Zoology and the Botanical Garden.

Pre-existing knowledge of French is not required but the successful candidate is expected to be able to teach in French within 2 years. She/he will also supervise Masters and PhD students and participate to other training activities.

The job description is available on the Internet site http://www.unil.ch/fbm/page64812.html . Further information may be obtained from the Chair of the Search Committee, Prof. Jan R. van der Meer (Jan-Roelof.VanDerMeer@unil.ch)

The applications, in English, will include the curriculum vitae, the list of publications with copies of the five most significant ones, a brief statement of the research program and teaching experience, as well as three references (names and contact information). They should be submitted online by August 16th 2013 as a single pdf file at www.unil.ch/iafbm/application . Seeking to promote an equitable representation of men and women among its staff, the University encourages applications from women.

– Tadeusz J. Kawecki Associate Professor Department of Ecology and Evolution University of Lausanne Le Biophore, CH 1015 Lausanne, Switzerland tadeusz.kawecki@unil.ch

tadeusz.kawecki@unil.ch

Lyon GroupLeaders EvolBiol

CALL for NEW RESEARCH GROUP LEADERS, LYON, FRANCE Deadline 15th of July 2013

The Institut de Génomique Fonctionnelle de Lyon (IGFL) currently hosts 13 groups (approx. 110 personnel). The Institute has just moved to a newly commissioned 3200 sq. m. building, within the multidisciplinary campus of Lyon-Gerland, and, in line with its expansion, is hiring additional groups.

Research at the IGFL focuses on the role of the genome in animal physiology, developmental biology and evolution. In addition, the IGFL is actively seeking to strengthen its research in bioinformatics and modelling at the genomic scale.

IGFL groups have full access to state-of-the-art core services, including high throughput sequencing technologies, X-Ray microtomography, 2D and 3D imaging and morphometrics, transgenic animal facilities (mouse, fish, drosophila), bioinformatics, mass spectrometry, proteomics, FACS sorting, histology and electron microscopy.

The IGFL proposes two distinct calls for outstanding young scientists wishing to start their own team as well as established group leaders interested in joining the IGFL:

#1-2013 Non-thematic call Group leaders with a strong interest in animal-based research falling within the scientific mission of the Institute - namely physiology and physiopathology, developmental biology and evolutionary sciences - may apply to this call.

#2-2013 Genomics Group leaders performing research on whole genome data analysis, gene regulatory networks, modelling of biological processes to understand genome structure and evolution may apply to this call. In addition to office space the Institute can accommodate the requirement for wet laboratory facilities.

Applications (in English, specifying the call reference in the subject line) should include curriculum vitae, a short description of achievements and records of self-financing, a proposed research program of max. 10 pages and contact details for 3 professional references. The deadline for applications is July 15th 2013. Please send as a single PDF named LASTNAME_IGFL_2013.pdf to direction.igfl@ens-lyon.fr Enquiries should also be directed to this address. http://igfl.ens-lyon.fr The IGFL is run by the Ecole normale supérieure de Lyon, the Centre National de la Recherche Scientifique, Université Lyon 1 and the Institut National de Recherche Agronomique.

fred <frederic.brunet@ens-lyon.fr>

MRC Edinburgh StaffBioinformatician

Staff Bioinformatician, MRC Human Genetics Unit (Edinburgh, UK)

The MRC Human Genetics Unit (HGU; http://www.hgu.mrc.ac.uk/) has an exciting opportunity for a bioinformatician, to work on prestigious projects at the cutting edge of biomedical science, as a member of our permanent staff. The post holder will be expected to interact with members of the Bioinformatics staff, the wider computational community and HGU scientific staff; initiating and working on diverse collaborative projects independently. The MRC HGU hosts a variety of internationally competitive groups working on major problems in human genetics and disease with excellent opportunities for high impact collaborations with leading researchers. The successful applicant will join a dynamic and expanding community of experimental and computational biologists in the MRC IGMM (http://www.igmm.ac.uk/), a new institute bringing together the MRC HGU, the Edinburgh Cancer Research Centre (http://www.ecrc.ed.ac.uk/) and the University of Edinburgh Molecular Medicine Centre (http://www.mmc.med.ed.ac.uk/). They will join our other computational biologists in the new Systems Medicine building, custom designed for computational biology, to open in 2015. Applicants should be able to demonstrate programming skills and possess published experience in the analysis of genome scale biological datasets, particularly high throughput sequencing data. We also envisage duties in the installation/ maintenance of bioinformatics applications and provision of advice/ training to users. This post would suit a biologist with good programming skills or a computer scientist with strong interests in biology/ bioinformatics. The closing date is 31st May 2013 and informal inquiries to Colin.Semple@igmm.ed.ac.uk are welcome. Candidates should apply via the University of Edinburgh jobs site quoting vacancy reference number 013670: https://www.vacancies.ed.ac.uk Colin A. M. Semple Head of Bioinformatics MRC Human Genetics Unit MRC Institute of Genetics and Molecular Medicine University of Edinburgh Tel: +44 (0)131 332 2471 x4034 Email: Colin.Semple@igmm.ed.ac.uk Web: http://www.hgu.mrc.ac.uk/Users/Colin.Semple/ Colin.Semple@igmm.ed.ac.uk

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Montpellier 5 InstCompBiol

:::::::::::::: TITLE ::::::::::::::

Young investigator positions at the Institute for Computational Biology of Montpellier (France)

:::::::::::::: BODY ::::::::::::::

FOR DIFFUSION AND APPLICATION!

The Institute for Computational Biology (IBC) of Montpellier is seeking to hire five young investigators, one for each of five work-packages (see below). These young researchers will benefit from an exceptional scientific environment combining the presence of numerous leading international biocomputational researchers at IBC with a vibrant community of biologists in Montpellier.

REQUIREMENTS and RESPONSIBILITIES

Applicants will typically have a PhD, a high level of publishing, strong communication skills, and a taste for multidisciplinary research. A post-doc experience in international research will be much appreciated. These young researchers will play a key role in the Institute life. Most of their time will be devoted to a scientific project. In addition, they are expected to actively participate in the coordination of workpackages, in the hosting of foreign researchers and in the organization of seminars and events (summer schools, conferences...). Positions are for up to 4 years with a salary above the French post-doc standard.

HOW TO APPLY

For more information and to apply for these positions:http://www.ibc-montpellier.fr/ Deadline: June 15, 2013

DETAILS OF EACH WORK PACKAGE

WP1: Algorithms for High Throughput Sequencing

This project aims at designing and developing new algorithms for the analysis of millions of sequences, involving complex techniques in text indexation, compression and algorithmics on classical or high performance computing architectures. These novel algorithms form the core of bioinformatics programs that will help investigating the transcriptome complexity. In the framework of a large cancer genomics project, we will exploit these programs to analyze over 100 tumoral genomes and transcriptomes as well as their normal counterparts. The candidate will participate in either of two aspects: (1) practical algorithms and indexing data structures for NGS processing; (2) bioanalysis of cancer genomes and transcriptomes.

WP2: Evolutionary genomics

This project involves evolutionary analyses of large-scale genomic data, at the interface between phylogeny and population genetics. The candidate will develop research on some of the following topics: inference of very large phylogenies, reconciliation of gene/species trees at a genomic scale, detection of selection, inference of population divergence, dating and migration studies, simulation-based inference. Application domains will be quite open, with emphasis on virus evolution and plant genomes. We are seeking a candidate with a strong background in mathematical and computational evolutionary biology, with interest in applications and software development.

WP3: Pathogen proteome annotation

This project aims at the development and integration of bioinformatics tools for an interdisciplinary project dealing with structural and/or functional annotations of pathogen proteomes. We are seeking a high level computer scientist with strong experience in bioinformatics; knowledge in 3D protein structures and/or statistical learning would be a plus. The successful candidate will have good knowledge in one or several of the following topics: statistical learning, hidden Markov models, pattern matching, 3D and geometry algorithmics, protein domains, unstructured regions, tandem repeats, gene ontology

WP4: 4D Image processing during plant and animal development

This project involves the Integration of 4D imaging data with functional genomics in plant and animal developmental biology. The candidate will contribute to the development of a software platform for image analysis. Two main directions are proposed: storage, annotation and handling of volumetric images obtained by confocal or light-sheet laser microscopy and development of a concept of 4D atlases, whereby cellular (e. g. geometry, mechanics) and molecular (e. g. gene expression) parameters can be projected onto "average" organ geometries. The final aim is to provide novel solutions to explore the genotype to phenotype relationships. Candidates will have a strong background in computer science and analysis of volumetric and segmented images.

WP5: Advanced Biological Databases in plant genomics

This project aims at the design and implementation of a data framework for plant genomics. We are seeking a candidate with strong experience in distributed data management, in particular data integration, a good grasp on implementation aspects and interest for biology applications.

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Olivier Gascuel

– Directeur de Recherche Institut de Biologie Computationnelle LIRMM, UMR 5506 CNRS - Université Montpellier 2 Case courrier 06011, 95 rue de la Galéra

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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

OregonStateU Teaching Evolution Ecampus

Greetings —

There is a job opening for a full-time Instructor to develop and teach two lower-division non-majors courses - one in evolution and one in ecology - as Ecampus (online) offerings at Oregon State University.

To review posting and apply, go to http://oregonstate.edu/jobs. Apply to posting #0010647. For full consideration, apply by June 1, 2013. OSU is an AA/EOE.

Contact me if you have questions about the position:

Dee Denver: denver[at]cgrb.oregonstate.edu

More details:

The Department of Zoology invites applications for a full-time (1.0 FTE), 12-month, fixed-term Instructor position. Reappointment is at the discretion of the Department Chair.

Position is responsible for the development and instruction of two lower-division Ecampus courses focused on introductory evolutionary biology and ecology. Position provides leadership and coordination of Zoology departmental Ecampus course offerings, in partnership with the OSU Ecampus office.

The Zoology Department receives support for its academic program from the College of Science. In addition to the faculty's activities in research and service, it has teaching responsibilities in nearly every undergraduate major at OSU. The department has developed an internationally recognized graduate program in conservation and evolutionary biology and marine ecology with faculty working in these areas at the level of the cell, organism, and community.

The College of Science provides a core instructional role at OSU, supporting the ideals of learning, discovery, and engagement that are the foundation of a land-grant university. The College embraces instruction and research, in disciplines ranging from the physical to the biological sciences, that are based in unbiased inquiry and a dedication to discovery and innovation. The College of Science is committed to partnering with industry and public agencies to address some of the most compelling challenges of today and tomorrow.

denvedee@cgrb.oregonstate.edu

PurdueU Lecturer EvolBiol

The Purdue University Department of Biological Sciences in West Lafayette, Indiana is advertising a Continuing Lecturer position. Applicants must have a Ph.D. in the biological sciences or related discipline and preferably two years of teaching experience at the university level. The successful candidate will teach lecture courses in a sophomore-level ecology & evolution class and introductory genetics for majors. The initial contract for this position is two years with potential of continuation based on performance.

Applications must be submitted electronically to https://hiring.science.purdue.edu as single PDF files that include a detailed curriculum vitae, names and addresses of three references, a 2-3 page summary of statement of teaching interests and/or philosophy. Inquiries should be directed to Continuing Lecturer Search Committee, Department of Biological Sciences, Purdue University, 915 West State Street, West Lafayette, IN 47907-2054 or emailed to search@bio.purdue.edu. Review of applications will continue until position is filled.

dbos@purdue.edu

RowanU Parttime TeachEvolution

Three-Quarter-Time Instructor/Assistant Professor in Biological Sciences, Rowan University, Glassboro, NJ

The Department of Biological Sciences at Rowan University invites applications for a one-year, 3/4-time Instructor / Assistant Professor position beginning Sept. 1, 2013. The successful candidate will teach a total of four courses and 18 instructor credits across the fall and spring semesters. A new contract may be available in the following year, contingent on position approval, course needs, and professional performance. Courses taught will include majors-level lab courses in cell biology and in one or more of the following specializations: genetics, microbiology or virology. The successful candidate will contribute appropriate service to the department, and will have the opportunity to pursue research or participate in collaborative research programs within our department and the University.

For more information on the position and how to apply, please see: http://www.rowan.edu/jobs/info.cfm?id=1627 Luke Holbrook, PhD Professor of Biological Sciences Rowan University

Science Hall 201 Mullica Hill Rd. Glassboro, NJ 08028

Phone: 856 256 4500 x3457 FAX: 856 256 4478 E-mail: holbrook@rowan.edu

holbrook@rowan.edu

UAlabama LabTech SuccessionDynamics

Research Technician in Community Ecology at The University of Alabama

The Howeth Laboratory at the University of Alabama invites applications for a full-time research technician in community ecology beginning August 15, 2013. The technician will be involved in projects which aim to understand (1) succession in pond metacommunities and (2) the role of metacommunity dynamics in affecting the establishment, spread, and impact of non-native species, using freshwater plankton communities as a model system. The position is for 12 months, with responsibilities divided equally between field and laboratory work. Field work may include out-of-state travel for several weeks, and mesocosm experiments at the University of Alabama Tanglewood Biological Station. Laboratory work may include identification and enumeration of zooplankton, culturing of zooplankton, water chemistry analyses, and microsatellite DNA analyses.

Required qualifications: BS or MS in Biology, Ecology, or related science. Ability to tolerate harsh field conditions when necessary. Basic computer skills and familiarity with major software programs (word processing and database management). Ability to interact congenially with students.

Preferred qualifications: Previous experience in freshwater ecology and/or molecular ecology.

Relevant Links:

Department of Biological Sciences: http://bsc.ua.edu/ Center for Freshwater Studies: http://as.ua.edu/cfs/ University of Alabama: www.ua.edu Tuscaloosa, Alabama is a vibrant university community with numerous cultural and recreational opportunities available. The newly constructed Tuscaloosa Amphitheater, located on the banks of the Black Warrior River and just minutes from the UA campus, brings a variety of shows and musicians to the city. Recreational activities such as canoeing and hiking are quite popular in the nearby Black Warrior and Sipsey River natural areas, and the Talladega National Forest.

Salary is commensurate with experience. Visit UA's staff employment website at http://jobs.ua.edu for more information and to apply. All applicants should submit a cover letter, a statement detailing relevant research experience, contact information for three references, and a CV. Job close date 05/30/2013. EOE/AA

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Jennifer Howeth, PhD Assistant Professor Department of Biological Sciences Program in Ecology, Evolution, and Systematics

University of Alabama Box 870206 1106 Bevill Building, 201 7th Ave. Tuscaloosa, AL 35487-0206

http://bsc.ua.edu/jennifer-howeth/
jghoweth@as.ua.edu

UAlabama ResTech DrosophilaGenetics

The University of Alabama is seeking qualified applicants for a Research Technician to work in a Drosophila genomics lab. The successful candidate will assist the Principal Investigator (Laura Reed) in a 5-year NIH funded project to map the genetic basis of dietary variation in endophenotypes (e.g. gene expression, metabolites) relating to diabetes and obesity in Drosophila melanogaster. Bachelor of Science degree or higher in a discipline related to the position and one year of relevant experience required; some experience working with molecular genetic techniques is required. Must be willing to make at least a two-year commitment to the position. Visit Employment Opportunities at http://jobs.ua.edu for more information and to apply. EEO/AA

Laura K. Reed Assistant Professor Dept. of Biological Sciences University of Alabama, Tuscaloosa Office: 2330 SEC, Lab: 2322 SEC Mailing address: Box 870344, Tuscaloosa AL 35487

office: 205-348-1345 lab: 205-348-1368

lreed1@bama.ua.edu http://flygxe.ua.edu/ “Reed, Laura” <lreed1@ua.edu>

UBritishColumbia BiologyDepartmentHead

The Irving K. Barber School of Arts and Sciences at the University of British Columbia, Okanagan Campus, invites applications for the position of Head of Biology. This administrative Unit is one of eight Units within the Irving K. Barber School of Arts and Science and has a total of 21 faculty members and 6 staff members. Graduate students have access to two vibrant graduate programs: the Biology graduate program and the Biochemistry and Molecular Biology graduate program. Undergraduate programs include majors in Biology, Biochemistry, Ecology and Evolutionary Biology, Microbiology and Zoology.

The ideal candidate will be in the early stages of the Full Professor rank, although a senior Associate Professor may also be considered. The Head^{1}s position includes a faculty appointment. We are seeking a candidate with demonstrated excellence in research, teaching, leadership and management skills, with proven ability to lead and motivate faculty, staff, and students. Field of research specialization can be related to any area of Biology (including Evolutionary Biology) or Biochemistry. Desirable attributes include a strong record of published research and external funding as well as prior experience in academic administration and undergraduate and graduate education.

The Head will provide administrative, intellectual, and academic leadership of the Unit and will serve on the Faculty^{1}s Leadership Team. The Head is expected to: (i) oversee the overall operation of the Unit, including the budget (ii) ensure that courses are suitably staffed (iii) take an active role in advancing the Unit^{1}s programs and activities through curriculum and program review, (iv) foster collegial interaction among faculty members, (v) mentor members of the Unit, (vi) conduct annual evaluations of each faculty member in the Unit, and (vii) serve as the advocate for Unit members within the Faculty and the University. Direct experience with managing reappointment, tenure and promotion processes and familiarity with budget processes are considered assets. As a faculty member of the Unit, the Head will be expected to maintain an active research program in his/her chosen field, to supervise graduate students, and otherwise contribute to the Unit^{1}s teaching programs.

The position of Head will be available July 1, 2014 with a five-year renewable term. The Head reports directly to the Dean of Arts and Sciences. UBC hires on the basis of merit and is committed to employment equity. All qualified persons are encouraged to apply. We especially welcome applications from members of visible minority groups, women, Aboriginal persons, persons with disabilities, persons of minority sexual orientations and gender identities, and others with the skills and knowledge to engage productively with diverse communities. Government regulations require that Canadians and permanent residents of Canada will be given priority. All appointments are subject to budgetary approval.

UBC is one of the world's top universities. The university has two distinct campuses, one in Vancouver and one in Kelowna. UBC^{1}s Okanagan campus, located in the city of Kelowna, at the heart of the Okanagan Valley has over 8,400 students in six Faculties, including strong graduate programs at all levels. Kelowna is connected by direct flights to major Canadian and USA cities and the region is considered one of the most desirable regions to live in Canada.

For more information about the Faculty, see http://www.ubc.ca/okanagan/academic/welcome.html How to Apply Applicants should provide: A cover letter that clearly identifies all related administrative experience, including a statement of the candidate^{1}s philosophy or approach to leadership; an up-to-date curriculum vitae; statements of a program of research and of teaching interests; evidence of teaching ability; and the name, title, and contact information of three referees. Following the initial review of applications, candidates selected for further consideration will be asked to provide letters from the referees. All documents must be submitted as e-mail attachments and sent to recruitment.bsas@ubc.ca. Preferred formats are Microsoft Word (.doc) and Adobe Acrobat (.pdf). Please put the competition title (Head, Unit 2-13) on the subject line of the e-mail and state whether you are currently legally entitled to work in Canada. The deadline for applications is August 31, 2013.

Please direct inquiries to: Associate Dean Barbara Rutherford, Irving K. Barber School of Arts and Sciences (barbara.rutherford@ubc.ca)

michael.russello@ubc.ca

UCalifornia Davis Bioinformatics

The Ross-Ibarra laboratory (www.rilab.org) at the University of California Davis is seeking a bioinformatician to head a project involving parentage analysis, imputation, and phasing of genomes from two large mapping populations in a study of inbreeding depression in maize and its wild relatives.

The position description and application can be found here:

www.employment.ucdavis.edu/applicants/-Central?quickFinde159

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

UColorado TeachingEvolBiol

Science Teaching Fellow

The Department of Ecology and Evolutionary Biology (EBIO), at the University of Colorado, Boulder, invites applicants for the position of Science Teaching Fellow to assist with enhancing teaching and learning in our undergraduate courses.

Candidates should hold a doctoral degree in Biology, Biology Education or a related field and have excellent organizational, interpersonal communication, team building and collaboration skills. The candidates primary interest and some experience should be in science education. Experience in developing active learning curricula and coaching educators is highly desirable.

The successful candidate will collaborate with new faculty towards the following goals: formulate learning goals, develop an active learning-based curriculum that aligns with the learning goals, provide feedback on faculty teaching practices, and assess learning gains.

The salary for this 1-year appointment will be competitive and commensurate with experience. Applicants should submit a single pdf containing their CV, a statement of teaching philosophy, and the names, phone numbers, and email addresses of three individuals who can serve as references to Andrew Martin at the following email address: am@colorado.edu. To ensure full consideration, applications must be received by June 30, 2013. We seek someone to fill this position prior to the beginning of the fall 2013 semester.

The University of Colorado at Boulder is an Equal Opportunity/Affirmative Action Institution committed to cultural diversity and compliance with the Americans with Disabilities Act. Women and minorities encouraged to apply. We invite applications from qualified candidates who share our commitment to diversity. The University of Colorado conducts background checks on all final applicants being considered for employment.

Andrew Martin Professor University of Colorado A mind once stretched by a new idea never regains its original dimensions.

Andrew Martin <Andrew.Martin-1@colorado.edu>

UCopenhagen Bioinformatics

Closing soon!!!

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/ KA-Marske@bio.ku.dk

UGeorgia ResearchTech

RESEARCH TECHNICIAN UNIVERSITY OF GEORGIA, ATHENS, GA

I anticipate hiring a research technician with an immediate start date. My laboratory conducts research in evolutionary and ecological genetics of invasive species.

Qualifications are an undergraduate degree in Biology or related field with 1 or more undergraduate or graduate courses in genetics, and some research experience. Experience with PCR and molecular biology protocols is necessary. Salary will be commensurate with experience.

I would prefer to hire a recently graduated undergraduate who is interested in working in an academic setting for at least a year before starting graduate school.

The working conditions, intellectual atmosphere, and facilities in Genetics at Georgia are excellent. Athens is a lovely and inexpensive place in which to live with all of the advantages of and culture of a 200 year-old university town. You may wish to look at the Department of Genetics' web site at: www.genetics.uga.edu . Applications will be accepted until a suitable candidate is found.

For more information, please contact me by e-mail at: mauricio@uga.edu

Interested persons should send by e-mail a letter of application, a CV and the name, phone number and e-mail address of 2 references.

Rodney Mauricio, Ph.D. Department of Genetics University of Georgia Athens, GA 30602-7223

Lab Web Page: http://www.genetics.uga.edu/-mauriciolab=0APIRE Grant Web Page: http://-www.genetics.uga.edu/pire

mauricio@uga.edu

UHelsinki ConservationBiol

University Lecturer conservation biology, with special emphasis on the ecological and evolutionary issues of conservation biology

Position announced on: May 13, 2013 Apply at latest on: Jun 14, 2013 Fixed-term: Permanent

Employer: Faculty of Biological and Environmental Sciences Department of Biosciences

The University of Helsinki is among the leading multidisciplinary research universities in the world and the most versatile institution of scholarship, education and intellectual stimulation in Finland. In addition to its 11 faculties, the University of Helsinki includes several independent institutes, some of which are jointly operated with other universities. Some 35,000 students are currently pursuing an undergraduate or postgraduate degree at the University.

The Department of Biosciences in the Faculty of Biological and Environmental Sciences, University of Helsinki, is Finland's largest and most prominent institution engaged in the research and teaching of the biosciences. The Department of Biosciences, based in the Viikki Science Park, is among the largest departments of the University. Its budget is EUR 24 million, and it employs over 300 people. The Department is divided into six divisions, namely those of biochemistry, ecology and evolutionary biology, physiology and neuroscience, plant biology, genetics, general microbiology. The Department coordinates the administration and provision of basic teaching for all students during the first few years of study, but each of the above major subject divisions are independently responsible for their teaching and research. The Department also offers a degree programme that provides students with the qualification of a biology teacher.

The Department of Biosciences invites applications for the position of

UNIVERSITY LECTURER

The field of the position is conservation biology, with special emphasis on the ecological and evolutionary issues of conservation biology.

The duties of the university lecturer include providing basic and intermediate level teaching, supervising and examining theses, conducting research in the field and attending to any other duties involving the discipline. Moreover, the duties include coordinating and developing teaching for international students.

According to the University of Helsinki Regulations, holders of university lectureships are required to possess an applicable doctoral degree, to have the ability to provide high quality research-based teaching and to supervise theses and dissertations. When assessing the qualifications of the applicants, attention shall be paid to scientific publications and other research results of scientific value, teaching experience and pedagogical training, the ability to produce learning materials, other teaching merits and, if necessary, a teaching demonstration.

University lecturers are required to be competent in the language in which they provide instruction. According to the Government Decree on Universities, university instructors must have at least satisfactory oral and written skills in Finnish and Swedish. Foreign citizens, non-native Finnish citizens or citizens who have not been educated in Finnish or Swedish may be exempted from this requirement without a separate application. To successfully attend to the duties of the position, appointees must also have good English skills.

The salary will be based on levels 5-7 of the job requirement scheme for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal work performance.

Applications must be accompanied by a CV, a list of publications and other documents that may be relevant to filling the position, or alternatively, an academic portfolio containing the above-mentioned documents. Applicants who do not intend to enclose an academic portfolio with their applications must enclose a brief written report of their qualifications which they deem relevant to the assessment of their teaching skills. Further information about the academic portfolio and assessment of teaching qualifications can be obtained from the Faculty Office or the Faculty's website, or from the following website: http://www.helsinki.fi/henkos/-academicportfolio/index.htm . Applications addressed to the head of the Department of Biosciences, together with the required enclosures, must be delivered to the following address: Registry of the University of Helsinki, P.O. Box 33 (Yliopistonkatu 4), 00014 University of Helsinki, Finland, or to hy-kirjaamo@helsinki.fi. The closing date for applications is June 14, 2013. (The Registry closes at 15.45 local Helsinki time.)

Further information may be obtained from Professor Veijo Kaitala, +358 9 19157723, veijo.kaitala@helsinki.fi.

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UOklahoma LabManager Metagenomics

Title of Position: Laboratory Manager - Research Associate

Position requires a Masters or higher degree in biological science related field, with at least five years of experience in genomics (metagenomics preferred). Strong organization skills and the ability to manage a genomics wet-lab is a must. Duties include next generation DNA sequencing library preparation, molecular cloning, extraction and amplification of degraded/low copy number DNA. Earliest start date: July 1, 2013. Salary: 50K plus fringe. Email resumes or CVs to Cecil M. Lewis, cmlewis@ou.edu, with "Laboratory Manager - Research Associate" in the subject line.

Located in Norman, Oklahoma, University of Oklahoma's Molecular Anthropology Laboratories specializes in anthropological genomics and metagenomics. Current projects include characterizing diverse host-associated microbiomes using biological samples collected from traditional indigenous communities, nonhuman primates, and archaeological "ancient" materials. An example of recent interviews: http:/-/ehp.niehs.nih.gov/121-a118/. Our labs are located in the SRTC (http://srtc.ou.edu/index.php), a new building with several research groups working in environmental genomics (e.g., http://ieg.ou.edu/) and genome sequencing (e.g., http://www.genome.ou.edu/-). Our building also houses part of OSCER, OU's supercomputer (http://www.oscer.ou.edu/). In 2008, CNN/Money Magazine ranked Norman as the sixth best small city within the United States.

cmlewis@ou.edu

UOulu Geneticist

Geneticist position at the University of Oulu, Finland

The Department of Biology at the at the University of Oulu (Finland) (www.oulu.fi/english/) invites applications for Senior research fellow position in genetics, a position for five years or permanent, depending on the qualifications. The duties include independent research, teaching, B.Sc., M.Sc. and Ph.D. student supervision and participation in departmental administration. The Biology Department has many research groups in and evolutionary and population biology and several in population genetics, with topics such as population genetics of adaptation of plants, and conservation genetics, statistical genetics. The applicant research should fit in this environment and complement the current research profile. In addition, the department includes animal physiologists and plant biologists. Please see details (in English) at http://www.hallinto.oulu.fi/yhallint/-kuulutus/26-04-13_sr_genetics.pdf .For further information, please be in touch with Outi.Savolainen@oulu.fi.

Outi Savolainen Department of Biology and Biocenter Oulu FIN-90014 University of Oulu +358(8)5531782

+358405168900 outi.savolainen@oulu.fi

Outi Savolainen <Outi.Savolainen@oulu.fi>

UPennsylvania Bioinformatics

Assistant Professor, Penn Institute for Biomedical Informatics

Posting Department:

Posted Date: 05/07/2013

Expire Date: 05/07/2015

To apply: http://www.med.upenn.edu/apps/faculty_ad/index.php/d3300

The Penn Institute for Biomedical Informatics at the Perelman School of Medicine at the University of Pennsylvania seeks candidates for an Assistant Professor position in the tenure track. The successful applicant will have experience in the field of bioinformatics research. Applicants must have an M.D. and/or Ph.D degree and have demonstrated excellent qualifications in research and education.

The faculty appointments will be at the Assistant Professor level in the tenure track in an appropriate department in the School of Medicine. Applicants are expected to establish robust independent funding for their research program.

This Institute is enabled by a recent multi-million dollar gift and focused on the science of biomedical informatics. The Institute will integrate informatics disciplines from bioinformatics, to translational, clinical, and public health informatics.

The University of Pennsylvania, founded by Benjamin Franklin, is a world-class research institution located near the center of Philadelphia. All of Penn's twelve schools are located within walking distance of one another. The Perelman School of Medicine at the University of Pennsylvania is one of the top ranked medical schools in the nation for research and NIH funding.

We seek candidates who embrace and reflect diversity in the broadest sense.

The University of Pennsylvania is an equal opportunity, affirmative action employer.

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/

tishkoff@mail.med.upenn.edu

URhodeIsland ConservationGenetics

Position #1 Research Associate I (NRS/Lab) position at the University of Rhode Island

Perform independent research work at the Regional Conservation Genetics Laboratory (RCGL) at the University of Rhode Island. Organize, coordinate, and supervise support staff, including volunteers and students, engaged on the project. This position is limited to 03/31/2014 with extension contingent on funding. Visit the URI jobs website at: https://jobs.uri.edu to apply and view complete details for job posting # (6001082). Please attach two documents (PDF) to the online Employment Application: (1) A cover letter, and (2) Resume, which includes the names and contact information of three references. Applications will close May 17, 2013. Only online applications will be accepted. The University of Rhode Island is an AA/EEOD employer and values diversity.

Office of Human Resources University of Rhode Island 80 Lower College Road Kingston, RI 02881 USA Phone: 401-874-2416 Fax: 401-874-5741 Humanres@etal.uri.edu

Position #2 Research Associate I (NRS/Field) position at the University of Rhode Island

Perform independent research work in support of the Regional Conservation Genetics Laboratory (RCGL) at the University of Rhode Island. Organize, coordinate, and supervise support staff, including volunteers and students, engaged on the project. This position is limited to 03/31/2014 with extension contingent on funding. Visit the URI jobs website at: https://jobs.uri.edu to apply and view complete details for job posting # (6001081). Please attach two documents (PDF) to the online Employment Application: (1) A cover letter, and (2) Resume, which includes the names and contact information of three references. Applications will close May 17, 2013. Only online applications will be accepted. The University of Rhode Island is an AA/EEOD employer and values diversity.

Office of Human Resources University of Rhode Island 80 Lower College Road Kingston, RI 02881 USA Phone: 401-874-2416 Fax: 401-874-5741 Humanres@etal.uri.edu

Sincerely, T.J.

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T.J. McGreevy Jr., Ph.D. Research Associate IV Director of the Regional Conservation Genetics Laboratory Department of Natural Resources Science Room 109 Coastal Institute in Kingston 1 Greenhouse Road University of Rhode Island Kingston, RI 02881 tjmcg@my.uri.edu office: (401) 874-4040 cell: (401) 481-6151 lab: (401) 874-5812

Thomas Mc Greevy Jr <tjmcg@my.uri.edu>

UTampa TeachingEvolBiol

Assistant Professor of Biology - Term

The Department of Biology in the College of Natural & Health Sciences at The University of Tampa invites applications for a full-time, renewable term (non-tenure-track) position as Assistant Professor beginning in August 2013. Position will have primary teaching responsibilities in Introductory Biology for science majors, non-science major courses, and potentially a course in the area of the applicants' expertise. Area of expertise for this position is open.

Review of applications will begin immediately and continue until the position is filled. Posting Date: 04-23-2013; Open until filled jobs.ut.edu/applicants/Central?quickFindQ856

Details below: The department is interested in attracting a broadly trained biologist to complement the existing faculty in biology. Opportunities for collaborative research involving undergraduates and current members of the faculty are possible using research space and equipment that may be made available by on-campus collaborators.

Candidates are expected to have a commitment to excellence in teaching and mentoring student research. A typical teaching load is 12 to 15 contact hours in a 14-week semester.

Ph.D. preferred (strong ABD/MS candidates considered), prior teaching and research experience with undergraduates is desirable. A personal commitment to quality undergraduate teaching and advising is essential.

The University of Tampa is a medium-sized comprehensive, private university that delivers challenging and high-quality educational experiences to a diverse group of learners. Located in the heart of one of the most dynamic commercial regions of Florida, the University has been providing education, training, and leadership skills to the Tampa Bay community through unique partnerships with business, government, the arts, and cultural entities for over 70 years. The University offers a wide array of study areas and pre-professional programs through a strong core curriculum rooted in the liberal arts, a residentially based educational experience, a commitment to an international focus, and a practical, experiential approach to learning. The University is growing and enrolls approximately 6900 students from 50 states and nearly 130 countries.

The College of Natural and Health Sciences offers rigorous, high quality curricula in biology, marine science, environmental science, chemistry, biochemistry, physics, forensic science, exercise science, public health, allied health, sport management and nursing; all designed to prepare students for challenges and opportunities that lie ahead. Our faculty are excellent teachers, both in the classroom and working with students on an individual basis. UT has invested heavily in the development of our college's teaching and research facilities and laboratories. Our college continually fosters relationships with organizations in the greater Tampa Bay area and elsewhere to provide students with the opportunity to pursue an internship, volunteer, or interact with professionals working in their chosen field. Each department also offers study abroad courses that students can take for credit toward their degree. For more information, see: http://www.ut.edu/natural-and-health-sciences . Applicants are electronic (see link below). Applicants will be requested to attach a cover letter, current curriculum vitae, a statement of research interest, teaching philosophy and a copy of your graduate transcript. In addition, applicants will be requested to enter name and email address for three (3) reference providers. Posting Date: 04-23-2013; Open until filled jobs.ut.edu/applicants/Central?quickFindQ856

nmb@berkeley.edu

UVirginia LabTech LizardEvol

The lab of Robert Cox in the Department of Biology at University of Virginia invites applications for a Laboratory Technician to assist with research on the evolution, ecology, and physiology of lizards. Research in the lab focuses on sexual conflict, sexual dimorphism, life-history evolution, quantitative genetics, animal physiology, and behavioral endocrinology.

The primary research responsibility is the care and maintenance of a large breeding colony of lizards, which includes training and coordinating student volunteers, overseeing the daily care of animals, maintaining equipment and cleaning cages, collecting and archiving data, and participating in research projects through data analysis and bench work potentially ranging from hormone assays to DNA extraction, PCR, and genotyping. Initial projects will be closely supervised with increased independence possible as experience and expertise are developed.

A Bachelor's degree in Biology or a related discipline is required at the time of hire. Strong organizational, computer, and communication skills are essential, and experience with animal care and basic molecular biology techniques are desirable.

Ideal start date would be between June and August of 2013. This position is for one year. Application materials should be received by May 16 for full consideration.

Further details and instructions for applying to this position can be found at the Jobs@UVa website:

https://jobs.virginia.edu Search for posting 0612071.

Questions about the position can be directed to Robert Cox (rmc3u@virginia.edu)

Questions about the application procedure can be directed to Mary Liberman (ml5ac@virginia.edu)

– Robert M. Cox Assistant Professor Department of Biology University of Virginia P.O. Box 400328 Charlottesville, VA 22904-4328

Office: (434) 982-1987 Lab: (434) 243-3399 047 Gilmer Hall http://faculty.virginia.edu/coxlab/ cox.robert.m@gmail.com

UZurich Evolution

The Faculty of Science at the University of Zurich invites applications for a

Professorship in Environmental Science / Ecology

at the Institute of Evolutionary Biology and Environmental Studies. The Institute conducts research in the fields of ecology, evolution, behaviour and the environment. We seek an outstanding and innovative ecologist who is familiar with evolutionary concepts. Examples of areas of interest are animal ecology, community ecology, conservation biology, and functional ecology.

The successful candidate will have a record of excellent research for their career stage. She or he will develop a strong, independent program of empirical research on animals or animal-plant interactions, and will contribute to graduate and undergraduate teaching (in English or German) in environmental science and ecology. The position will be filled preferentially at the level of associate or tenure-track assistant professor.

The University of Zurich provides generous research support, including earmarked funds for personnel and running expenses, and competitive start-up packages. Zurich offers a stimulating scientific environment, and extensive opportunities for collaborations. Switzerland provides excellent opportunities for external funding of research.

Application packages should include a cover letter, a full curriculum vitae (see http://www.ieu.uzh.ch/-static/documents/ for guidelines), a vision statement of research interests and the names and addresses of three potential referees. Applications should be addressed to Prof. Dr. Michael O. Hengartner, Dean of the Faculty of Science, University of Zurich, and submitted as a single PDF document at www.mnf.uzh.ch/ese by 20 June 2013.

For further information, please contact Prof. Dr. Barbara König, Institute of Evolutionary Biology and Environmental Studies, at barbara.koenig@ieu.uzh.ch, or visit the homepage at www.ieu.uzh.ch . The University of Zurich is an equal opportunities employer. Applications from women are particularly encouraged.

lukas.keller@ieu.uzh.ch

UppsalaU 10 EvolBiol

10 TENURE-TRACK ASSISTANT PROFESSORSHIPS OPEN AT UPPSALA UNIVERSITY

The Faculty of Science and Technology at Uppsala University makes a unique effort by seeking 10 junior research scientists at the very foremost international level within all of science and technology. The level of hire is equivalent to the US assistant professorship or the UK associate senior lecturer, with the possibility of promotion to associate professor / senior lecturer after four years of employment. The positions are open to any area of research within natural sciences and technology, including evolutionary biology broadly defined, and can be placed at any of our 10 departments. For EvolDir subscribers, these positions offer a possibility of becoming affiliated with our Evolutionary Biology Centre (see below).

Excellence and potential in research and teaching are the prime selection criteria. Each position comes with significant start-up funds. To be eligible, applicants must have received their doctoral degree no more than 7 years prior to the application deadline, which is June 23, 2013.

Uppsala University is the oldest university in Scandinavia and is ranked among the top-100 universities in the world. It is a complete university with all three major disciplinary domains and 10 different Faculties represented. The Faculty of Science and Technology has excellent infrastructure and laboratory facilities at dedicated campus areas where the working atmosphere is truly international, with regular recruitment of PhD students, post-docs and faculty from abroad. Uppsala is a vibrant college town conveniently situated close to Stockholm (and even closer to the Arlanda airport) with beautiful and easy accessible surroundings.

For evolutionarily oriented scientists, positions would be placed at our Evolutionary Biology Centre (EBC). EBC is a vibrant international research environment that hosts what might be the largest aggregation of evolutionary biologists in the world. Here, the Department of Ecology and Genetics (IEG) houses many renowned research groups covering a wide range of research themes in evolutionary ecology, evolutionary biology, genetics and genomics, limnology, biogeochemistry, conservation biology and molecular evolution.

More information about IEG can be found at http://www.ebc.uu.se/Research/IEG/ More information about EBC can be found at http://www.ebc.uu.se/ More information about the positions and research in science and technology in Uppsala can be found at http://teknat.uu.se/forskning/oppna-lektorat/ More information about Uppsala University can be found at http://www.uu.se A full announcement of these positions, including a description of the application procedure, is available at http://www.uu.se/jobb/teacher/annonsvisning?tarContentId=242814&languageId=1 We warmly welcome applications from candidates within the evolutionary biology community!

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Prof. Göran Arnqvist Animal Ecology Department of Ecology and Genetics Evolutionary Biology Centre University of Uppsala Norbyvägen 18D SE - 752 36 Uppsala Sweden

Email: Goran.Arnqvist@ebc.uu.se Phone: +46-(0)18-471 2645 Cell phone: +46-(0)70-2935032 Fax: +46-(0)18-471 6484 Homepage with PDF reprints and more at: http://www.anst.uu.se/goarn789/index.html Goran.Arnqvist@ebc.uu.se

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Vienna EvolutionaryPhysiology

In order to further develop the cooperation in organismic biology between the University of Vienna and the University of Veterinary Medicine, Vienna, and to strengthen integrative biology, both universities agreed to establish a joint professorship. They hereby announce the position of a

Full Professor of Physiology with a focus on Ornithology

(full-time permanent position under private law - University Law 2002 §98). Both universities intend to increase the number of women on their faculties, particularly in high-level positions, and therefore specifically invite applications by women. Among equally qualified applicants women will receive preferential consideration.

The applicant must have an outstanding record in systemic physiology of birds, ideally in combination with cellular and molecular mechanisms. A particular focus should be on the physiology of seasonal processes of birds and its relation to migration. We search for a researcher who combines skills in physiology, a systems-biology approach across levels of organization, and a lively interest in studying animals in their natural environments.

The applicant's expertise should also serve to complement existing research groups in the Department of Integrative Biology and Evolution of the University of Veterinary Medicine and in the Center of Organismal Systems Biology of the Faculty of Life Sciences of the University of Vienna, working in the fields of physiology, ecology, evolution and animal behaviour. Along with the establishment of a bird physiology research program, the applicant will lead the newly established Center for avian migration of Austria ("Österreichische Vogelwarte"). Further, the applicant is expected to participate in the curricula of BSc, MSc and diploma study programs of both universities. The documentation of adequate teaching experience (habilitation or equivalent) is expected. Both universities of Vienna are committed to expand English teaching. Successful candidates will have the following qualifications:

* PhD and post-doctoral experience at a university or other research institution (Austrian or equivalent international academic degree in the relevant field) * Outstanding research and publication record, with an excellent reputation as an active member in the international academic community (Habilitation (venia docendi) or equivalent international qualification in the relevant field is desirable) * Experience in designing, procuring and directing major research projects, and willingness and ability to assume the responsibility of team leadership * The ability to acquire third party funding for financing research in a substantial amount * Experience in university teaching, and willingness and ability to teach at all curricular levels, to supervise theses, and to further the work of junior academic colleagues * Experience in personnel management, organizational and communication skills

Both universities expect the successful candidate to acquire, within three years, proficiency in German sufficient for teaching in Bachelor programmes and participation in committees.

The University of Vienna and the University of Veterinary Medicine, Vienna offer:

* Attractive terms and conditions of employment with a negotiable and performance-related salary, associated with a retirement fund * a "start-up package" for the initiation of research projects * an attractive and dynamic research location in a city with a high quality of life and in a country with excellent research funding provision * Grant for relocation to Vienna, where appropriate

Candidates should send an application containing at least the following documents:

* Academic curriculum vitae * Brief description of current research interests and research plans for the immediate future * List of publications together with

a) specification of five key publications judged by the applicant to be particularly relevant to the advertised professorship together with an explanation of their relevance

b) PDF versions of these five publications provided either as email attachments or through URLs of downloadable copies

* List of talks given, including detailed information about invited plenaries at international conferences * List of projects supported by third-party funds * Short survey of previous academic teaching and list of supervised PhD theses

University professors will be classified according to the Collective Bargaining Agreement<http://personalwesen.univie.ac.at/kollektivvertrag-/mitarbeiterinnengruppen/> for University Staff into the salary group A1. The salary will be individually negotiated under consideration of the previous career development and in case of an appointment from

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Vienna ResAssoc EvolutionaryModeling

University Assistant (= Research Associate/Senior Postdoc), 6 years in Evolutionary Modeling at the University of Vienna

The mathematics and biosciences group (MaBS) at the University of Vienna is looking for a strong and highly motivated candidate for a university assistant position in evolutionary modeling. The research focus is flexible and includes work in population genetics or genomics, quantitative genetics, and evolutionary ecology. See the MaBS homepage (www.mabs.at) for further information on our research interests.

In recent years, Vienna has developed into one of the leading centers in evolutionary biology (www.evolvienna.at). In addition to a stimulating scientific environment, Vienna also offers an extraordinarily high quality of life. Affordable housing, excellent public transport, great restaurants, a range of international schools, two operas, two music centers, many theaters and museums in combination with a pleasant climate make Vienna one of the most attractive cities in Europe.

The successful candidate will have a record of high quality research in evolutionary modeling. S/he is expected to develop and maintain an independent research profile and to attract extramural funding. In addition to research, the candidate will contribute to teaching and supervise students. The position will be offered for 6 years and comes with a competitive salary. The starting date is October 2013 or later (negotiable).

Formal requirement is a PhD and a strong background and interest in quantitative evolutionary research (analytical or computational modeling). Prior postdoc experience and the proven ability to attract funding are desirable. The working language is English, German skills are not essential.

Applications should include: # Cover letter # CV with publication list and grants, # summary of past and future research plans, # teaching experience, # names and email addresses of three potential referees.

Full applications (preferably as a single pdf) should be sent via the Job Center to the University of Vienna (http://jobcenter.univie.ac.at, email: jobcenter@univie.ac.at), with cc to Joachim Hermisson (joachim.hermisson@univie.ac.at) # no later than June 9th, 2013 # referenced to the identification number 3988. Informal inquiries (encouraged) should be sent to Joachim Hermisson.

Joachim Hermisson Professor for Mathematics and Biosciences University of Vienna Department for Mathematics Nordbergstr. 15, 1090 Vienna, Austria and Max F.Perutz Laboratories Dr.-Bohrgasse 9, 1030 Vienna, Austria phone: +43 (0) 1 4277 50648 email: joachim.hermisson@univie.ac.at www.mabs.at joachim.hermisson@univie.ac.at

Other

ASN regional meetings

The American Society of Naturalists (ASN) invites organizers of local or regional conferences specializing in the areas of ecology and evolution to apply for funds to enhance and support student participation in their meetings.

Previous awards in the range of $500-$1500 have been used to support plenary speakers, provide student presentation awards, and reduce registration fees for ASN student members.

Please send a short letter describing the intended uses of funds to the chair of the ASN Regional Liaison Committee, Mike Whitlock (whitlock@zoology.ubc.ca). Requests should be made at least a month before the registration opens for the meeting and include information about the expected size and focus of the meeting. Informal inquiries in advance of a written proposal are welcome.

Michael Whitlock whitlock@zoology.ubc.ca

Department of Zoology - University of British Columbia 6270 University Blvd, Vancouver, BC V6T 1Z4 CANADA phone: (604) 822-2069 FAX: (604) 822-2416

Michael Whitlock <whitlock@zoology.ubc.ca>

BBSRC futureFunding EvolBiol

Dear all,

One of the major UK Research Councils, the Biotechnology and Biological Sciences Research Council, is asking for opinions on what the most important research areas and technological developments in biosciences might be over the next five to 10 years. The BBSRC is an important source of funding in the UK for evolutionary biology (especially evolutionary genetics) and animal behaviour, and this survey provides us in the evolution community with the opportunity to highlight the importance of understanding evolutionary change. Without appreciating the role of evolution, many of the proposed solutions to the crises of food security, climate change, and emerging diseases and pests, may fail to deliver.

The BBSRC says the survey results will inform its long-term strategic plan and will be discussed by the council and its advisory network. Anyone can take part in the survey, but the BBSRC says it is particularly keen to hear from PhD students and postdoctoral researchers (so do please pass it on).

The survey is open until 3 June and can be accessed at:

http://www.bbsrc.ac.uk/news/policy/2013/130517-n-strategic-workshop-survey.aspx Dr David M Shuker Lecturer in Behavioural Ecology School of Biology University of St Andrews St Andrews KY16 9TH United Kingdom

dms14@st-andrews.ac.uk

Cameroon VolFieldAssistant PopBiology

VOLUNTEER FIELD ASSISTANT for population biology and behavioral ecology fieldwork in CAMEROON, Sept. through Dec. 2013

We are seeking a field assistant for three months (mid-September through mid-December) to help with a host-parasite mimicry study on the brood parasitic indigobirds and their hosts the estrildid finches. Fieldwork will be centered around a small town in central CAMEROON. The objective of the study is to gain an understanding of the evolution of mimicry between the parasite nestlings and the host nestlings in sympatric species. Fieldwork will include nest searching, song recording and mist-netting birds.

Applicants must be willing and able to walk long distances in very hot, dry weather and to tolerate rustic accommodations. Previous field experience with birds is a plus. Assistants must provide their own airfare to Cameroon, however travel within Cameroon, room, and board will be provided.

Please email a cover letter that addresses your qualifications for this position, a CV with undergraduate GPA, and contact information for 3 references. Review of applications will begin immediately and continue until position is filled.

Email materials and questions to Allison Lansverk, lansverka12@students.ecu.edu.

“Lansverk, Allison” <lansverka12@students.ecu.edu>

Campanula samples

Dear EvolDir members

We are starting a project on the evolutionary history and biogeography of the Campanula rotundifolia group (angiosperm, Campanulaceae), which includes some 50-60 morphologically-related taxa with different ploidy levels.

We are looking for leaf tissues and seeds from populations sampled across the European mountain ranges (i.e. between the Spanish Sierra Nevada and the Carpathians) for next-generation sequencing and flow cytometry analyses.

We would like to ask you for help with plant collection in the field. >From each population, we need EITHER well-dried leaf material (silica gel can be provided upon request) from 5 individuals and a well- preserved herbarium voucher, OR 5 mature fruits (capsules) from 5 different individuals. The plants belonging to this group are generally easy to separate from other Campanula species (a specific determination is not necessary at that stage). A detailed sampling protocol will be sent to all people willing to support this project.

It would be amazing if you could contribute with some samples growing close to your working place or collected during forthcoming field trips. Contact addresses and plant localities are also highly appreciated.

Many thanks in advance for your help!

Best wishes,

Guilhem Mansion (1) Ludo Mueller (2) Federico Luebert (2)

(1) Freie Universität Berlin, Botanischer Garten und Botanisches Museum Berlin-Dahlem, Königin-Luise-Straße 6 - 8, 14195 Berlin, Germany (E-mail: g.mansion@bgbm.org) (2) Freie Universität Berlin, Institut für Biologie - Botanik, Altensteinstraße 6, 14195 Berlin, Germany (E-mail: ludo.muller@fu- berlin.de; fluebert@zedat.fu-berlin.de)

Annex - Species included in the Campanula rotundifolia group C alaskana (A. Gray) Wight C albanica Witasek C baumgartenii Becker C baumgartenii subsp. beckiana (Hayek) Podlech C bertolae Colla C bohemica Hruby C caespitosa Scop. C cantabrica Feer C carnica Schiede C carnica subsp. puberula Podlech C cochleariifolia Lam. C excisa Schleich. C ficarioides Timb.-Lagr. C forsythii (Arcang.) Podl. C fritschii Witasek C gentilis Kovanda C giesekiana Vest C gracillima Podl. C hercegovina Degen & Fiala C herminii Hoffmanns. & Link C hispanica Willk. C intercedens Witasek C jaubertiana Timb.-Lagr. C jurjurensis Pomel C justiniana Witasek C longisepala Podl. C macrorhiza Gay ex A. DC. C marcenoi Brullo C marchesettii Witasek C micrantha Bertol. C moravica (Spitzner) Kovanda C petiolata A. DC. C pindicola Aldén C pollinensis Podl. C praesignis Beck C precatoria Timb.-Lagr. C pseudostenocodon Lacaita C pulla L. C raineri Perpenti C rhomboidalis L. C romanica Savul C rotundifolia L. C ruscinonensis Timb.-Lagr. C sabatia De Not. C scheuchzeri Vill. C serrata (Kit.) Hendrych C serrata subsp. recta (Dulac) Podlech C stenocodon Boiss. & Reuter C tanfanii Podl. C tatrae Borbas C trojanensis Kovanda & Ancev C velebitica Borbás C willkommii Witasek C witasekiana Vierh. C xylocarpa Kovanda

Dr Guilhem Mansion

Botanischer Garten und Botanisches Museum Berlin-Dahlem Freie Universität Berlin Königin-Luise-Straße 6 - 8 14195 Berlin

http://www.bgbm.fu-berlin.de/bgbm/STAFF/wiss/-Mansion/default.htm Email: g.mansion@bgbm.org Tel.: +49 30 838 50 128 Fax: +49 30 838 50 218

“Mansion, Guilhem” <g.mansion@BGBM.ORG>

ConGenOmics TravelGrants

TravelGrants - ConservationGenomics

Dear colleagues,

The European Research Networking Programme “ConGenOmics”, supported by the European Science Foundation, invites applications for travel grants intended to foster collaborations between European researchers working on topics related to the Programme.

We will support the exchange of researchers, ideally targeting at early careers researchers such as PhD students and postdocs. We invite applications for short visits (1-2 weeks) as well as longer exchange visits (up to 4 months) to foster scientific interactions between institutions from different countries. The planned visits should be directly relevant to the scope of the ConGenOmics network, which include topics such as:

- Development and transfer of genomic knowledge and approaches in a conservation context

- Experimental study of the (genomic) mechanisms behind important biological processes of relevance for conservation

- Application and development of data handling and processing strategies in conservation genomics

- Application of community and metagenomics in conservation biological context

After assessment of scientific merit and relevance to the ConGenOmics network, priority will be given to applications in the following order:

- knowledge exchange between contributing countries

- knowledge exchange between a contributing country and a non- contributing ESF member country or the associated USA Ecogenomics network Ecological Genomics Institute (EGI) at Kansas State University (KSU).

- knowledge exchange between a contributing country and a non-ESF member country in Europe

- knowledge exchange between a contributing country and any country not covered by 1-3

Further information and instructions on how to apply are available at

http://www.ru.nl/congenomics/grants-application/-travel-grants/ Deadline for submission: 31 May

2013

philippine.vergeer@wur.nl

E-Z96 Plant DNA Kit

Dear evoldir members, anybody has used the Plant DNA kit E-Z 96of OMEGA ?, What about the amount and quality of the DNA extracted?

Thank in advance,

Miguel Angel González– Associate ResearcherDepartment of Molecular Biodiversity and DNA BankJardín Botánico Canario "Viera y Clavijo"Unidad Asociada al CSICCabildo de Gran Canaria

canariensis750@hotmail.com

Evolution Video Contest Deadline May31

NESCent Evolution Film Festival - Submission Deadline Approaching (May 31st)!

Scientists and science educators of all stripes (students, postdocs, faculty, and full- or part-time science communicators) 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, graduate - your 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>

Evolution deception

Evolutionary consequences of deception: Call for submissions

The Journal CURRENT ZOOLOGY (ISSN 1674-5507, http://www.currentzoology.org) is preparing one special issue, Evolutionary consequences of deception, for the first issue of 2014. Deadline for abstract submission: July 1 , 2013; Deadline for manuscript submission: Sept 10, 2013.

Title and abstract submissions should be sent to the guest editors, Dr. Lindstedt-Kareksela Carita <carita.a.lindstedt@jyu.fi> and Dr. Mikael Mokkonen >. You may send your manuscript now or by the deadline. Manuscripts should be submitted to the special column via CURRENT ZOOLOGY webpage at http://www.currentzoology.org, or via ScholarOne Manuscripts http://mc03.manuscriptcentral.com/currentzoology. Manuscripts received after the deadline will be considered as submissions for regular issues.

Submitted papers should not have been published previously, nor will be under consideration for publication elsewhere. Submitted manuscripts are accepted with the understanding that they are subject to peer review and editorial revision. There are no publication or processing charges. Please visit the Instructions for Authors before submitting a manuscript (http://www.currentzoology.org/instruct.asp . Dr. Carita Lindstedt-Kareksela

Department of Biological and Environmental Sciences University of Jyväskylä P.O. Box 35 FIN-40014 University of Jyväskylä email: carita.a.lindstedt@jyu.fi

Experimental design EEB textbook answers

... "Experimental Design for the Life Sciences" by Graeme Ruxton and Nick Colegrave, published by Oxford. This book has been advocated by many people (26 so far!, actually almost everyone who has replied to my original email). It seems to be the community's clear favorite. Some folks suggested complementing it with some selected readings from here and there, most notably with Hurlbert's 1984 paper of Pseudoreplication. Now let's see what my students say... Rafa

——– Mensaje original ——– Asunto: introductory text for experimental design in EEB Fecha: Mon, 22 Apr 2013 19:17:23 +0200 De: Rafael Rubio de Casas <rubiodecasas@ugr.es> Para: evoldir@evol.biology.mcmaster.ca

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

rubiodecasas@ugr.es

Fish pathogen samples

I am looking for DNA samples from two different fish pathogens to be used as positive controls for environmental sampling. The pathogens of interest are Flavobacterium psychrophilum and Saprolegnia ferax. If you have DNA samples that you would be willing to donate, or if you can suggest someone for me to contact, please send me an email (matt.lemay@ubc.ca).

Best regards,

Matt Lemay

PhD Candidate, University of British Columbia (Okanagan Campus)

matt.lemay@ubc.ca

Invisorb DNAPlantKit

Dear evoldir members, since there are few people that have replied about the Plant DNA kit E-Z 96of OMEGA, and the memebers that have used this kit have not obtained "excellent" results. Has anyone used the DNA extraction kit of Invisorb - DNA Plant HTS 96 kit/C?, and what about the amount and quality of the DNA extracted?

Thank in advance, Miguel Angel

– Associate ResearcherDepartment of Molecular Biodiversity and DNA BankJardín Botánico Canario "Viera y Clavijo"Unidad Asociada al CSICCabildo de Gran Canaria

canariensis750@hotmail.com

Jaenike 1978 Evo Theo

Dear all,

I am looking for a often-cited, but hardly accessible paper by John Jaenike (1978, An hypothesis to account for the maintenance of sex within populations. Evol. Theor. 3: 191-194.) If you by any chance have a pdf for this paper in your collection could you please send me a copy?

Many thanks, Yun

ytao3@emory.edu

LGBTQ

Folks,

I'm collaborating on a survey of the experiences of LGBTQ individuals working in science, tech, engineering, and math, and I'm hoping that the EvolDir community will help us share it with as many people as possible. We're using a "snowball sample" distribution model, in which we as respondents to help distribute links to the survey to their own professional and personal networks, so we can hear from as many people as possible.

There's more information below my signature, or you can go directly to the survey website, www.queerstem.org, to learn more, take the survey, and find out how to help spread the word.

thanks! Jeremy Yoder

—- Jeremy B. Yoder Postdoctoral Associate University of Minnesota Department of Plant Biology

www.jeremybyoder.com jbyoder@umn.edu

Sent with Sparrow (http://www.sparrowmailapp.com/?sig)

In the fields of science, technology, engineering and mathematics (STEM), the social experiences of lesbian, gay, bisexual, transgendered, or queer (LGBTQ) professionals are often overlooked. Those of us who work in STEM research or teaching know that LGBTQ colleagues are out there, if we know where to look, but we know very little about the LGBTQ folks who work in STEM, as a group. Basic, general information regrading the following questions is hard to come by:

What do we study? What kinds of institutions do we work at? What kinds of communities do we live in? What degree of acceptance and support have we found in our chosen career fields?

We are conducting a new, nationwide survey to begin to answer some of these questions, by eliciting feedback from as large a sample of LGBTQ folks working in STEM fields as possible. By participating, you will contribute to efforts to document the contributions of LGBTQ individuals to STEM fields and inform advocacy efforts to improve occupational experiences.

Although we welcome as much feedback as possible, please note that this survey is primarily targeted toward individuals who have completed an initial Bachelor's or Technical degree and are working in a STEM field within or outside of academia. Undergraduate experiences are unique and several quality studies exist regarding LGBTQ identity across fields of study at the postsecondary level–with this survey we aim to fill a different gap in the field.

The survey should take about 15-20 minutes to complete, and will ask about your research, your career path, your gender identity and sexual orientation, and your experience at the institution where you work and the community in which you live.

Thank you in advance for your valuable feedback!

Take the survey here: http://www.queerstem.org/p/take-survey.html jbyoder@gmail.com jbyoder@gmail.com

LilyLeafBeetle samples

Dear Evoldir members,

We are investigating the route(s) of invasion of the lily leaf beetle (Lilioceris lilii) in North America.

We would be grateful to anyone willing to send us ethanol-preserved samples (15-30 individuals) from Eurasia.

This conspicuous red insect lives exclusively on lilies (Lilium) and fritillary (Fritillaria), you may have seen it in your garden or in public parks.

(http://invasives.biodiversityireland.ie/wp-content/uploads/lily_leaf_beetle-U.S-fact-sheet.pdf)

Please contact me for further information ('collection kit', mailing addresses, etc).

Alessandro Dieni, Candidat Msc.

Laboratoire Jacques Brodeur - Institut de Recherche en Biologie Végétale Université de Montréal 4101 Sherbrooke Est - Bureau G202 Montréal, Qc, Canada, H1X 2B2

Téléphone (514) 343-6111 #82548 Courriel : alessandro.dieni-lafrance@umontreal.ca

Alessandro Dieni <a.dieni.umontreal@gmail.com>

Megabalanus coccopoma Micros

EvolDir,

I am working on the population genetic structure of the Titan Acorn Barnacle, Megabalanus coccopoma. Currently we are hoping to discover if microsatellites have already been designed for this species. If you have any knowledge of microsatellite primers for this species or if you know of a primers for a related species that have worked with M. coccopoma I would love to hear from you.

Thanks, Alicia Reigel

Alicia Reigel Georgia Southern University ar04609@georgiasouthern.edu

Alicia Reigel <ar04609@georgiasouthern.edu>

NGS dataset inquiry

Dear all,

My name is Enrique Gonzalez and I am developing a pipeline to analyse population structure from NGS dataset as part of my PhD thesis. I was searching for several NGS raw files (in .fna and .qual or .fastq) to test my pipeline, but I didn't find nothing. I only found papers on this topic and supplementary material are tables and more tables.

Do you have these kind of files? If you have fasta and quality files (or fastq files), could you use your data to test it, please?

Thanks for your attention and sorry for the inconveniences

Best regards,

Enrique

Enrique Gonzalez-Tortuero Department Biology II Evolutionsökologie Ludwig-Maximilien-University, Munich Grosshaderner Strasse 2 82512 Planegg-Martinsried, Germany email: tortuero@bio.lmu.de

Enrique Gonzalez Tortuero <tortuero@biologie.uni-muenchen.de>

Paper by Muck Lampert

Dear Members,

does any one have access to the paper

P Muck, W Lampert. 1984 An experimental study of the importance of food conditions for the relative abundance of calanoid copepods and cladocerans. I. Comparative feeding studies with Eudiaptomus gracilis and Daphnia longispina. Archiv für Hydrobiologie. 66 (2) 157-179.

If so, I would be grateful if you could send me a pdf copy of the paper.

Best regards

Miguel

Miguel Barbosa Visiting Postdoctoral Researcher Scottish Oceans Institute School of Biology University of St Andrews KL16 8LB Scotland

“Miguel Barbosa(Gmail)” <migosas@gmail.com>

Phyloseminar PhilHugenholtz Jun27

Next talk: Carl Woese's grand view of life that just keeps getting grander“ Phil Hugenholtz (University of Queensland)

Most microorganisms cannot be grown in pure culture (or at least not easily). This has been apparent for decades by comparing the number of cells seen under a microscope to the fraction of those cells that will grow into colony forming units (typically <1%). The objective classification of cellular life by comparative rRNA analysis pioneered by Carl Woese provided the first grand view of the tree of life and also provided the reference framework upon which his friend and colleague, Norman Pace, developed ways to directly survey microbial communities via their rRNA sequences without the need to grow them. This put our degree of ignorance of the microbial world into perspective: dozens of major microbial lineages have emerged over the last 20 years that lack even a single cultured representative. New approaches, such as deep metagenomics and single cell genomics, are now transforming the rRNA-based phylogenetic outlines of the tree of life into a fully-fledged genome-based view of the tree. I will present a recent snapshot overview of the genome tree of the bacterial and archaeal domains and examples of functional insights in the context of a more complete view of microbial evolution.

West Coast USA: 16:00 (04:00 PM) on Thursday, June 27 East Coast USA: 19:00 (07:00 PM) on Thursday, June 27 UK: 00:00 (12:00 AM) on Friday, June 28 France: 01:00 (01:00 AM) on Friday, June 28 Japan: 08:00 (08:00 AM) on Friday, June 28 New Zealand: 11:00 (11:00 AM) on Friday, June 28

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

SNP heat stress

Dear All,,

I am about develop a project detecting heat stress genes in local sheep. I hope that an advice is avilabe about SNP chips or specific marker primers that could do so.

Are you awarewhether SNP chips of Sheep consortium/Illumina could do so.

Kindest regards,

Raed

Dr. Raed Al-Atiyat Animal Breeding and Genetics Animal Sci. Dep., Agriculture Faculty Mutah University, Jordan. Ph(W): +962 3 2372380 Ext 6555 Fax: +962 3 2323 154 Mobile: +962 777926168

Raed al-atiyat <ratiyat2003@yahoo.com.au>

Software BORICE

Dear EvolDir,

I would like to announce the release of the BORICE 1.0 software package. BORICE (Bayesian Outcrossing Rate and Inbreeding Coefficient Estimation) is free software developed to estimate the mean outcrossing rate and inbreeding coefficient of populations from progeny arrays using Bayesian methods. BORICE is compatible with both Windows and Mac OS X. To learn more about how this software works, its uses, and for the purposes of citing this software, please refer to the following publication:

Koelling, V. A., P. J. Monnahan, and J. K. Kelly. 2012. A Bayesian method for the joint estimation of outcrossing rate and inbreeding depression. Heredity 109: 393-400. doi:10.1038/hdy.2012.58

The BORICE software and supporting documents can be downloaded at: http://www2.ku.edu/~eeb/faculty/kellyj.shtml Vanessa Koelling IRACDA Postdoctoral Fellow The University of Kansas Dept. of Ecology and Evolutionary Biology 5032 Haworth Hall 1200 Sunnyside Ave. Lawrence, KS 66045 vkoelling@ku.edu 785-864-3848

vkoelling@ku.edu

nextRAD

SNPsaurus announces launch of nextRAD genotyping

Enables genotyping by sequencing on low input samples

May 15, 2013. SNPsaurus, a genomic services company based in Eugene, Oregon, today announced the launch of their nextRAD genotyping platform. The nextRAD (Nextera-tagmented reductively-amplified DNA) marker platform is designed for genotyping large populations and for samples with limited availability of genomic DNA.

“The distinguishing feature of nextRAD compared to other genotyping-by-sequencing methods is that it does not use restriction enzymes to reduce the complexity of the genome.” said SNPsaurus founder Eric Johnson. “This allows us to make high quality sequencing libraries that sample thousands to hundreds of thousands of loci across a genome from less than 10 ng total genomic DNA.”

Director of Research Paul Etter said, “We tried to design nextRAD for the rapidly increasing capabilities of next-generation sequencers. It has the throughput for genotyping thousands of samples because of the streamlined protocol and the ability to multiplex hundreds of samples in a lane of a sequencer.”

SNPsaurus also unveiled their nextRAD Project Explorer, at http://snpsaurus.com/project/, an online tool for exploring the parameters of a genotyping project, from low-coverage mapping of recombinant inbred lines to high-coverage genotyping for creating genetic maps, and getting a project price estimate.

SNPsaurus has licensed nextRAD technology from the University of Oregon.

About SNPsaurus

SNPsaurus is a privately owned genomic services company founded in 2013. Based in Eugene, Oregon, SNPsaurus works with researchers to rapidly provide high-quality genotyping data.

contact:

Eric Johnson, founder

<eric@snpsaurus.com>

PostDocs

Ames Iowa InfluenzaEvolution

Post Doctoral Associate Vacancy

The vacancy is assigned to the Intervention Strategies to Control Viral Diseases of Swine project, Virus and Prion Research Unit, National Animal Disease Center, Ames, Iowa. The incumbent's overall responsibility is to evaluate the genetic evolution of influenza A viruses (IAV) identified in the US Department of Agriculture (USDA) swine influenza virus (SIV) surveillance system by sequence analysis and computational biology tools and pair with in vitro and in vivo characterization of selected viruses. Identifying the relative representation of subtypes, phylogenetic types, and whole genome variants in the swine population in geographic and temporal contexts will allow monitoring of the genetic evolution of IAV in swine. The resulting data will provide scientific based approaches for IAV intervention strategies, vaccine and diagnostic test development, and pandemic preparedness. The research assignment requires a PhD degree with emphasis on bioinformatics and computational biology with additional knowledge of virology, microbiology, and research techniques.

The incumbent's specific objectives within the research assignment are to:

1. Participate with a team of virologists, diagnosticians, and bioinformaticists to assemble, validate, and deposit fully assembled sequences into GenBank or other selected databases from high throughput next generation sequence techniques and/or traditional Sanger sequencing. 2. Conduct computational evolutionary biology analyses with fully assembled swine IAV sequences in the context of contemporary and historical isolates for determination of phylogenetic relationships, lineages, interspecies transmission, and/or reassortment events. Adapt existing database(s) for efficient management of swine IAV surveillance data. 3. Interact and liaise with National Veterinary Services Laboratory staff to transfer knowledge and skills as appropriate, with National Surveillance Unit staff for data management, and with NADC scientific staff for associated in vitro and in vivo study of select SIV isolates.

Contact: Amy L. Vincent DVM, PhD National Animal Disease Center, USDA-ARS 1920 Dayton Avenue Ames, IA 50010

(515) 337-7557 amy.vincent@ars.usda.gov

Amy L. Vincent DVM, PhD National Animal Disease Center, USDA-ARS 1920 Dayton Avenue Ames, IA 50010

(515) 337-7557 amy.vincent@ars.usda.gov

"Vincent, Amy" <Amy.Vincent@ARS.USDA.GOV>

AuburnU Phylogenomics

Postdoctoral Fellow in Metazoan Phylogenomics at Auburn University

We are looking for a postdoc to work on phylogenomics analyses of higher-level metazoan groups, especially annelids. The successful candidate should have knowledge of high-throughput sequencing (i.e., Illumina and/or comparable) approaches for transcriptome and genomic data. They will be expected to be proficient with shell scripting, BioPerl, and/or Biopython. Duties will include pipeline development, analyses of existing and/or new data, and assisting others with bioinformatics needs. The individual will be expected to produce first-authored papers as well as collaborate on others. This is a one-year position with the possibility of renewal pending satisfactory work.

The laboratory is jointly operated by Dr. Scott Santos and Dr. Ken Halanych. Information about the laboratory can be founds at:

http://www.auburn.edu/academic/cosam/-departments/biology/molette_lab/index.htm Applicants must have a Ph.D. in an appropriate field. The candidate selected for this position must be able to meet eligibility requirements to work in the United States at the time the appointment is scheduled to begin, continue working legally for the proposed term of employment; excellent communication skills required. Women and minorities are strongly encouraged to apply.

This announcement is informal in nature and candidates of interest will be asked to submit a formal application for complete consideration.

If interest please send a CV and a statement of interest to Ken Halanych at Ken@auburn.edu (please note our mail system is limited to 25Mb messages). Review of applications will begin 20 May 2013, and will continue until a suitable applicant is found.

Kenneth Halanych <ken@auburn.edu>

Berlin ConservationGenetics Repost

Because of formatting errors in the previous announcement, this is a repost of an announcement for a vacant postdoc position at the Freie Universitat Berlin:

Full time position (E 13 TV-L FU), limited to 1 year

The Botanic Garden and Botanical Museum Berlin-Dahlem is carrying out research projects and conservation measures on threatened plants of Germany. The core of these activities is formed by a new research and development project that has been developed in cooperation with and is financed by the German Federal Agency for Nature Conservation. Within this project, a selection of threatened plants that are native in Germany will be analyzed with molecular methods. Based on the genetic variability and phylogeographic history of populations, conservation scenarios will be elaborated. The project has been developed in cooperation with and is financed by the German Federal Agency for Nature Conservation.

We are currently seeking a dedicated postdoc for developing a scientific program on “In situ and ex situ conservation of plants” for our institution and linking it up with existing projects and activities in our focal area “Biodiversity of the Euro-Mediterranean Area” and in the “Dahlem Seed Bank”. Within this framework, the successful applicant will be supported in conducting own research in conservation genetics and in raising additional funds for the continuation of his/her work at our institution.

Requirements:

University degree in biology or related fields Desired qualifications:

Knowledge and deep interest in conservation genetics

Experience with relevant methods in populations genetics and phylogeography, e.g. AFLP and microsatellite screening

Good general knowledge of statistics and statistical software (e.g. R)

Very good command of German and English

Motivation and ability to work in an interdisciplinary team

Please send your application and documents (CV, certificates) with the reference code “Ex-Situ/In-Situ” until 27 May 2013 to:

Freie Universitat Berlin Zentraleinrichtung Botanischer Garten und Botanisches Museum - AV - Konigin-Luise-Str. 6-8 14195 Berlin

For further information please contact Dr Cornelia Loehne (c.loehne@bgbm.org; Tel. +49 30 838 50135). The original announcement (in German) can be found here: http://www.fu-berlin.de/-service/stellen/st_2013/st_20130429.html Ludo Muller <ludo_muller@yahoo.com>

Berlin PostdocConservationGenetics

Full time position (E 13 TVâL FU), limited to 1 year

The Botanic Garden and Botanical Museum BerlinâDahlem is carrying out research projects and conservation measures on threatened plants of Germany. The core of these activities is formed by a new research and development project that has been developed in cooperation with and is financed by the German Federal Agency for Nature Conservation. Within this project, a selection of threatened plants that are native in Germany will be analyzed with molecular methods. Based on the genetic variability and phylogeographic history of populations, conservation scenarios will be elaborated. The project has been developed in cooperation with and is financed by the German Federal Agency for Nature Conservation.

We are currently seeking a dedicated postdoc for developing a scientific program on “In situ and ex situ conservation of plants” for our institution and linking it up with existing projects and activities in our focal area “Biodiversity of the EuroâMediterranean Area” and in the “Dahlem Seed Bank”. Within this framework, the successful applicant will be supported in conducting own research in conservation genetics and in raising additional funds for the continuation of his/her work at our institution.

Requirements:

University degree in biology or related fields Desired qualifications: Knowledge and deep interest in conservation genetics Experience with relevant methods in populations genetics and phylogeography, e.g., AFLP and microâsatellite screening Good general knowledge of statistics and statistical software (e.g., R) Very good command of German and English Motivation and ability to work in an interdisciplinary team

Please send your application and documents (CV, certificates) with the reference code “ExâSitu/InâSitu” until 27 May 2013 to:

Freie UniversitaÌt Berlin Zentraleinrichtung Botanischer Garten und Botanisches Museum â AV â KoÌniginâLuiseâStr. 6â8 14195 Berlin

For further information please contact Dr Cornelia LoÌhne (c.loehne@bgbm.org; Tel. +49 30 838 50135). The original announcement (in German) can be found here: http://www.fu=E2=80=-90berlin.de/service/stellen/st_2013/st_20130429.html ludo.muller@fu-berlin.de

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CSIRO Canberra GenomicsAustralianFinches

Advertised Job Title: OCE Post Doc fellow in Evolutionary Rescue through Physiological Genomics of Australian Finches Salary Range: $81K to $88K plus up to 15.4% Superannuation Location:Australian National Wildlife Collection, Crace, Australian Capital Territory Tenure: 3 years Relocation Assistance: May be provided to the successful candidate Residency Status: All Candidates

Role Overview:

CSIRO offers PhD graduates an opportunity to launch their scientific careers through our Office of the Chief Executive (OCE) Postdoctoral Fellowships. Successful applicants will work with leaders in the field of science and receive personal development and learning opportunities.

Applications are invited for a three-year OCE Postdoctoral Fellowship in Evolutionary Rescue (ER). ER posits that evolution might occur sufficiently fast to arrest population decline under new environmental challenges and allow population recovery before extinction occurs. It stresses short-term evolutionary dynamics and focuses on genetic variants of large effects and absolute rather than relative fitness. This project addresses an emerging key area in Evolutionary Rescue - the genetic and genomic mechanisms of adaptation to climate change. It will use the tools provided by the published, annotated Zebra Finch genome as [3]roadmap[2] for genomic study of how the 17 other native Australian and five introduced finches have adapted to diverse climates. For example, two native species are confined to the continent[1]s wettest temperate forests, one to tropical forests, nine to monsoonal savannas, two to arid deserts and four to inland eastern Australia. Australian finches, therefore, are a comparative system with which we can explore genomic underpinnings of traits important in adaptation to climate change and gene-environment interactions in natural populations.

Duties and Key Result Areas:

The Postdoctoral Fellow will be mentored but will be responsible for:

-performing high-throughput genotyping and detection of thousands of single-nucleotide polymorphisms (SNPs) in up to 30 individuals across the geographical ranges of at least two finch species from arid, tropical and temperate climates -identify genomic regions under selection by outlier analysis or other methods to identify sites with high diversification relative to the finch species' genome -screening for patterns of gene expression across the geographical and climatic ranges of the finch species; -seek correlations among patterns of gene expression, outlier loci and environmental variables across species to pinpoint genomic regions of interest to climatic adaptation. -test whether genes and gene functions are differentially expressed and present/absent in species living in different climatic regimes (e.g., tropical and arid versus temperate zones). -Work with other team members and provide support and/or supervision of junior staff or students, etc. -Produce high quality scientific and technical outputs including journal articles, conference papers and presentations, patents and technical reports. -Develop innovative concepts and ideas for further research. -Regularly review relevant literature and patents. -Contribute to the effective functioning of the research team and help deliver upon CSIRO[1]s organisational objectives. -Participate in CSIRO[1]s postdoctoral training program.

*CSIRO's postdoctoral training program is a structured training program that will be developed between you and a CSIRO scientist. The program will allow you to further develop your skills in research, planning, management and communication. Training and development plans will be designed to develop fellows[1] capabilities to the level expected of an independent researcher. Each plan will include on-the-job and course-based development encompassing:

-Discipline-specific techniques and protocols -Professional growth -Project management -Communication and influencing skills -Working and collaborating with others

For further information please see http://-www.csiro.au/Portals/Careers/Postdoctoral-Fellowships/Postdoctoral-F ellowships.aspx

Selection Criteria: Please note: Under CSIRO policy only applicants who meet all the essential criteria can be appointed

Pre-Requisite: A PhD, or will shortly satisfy the requirements for a PhD degree, in a relevant scientific discipline. Owing to the terms of CSIRO Postdoctoral Fellowships, you must not have more than 3 years relevant post doctoral experience.

Essential Criteria:

1.Demonstrated ability to conduct innovative research in vertebrate genomics and informatics. 2.Demonstrated ability to develop experimental plans and pursue novel research approaches. 3.Demonstrated originality, creativity and innovation in solving problems and introducing new directions and approaches.

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CSIRO Canberra GenomicsClimateAdaptation

Advertised Job Title: OCE Postdoctoral Fellow ' Genomics of Climate Adaptability

Salary Range: $81K to $88K plus up to 15.4% Superannuation Location:Black Mountain, Canberra, Australia Tenure: Specified Term of 3 years Relocation Assistance: May be provided to the successful candidate

Residency Status: All Candidates

Role Overview: CSIRO offers PhD graduates an opportunity to launch their scientific careers through our Office of the Chief Executive (OCE) Postdoctoral Fellowships. Successful applicants will work with leaders in the field of science and receive personal development and learning opportunities.

The Position: There is mounting evidence for large differences between species in their ability to adapt to climate change. On one hand some climate specialists' confined to tropical or semi-tropical rainforest habitats may have negligible ability to adapt to altered climate regimes (see eg Nature 470: 479; Science 325:1244). On the other hand some generalist species may become invasive in the disrupted ecosystems generated by climate change. There would clearly be profound consequences for biodiversity management strategies if these patterns prove to be general phenomena.

CSIRO, University of Melbourne and Monash University have therefore begun a large, multidisciplinary collaboration to test a range of species for their phenotypic and genotypic abilities to adapt to altered climates, and to determine the genomic basis for these abilities. The initial focus has been on 20 Drosophila species but we are also extending our work to other species, including bactroceran fruit flies. The current position focuses mainly on potentially invasive species, including a mix of Drosophila and Bactrocera. Your primary responsibilities will include bioinformatic and biostatistical analyses of genome data but you will also have the opportunity to contribute to empirical studies, including some complementary metabolic work.

Duties and Key Result Areas:

The Postdoctoral Fellow will be mentored but will be responsible for:

- Undertake research on the comparative genomics of climate stress responses in Drosophila and Bactrocera. -Develop innovative concepts and ideas for further research. -Under broad supervision, assist in the planning and preparation of research proposals and carryout investigations requiring originality, creativity and innovation. -Cooperate with others to build an effective research team. -Work with other team members and provide support and/or supervision of junior staff or students, etc. -Produce high quality scientific and technical outputs including journal articles, conference papers and presentations, patents and technical reports. -Regularly review relevant literature and patents. -Contribute to the effective functioning of the research team and help deliver upon CSIRO^{1}s organisational objectives. -Participate in CSIRO^{1}s postdoctoral training program.*

*CSIRO's postdoctoral training program is a structured training program that will be developed between you and a CSIRO scientist. The program will allow you to further develop your skills in research, planning, management and communication. Training and development plans will be designed to develop fellows^1 capabilities to the level expected of an independent researcher. Each plan will include on-the-job and course-based development encompassing:

-Discipline-specific techniques and protocols -Professional growth -Project management -Communication and influencing skills -Working and collaborating with others For further information please see http://www.csiro.au/Portals/Careers/Postdoctoral-Fellowships/Postdoctoral-F ellowships.aspx

Selection Criteria:

Please note: Under CSIRO policy only applicants who meet all the essential criteria can be appointed

Pre-Requisite: A PhD, or will shortly satisfy the requirements for a PhD degree, in a relevant scientific discipline. Owing to the terms of CSIRO Postdoctoral Fellowships, you must not have more than 3 years relevant postdoctoral experience.

Essential Criteria:

1.Demonstrated ability to conduct innovative research in genome bioinformatics / biostatistics and preferably also some training in biochemistry. 2.Demonstrated ability to develop experimental plans and pursue novel research approaches. 3.Demonstrated originality, creativity and innovation in solving problems and introducing new directions and approaches. 4.Ability to work with a broad range of people from varying research backgrounds and evidence of strong oral and written communication skills, including the ability to publish the results of scientific research in scientific journals. 5.Demonstrated ability to work independently under minimal supervision while contributing to overall team performance and proven ability to meet performance deadlines during the course of the project.

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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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Cleveland PlasmodiumPopulationGenomics

Postdoctoral researcher - Plasmodium genomics

A postdoctoral position is available to work on Plasmodium vivax population genomics with David Serre (http://www.lerner.ccf.org/gmi/serre/) at the Cleveland Clinic Genomic Medicine Institute.

P. vivax is the main cause of malaria outside Africa but little is known about its biology since the parasite cannot be easily propagated in vitro. In the frame of a NIH-funded project, we are sequencing parasite genomes from blood samples of infected Cambodian patients to better characterize genetic diversity and organization of the P. vivax population and identify genetic loci underlying resistance to antimalarial drugs. Possibilities also exist for a successful candidate to develop new projects related to the overall goals of this research.

An ideal candidate would have prior experience with next-generation sequencing data, strong quantitative, computational and programming skills, and a record of published work in population genetics. Applicant should hold a Ph.D. in Biology, Genetics, Bioinformatics, Statistics or a related field, as well as strong written and oral communication skills. The position is available immediately.

Applicants should send a single pdf including a CV, contact information for three references, and a cover letter to serred@ccf.org

serred@ccf.org

CornellU CassavaGenomicSelection

Postdoctoral Associate: Genomic Selection in Cassava

A Postdoctoral Associate position is available to work in the area of genomic selection in the Department of Plant Breeding and Genetics at Cornell University. This position is part of an exciting international project to implement genomic selection in cassava led by Jean-Luc Jannink. The goal of this project is to increase the rate of genetic improvement of cassava for farmers in sub-Saharan Africa. Although the project is applied, we will be collecting a lot of sequence and phenotype data that can also be used to explore more basic issues in quantitative genetics and methods for genomic prediction, genotype imputation etc. Information about the project can be found at http://www.nextgencassava.org . The ideal candidate will have expertise in statistical genomics and plant breeding. Responsibilities will include independent research in development and evaluation of prediction models, analysis of empirical data, and training of scientists and students. Programming skills and working knowledge of mixed models are desirable, as are good communication skills, including preparation of manuscripts and the ability to explain complex material to non-experts, and knowledge of plant breeding practices. The position will involve close collaboration with the bioinformatics team and with cassava breeders in Nigeria and Uganda. Travel to Africa will be expected.

The position is available July 1. Applications will be reviewed until a suitable candidate is found. The initial appointment will be made for one year, with renewal contingent on satisfactory performance (the project is funded until 2017). Cornell is an equal opportunity employer.

Inquiries or applications can be sent to Martha Hamblin (mth3@cornell.edu).

A list of publications from the Jannink group can be found at http://www.ars.usda.gov/pandp/people/-people.htm?personid=40650 Martha Hamblin

"Martha T. Hamblin" <mth3@cornell.edu>

DalhousieU AppleGenomics

The Myles lab at Dalhousie University (www.cultivatingdiversity.org) invites applications for a postdoctoral position in apple genomics.

The position is available from July 1st, 2013 for a duration of 2 years with the possibility of extension.

We are seeking a postdoc to work on the analysis of genotyping-by-sequencing (GBS) data generated from a diverse collection of more than 1000 apple cultivars. The successful applicant will have extensive experience with computer programming and will preferably have experience with Java and at least one other programming language. No previous experience in agriculture is required. The aim of the project is to develop novel imputation algorithms that will allow us to better exploit GBS data. Experience handling next-generation DNA sequence data and software development will be considered a major asset. We will also use these data to elucidate the evolutionary history of apples, so experience with population genetics and evolutionary analyses of genome-wide polymorphism data will also be considered an asset.

The location of the lab is in Kentville, Nova Scotia, Canada, but we will consider applicants who wish to work remotely. For more information about the Myles lab, please visit:

www.cultivatingdiversity.org Interested applicants can send a cover letter and a CV to jobs@cultivatingdiversity.org–

Sean Myles Assistant Professor Canada Research Chair in Agricultural Genetic Diversity Faculty of Agriculture Dalhousie University Mobile: 902-690-7093 Lab Manager: 902-365-8463 Fax: 902-679-2311 www.cultivatingdiversity.org sean.michael.myles@gmail.com

DurhamU PopGenomics

Deadline for Post-Doctoral Research Associate position in Population Genomics extended to 24 May 13

PDRA Position at Durham University

Post-Doctoral Research Associate position in Population Genomics for the project "Adaptation and drift in the deep sea - investigating the evolution of diversity in a 'uniform' environment". This is a 3-year position funded by the Natural Environment Research Council (NERC) to investigate the population genomics and phylogenetics of deep sea fish species in the genus Coryphaenoides. Single nucleotide polymorphisms (SNP) will be developed by RAD tag sequencing for two focal species (DNA from 400+ individuals already available in the lab archive), one found in deep demersal habitat, and the other in the abyss. Population genomic analysis will investigate evolutionary processes generating diversity at both neutral and functional loci (e.g. functional loci associated with adaptation to depth). Phylogenetic analyses will compare neutral and functional loci for phylogenies constructed using DNA from 50-60 congeneric species that inhabit a range of depths, from 500-1000m down to the abyss at 4-5 km.

The ideal candidate will have experience with next generation sequencing methodologies and genome analysis software, be able to use script writing languages (such as Perl or Python), and have a general understanding of bio-informatics associated with the analysis of second generation DNA sequence data. Candidates who have some relevant experience and the background to allow them to learn these methods will also be considered. The candidate should also have skills associated with the use of population genetics and phylogenetic software packages, and there will be some labwork associated with DNA amplification and preparation for Sanger sequencing.

The project is a collaboration between the Molecular Ecology Group in Durham and the Centre for Genomic Research in Liverpool, to begin on 29 July 2013. The Post-doc will be based in Durham (UK), but the position is open to all nationalities. A PhD in a related field is required and relevant post-doctoral experience and publications highly desirable.

Contact Rus Hoelzel if you have any questions, and to apply please send your c.v., a cover letter, and have three letters of reference sent to Prof. Hoelzel at a.r.hoelzel@dur.ac.uk.

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

ETH Zurich 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.

Christoph.Vorburger@eawag.ch

Europe PlantEvolution

Our fellowship programme is open to all fields of plant sciences, including but not limited to evolutionary biologists.

PLANT FELLOWS - The International Post doc Fellowship Programme in Plant Sciences

Next deadline for applications: 24th June 2013 at 17.00.00, Zurich local time

PLANT FELLOWS is an international post doc fellowship programme in the field of plant sciences co-funded by the SEVENTH FRAMEWORK PROGRAMME (FP7) Marie Curie Actions ' People, Co-funding of Regional, National and International Programmes (COFUND) and is centrally managed at the Zurich-Basel Plant Science Center: www.plantsciences.ch It is offering post-doc fellowships between 12 and 24 months, spread between three different mobility schemes (incoming, outgoing and reintegration) at more than 20 universities, research institutions and industry partners all over the world. The fellows of the programme can benefit from a postdoc training programme including transnational mobility, industrial placements, career events and courses dedicated to training in en trepreneurship and complementary skills.

PLANT FELLOWS is open to all fields of research in plant sciences and to applicants of any nationality fulfilling the following eligibility criteria: - Only experienced researcher can benefit from the PLANT FELLOWS programme. Thus the applicant must, at the time of recruitment be in possession of a doctoral degree or have at least four years of full- time equivalent research experience. Both options need to be verified by certificates, which will be reviewed by the selection committee. - At the date for application submission, the applicant must not have resided or carried out his/her main activity (e.g. work, studies) in the country of the host organisation for more than 12 months in the 3 years immediately prior to the application submission. - The transnational mobility shall come under one of the following 3 fellowship schemes: incoming, outgoing or re-integration mobility.

The general eligibility criteria are set out in the PLANT FELLOWS guide for applicants available at the PLANT FELLOWS website: www.plantfellows.ch The applicant shall be available for the post within 5 months after receiving the notification of acceptance of application.

The application for a PLANT FELLOWS post doc fellowship needs to be submitted electronically via an online application system at the PLANT FELLOWS website.

The forms of grants and maximum reimbursement rates, which will be offered, are specified in the PLANT FELLOWS guide for applicants.

Do not hesitate to contact the programme officer Mrs. Romy Kohlmann (info-at-plantfellows.ch) for any further questions.

To learn more about the programme activities, the application and selection procedures as well as the host organisations please visit: www.plantfellows.ch Romy Kohlmann, M.A. ' Programme Officer PLANT FELLOWS - Zurich-Basel Plant Science Center - ETH Zürich, LFW B 51 - Universitätstrasse 2 - 8092 Zürich phone: 0041 44 632 47 96 - fax: 044 632 18 26 (Monday-Thursday)

Kohlmann Romy <romy.kohlmann@usys.ethz.ch>

FUBerlin PhylogenomicsOfNymphaeales

We are looking for a postdoctoral researcher to work on chloroplast phylogenomics of Nymphaeales at the Freie Universitaet Berlin (Germany). The project is supervised by Prof. Thomas Borsch (http://www.bcp.fu-berlin.de/biologie/arbeitsgruppen/botanik/ag_borsch/index.html) and will be executed in collaboration with the Berlin Centre for Genomics in Biodiversity Research (BeGenDiv; http://www.begendiv.de). It is a full-time position (40 hours/week) that will initially be limited to 2 years and that includes teaching at the Bsc and/or MSc level (max. 4 hours/week). The salary will be calculated according to E 13 TV-L. Starting date: June 2013, or soon thereafter.

Requirements: - PhD in Biology or similar discipline - Experience in phylogenetics/-genomics - Good knowledge about systematics and diversity of flowering plants - Good statistical knowledge and experience with handling large datasets - Good knowledge of German and English, both written and spoken

Applications should include a motivation letter, detailed CV and the contact details of at least two referees, and can be sent to:

FU Berlin Institut fuer Biologie - Botanik Prof. Dr. Thomas Borsch Altensteinstr. 6 14195 Berlin

or by E-mail to: systbot@zedat.fu-berlin.de.

Deadline for applications is June 7, 2013 and informal inquiries are welcome at t.borsch@bgbm.org.

ludo_muller@yahoo.com

Germany 3 FungalGenomics

The LOEWE Excellence Cluster for Integrative Fungal Research (IPF), a joint initiative of four universities and Senckenberg invites applications for “Three Postdoctoral Fellowships in Functional Genetics or Genomics of Fungi”

The positions are available from 1st of July 2013 to 30st of June 2015, with a possibility of extension for 6 months.

We are seeking a highly motivated individual whose research will be adding significantly to the LOEWE excellence cluster 'Integrative Fungal Research (IPF)'. The aim of the cluster is to synergistically tie together biodiversity, genetics and applied biochemistry/biotechnology.

The IPF is equipped with state of the art scientific instrumentation and offers an ideal environment for young researchers. It is envisaged that the successful applicants will develop their scientific profile and independence and will develop a vigorous research agenda. Apart from a competitive allowance the fellowship also includes a core funding for research and comes with special benefits for young researchers with children. International applications are especially welcome.

The successful applicant will have a strong background in functional genetics/genomics of fungi or fungal analogues. Expertise in genome analyses, developmental biology, heterologous expression, functional assays, or related topics is welcome.

We expect a solid publication record, good written and oral communication skills in English, and the capability of developing and testing scientific hypothesis and to explore new areas of research. The willingness to write research proposals is beneficial. Experiences in acquiring extramural funding are a plus. The fellowship allowance depends on previous experience and scientific excellence. The selection committee will pay special attention to the research proposal. Projects with links to biodiversity or biotechnology will be especially welcome.

If interested, please contact Prof. Dr. Marco Thines (marco.thines@senckenberg.de) and submit your application including a cover letter, CV, statement of research achievements, a detailed proposal of future research (about three pages) certificates (PhD, MSc, BSc, or similar), and the names of three scientists who could provide references. Applications should be submitted as a single PDF file.

Review of applications will start on the 18th of May 2012 and will continue until all positions have been filled.

Jenny Koeppchen

Jenny Koeppchen <Jenny.Koeppchen@senckenberg.de>

Grenoble MicrobialEvolution

A post-doctoral position is available for three years with Dominique Schneider in the Laboratory "Adaptation and Pathogenicity of Microorganisms", University Joseph Fourier, Grenoble, France. The position is part of a European research project, called EvoEvo, with four other partners (Guillaume Beslon INRIA Lyon, Santiago Elena CSIC Spain, Susan Stepney University of York, Paulien Hogeweg University of Utrecht).

Evolution is the major source of biological complexity on Earth, at the origin of all the species we can observe, interact with or breed. At a shorter scale, evolution is at the heart of the adaptation process for many species, in particular microorganisms (e.g. bacteria and viruses...). Microbial evolution not only results in the emergence of the species itself but also contributes to real-time adaptation of the organisms when facing perturbations or environmental changes. Thus, these organisms are not only organized/by/ evolution, they are also organized/to/ evolve. Molecular systems that are involved in the evolutionary process are themselves shaped by past evolution. This implies that evolution is able to influence its own course. This evolution of evolution ("EvoEvo") is at the heart of many phenomena overlooked by evolutionary algorithms, like second-order evolution, evolution of robustness, of evolvability, of mutation operators and rates, co-evolution... Yet, all these processes are at work in living organisms including bacteria and viruses, accelerating their evolution and enabling them to adapt rapidly and efficiently to environmental changes like new drugs, to fight the immune system or to colonize diverse ecological niches.

In our laboratory in Grenoble, the project will consist in observing, quantifying and characterizing "evolution of evolution" in microorganisms at the level of genomes, biological networks and populations. We will address experimentally the pace of evolution of microorganisms and relate it to their robustness, evolvability and open-endedness. In particular, we will address the relationship between robustness and evolvability by directly testing whether more robust genotypes are also more evolvable or, by contrast, whether they adapt in a slower pace to new environmental conditions. We will tackle these issues using the longest-running evolution experiment from Richard Lenski with/Escherichia coli/. It provides a powerful methodology to analyse the molecular basis of adaptation and to draw a rigorous phenotype-to-genotype map. We will gain a better understanding of the "evolution of evolution" phenomenon that is still poorly understood. EvoEvo will contribute evolutionary theory by allowing understanding of the surprisingly high pace of evolution of microorganisms. It will enable us to understand if/when/how the characteristics of the genotype-to-phenotype mapping are selected in real evolving systems that have to adapt to new conditions.

Candidates must have a Ph.D. in Genetics, Molecular and Evolutionary

Biology, or related fields. Expertise in molecular biology, genome sequencing, and global transcription profiles is requested. In addition, the candidates should have computational skills for analyses of genome sequences and transcription profiles.

To apply, please submit applications by e-mail to Dominique Schneider, including (1) a CV, (2) a brief statement of past accomplishments and PDFs of most relevant publications, (3) research interests and (4) names and contact information of three referees.

Dominique Schneider Laboratoire Adaptation et Pathogénie des Microorganismes CNRS UMR5163 Université Joseph Fourier Institut Jean Roget Domaine de la Merci BP170 38042 Grenoble Cedex 9 France

Phone: +33 (0) 4 76 63 74 90 Fax: +33 (0) 4 76 63 74 97 E-mail: dominique.schneider@ujf-grenoble.fr

Dominique Schneider <dominique.schneider@ujf-grenoble.fr>

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 from 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>

INRIA Lille France Statistical genomic rearrangement

Postdoctoral position in Statistical genomic rearrangement in Lille/France

A postdoctoral position is available within the BONSAI team, a bioinformatics research group between INRIA Lille - Nord Europe and LIFL (UMR 8022 CNRS, University Lille, France). - Duration : 12 months - Starting date : between June 2013 and October 2013

Description

The position is funded by a Nord-Pas-de-Calais region grant for a scientific project on the application of Bayesian models and Markov chains Monte Carlo (MCMC) sampling techniques to the analysis of genomic rearrangements.

The successful candidate will work on exploring and developing new Bayesian probabilistic models for the analysis of genome evolution based on the evolution of genomic breakpoints.

Application

The ideal candidate should hold: - either a PhD in Probability and Statistics with a taste for applications in bioinformatics, - or a PhD in Computer Science / Computational Biology with an expertise in Probability and Statistics.

If the Ph.D. thesis is not yet defended, the candidate should provide the planned defense date.

Before applying, candidates should email their detailed CV with a list of publications, and a short description of their current research interests and future research plans to Aida.Ouangraoua@inria.fr .

- Application deadline: May 20, 2013. http://tinyurl.com/dxlh4s4 aida.ouangraoua@inria.fr

ImperialCollege London MicrobialCommunityEvolution

Salary £32,100 - £40,720 per annum (maximum starting salary £34,720)

We are looking for a Research Associate who will lead large-scale, high-throughput eco-evolutionary experiments using bacteria collected from natural environments.

Laboratory studies of adaptation to novel environments are well documented, but very little is known about how species evolve in nature. This position offers the opportunity to combine field and laboratory investigations of how microbes adapt to changing environments. Previous research in the group has shown that, while interactions among random collections of microbes tend to be competitive (Foster & Bell, 2013, Current Biology, 22: 1845), positive interactions emerge when microbial strains coevolve in closed microcosms (Lawrence et al. PLoS Biology, 2013, 10: e1001330). The project will build on these results by investigating how bacterial species adapt while they are embedded within complex communities containing hundreds or thousands of species.

The project will complement ongoing research being undertaken in Professor Barraclough's and Dr Bell's research groups, which investigate the biodiversity and evolution of microbial communities, and will be based at the Silwood Park Campus.

You must have a PhD (or equivalent) in microbiology, evolution, ecology, or a closely related discipline and a strong background in experimental microbial ecology. Experience of conducting large-scale ecological experiments is also essential.

Experience in molecular microbiology, including next-generation sequencing, and diversity surveys using 16S sequencing is desirable. Experience of statistical analysis of complex ecological datasets using R or similar software would also be an advantage.

You must have excellent verbal and written communication skills, and be able to write clearly and succinctly for publication. You must also be able to relate well with others, form positive relationships with a wide range of people and to work as part of a team, as well as independently. The ability to develop and apply new concepts and have a creative approach to problem-solving will be required.

Closing Date

Our preferred method of application is online via this website:

https://www4.ad.ic.ac.uk/OA_HTML/OA.jsp?page=3D/oracle/apps/irc/candidateSelfService/webui/VisVacDispPG&akRegionApplicationId=821&transactionid=1394171123&retainAM=Y&addBreadCrumb=S&p_svid=41105&p_spid=1629668&oapc=7&oas=UqKhtoBHrugbHmgRICYJw. . Should you have any administrative queries please contact: Mrs Diana Anderson - 020 7594 2207 or email d.anderson@imperial.ac.uk

t.barraclough@imperial.ac.uk

Jyvaskyla Finland BacterialEvolution

Postdoc position University of Jyväskylä:

We are searching for a candidate for a postdoctoral position at the Department of Biological and Environmental Science, University of Jyväskylä, Finland. The work would involve development of qPCR for the fish pathogen Flavobacterium columnare to study the effect of strain competition on the evolution of virulence under varying resource conditions. The position is for 2 years, starting preferably in August, 2013.

Please send letters of interest and CV (single pdf file) to jouni.k.taskinen@jyu.fi and/or katja.pulkkinen@jyu.fi

Short description of the project can be found at http://users.jyu.fi/˜pukaan/research.html katja.pulkkinen@jyu.fi

KansasStateU Phylogenetics

Postdoctoral Research Associate – Phylogenetics and Polyploidy

A two-year postdoctoral position is available in the laboratory of Dr. Carolyn Ferguson in the Division of Biology at Kansas State University (Manhattan, Kansas). The successful candidate will investigate phylogenetics of several polyploid complexes in the genus *Phlox *(Polemoniaceae) using both traditional and next-generation sequencing approaches. This research contributes to a collaborative project focused on polyploidy and aspects of diversity in *Phlox* in the southwestern U.S. (including studies in phylogenetics, population genetics, morphology, ecology and taxonomy). The postdoctoral researcher will work under the mentorship of the PI, and will interact with collaborating investigators as well as graduate and undergraduate students. Minimum qualifications: a Ph.D. (by start date) with emphasis on Systematics, Evolutionary Biology or related discipline. Preferred qualifications: strong molecular biology laboratory skills; and excellent writing and interpersonal skills. The salary is $40,000 plus benefits, with the position available on a 12-month appointment contingent on need for services and funding. The position is available immediately but the start date is flexible. Review of applications will begin 20 May 2013, and continue until the position is filled. To apply, send a cover letter, CV, up to three publications, and arrange to have two letters of reference sent to biology@ksu.edu. Inquiries are welcomed and should be addressed to Carolyn Ferguson, ferg@ksu.edu. Kansas State University is an equal opportunity employer and actively seeks diversity among its employees. Background check required.

Carolyn J. Ferguson Associate Professor Curator of the Herbarium (KSC) Division of Biology Kansas State University Manhattan, KS 66506-4901 ph: 785-532-3166 ferg@ksu.edu

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LBBE Lyon AncestralGenomes

Integrative methods for reconstructing ancestral genomes

A 2 year (+1) post-doctoral position is available to work on integrative methods for reconstructing ancestral genomes in the Bioinformatics and Genome Evolution (BGE) group at the LBBE in Lyon, France (http://lbbe.univ-lyon1.fr/?lang=en).

The researcher will work in collaboration with Vincent Daubin, Bastien Boussau, Gergely Szollosi and Eric Tannier, in the context of the ANCESTROME project. ANCESTROME (http://ancestrome.univ-lyon1.fr) is a large collaborative project funded by the French National Research Agency .

The project aims at building integrative models and studying the genomes of extant living organisms to reconstruct evolutionary intermediates together with the evolutionary processes that have generated them. A critical step in the development of methods to reconstruct the evolution of genomes is the modeling of the processes that relate gene phylogenies to species phylogenies. We have developed methods for integrating events of gene duplication, gene loss and lateral gene transfer in the simultaneous reconstruction of species and gene histories. These methods yield much better estimates of the gene content of ancestral genome, and hence open the door to accurate reconstructions of ancestral species characteristics. These include not only cellular and genome organization, or metabolic capabilities, as deduced from genome content, but also virtually any internal or external factor that has left a trace in the genomic record, in particular details of the environment to which the species has adapted, its resources, symbionts or demography.

In a series of recent papers, we have used probabilistic models and high performance computing methods on the HOGENOM (http://pbil.univ-lyon1.fr/databases/hogenom/acceuil.php) database to start exploiting genomes as documents of evolutionary history (see references below).

Possible avenues of research include:

- Reconstructing ancestral genomes, phenotypes and environments

- Modeling coevolution of genes and genomes...

The successful candidate will have a strong background in computational biology or probabilistic models. Good programming skills are essential. A good understanding of the concepts of evolutionary biology is a plus.

The LBBE offers a highly stimulating scientific environment, and Lyon is a lively, beautiful, history rich city (see http://whc.unesco.org/en/list/872/) with great food. The researcher will also have the opportunity to visit collaborating labs in the no less interesting cities of Budapest and Berkeley.

Please send a CV and motivation letter including references to Vincent Daubin (vincent.daubin@univ-lyon1.fr) and Bastien Boussau (bastien.boussau@univ-lyon1.fr).

Keywords: Probabilistic Models, Phylogenetics, Evolution of Life on Earth, Evolutionary Genomics, Coevolution, HPC

References: - Szöllosi GJ, Tannier E, Lartillot N, Daubin V. Lateral Gene Transfer from the Dead. Syst Biol. 2013 May 1;62(3):386-397. - Boussau B, Szöllosi GJ, Duret L, Gouy M, Tannier E, Daubin V. Genome-scale coestimation of species and gene trees. Genome Res. 2012 Nov 6. - Szöllosi GJ, Boussau B, Abby SS, Tannier E, Daubin V. Phylogenetic modeling of lateral gene transfer reconstructs the pattern and relative timing of speciations. Proc Natl Acad Sci U S A. 2012 Oct 23;109(43):17513-8. - Bérard S, Gallien C, Boussau B, Szöllo“si GJ, Daubin V, Tannier E. Evolution of gene neighborhoods within reconciled phylogenies. Bioinformatics. 2012 Sep 15;28(18):i382-i388. - Abby SS, Tannier E, Gouy M, Daubin V. Lateral gene transfer as a support for the tree of life. Proc Natl Acad Sci U S A. 2012 Mar 27;109(13):4962-7. - Szöllosi GJ, Daubin V. Modeling gene family evolution and reconciling phylogenetic discord. Methods Mol Biol. 2012;856:29-51. - Abby SS, Tannier E, Gouy M, Daubin V. Detecting lateral gene transfers by statistical reconciliation of phylogenetic forests. BMC Bioinformatics. 2010 Jun 15;11:324. - Boussau B, Daubin V. Genomes as documents of evolutionary history. Trends Ecol Evol. 2010 Apr;25(4):224-32. - Penel S, Arigon AM, Dufayard JF, Sertier AS, Daubin V, Duret L, Gouy M, Perrière G. Databases of homologous gene families for comparative genomics. BMC Bioinformatics. 2009 Jun 16;10 Suppl 6:S3.

Vincent Daubin <daubinster@gmail.com>

Melbourne MCRI StatisticalGenetics

Post-doc, Statistical Genetics Murdoch Childrens Research Institute

Position Title Postdoctoral Research Assistant (Ref# 724/2013) Position Description See http://www.mcri.edu.au/careers-students/careers/current-vacancies/ Group Statistical Genetics Employer Murdoch Childrens Research Institute Location (Melbourne) Royal Children's Hospital, Parkville, Victoria Work Type Full-time Classification MCRI Research Scale (AUD 75,404 - 80,939 p.a. plus superannuation and salary packaging benefits) Closing Date 7 June 2013

Applications are invited for a Post-doctoral Researcher to join the Statistical Genetics Group at the Murdoch Childrens Research Institute, headed by Dr Stephen Leslie. The group's work focuses on methodological developments for the analysis of high throughput genetic data and the application of these methods to studies of disease and natural population variation. These methods typically combine modern computationally-intensive statistical approaches with insights from population genetics models. Specifically the group works on statistical methods for imputing immune system (and other) genes from incomplete genetic data; the application of these methods to studies of autoimmune and other diseases; methods for detecting and controlling for population stratification; and understanding the causes and consequences of genetic variation in populations. The group has strong established collaborations with the Donnelly and McVean groups at the Wellcome Trust Centre for Human Gene tics in Oxford.

The position involves working on problems at the cutting edge of human genetics, and represents an exciting opportunity for a statistical geneticist, or someone with a strong statistical background and skills wishing to move into this field. The successful applicant will work on developing statistical methods for detecting and controlling for population stratification, with particular focus on incorporating such methods into genetic (and in particular genome-wide) association studies. The appointee will also contribute to other research projects in statistical genetics as directed by the group leader. He/ she will be encouraged to develop his/ her independent research projects where appropriate.

We are seeking a highly motivated scientist, with a PhD in statistics or a closely related area. Applications are encouraged from people who can demonstrate a strong statistical or other quantitative background and wish to move into statistical genetics research. Ideally you will have experience of genetic analyses but this is not essential. You must have considerable programming experience with a low level language (e.g. C, C++) and preferably also with the statistical software R. The successful applicant will have an aptitude for visualizing data, problem solving and careful statistical analysis. You should be able to work alone and collaboratively, and be able to digest and communicate scientific ideas effectively. The position is available for two years with the possibility of extension.

Informal enquires can be directed to Stephen Leslie (stephen.leslie@mcri.edu.au).

Applications close at 9am Friday 7th June 2013. Late applications will not be considered.

REF: 724/2013

Please send written applications (in PDF format) addressing the Key Selection Criteria (see http://www.mcri.edu.au/careers-students/careers/current-vacancies/), Academic Transcripts, Cover Letter and CV containing details of 3 referees, quoting the above mentioned reference number to Human Resources via recruitment@mcri.edu.au.

stephen.leslie@mcri.edu.au

MountSinai NewYork EvolutionaryMedicineInformatics

Postdoctoral Scholar in Evolutionary Medicine and Informatics

We are currently accepting applications for post-docs combining computational genomics, molecular evolution, and disease biology. Candidates should have a Ph.D. in biology, genetics, computer science, statistics, bioinformatics, computational biology, or a related field and knowledge of molecular evolution. Knowledge or experience in complex genetic traits and network biology are a plus. The ideal candidate for this position will have substantial input to the specific nature of the research project. However, the project should broadly fit within the lab's goals of understanding how evolution plays a role in shaping and understanding complex health traits. There are opportunities to develop novel integrative evolutionary methods, analyze clinical genomic data, and to work on evolutionary analysis projects that could have a direct impact on human health.

Interested candidates should send a CV and a short (1 page) description of both research interests and ideas for possible projects to me at dudleylabmssm@gmail.com. Review of applications will begin in April 2013, and will continue until the position is filled.

Joel Dudley, PhD Director of Biomedical Informatics Assistant Professor of Genetics and Genomic Sciences Institute for Genomics and Multiscale Biology Icahn School of Medicine at Mount Sinai http://research.mssm.edu/dudley/ http://www.linkedin.com/in/joeldudley joel.dudley@gmail.com

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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>

SangerInst ComparativeGenomics

THREE-YEAR POST-DOCTORAL FELLOWSHIP IN COMPARATIVE GENOMIC INSIGHTS INTO PARASITE GENOME FUNCTION

Applications are invited for a three-year post-doctoral fellowship held jointly at the Sanger Institute and European Bioinformatics Institute under these institutes' "ESPOD" fellowship programme (http://www.ebi.ac.uk/research/postdocs/espods).

The above webpage includes a link to an abstract of this project (and others in the programme). Full project details are available at http://www.ebi.ac.uk/sites/ebi.ac.uk/files/groups/research_office/Goldman-Berriman.pdf The successful candidate will work in the Goldman Group at EMBL-European Bioinformatics Institute (http://www.ebi.ac.uk/research/goldman) and Matt Berriman's Parasite Genomics group at the Sanger Institute (http://www.sanger.ac.uk/research/projects/parasitegenomics).

Applications should be sumitted by e-mail to the EBI Research Office <roffice@ebi.ac.uk> by 26 July 2013.

Nick Goldman tel: +44-(0)1223-492530 EMBL - European Bioinformatics Institute fax: +44-(0)1223-494468 Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK

goldman@ebi.ac.uk

StanfordU AntEvolution

A postdoctoral position is available in the Gordon lab in the Department of Biology at Stanford University. The project will involve developing and testing models of how ants assess interaction rate. The ideal candidate will have experience in behavioral experiments with ants (or other insects) and some background in mathematics or computer science. The position is for a recent Ph.D. for one year with a possibility of renewal. Interested candidates should contact Deborah Gordon by email (dmgordon@stanford.edu). Please include a single PDF attachment containing your CV, a brief description of past research accomplishments and future goals, and the names and email addresses of 2 potential references.

Deborah M Gordon Professor, Dept of Biology Stanford University http://www.stanford.edu/~dmgordon "Deborah M. Gordon" <dmgordon@stanford.edu>

StellenboschU PotatoGenomics

Postdoctoral position available in the Department of Genetics, Stellenbosch University (20 May 2013)

A postdoctoral position is available in the Molecular Plant and Animal Research Group, Department of Genetics, Stellenbosch University with the focus on "Association mapping in Potato for advancement of Marker Assisted Selection for specifically Potato Virus Y disease resistance in South Africa". This project is a collaborative effort with Agrocorp and Tubertek South Africa.

Breeding for enhanced cultivars in potato is a necessary, but time consuming process encumbered by the polyploid, heterozygous, non-inbred and clonal nature of the crop. With the sequencing and publishing of the potato genome in 2011 and associated marker development [mainly of Single Nucleotide Polymorphism (SNP) markers] the potential for molecular breeding in the crop has been enhanced. The development of an 8300 SNP array with genome-wide marker coverage attests to this.

Disease resistance is one of the main breeding aims for many crops, as it is for potatoes. The nature of this resistance can vary from simple, Mendelian, single gene, vertical resistance to more complex, multi-gene (quantitative traits), horizontal resistance. Although work has been done on many single genes, quantitative trait loci (QTL) work is a laborious process, which in the past mainly relied on the creation of segregating mapping families. Quantitative variation is however proposed to be a more durable form of resistance as is has been shown that pathogens could potentially more easily overcome single gene resistance.

During the past decade, association mapping, commonly applied in human- and livestock genetics, has shown greater promise and power for the genomic mapping of complex quantitative traits in plants as compared to traditional linkage mapping.

It is the aim of this study to combine the potential and power of association mapping to identify genetic markers (SNPs) showing association with phenotypic variance mostly related to disease traits (specifically to potato virus Y) in order to expedite the process of marker assisted selection in this species for growth under South African conditions. To this effect we will make use of the recently published and developed genome sequence and SNP Infinium array developed by the SOLCAP community.

The successful candidate will primarily be responsible for: 1) Phenotypic evaluations, SNP data analysis and association mapping of potato cultivars in terms of Potato Virus Y resistance. 2) Identifying a set of markers associated with PVY resistance (known and novel QTL). 3) Development of robust marker assay to test for associated phenotypes in South African cultivars. 4) Advancement of marker assisted breeding of PVY resistance in South African potato breeding.

Minimum requirements: PhD with specialization in association mapping or any closely related discipline. Candidates should have proficiency in the relevant software packages, and experience with handling and analysing large scale SNP data. Experience within the field of potato genetics in general and potato virus studies in particular would serve as a strong recommendation. The ideal candidate should also have proven project management experience and ability to set deadlines and meet milestones.

This position is available for 3 years and commencement of duties is set for September 2013.

Interested researchers are requested to send their CV including details of at least 2 references to Prof. Rouvay Roodt-Wilding at roodt@sun.ac.za

Closing date: 10 June 2013

"Roodt-Wilding, R <roodt@sun.ac.za>" <roodt@sun.ac.za>

Switzerland Evolutionarydynamics

A collaborative research team led by Blake Matthews, Ole Seehausen, and Bernhard Wehrli are seeking a postdoctoral researcher with a background and interest in evolutionary biology, community ecology, and/or ecosystem science.

The aim of the project is to understand the interaction between eco-evolutionary dynamics and the functioning of aquatic ecosystems. Specifically, we are interested in how organism-mediated changes to the temporal and spatial heterogeneity of ecosystems can alter environmental sources of selection, so as to either promote or constrain further adaptive evolution. The project involves large-scale eco-evolutionary experiments that address fundamental links between the ecology and evolution of food webs and the physical environment and biogeochemistry of aquatic ecosystems. An ideal candidate would have some experience with next generation sequencing methodologies and strong analytical abilities for the analysis of ecological communities.

Eawag's Center for Ecology, Evolution & Biogeochemistry (CEEB) is located on the shore of Lake Lucerne in Switzerland, and is a strong nucleus of Eawag research groups aimed at integrating evolutionary biology, community ecology, and ecosystem science http://www.eawag.ch/forschung/cc/ceeb/-index_EN. The postdoc will interact with a diverse range of researchers studying community ecology, evolutionary biology, ecological genetics, ecosystem science, and applied environmental science.

The starting date for the postdoc is flexible, but a starting date in 2013 is preferred. Applications should include a cover letter, a curriculum vita, and the names of three references. Copies of 3-5 prior publications will also be considered if made available via PDF.

Please submit your application by 1 July 2013. Applications must be submitted online via this link: http://-internet1.refline.ch/673277/0201/++publications++/-1/index.html For further information: please contact Blake Matthews by email (blake.matthews@eawag.ch), or visit our webpages below.

Blake Matthews: http://homepages.eawag.ch/-~matthebl/Welcome.html Ole Seehausen: http:/-/www.eawag.ch/about/personen/homepages/-seehauso/index_EN Bernhard Wehrli: http://-www.eawag.ch/about/personen/homepages/wehrli/-index Blake.Matthews@eawag.ch

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SydneyAustralia GenomeEvolution

The Darling lab at the University of Technology Sydney, in collaboration with Dr. Erik Matsen's group at Fred Hutchison Cancer Research Center, is exploring statistical inference algorithms for the next generation of genome evolution models. We have the opportunity to support an inspired postdoctoral researcher to join in this effort. In this role you would develop novel statistical methods and software to analyze genomes and metagenomes in forensic and environmental systems. You would be developing scalable approaches to Bayesian inference of phylogenetic models of genome evolution. Approaches of interest include Sequential Monte Carlo methods, Variational Bayes, hybrid SMC/MCMC approaches, and approximate Bayesian methods.

As a Postdoctoral Research Associate experience and qualifications will include (but not be limited to):

* Ph.D in computer science, statistics, bioinformatics, or quantitative population genetics * Knowledge of Bayesian phylogenetic inference * Strong computational, mathematical and/or statistical skills * Software engineering in C++, Java or Python

UTS offers a friendly and collaborative work culture at its city campus, which is undergoing an exciting redevelopment program. The appointee will join a committed and energetic team within the ithree institute of the Faculty of Science.

Salary: $65,539 - $79,822pa. plus 17% superannuation.

See the UTS page for further information and to apply: http://www.jobs.uts.edu.au/job/job_details.cfm?id=-813415 Contact Aaron Darling with questions: aaron.darling@uts.edu.au

– Aaron E. Darling, Ph.D. Associate Professor, ithree institute University of Technology Sydney Australia

http://darlinglab.org twitter: @koadman

aaron.darling@uts.edu.au

UArizona Evolability

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 EEB department in Tucson was ranked in the top

10 by US News & World Report.

The Masel group's main research interests are in robustness and evolvability, using a mixture of analytical theory, bioinformatic and simulation approaches. In previous work (Rajon & Masel 2011 PNAS), we explored the evolutionary consequences of the simple fact that all molecular processes, from transcription to protein interactions, are subject to errors. The evolution of error rates is bistable. One attractor represents a global proofreading solution that avoids making errors at many loci at once, the other a local robustness solution, where errors happen at high rates but the consequences of each error have evolved, one locus at a time, to be benign. Populations that evolved the local solution were much more evolvable, with selection acting on the consequences of errors acting as a playground to explore and prescreen possible future mutations.

We are looking for a postdoc to extend this and related work (Rajon & Masel 2013 Genetics) to examine sexual as well as asexual populations, and to test the controversial hypothesis of the adaptive evolution of evolvability. In other words, might the high evolvability of local solutions cause their prevalence to increase?

A strong quantitative background, good programming skills, and previous modeling experience are all required. A background in evolutionary theory is strongly preferred. Some interest in the molecular biology of transcription, translation, protein folding and binding, and the errors in each of these processes is an advantage. The position is available starting August 26, 2013, and is renewable, with funding secured for at least two years.

Contact Joanna Masel at masel@u.arizona.edu for more information and/or to apply.

masel@email.arizona.edu

UArizona VertebratePhylogenomics

Postdoctoral position in vertebrate phylogenomics and evolution at the University of Arizona

A postdoctoral position is available in the recently relocated laboratory of John Wiens in the Department of Ecology and Evolutionary Biology at the University of Arizona (http://www.wienslab.com/Home.html). The successful applicant will work on one (or more) of several projects related to the phylogenomics and evolution of reptiles and amphibians. The successful applicant will be expected to generate first-authored papers and will have the opportunity to collaborate on many others. The position should be for two years (given a successful first year), starting in the fall of 2013.

Candidates must have a Ph.D. in evolutionary biology (or a related field) by the time the position starts. The ideal candidate will have experience in next-generation sequencing and the associated computational approaches for analyzing these data, as well as interest in phylogenetics and comparative approaches in evolution and ecology. Experience with reptiles and amphibians is desirable but not necessary. Demonstrated skills in writing and data analysis will factor heavily in selecting candidates, as will creativity, research productivity, and the ability to learn new approaches and to work well with others.

The EEB department at the University of Arizona is currently ranked as one of the top ten in the country. Tucson is a fun town surrounded by amazing scenery and biodiversity (with mountain wilderness areas on three sides), and has an incredible herpetofauna.

Review of applications will begin June 1, 2013 and will continue until the position is filled. I hope to have the opportunity to meet with some candidates for the position at the Evolution meetings in Snowbird, Utah (June 22V26).

To apply, please send electonically a cover letter (including research interests and relevant experience), full CV, three PDF reprints, and contact information for two references to: wiensj@email.arizona.edu

John J. Wiens Professor Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721-0088

E-mail: wiensj@email.arizona.edu Web: http://www.wienslab.com/Home.html John Wiens <wiensj@life.bio.sunysb.edu>

UBielefeld EvolutionSalamanders

University of Bielefeld, Department of Animal Behaviour, Unit Molecular Ecology and Behaviour, Germany

Application deadline: June 7th 2013

We are looking for a highly motivated postdoc to join our research team, to study mechanisms and processes of parallel habitat adaptation in the fire salamander.

The research will be carried out in the framework of the German-Israeli Project Cooperation (DIP) financed by the German Research Foundation (DFG) genomics: analysis of gene expression underlying parallel habitat adaptation in distinct salamander species.

Although a lot of data on the consequences of habitat adaptation at the phenotypic and population structure levels are available, we are currently missing deeper insights into the genetic architecture of habitat-dependent adaptation. The study of parallel adaptive evolution is very promising to identify genes and underlying genetic mechanisms of how individuals can adapt to different environmental conditions. Due to their fascinating breadth of habitat-specific adaptations as well to aquatic and terrestrial habitats, amphibians provide ideal systems to study the impact of ecological adaptation on the genome level under natural conditions. In the past, we have intensively studied the ecology and population genetics of two distinct species of fire salamanders V Salamandra salamandra in Germany and Salamandra infraimmaculata in Israel, with a special focus on how larvae can adapt to the different conditions experienced until metamorphosis in contrasting habitats such as streams and ponds. This international cooperative research program is aimed to extend and to combine the ecological-genetic framework of parallel habitat adaptation in the fire salamander exemplified for two distinct species to the level of the transcriptome and gene expression analysis. By characterizing the ecological conditions of parallel habitat adaptation in these two species and by simultaneously screening a large number of genes for patterns of evolutionary divergence, we aim to link the ecology of habitat adaptation and gene expression patterns to a very detailed extent.

The postdoc candidate will join an international team of leading scientists in the field of Ecology (Prof. Dr. Leon Blaustein, University of Haifa), Molecular Ecology (Dr. Sebastian Steinfartz, University of Bielefeld), Evolutionary Genomics (Dr. Arne Nolte, Max-Planck Institute of Evolutionary Biology), Evolution and Bioinformatics (Prof. Dr. Alan Templeton, University of Haifa) and River Ecology (Prof. Dr. Markus Weitere, Helmholtz-Centre for Environmental Research - UFZ). Moreover she/he will strongly interact with two other postdoc researchers, one in genomics and one in bioinformatics, as well as with involved PhD students based in Germany and in Israel. The candidate is expected to perform intensive first hand ecological characterizations of larval habitat structure (e.g. niche modelling) and habitat analysis by performing stable isotope analysis to infer food web structure for larval habitats in Germany and in Israel. These analyses will be crucial to understand and interpret observed gene expression patterns of larvae from these habitat types and to be able to connect gene expression data with the observed ecology of the larvae. The successful candidate is furthermore expected to work closely together with the ecologically oriented PhD student in the project. The PhD student will mainly focus on the impact of certain habitat specific selection pressures (e.g. desiccation risk, flush floods, predators, etc.) on the larvae and how these impact gene expression.

We expect applications from highly motivated and qualified young scientists holding a PhD, preferably with a postdoc experience, but most importantly with a strong research background and interest in ecology and evolution of organisms and experience with genetic/genomic methods. Experience with amphibians would be desirable, but is not mandatory. The candidate is supposed to be based in Germany. However, as this project involves intensive fieldwork also in Israel, the candidate should be highly flexible and willing to live for some months also abroad. The position will come with a full TV-L E13 salary with a gross income around 59,000 £á/year. The position is initially scheduled for two years with the option for a prolongation of one year.

Please send your application until June 7th, including a curriculum vitae, copies of academic certifications including PhD certification, PhD thesis, a letter of motivation why you are interested in the project and addresses (e-mail addresses and telephone numbers) of two referees as a merged PDF to:

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

We expect to contact/interview candidates starting from the middle of June on.

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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

UCalifornia Berkeley InvasionEvolution

Invasions, interactions and global change

Two postdoctoral positions are available at the University of California, Berkeley, to conduct bridging research connecting the themes of invasion biology, species interactions and global change, focused on the San Francisco Bay Area. On-going projects include studies of interactions of plants with their symbionts and diseases, insect herbivores and their natural enemies, as well as associated economic impacts. Ecosystems under study include those associated with legumes, grapes, and olives, but also natural systems and the urban/natural interface. Research in other relevant areas and systems is also encouraged, including quantitative analyses of community structure in space and time and novel approaches for the study of invasions, including citizen science.

This project is part of the Berkeley Initiative for Global Change Biology (BiGCB). It is one of seven integrated research projects focused on global change forecasting for California ecosystems. Project leaders include Ellen Simms, George Roderick, Wayne Sousa, Rodrigo Almeida, Nick Mills, and David Zilberman. Associated departments include Integrative Biology, Environmental Science Policy and Management, and Agricultural and Resource Economics.

Details: - Each postdoc will be for 1 year, but renewable for up to 2 years. - Expectations for the position include relevant research and coordinating a graduate seminar. - Connections with on-going projects is encouraged. Please contact individual project leaders using website links above. - The scholars will also be required to participate in and collaborate with other projects associated with the Berkeley Initiative in Global Change Biology (BiGCB). - Salary is commensurate with experience as set by UC policies (see http://vspa.berkeley.edu/-postdocs). - Start date: 1 July 2013, or negotiable.

Requirements: - Ph.D. in relevant field. Successful candidates must start appointment before accruing more than three years of research experience since receipt of Ph.D. - Demonstrated ability to communicate effectively in both writing and speaking, through publications and contributed talks. - Expertise in area relevant to project.

To apply: Send the following as attachments to an email with the header “Invasion Postdoc” to globalchange@berkeley.edu. Applications will be accepted starting today (1 May).

1. Statement of research interests (no more than 3 pages), including summary of Ph.D. project. 2. CV including education, publications, contributed papers. 3. Names and email addresses of 3 people who have agreed to provide letters of recommendation if asked.

Deadline: The First Review Date of applications is 22 April 2013.

roderick@berkeley.edu

UCollege London Bioinformatics

Dear all,

UCL’s Research Department of Genetics, Evolution and Environment invites expressions of interest from potential applicants to NERC’s Independent Research Fellowships in Bioinformatics.

NERC has recently launched a research programme in “Mathematics and Informatics for Environmental ’Omic Data Synthesis” and funds 5-year fellowships for early-career scientists wishing to establish independent research groups. More information on the scheme and the background of the programme can be found on the NERC website (http://www.nerc.ac.uk/research/programmes/-omics/events/ao-bioinformaticsfellowships.asp).

If you have the appropriate expertise and would like to apply for a fellowship hosted in our department, please get in touch with Max Reuter (m.reuter@ucl.ac.uk). We will support selected candidates through all stages of their application.

Our department fosters young talent and provides a stimulating and multi-discilinary research environment. It has strengths in evolutionary and statistical genetics, genomics, evo-devo and environmental and biodiversity research. For more information about our research, please visit the department’s website (http://-www.ucl.ac.uk/gee/) as well as those of departmental sub-nuits including the UCL Genetics Institute (http:/-/www.ucl.ac.uk/ugi/) and the Centre for Biodiversity and Environment Research (http://www.ucl.ac.uk/-cber/).

Best regards, Max

Max Reuter

Research Department of Genetics, Evolution and Environment Faculty of Life Sciences University College London Darwin Building Gower Street London WC1E 6BT, UK

Phone: +44-20-76792201 (internal 32201)

Lab: http://www.homepages.ucl.ac.uk/ ˜ ucbtmre/-

Labsite/ Department: http://www.ucl.ac.uk/gee Centre for Ecology and Evolution: http://www.ceevol.org.uk m.reuter@ucl.ac.uk

UEdinburgh EvolBiol

Postdoctoral Researcher, University of Edinburgh

Applications are invited for a 5-month appointment as Post-doctoral Researcher based in the Institute of Evolutionary Biology, University of Edinburgh. The position is funded by a Wellcome Trust project grant.

Applicants should have, or shortly obtain, a PhD in evolutionary genetics or bioinformatics and have experience in computer programming and population genetics or molecular evolution. The project aims to increase the understanding of the nature and strength of natural selection operating in various kinds of functional elements of the mammalian genome. In particular, the post holder could work on the evolutionary genetics of adaptation in the murid genome by analysis of next-generation sequence data of multiple individuals sampled from natural populations.

Informal enquiries can be made to peter.keightley.ed.ac.uk

Peter Keightley Professor of Evolutionary Genetics Institute of Evolutionary Biology University of Edinburgh West Mains Rd Edinburgh EH9 3JT UK http://homepages.ed.ac.uk/eang33/ Full applications by 24th June 2013 can be made under reference 014484 at https://www.vacancies.ed.ac.uk/ peter.keightley@ed.ac.uk

UIdaho PlantPhylogenetics

Postdoctoral Research Position at the University of Idaho - Phylogeny and Evolution Castilleja (paintbrushes)

Position Description: The postdoctoral researcher will work in the lab of David Tank (http://phylodiversity.net/dtank/) to study diversification dynamics in the diverse North American clade of Castilleja (Orobanchaceae). The postdoc will focus on assembly and analysis of next-generation sequencing data using subgenomic approaches (microfluidic PCR, sequence capture) and phylogenetic comparative analysis of biogeographic, morphological, and ecological data, especially in relation to polyploidy. Research will require the integration of cytological, morphological, ecological, and molecular phylogenetic approaches.

In addition, the postdoc will have the opportunity to participate in teaching a 2-week Advanced Field Botany course for upper division undergraduates and early career graduate students. More information about the course can be found at http://webpages.uidaho.edu/dtank/AFB/ Required Qualifications: Ph.D. in Botany, Biology, Evolution, or related discipline.

Preferred Qualifications: Experience with molecular phylogenetics, next-generation sequencing data, phylogenetic comparative methods, and at least basic computational experience (e.g. Unix, R, Python). Evidence of strong writing and communication skills.

The position is available starting immediately, but the start date is flexible. The appointment is for one to three years, with annual extensions dependent on satisfactory performance.

Please apply by sending a cover letter, CV, and contact information for three references to David Tank (dtank@uidaho.edu). General inquiries are welcome.

David C. Tank Assistant Professor & Director, Stillinger Herbarium University of Idaho 208.885.7033 dtank@uidaho.edu http://www.phylodiversity.net/dtank/ dtank@uidaho.edu

UInnsbruck Bioinformatics

PostDoc: UInnsbruck.Bioinformatics

MOLECULAR ECOLOGY, INSTITUTE OF ECOLOGY, UNIVERSITY OF INNSBRUCK PostDoc position

We seek to hire a PostDoc with training in bioinformatics. The position is a 36-months position at the Molecular Ecology group of the Institute of Ecology, starting from 1 March 2014. Centering on the Alpine Space, the group's mission is interdisciplinary research, embedded in international collaboration networks. A list of research topics can be found at: http://www.uibk.ac.at/ecology/forschung/-

molecular_ecology.html.en. The successful candidate will participate in the next-generation sequencing of Alpine insects.

Responsibilities 1. de-novo assembly and annotation of ant and Drosophila transcriptomes and genomes, using mainly Illumina data 2. analysis of genome sequences of pooled individuals, including search for selection signatures 3. provision of advice / training to users in analysing high-throughput sequencing data and participation in other bioinformatics tasks as need arises in the group 4. participation in manuscript writing 5. participation in preparing grant applications 6. contact and collaboration with a range of scientists and laboratory technicians at the Faculty of Biology in Innsbruck, at other Austrian research facilities, and internationally

Selection criteria A. PhD degree in bioinformatics or equivalent area B. published research experience in bioinformatics, especially in the de-novo assembly and annotation of genomes using high-throughput sequencing data C. excellent skills in the installation / maintenance of Linux systems for bioinformatic purposes D. proficiency in Biopython, R, scripting languages (e.g. awk, Perl) E. experience in the use of relevant software packages for transcriptome and genome analysis (e.g. Trinity, Mira, SOAPdenovo, SAMtools) F. ability to work as part of a multi-disciplinary team G. ability to work independently H. very good knowledge of English

Salary The annual gross salary is Euro 47,765.20. The contract includes health insurance and 5 weeks of holidays annually.

How to apply To apply, please submit by E-mail to <birgit.schlick-steiner@uibk.ac.at>: a cover letter, systematic point-by-point replies as to your readiness for the responsibilities and how you meet the selection criteria, brief statement of research interests, curriculum vitae, and complete list of publications. Also, arrange for at least one letter of recommendation to be sent to <birgit.schlick-steiner@uibk.ac.at> Applications must be written in English. Review of applications will begin immediately and continue until a suitable candidate has been found. The University of Innsbruck is striving to increase the percentage of female employees and therefore invites qualified women to apply. In the case of equivalent qualifications, women will be given preference. An offer of employment is contingent on a satisfactory pre-employment background check.

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

More information needed? For more information, please contact: Birgit Schlick-Steiner <birgit.schlick-steiner@uibk.ac.at>

Birgit C. Schlick-Steiner Professor of Molecular Ecology

Institute of Ecology University of Innsbruck Technikerstr. 25 6020 Innsbruck, Austria Phone: +43 512 507-51750 Fax: +43 512 507-51799 http://www.uibk.ac.at/ecology/forschung/molecular_ecology.html.en Birgit.Schlick-Steiner@uibk.ac.at

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UMelbourne EvolutionCooperation

RESEARCH FELLOW Department of Zoology Faculty of Science The University of Melbourne, Australia

Salary: AUD$61,138 - AUD$82,936 p.a. (PhD entry level AUD$77,290 p.a.) plus 9% superannuation An exciting opportunity at the University of Melbourne to join a group investigating the nature and role of chemical signals and sensory conditions in the evolution of cooperation in an ant/lycaenid butterfly mutualism. You will undertake field-work in Queensland, New South Wales, and Victoria, and may also be involved in laboratory work at Harvard University.

Employment Type: Full-time (fixed-term) position available until 30 June 2015

Enquiries only to: Prof Mark Elgar Tel +61 3 8344 4338 Email m.elgar@unimelb.edu.au

Close date: 23 June 2013

For position information and to apply online go to www.hr.unimelb.edu.au/careers, click on 'Search for Jobs' and search under the job title or job number 0031438.

advertising-hr <advertising-hr@unimelb.edu.au>

UMichigan PopulationGenomics

Postdoctoral Associate in Population Genomics

Postdoctoral positions are available with Jeffrey Kidd in the Department of Human Genetics and Department of Computational Medicine and Bioinformatics at the University of Michigan Medical School. These positions are focused on population genomic analysis to learn about the demographic history of populations and species and how demography interacts with selection to create observed patterns of variation. Multiple projects are available in a number of systems, including human populations (particularly African populations), dogs, and other species.

Qualifications The applicant should have a Ph.D. in genetics, ecology and evolution, anthropology, molecular biology, bioinformatics, computational biology or a related field and have experience in the analysis of genome-wide data. Excellent written and oral communication skills are required.

Successful applicants will be part of a cutting-edge research program in genomics with ample opportunities for collaboration with researchers at the University of Michigan and around the world.

To apply, send a CV, cover letter describing your research experiences and ongoing research interests, and contact information for up to three references to Jeffrey Kidd at jmkidd@umich.edu

jmkidd@med.umich.edu

UOklahoma MetagenomicBioinformatics

Title of Position: Post-doctoral Fellow (bioinformatics emphasis) - Research Associate

Position text: Position requires previous bioinformatics training, with emphasis in metagenomics and analysis of next-generation DNA sequencing data (HiSeq/MiSeq preferred). Proficiency with programming languages "R" and either Perl or Python are expected. Earliest start date: July 1, 2013. Salary: 60K plus fringe. Email resumes or CVs to Cecil M. Lewis, cmlewis@ou.edu, with "Post-doctoral Fellow (bioinformatics emphasis) - Research Associate" in the subject line.

Located in Norman, Oklahoma, University of Oklahoma's Molecular Anthropology Laboratories specializes in anthropological genomics and metagenomics. Current projects include characterizing diverse host-associated microbiomes using biological samples collected from traditional indigenous communities, non-human primates, and archaeological "ancient" materials. An example of recent interviews: http://ehp.niehs.nih.gov/121-a118/. Our labs are located in the SRTC (http://srtc.ou.edu/index.php), a new building with several research groups working in environmental genomics (e.g., http://ieg.ou.edu/) and genome sequencing (e.g., http://www.genome.ou.edu/). Our building also houses part of OSCER, OU's supercomputer (http://www.oscer.ou.edu/). In 2008, CNN/Money Magazine ranked Norman as the sixth best small city within the United States.

cmlewis@ou.edu

UPorto LivestockPopulationGenomics

TWO POST DOCTORAL RESEARCH ASSOCIATES IN BIOINFORMATICS AND POPULATION GENETICS

The Population Genomics and Traits Group at CIBIO-University of Porto (http://cibio.up.pt) is seeking candidates for two Posdoctoral fellowships. The successful candidates will be expected to engage in a vigorous basic and applied research program focused on NGS (next generation sequencing) and SNPchip data from several domestic species and their wild relative species. The initial appointment to this position is for three years with a possible extension to six years. Requires a PhD in biology field or computer sciences with a solid background on population genetics and evolution as well strong experience with bioinformatics programming languages in a unix environment (Perl, Python, Javascript, SQL) and compiled languages (e.g. C++), relational databases, and construction of computational pipelines. Ability to work independently and with theoretical and empirical population genetics researchers is important.The projects, which include SNPChip, and Pool-Seq data require exper ience in working with large SNP data sets and sequence data. Good programming skills and familiarity with the available analysis tools are essential. The goal of the research is to test hypotheses related to animal domestication and molecular adaptation of populations and species to extreme environments. The postdoctoral research will be mainly focused in population genomics, selection, and demography of wild/domestic (livestock) species their parasites from all over the world. This work will include a large amount of data analysis, simulation, and bioinformatics. Several interesting datasets are in hand, which will allow the postdoc to analyze data and publish quality manuscripts relatively quickly to advance the field.

Instructions to Applicants: Applicants should submit by email a cover letter describing interests, skills (including any specific experience with the job responsibilities listed above), prior scientific experience (at least 1 year of posdoc and not less than 5 published papers), and 3 publications (.pdfs) from peer-reviewed journals (one at least as first author), their CV, and the names and contact information of 2 people who can provide letters of reference. Applications as well as demands for further information should be sent to Albano Beja-Pereira to the following email address: posdoc_call2012@cibio.up.pt

The successful candidate will apply to the Portuguese National Science Agency (FCT) and it's expected to start working in the first months of 2014. Fellowship wage will be 1495 euros /month (tax-free), with social security and national health system assess included.

Application review will start at June 15, 2013 and continue until the position is filled.

albanobp@fc.up.pt

UToronto MutualismEvolution

Postdoctoral Position in the Ecology or Evolution of Mutualism

A postdoctoral position is available in the Frederickson Lab in the Department of Ecology and Evolutionary Biology at the University of Toronto. My lab conducts research on the ecology and evolution of mutualism in a range of systems, especially protective ant-plant mutualisms, seed dispersal by ants, and, increasingly, interactions between bacteria and their plant or insect hosts.

The ideal candidate will have a clear intellectual vision of promising directions and unresolved fundamental questions in mutualism ecology or evolution. Projects may involve greenhouse or molecular work, field experiments, or behavioral research on live ant colonies in the lab. Lab members currently do field research at the University of Toronto's field station, the Koffler Scientific Reserve at Jokers Hill (ksr.utoronto.ca), as well as in the Peruvian Amazon and elsewhere.

The successful candidate will primarily conduct independent research and work towards publishing in peer-reviewed journals; the postdoc will also be expected to mentor students and to perform some light administrative duties. The position is for 1 year, with the possibility of a second year depending on both progress and available funding. The preferred start date is August 1, 2013, but the position could start as early as July 1, 2013 or as late as January 1, 2014. The salary is $40,000 Canadian a year.

Interested candidates should contact me by email (m.frederickson@utoronto.ca). Please include a single PDF attachment containing your CV, a brief description of past research accomplishments and future goals, and the names and email addresses of 2 potential references.

Toronto is a vibrant, multicultural city on the shore of Lake Ontario, with a high quality of life. The EEB department is home to an interactive, collegial group of ecologists and evolutionary biologists, and currently supports a strong group of postdoctoral fellows with diverse research interests.

– Megan Frederickson Assistant Professor Department of Ecology and Evolutionary Biology University of Toronto 25 Harbord Street Toronto, Ontario, M5S 3G5, Canada Email: m.frederickson@utoronto.ca Web: mutualism.ca

m.frederickson@utoronto.ca

UTuebingen EvolutionFishFluorescence

Two Year Postdoctoral Academic Associate in the field of fish visual ecology

The successful candidate will be integrated in an ongoing research programme within the Animal Evolutionary Ecology unit. We study the function and evolution of fish fluorescent patterns using state-of-the-art spectrometry equipment, microscopy and fish keeping infrastructure. The successful candidate is expected to develop a high-profile research programme and contribute to our teaching in marine visual ecology. The successful candidate should have a PhD in relevant fields such as e.g. theoretical and empirical analysis of light in marine environments, fish tissue pigmentation, fish colour vision or fish neuroanatomy.

We cooperate with other groups with complementary expertises, both nationally and internationally. The teaching load is 60 h during winter and summer term each.

The employment will be effected by the central administration of the university. The position is fulltime and limited up to two years. The pay scale classification refers to the German federal public service scale 13 (TV-L).

Disabled candidates will be given preference over other equally qualified applicants. The University seeks to raise the number of women in research and teaching and therefore urges qualified women to apply.

Please send a single PDF to office.michiels@biologie.uni-tuebingen.de including a motivation letter as well as a full CV. Please include details on research interests and accomplishments, teaching experience, external funding plus names and email addresses of at least two referees. Closing date for applications is 1 July 2013. Earliest appointment is 1 October 2013.

Prof. Dr. N. Michiels, University of Tübingen, Faculty of Science, Institute of Evolution and Ecology, Animal Evolutionary Ecology, Auf der Morgenstelle 28, 72076 Tübingen, Germany

Nico Michiels <nico.michiels@gmail.com>

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.

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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

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UUtah EvolutionPlantHerbivore

Postdoctoral position, May, 2013: The Kursar/Coley lab is looking for a Ph.D. in evolution or ecology with an interest in plant-herbivore interactions. Useful, though not essential, is a background in chemistry, including analytical chemistry, metabolomics, chemoinformatics, or the analysis of large data sets from LC-MS or GC-MS.

The primary responsibility will be the analysis by LC-MS of the secondary metabolites, including non-protein amino acids, saponins and highly diverse phenolics, of multiple species in a genus of tropical tree, Inga, in a project funded by NSF. Our lab owns and has full-time access to a Waters I-class UPLC with a Xevo-G2 Q-ToF detector. The position also entails care of the LC-MS. All maintenance is covered by contract. The ideal candidate will have an excellent record of publication. The position also entails interacting with graduate students and co-supervision of undergraduates.

We study the divergence of defenses in a phylogenetic context among species of the tropical tree genus, Inga, a process that may be central to speciation and coexistence. The position is flexible such that, in addition to the core metabolomics goals, one also may focus on related aspects of particular interest to the candidate.

The University of Utah encourages applications from individuals with disabilities, minorities, veterans, and women and is an equal opportunity and affirmative action employer.

The position is available on September 1 for an initial period of 1 year, with an option of up to 1 additional year. Salary (plus full benefits) will be commensurate with experience and qualifications. Please provide a CV, the contact information for three references, and a short (500- to 1000-word) statement regarding your future, long-term goals. Address questions and applications to Tom Kursar at kursar@biology.utah.edu http://biologylabs.utah.edu/coley Closing: July 15.

Renae Curtz <renaecurtz@biology.utah.edu>

UWisconsin Madison PopulationModeling

Post Doctoral Fellow - Population Modeling

Department of Forest and Wildlife Ecology, University of Wisconsin-Madison, Madison, Wisconsin

PROJECT DESCRIPTION: The successful candidate will work on a NSF-funded project to develop a Bayesian population model that incorporates information on the spatial distribution of related individuals derived using genetic methods. The post-doc will be housed at Groningen University in the Netherlands, but will be a University of Wisconsin-Madison employee and collaborate with faculty at both universities.

REQUIREMENTS: Applicants should have a doctoral degree in quantitative ecology, biostatistics, population genetics, or closely related discipline by the start date. A strong publishing record, programming experience (Python, Perl, and/or C), population genetics background, and population modeling skills are essential.

SALARY AND CONDITIONS: The position will be available Sept 1, 2013 and the duration of the appointment is 13 months. Salary will be $44,000 per year plus benefits.

APPLICATION/CONTACT INFORMATION: Applicants should send a cover letter, curriculum vitae, and contact information for three references in a single pdf-file to Dr. Zach Peery at mpeery@wisc.edu. The CV should contain a list of publications and information describing relevant skills and experience. Reviews of material will begin June 30, 2013 and continue until a suitable candidate is found.

Zach Peery Graduate Research Assistant Department of Forest and Wildlife Ecology University of Wisconsin Russell Labs 1630 Linden Dr. Madison, WI 53706

rickaes@gmail.com

Vanderbilt EvolutionPregnancy

A postdoctoral position is available to join a new collaboration between the Abbot and Rokas labs at Vanderbilt University. We are seeking candidates with strong backgrounds in evolutionary genetics and genomics, with expertise in statistical/computational/quantitative genetics. The primary appointment will be in the Abbot lab, but the candidate will join a team of faculty, postdocs, graduate students, and technicians in Biological Sciences at Vanderbilt. The Abbot lab studies social evolution and species interactions between insects and microbes, using a variety of evolutionary and molecular approaches.

The candidate will be encouraged to develop independent research and training directions. However, the candidate will be a primary associate in Abbot & Rokas' team working in a new March of Dimes-funded transdisciplinary Center, the goal of which is to elucidate the biology of birth timing and the pathogenesis of preterm birth to allow evidence-based development of preventative measures (http:/-

/www.marchofdimes.com/news/11085.html). Preterm birth is a frequent and often devastating adverse outcome of pregnancy, and the single most challenging problem in modern obstetric practice and child health. As part of the new Center, the Abbot & Rokas labs are developing the computational and conceptual tools necessary for generating a comprehensive evolutionary synthesis of human pregnancy. Our goal is to generate a set of database tools that will build bridges between evolutionary biologists, geneticists, developmental biologists, physiologists, obstetricians, and social anthropologists, and to exploit the power of cross-species comparisons and macroevolutionary history in order to elucidate human birth timing and disease susceptibility.

The Department of Biological Sciences at Vanderbilt University has a diverse research faculty. The department is centrally located on the main campus, and adjoins the Vanderbilt University Medical Center. Vanderbilt researchers enjoy the participation of excellent undergraduates and the resources of a thriving medical center. Our campus is located in the heart of Nashville, an up-and-coming, yet friendly and inexpensive city situated amidst the rolling hills of biologically diverse middle Tennessee. Candidates should send a CV and contact information for three references to Dr. Patrick Abbot, patrick.abbot@vanderbilt.edu. The position is effective immediately / July 1ST 2013 onward.

Patrick Abbot Department of Biological Sciences Vanderbilt University, Nashville, TN 37235 Tel. 615.936.2550 patrick.abbot@vanderbilt.edu http://vanderbilt.edu/abbotlab/Home.html See also: Antonis Rokas (http://as.vanderbilt.edu/rokaslab/)

patrick.abbot@Vanderbilt.Edu

Vienna DrosophilaAdaptationGenetics

A postdoctoral position is available at the Institute of Population Genetics, Vetmeduni Vienna (Austria). The research focus of the Institute of Population Genetics is on understanding the genetics of adaptation. This central question in evolutionary biology is being tackled using up-to-date methods and a variety of approaches, including experimental evolution, quantitative genetics, functional genetics, empirical population genetics, bioinformatics and statistics.

The successful candidate will have access to an excellent data set on thermal adaptation in Drosophila including:

1) Genome-wide polymorphism data from laboratory selection experiments exposing Drosophila to different temperature regimes.

2) Gene expression data of Drosophila populations evolved to different temperatures in the laboratory

3) GWAS data for traits related to thermal adaptation

4) Genome-wide polymorphism data for natural populations from environments with different temperatures

We are searching for a candidate with a keen interest to understand adaptation in Drosophila by combining information from these proprietary data sets. Given the scale of the experiment, sound statistical knowledge is beneficial and programming skills are essential.

In recent years, Vienna has developed into one of the leading centers in evolutionary biology (http://www.evolvienna.at). In addition, Vienna is home to the VDRC Stock Center, and a high-profile Drosophila research community, most notably at the IMP (http://www.imp.ac.at/) and the IMBA (http://www.imba.oeaw.ac.at/). In addition to a stimulating scientific environment, Vienna also offers an extraordinarily high quality of life. Affordable housing, excellent public transport, great restaurants, a range of international schools, two operas, two music centers, many theaters and museums in combination with a pleasant climate make Vienna one of the most attractive cities in Europe.

The position is available from July 2013. The application should be emailed to christian.schloetterer@vetmeduni.ac.at as a single pdf containing CV, list of publications, a statement of research interests, and the names of three references with contact details. While the search will continue until the position is filled, applications should be received by June 8, 2013 to ensure full consideration.

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

WorkshopsCourses

Barcelona PhylogeneticMorphometrics Sep3-6 2

Dear colleagues:

Last call for registration to the course “GEOMETRIC MORPHOMETRICS AND PHYLOGENY- Fourth edition”. End of registration with reduced fee May Th.

INSTRUCTOR: Dr. Chris Klingenberg (University of Manchester, UK) .

DATES: September 3-6, 2013; 30 teaching hours.

PLACE: Els Hostalets de Pierola, Barcelona (Spain).

Organized by: Transmitting Science, the Institut Catalá de Paleontologia Miquel Crusafont and the Council of Hostalets de Pierola.

More information: http://www.transmittingscience.org/courses/gm/gm-and-phylogeny/ or writing to courses@transmittingscience.org

This workshop provides an overview of the interface between geometric morphometrics and phylogenetics. It aims to give an overview of the different approaches and methods that link the two fields and to enable participants to apply them to their own research problems. Lectures that introduce concepts and methods are integrated with demonstrations of software that put them into practice right away. The main emphasis is on mapping shape data on existing phylogenies to reconstruct the evolutionary history of shape diversification, as well as comparative methods that take phylogeny into account. To enhance the practical approach of the workshop, participants are encouraged to bring their own data to conduct analyses and discuss results.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Soledad De Esteban Trivigno, PhD.

soledad.esteban@transmittingscience.org

China Conservation Oct19-Nov30

A field course is due to be running in Xishuangbanna, China this year Registration is now open, and a limited number of scholarships are available http://www.pfs-tropasia.org/2013/05/afec-x-china-2013/

alice Hughes <dr_achughes@hotmail.co.uk>

CostaRica Amphbian Jul29-Aug12

Hello,

Below is a brief description of the Organization for Tropical Studies' Microbial Ecology of Amphibian Decline, an upcoming graduate-level specialty course which will be taught in Costa Rica from July 29 - August 12, 2013. The course is worth 2 graduate academic credits transferable to all institutions within the Organization for Tropical Studies consortium, which includes over 50 universities in the USA, Latin America, South Africa and Australia. This course may be of interest to students in the fields of microbial ecology, amphibian ecology, vertebrate survey techniques, disease ecology and amphibian decline, emphasizing on modern approaches: genomics, proteomics and metabolomics.

http://ots.ac.cr/images/downloads/education/-graduate/specialty-courses/amphi biandecline.pdf

Your circulation of this material among graduate students in different departments and programs would be greatly appreciated.

Many thanks!

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Microbial Ecology of amphibian decline

Microbes are essential components of the environment because they provide key services that support ecosystem functioning. Our ability to understand these microbes has advanced substantially due to the recent development of rapid, low-cost, high-throughput sequencing. Entire microbiomes can now be characterized to understand both the identity and function of microbes within these communities. As a result, we are now gaining insights into microbial communities that are associated with animals. These recent developments in technology poise the field of microbial ecology to make important discoveries and advances regarding their relationship to amphibian decline.

This course will present students with a variety of topics relevant to the microbial ecology of amphibian decline, emphasizing on modern OMICS approaches (genomics, proteomics and metabolomics). During the first part of the course at La Selva Biological Station, students will learn to identify and sample amphibians in the field, detect by culture dependent and molecular techniques of both symbiotic and pathogenic microbes including Batrachotrychium dendrobatidis (Bd) and ranavirus, as well as build phylogenetic trees and analyze complete genomes of these microbes. At the end of this period, students will be able to design their own hypotheses and test them the following week at the University of Costa Rica, employing a combination of genetic, proteomic and metabolomics approach.

Course Content

Through fieldwork, computer-based and laboratory analyses, this course will help students gain basic knowledge and hands-on experience in the following diverse fields: amphibian ecology, vertebrate survey techniques, disease ecology, isolation and laboratory culture of amphibian pathogens, microbial ecology and diversity, host-microbe symbioses, molecular biology, phylogenetics, next generation sequencing technologies, comparative genomics, proteomics and metabolomics.

Participants

The course will be held in Costa Rica and is limited to 20 students. We anticipate that half of the students will come from Latin American institutions and about half from U.S. institutions. All participants should be fluent in English. A working knowledge of Spanish would be useful.

The course is intended for graduate students with an interest in amphibian conservation, microbial ecology or global change biology.

Course Instructors: Adrian Pinto Director, Microscopic Structures Research Center. Course Coordinator.

Ibrahim Zuñiga Microscopic Structures Research Center. Microbiology research.

Invited Faculty

Bruno Lomonte Instituto Clodomiro Picado, Proteomic research.

Godofredo Solano Centro de Investigaciones en Productos Naturales. Metabolomics research.

Gilbert Alvarado, DVM Microscopic Structures Research Center. Pathology research.

Gabriel Vargas, Microscopic Structures Research Center. Bioinformatics research.

Juan Abarca Microscopic Structures Research Center. Field research.

Course dates: July 29 - August 12, 2013 (arrive July 28, depart 13 August)

Application Deadline: June 14, 2013. For priority consideration, followed by open enrollment until filled.

Tuition: OTS consortium applicants $2300; non-member applicants $2900

Tuition includes: all lodging (hotel and biological research stations), all meals, all transportation within Costa Rica, all course materials (sample equipment and lab). Does not cover personal expenses or airfare.

Partial need-based scholarships are available; priority given to OTS consortium and Latin American applicants.

For more information please consult the OTS website www.ots.ac.cr

or write to Andrés Santana andres.santana@ots.ac.cr or Barbara Lewis barbara.lewis@ots.ac.cr for application information

andres.santana@ots.ac.cr

CostaRica AmphibianDecline Jul29-Aug12

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http://ots.ac.cr/images/downloads/education/-graduate/specialty-courses/amphi biandecline.pdf

or

http://bit.ly/10MDY4T

Your circulation of this material among graduate students in different departments and programs would be greatly appreciated.

Many thanks!

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Microbial Ecology of amphibian decline

Microbes are essential components of the environment because they provide key services that support ecosystem functioning. Our ability to understand these microbes has advanced substantially due to the recent development of rapid, low-cost, high-throughput sequencing. Entire microbiomes can now be characterized to understand both the identity and function of microbes within these communities. As a result, we are now gaining insights into microbial communities that are associated with animals. These recent developments in technology poise the field of microbial ecology to make important discoveries and advances regarding their relationship to amphibian decline.

This course will present students with a variety of topics relevant to the microbial ecology of amphibian decline, emphasizing on modern OMICS approaches (genomics, proteomics and metabolomics). During the first part of the course at La Selva Biological Station, students will learn to identify and sample amphibians in the field, detect by culture dependent and molecular techniques of both symbiotic and pathogenic microbes including Batrachotrychium dendrobatidis (Bd) and ranavirus, as well as build phylogenetic trees and analyze complete genomes of these microbes. At the end of this period, students will be able to design their own hypotheses and test them the following week at the University of Costa Rica, employing a combination of genetic, proteomic and metabolomics approach.

Course Content

Through fieldwork, computer-based and laboratory analyses, this course will help students gain basic knowledge and hands-on experience in the following diverse fields: amphibian ecology, vertebrate survey techniques, disease ecology, isolation and laboratory culture of amphibian pathogens, microbial ecology and diversity, host-microbe symbioses, molecular biology, phylogenetics, next generation sequencing technologies, comparative genomics, proteomics and metabolomics.

Participants

The course will be held in Costa Rica and is limited to 20 students. We anticipate that half of the students will come from Latin American institutions and about half from U.S. institutions. All participants should be fluent in English. A working knowledge of Spanish would be useful.

The course is intended for graduate students with an interest in amphibian conservation, microbial ecology or global change biology.

Course Instructors:

Adrian Pinto Director, Microscopic Structures Research Center. Course Coordinator.

Ibrahim Zuñiga Microscopic Structures Research Center. Microbiology research.

Invited Faculty

Bruno Lomonte Instituto Clodomiro Picado, Proteomic research.

Godofredo Solano Centro de Investigaciones en Productos Naturales. Metabolomics research.

Gilbert Alvarado, DVM Microscopic Structures Research Center. Pathology research.

Gabriel Vargas, Microscopic Structures Research Center. Bioinformatics research.

Juan Abarca Microscopic Structures Research Center. Field research.

Course dates: July 29 - August 12, 2013 (arrive July 28, depart 13 August)

Application Deadline: June 14, 2013. For priority consideration, followed by open enrollment until filled.

Tuition: OTS consortium applicants $2300; non-member applicants $2900

Tuition includes: all lodging (hotel and biological research stations), all meals, all transportation within Costa Rica, all course materials (sample equipment and lab). Does not cover personal expenses or airfare.

Partial need-based scholarships are available; priority given to OTS consortium and Latin American applicants.

For more information please consult the OTS website www.ots.ac.cr

or write to Andrés Santana andres.santana@ots.ac.cr or Barbara Lewis barbara.lewis@ots.ac.cr for application information

andres.santana@ots.ac.cr

KazimierzWielkiU EstimatingPlantMatingSystem Jun3-6

"Estimating mating system and gene flow in plants, with special emphasis to trees"

Dates: 3-6.06.2013

Venue: Kazimierz Wielki University, Institute of Experimental Biology

Chodkiewicza 30, Building F, Bydgoszcz, Poland

Website: http://www.gene-flow.ukw.edu.pl/index.htm

This workshop is a unique opportunity to broaden knowledge and experience on how to study mating patterns and gene flow in plants. The workshop is offered for students, post-docs and interested researchers from the partner institutions of EVOLTREE Network. Registration will be on the first-in first-served basis. The number of attendants is limited to about 20 persons. If less than 20 persons will register from within EVOLTREE, other people from outside the network will be welcomed. There is no registration fee.

The following subjects are intended to be discussed: Introduction to mating systems and gene flow; Microsatellites as genetic markers for estimating mating system and gene flow; Indirect inferences on gene flow based on spatial genetic structure; Indirect assessment of gene flow based on pollen pool structure (Two-Gener/KINDIST); Correlated mating systems; Principles of paternity analysis; Spatially explicit models for pollen dispersal; Inverse modeling of propagule dispersal; Inference on pollen and seed dispersal based on naturally established seedlings; 'Among population dispersal' - assignment methods as a tool for long distance gene flow estimation; Current limitations and future perspectives on estimating gene flow.

The workshop will be organized into morning and afternoon sessions. Morning sessions will provide theoretical knowledge on the methodology and statistical procedures used in mating system and gene flow studies. In the afternoon sessions, there will be computer lab where specific software used for estimation of gene flow will be presented and some examples of gene flow studies provided. This is a lab with hands-on the computers so each participant will be able to get training on the software (Spagedi, Kindist, Cervus, NM+). We expect that there will be also time for consultations with lecturers on specific topics interested for the participants. One all-day field trip is planned.

Up to 30 participants (based on first-on, first-served basis) are welcome.

Registration deadline: April 30th , 2013 (now extended until full board completed)

Lecturers (confirmed):

Olivier Hardy (University of Brussels, Belgium)

Juan Jose Robledo-Arnuncio (CIFOR-INIA, Spain)

Igor J. Chybicki (Kazimierz Wielki University, Poland)

El¿bieta Sandurska (Kazimierz Wielki University, Poland)

Jaros³aw Burczyk (Kazimierz Wielki University, Poland)

Organizing committee:

Chair: Jaroslaw Burczyk [burczyk@ukw.edu.pl]

Registration, travel and accommodation assistance:

Sandra Jankowska- Wróblewka [jankowska-wroblewska@ukw.edu.pl]

Micha³ Chmielewski [chmielewski@ukw.edu.pl]

Local support:

Ewa Sztupecka [sztupecka@ukw.edu.pl]

Katarzyna Kowalkowska [kasiakow@ukw.edu.pl]

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+48-52-3419197

Fax: +48-52-3419184

www(dot)ukw(dot)edu(dot)pl

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Jarek Burczyk <burczyk@ukw.edu.pl>

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

stephan.peischl@iee.unibe.ch

LakeheadU AncientDNA variable

Practical DNA Training Program:

A two-week (9 business days) intensive laboratory-based training program designed to teach participants the fundamentals of molecular techniques including DNA extraction, amplification (using PCR), sequencing and interpretation.

This training program is offered at various times throughout the year and we will work with you to find a suitable time for training.

Special Offer: Save the Tax! Save $455.00 by attending the Practical DNA Training Program June 17-27, 2013.

For more information please contact us at 807-343-8877 or paleodna@lakeheadu.ca or visit our website www.ancientdna.com and click on 'Training Programs'.

Thank you.

Karen.

– Karen Maa Administrative Assistant Paleo-DNA Laboratory 1294 Balmoral Street, 3rd Floor Thunder Bay, Ontario P7B 5Z5 Telephone: 1-866-DNA-LABS or 1-807-343-8616

Karen Maa <kmaa@lakeheadu.ca>

Madrid MasterEvolutionaryBiol Autumn

Dear EvolDir members:

The Master in Evolutionary Biology at Complutense University of Madrid (Spain) is about to open its application period for the new course, starting in autumn 2013.

The Master is an official postgraduate program directed to students seeking a comprehensive introduction to the major questions in evolutionary biology. To complete the program, students have to complete 60 ECTS credits. All students take four compulsory courses (The genetic basis of evolution, Natural selection and adaptation, Phylogenetic Systematics, Patterns and processes in macroevolution, each 6 ECTS) and produce a Master's Thesis (12 ECTS). The program is completed with four other 6-credit courses, to be chosen among the following: Molecular phylogenies, Phylogeography and its applications, Animal phylogeny, Evolution and phylogeny of plants, Life-history evolution, Mechanisms of speciation in plants, Principles of experimental design in ecology, Data analysis in ecology and evolution, Methods in evolutionary biology.

Information about the Master: http://www.ucm.es/-info/zoo/evolucion/inicio.html Prospective students should submit applications 21 May 2013 - 17 Jun 2013 (there may be another application period in autumn, which will open only if there are available places: 4-11 Sep 2013). All required information about the documents required to complete applications is available at the university website.

Best regards,

Javier Pérez-Tris

jperez@bio.ucm.es

jperez@ucm.es

MaxPlanckInst Leipzig LanguageEvolution Dec2-3

CALL FOR PAPERS Workshop: Talking Neolithic: The Indo-European Homeland Problem versus the Origin(s) of the First European Farmers Venue: Max Planck Institute for Evolutionary Anthropology Date: December 02-03, 2013

ORGANIZERS: Bernard Comrie (Max Planck Institute for Evolutionary Anthropology), Guus Kroonen (Copenhagen University)

CONFIRMED INVITED SPEAKERS Dr. P. Heggarty (MPI EVA Leipzig) Prof. M.A. Jobling (University of Leicester) Prof. J.P. Mallory (Queens University) Prof. J. Salmons (University of Wisconsin) Prof. P.C.H. Schrijver (Utrecht University)

CONTEXT In recent years, the study of archaeological DNA and strontium isotopes has been shedding more and more light on the origins and migrations of the first European farmers. The evidence now seems to confirm that the dispersal of agricultural techniques from Anatolia to Central and Northwest Europe was not merely cultural, but truly $B!H(Bdemic$B!I(B, i.e. induced by migrating farmers.

At the background of this, the debate on the location of the Indo-European homeland recently sparked into life again. In 2012, the widely supported theory that the Indo-European languages reached Europe during a Bronze Age expansion wave from the Ukrainian steppes was challenged once more by the rival Out-of-Anatolia hypothesis. This hypothesis, which claims that the

Indo-Europeans spread from Anatolia in the wake of agriculture, gained world-wide media attention after its implementation in a new model for language expansions. Meanwhile, current research on the pre-Indo-European loanwords in Germanic, Celtic, Greek and Latin reveals that the separate Indo-European dialects borrowed a significant part of their agricultural terminology from extinct Neolithic languages. This seems to suggest that the Indo-Europeans and the earliest European farmers were two culturally and linguistically distinct groups.

The questions that thus arise are: $B!H(BExactly how agricultural were the Indo-Europeans and how Indo-European were Europe$B!G(Bs first agriculturalists?$B!I(B

CALL The international workshop Talking Neolithic aims at creating an interdisciplinary focus on the European Neolithic in order to tackle 1. the Indo-European homeland problem and Indo-European expansions, in particular from the perspective of 2. the origin and nature of extinct prehistoric European languages, and 3. the spread of agriculture and/or the first European agriculturalists. The objective is to compare findings from different historical disciplines and unite them into a cross-disciplinary perspective. Within this framework, linguists, geneticists and archaeologists are invited to submit a paper of no longer than 20 minutes on any of these three or closely related topics. Abstracts should not exceed 400 words, fit on a single page, and must be sent to Guus Kroonen (guus(a)hum.ku.dk) no later than June 1, 2013. Please be sure to include your name, institute and contact information (land and e-mail address).

Guus Kroonen <Guus@hum.ku.dk>

Montana ConGen Sep2-7

ConGen 2013 Population Genomic Data Analysis Course http://www.popgen.net/congen2013/ Recent Approaches for Estimation of Population Structure, Gene-flow, Landscape Genomics, Selection Detection, and the Analysis of Next-Gen Sequence Data.

2-7 September 2013 Flathead Lake Biological Station, Montana, USA http://www2.umt.edu/flbs/ Applications for 2013 edition are now open!

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genomics of natural and managed populations. Emphasis will be on next generation sequence data analysis (RADs, exon capture, and whole genome sequence analyses) and interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers (students/participants) and leaders in conservation genomics to help develop the "next generation" of conservation geneticists. We will identify and discuss developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 25-30 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students at the end of their degree program).

Course/Workshop Format: For each subject, we typically provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and lodging together of the instructors and students in the same location (the beautiful Flathead Lake field station) will allow for extensive exchange and facilitate learning.

Cost (before July 1st): $US 1,300 - which includes all lodging, meals (& coffee breaks etc.), transportation (to/from airport and Glacier National Park), a field trip to Glacier Park, and power point slide shows of all lectures (as well as audio-visual recordings of each lecture, including "question & answering sessions"). USD $1,500 if payment after July 1st.

Deadline for application is 1 July, 2013

More information on http://www.popgen.net/-congen2013/ tiagoantao@gmail.com

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Montana Congen PopulationGenetics Sep2-7

ConGen 2013 Population Genomic Data Analysis Course http://www.popgen.net/congen2013/ Recent Approaches for Estimation of Population Structure, Gene-flow, Landscape Genomics, Selection Detection, and the Analysis of Next-Gen Sequence Data.

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Deadline for application is 1 July, 2013

More information on http://www.popgen.net/congen2013/ tiagoantao@gmail.com

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NESCent EvolutionaryQuantGenetics Aug5-10

Title: Evolutionary Quantitative Genetics Instructors: Stevan Arnold, Joe Felsenstein, Thomas Hansen, Trudy Mackay, Brian O'Meara, Patrick Phillips, Liam Revell, Josef Uyeda Dates: August 5-10, 2013 Application review begins: June 1, 2013 Website: academy.nescent.org Where: National Evolutionary Synthesis Center, Durham, NC, USA

As part of the NESCent Academy, we are pleased to open applications for Evolutionary Quantitative Genetics. In this workshop we will review the basics of theory in the field of evolutionary quantitative genetics and its connections to evolution that is observed at various time scales. Quantitative genetics deals with the inheritance of measurements of traits that are affected by many genes. Quantitative genetic theory for natural populations was developed considerably in the period 1970-90 and up to the present time. It has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements. Textbooks have not kept pace with these developments, and currently few universities offer courses in this subject aimed at evolutionary biologists. There is a need for evolutionary biologists to understand this field because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics. This workshop aims to fill this need by reviewing basic aspects of theory and illustrating how that theory can be tested with data. Participants will learn to use R, an open-source statistical programming language, to build and test evolutionary models. The intended participants for this workshop are graduate students, postdocs, and junior faculty members in evolutionary biology.

The course is co-sponsored by the American Society of Naturalists, and reduced tuition will be offered to participants who are ASN members.

Questions? email academy@nescent.org

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karen.cranston@gmail.com

@kcranstn

Karen Cranston <karen.cranston@gmail.com>

NESCent OntologiesEvolutionaryBiol Jul29-Aug3

Title: Ontologies for evolutionary biology Instructors: Melissa Haendel, Matt Yoder, Jim Balhoff, Erik Segerdell Dates: July 29-August 3, 2013 Application review begins: June 1, 2013 Website: academy.nescent.org Where: National Evolutionary Synthesis Center, Durham, NC, USA

Evolutionary research has been revolutionized by the explosion of genetic information available, and ontologies must play a central crucial in relating this knowledge to observable diversity. Ontologies provide scaffolding that interconnects many kinds of observations; across species, they provide evolutionary, developmental, and mechanistic insights. The theme for this year's course is 'enrichment'. We aim to help participants enrich their research through the use of ontologies, to enrich existing ontologies with new content, and to bring new domain expertise to the ontology community.

The course will start with introduction to ontology development and design (using OWL, Protege), including best practices for community interoperability. We will explore, explain, and demonstrate how ontologies are being used within the field of evolutionary biology. We will then focus on providing new material for and conceptual links between key existing ontologies and biodiversity informatics. Specifics will include strategies for ontology integration, mash-up of data using different ontologies, visualization tools, data stores leveraging ontologies, limits to ontological expression, and ontology manipulation tools and tricks. Following the introductory materials, we will apply what we have learned in the context of individual research projects and participants should come prepared with a research problem that they would like to use ontologies to help address.

Questions? email: academy@nescent.org

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karen.cranston@gmail.com @kcranstn

Karen Cranston <karen.cranston@gmail.com>

NESCent Durham GMODSummerSchool Jul19-23

Learn how to get started with GMOD's toolkit for genetics and genomics, GMOD in the Cloud!

July 19-23, 2013; NESCent, Durham, North Carolina http://gmod.org/wiki/2013_GMOD_Summer_School The 2013 GMOD Summer School is the best way to get to grips with GMOD in the Cloud, GMOD's suite of genomic and genetic software. Over five days, attendees will learn how to install, configure, and run popular GMOD software for visualization, storage, and dissemination of genetic and genomic data. The following software is covered:

- Chado, a species-independent database schema covering many areas of genetic and genomic data; - GBrowse, the ubiquitous genome browser; - GBrowse syn, a synteny browser built on GBrowse; - Galaxy, analysis and computation pipeline; - JBrowse, genome browsing evolved; - MAKER, automated annotation pipeline; - Tripal, a slick web interface for displaying and editing data from Chado; and - WebApollo, distributed community genome annotation tool (built on JBrowse).

There are additional sessions on setting up a GMOD in the Cloud virtual machine in the Amazon cloud, and common file formats.

Courses are taught by members of the software development teams, and there are work sessions in the evenings for participants to talk to the developers or apply what they have been taught to their own data.

For more information and to apply, visit http://gmod.org/wiki/2013_GMOD_Summer_School. There are some scholarship funds available for those from underrepresented minorities.

All applications should be in by June 10th. If you have any questions, please contact the GMOD help desk at help@gmod.org.

Hope to see you there!

Thanks, Amelia Ireland GMOD Community Support http://gmod.org || @gmodproject

amelia.ireland@gmod.org

Portugal Evolution Jul15-19

CALL FOR STUDENTS: 1st International SUMMER School on Evolution

Early Bird Registration deadline coming up!

July 15th - 19th, 2013 | Ciência Viva Knowledge Pavilion, Lisbon, Portugal Website: http://evolutionschool.fc.ul.pt/summer Early Bird registration until May 31st, 350 euro Late Registration until June 15th, 450 euro

About the courses

Module 1: EVOLutionary theory Courses are taught by: Luís Villarreal, Ilya Tëmkin, Frietson Galis.

Module 2: sociocultural Evolution Courses are taught by Fiona Jordan, Marion Blute, Nathalie Gontier & Emanuele Serrelli.

Module 3: philosophy of biology Courses are taught by Derek Turner, Frédéric Bouchard, Michael Ruse.

The course program is online at: http://evolutionschool.fc.ul.pt/summer/sub/pro/program.php All courses are taught at a level accessible to Master, PhD and post-doctoral students in the exact, life, human and sociocultural evolutionary sciences. Students of evolutionary biology, evolutionary developmental biology, virology, paleontology, evolutionary linguistics, evolutionary anthropology, and philosophy of biology will especially benefit from these courses. Students will be provided a mandatory reading list which will form the basis of lectures and discussions. There are neither examinations nor paper assignments.

REGISTRATION FEE 350 euro for the whole week, regardless the number of courses you chose.

HOW TO ENROLL You can enroll for a specific module (therefore following a 30-hour course on the subject) or you may choose three courses of your specific interest.

About the SUMMER School The School is organized by the Applied Evolutionary Epistemology Lab of the Centre for Philosophy of Science of the University of Lisbon, in collaboration with Ciência Viva and with the support of the John Templeton Foundation.

SUBSCRIBE TO THE SUMMER SCHOOL MAILINGLIST http://eepurl.com/n2EGb Websites http://evolutionschool.fc.ul.pt, http://appeel.fc.ul.pt

Find us on Facebook https://www.facebook.com/events/374500115949579

appeelannouncements@fc.ul.pt

Poznan Poland Bioinformatics Aug19-23

Category: Course Topic: Poznan Summer School of Bioinformatics 2013

Dear colleagues,

We are extremely happy to announce 10th edition of Poznan Summer School of Bioinformatics. This meeting takes place in Faculty of Biology at Adam Mickiewicz University in Poznan (Poland) from 19th to 23rd August 2013. This year the course will cover several areas of research at the interface between molecular biology and evolution focusing on using genetic and genomic data to infer phylogenetic relationships, identify unknown samples, gain knowledge about mechanisms of molecular evolution. The course is tailored for those who already have some basic knowledge in bioinformatics and find it necessary and interesting to learn more about bioinformatics applications in molecular evolution and phylogenomics. The course consists of lectures and hands-on - this combination should fit best your needs as you have a chance to try out the discussed methods yourself.

For further information please visit our website: http://bioinformatics-school.pl Please forward this announcement to anyone who might be interested.

Best regards, PSSB Organizing Committee Contact: genomics@amu.edu.pl

Bioinfo School <genomics@amu.edu.pl>

Shenzhen HumanPopulationGeneticAnalyses Oct14-18

Centre for Bioinformatics at University of Copenhagen and Beijing Genomics institute invites you to a PhD

Course in

Human Population Genetic Analyses

with an emphasis on Next-Generation Sequencing Data.

Dates: Oct 14-18, 2013. Venue: Beijing Genomics Institute, Shenzhen, China.

This course provides a one week comprehensive introduction to a number of topics and common research tools used in analyses of human population genetic data, including genetic drift, coalescence theory, population structure, natural selection, linkage disequilibrium, association mapping and admixture analyses. Using computer exercises students will be familiarized with common research tools including IM, Structure, PLINK, ANGSD, and pipelines for analyzing Next Generation Sequencing data. The fee for the course is $200 (waived for students from BGI or Department of Biology, University of Copenhagen) and includes dormitory style accommodation and food.

Instructors: Rasmus Nielsen, Noah Rosenberg, Anders Albrechtsen, Ida Moltke and Thorfinn Korneliussen.

For sign up and questions, please email: cphsummercourse@gmail.com. Registration deadline: September 1st 2013.

Rasmus Nielsen

rasmus_nielsen@berkeley.edu

UNordland NGSofNonmodelOrganisms Jun11-18

PhD course: high throughput sequencing of non-model organisms

Time: June 11-18, 2013

At: Faculty of Biosciences and Aquaculture, University of Nordland

High throughput sequencing technologies are being applied to a wide range of important topics in biology. However, the analyses of non-model organisms, for which little previous sequence information is available, pose specific problems. This course will address the specific strengths and weaknesses of alternative HTS technologies, the computational resources needed for HTS, and how to analyze non-model species using HTS. The course consists of a practical training module on the Ion Torrent PGM, HTS bioinformatics training, and lecturing/seminars of HTS approaches specifically targeting non-model organisms.

Find more information and application form on our web pages < http://www.uin.no/omuin/fakulteter/-fba/phdakvakultur/courses/Pages/High-throughput-sequencing-of-non-model-organisms.aspx >.

The registration deadline is May 29.

If you think anyone in your network would be interested in the course, please forward this information to them!

[cid:103113605@18052011-19E4] Best regards, Ms. GÃril FrÃmyr Borgen PhD coordinator Faculty of Biosciences and Aquaculture Phone: 75517351 E-mail: gfb@uin.no http://www.uin.no

GÃril FrÃmyr Borgen <Goril.Fromyr.Borgen@uin.no>

Valencia GenomicsHealth Jun24-Jul26

Applications are now open for the Third Edition of the CSISP Summer School. These courses are addressed at students and professionals in the biomedical, public health and related disciplines in biology and medicine. The school will run from June 24 until July 26, 2013 and will be focused on “Genomics and Health”. Further information can be obtained at http://www.csisp.gva.es/en/summer-school We look forward seeing you in Valencia!

Fernando Gonzalez.

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Prof. Fernando Gonzalez Candelas Catedrático de Genética / Professor of Genetics Unidad Mixta Genómica y Salud CSISP-UV/Instituto Cavanilles Universitat de Valencia Phone: (+34) 963543653 - 961925961 C/ Catedrático Jose Beltran, 2 FAX: (+34) 963543670 E-46980 Paterna (Valencia) SPAIN e-mail: fernando.gonzalez@uv.es http://www.uv.es/-%7Egonzalef/index.htm ResearcherID: G-5681-2010

fernando.gonzalez@uv.es

Venice EvoDevo Sep23-27

Summer School on Evolutionary Developmental Biology Conceptual and Methodological Foundations

3rd Edition: From Gene Networks to Organismal Systems

Venice, 23-27 September 2013

Organizers: Alessandro Minelli, Gerd B. Müller and Giuseppe Fusco School director: Johannes Jaeger

School sponsors: Istituto Veneto di Scienze, Lettere ed Arti, Venice and Konrad Lorenz Institute for Evolution and Cognition Research, Vienna. Location: Istituto Veneto di Scienze, Lettere ed Arti, Palazzo Franchetti, Venice

Taching panel: J. Jaeger, School Director (Centre for Genomic Regulation - CRG, Barcelona), C. Alonso (University of Sussex), P. Beldade (Instituto Gulbenkian de Ciência, Lisbon), G.E. Budd (University of Uppsala), G. Fusco (University of Padova), G. Giribet (Harvard University), V. Grieneisen (John Innes Centre, Norwich), R. Jenner (Natural History Museum, London), A. McGregor (Oxford Brookes University), A. Minelli (University of Padova), C. Mirth (Instituto Gulbenkian de Ciência, Oeiras), G.B. Müller (Konrad Lorenz Institute, Vienna)

Deadline for applications: May 30th 2013

For details, visit http://extra.istitutoveneto.it/-EDB2013/ Giuseppe Fusco Department of Biology University of Padova Via U. Bassi 58/B I-35131 Padova Italy tel. +39.049.827.6238 fax +39.049.827.6230 e-mail giuseppe.fusco@unipd.it webpage http://-dept.bio.unipd.it/fusco

Giuseppe Fusco <giuseppe.fusco@unipd.it>

Vienna eFLOWERSummerSchool Jul3-10

Dear colleagues,

Applications are invited for the first eFLOWER Summer School to take place in Vienna, Jul. 3-10, 2013. All detail are below and on our website (www.eflower.org).

Do not hesitate to pass this along to any potentially interested students.

Kind regards,

Hervé

ORGANIZERS: Hervé Sauquet (Univ. Paris-Sud) and Jürg Schönenberger (Univ. Vienna)

LOCATION: Faculty Centre of Biodiversity, University of Vienna, Rennweg 14, A-1030 Wien, Austria

DATES: 3-10 July 2013 (six working days); the weekend (6-7 July) may be used to explore Vienna

NUMBER OF PARTICIPANTS: 12

PURPOSE: To speed up data entry in the PROTEUS database in order to reach the first targets of the eFLOWER project (www.eflower.org). The School will consist primarily in massive entry of floral trait data, based on published descriptions, for a target list of species representing all angiosperm families, assisted by eFLOWER project coordinators, and interspersed with lectures by experts on a diversity of relevant topics for the project. Preliminary analyses and exciting new results will be expected and presented by the end of the School. All participants (PhD students, master students) will be offered co-authorship on the eFLOWER paper using the data from the School and have the chance to use PROTEUS for their own projects in their home labs as well as to continue collaborating on eFLOWER. The School offers a unique opportunity to learn about floral structure and evolution, angiosperm phylogeny, and contemporary macroevolutionary methods; great networking opportunity for students in an informal and friendly atmosphere.

INVITED SPEAKERS: Peter Endress (University of Zurich), Maria von Balthazar (University of Vienna), Susana Magallón (Universidad Nacional Autónoma de México), Brian O'Meara (University of Tennessee; virtual lecture).

PROFILE OF PARTICIPANTS: We target primarily early PhD students as well as master students with some knowledge of plant morphology, systematics, and phylogenetics. Students of flowering plant Evo-Devo are also welcome to apply.

APPLICATION: To apply, send a letter of motivation and your CV in a single PDF file to herve.sauquet@u-psud.fr and juerg.schoenenberger@univie.ac.atby 31 May 2013. Your letter should be no more than one page and explain clearly why you think the eFLOWER Summer School will be beneficial to your research and how you think your experience and expertise will benefit the project.

COSTS: Each participant will receive a travel grant for up to 250 Eur. Accomodation in a nearby youth hostel (including breakfast) will be covered by the School. Other meals and travel insurance are not included and need to be covered by the participants themselves.

Hervé Sauquet

Maître de Conférences / Assistant Professor Université Paris-Sud 11 Lab. Écologie, Systématique, Évolution (ESE) CNRS UMR 8079, bât. 360 91405 Orsay, France Tel/Fax: +33 169154991/+33 169154697 E-mail: herve.sauquet@u-psud.fr www.eflower.org herve.sauquet@gmail.com

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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.