EvolDir

June 1, 2012

Month in Review

Foreword

This listing is intended to aid researchers in population genetics and evolution. To add your name to the directory listing, to change anything regarding this listing or to complain please send me mail at Golding@McMaster.CA.

Listing in this directory is neither limited nor censored and is solely to help scientists reach other members in the same field and to serve as a means of communication. Please do not add to the junk e-mail unless necessary. The nature of the messages should be "bulletin board" in nature, if there is a "discussion" style topic that you would like to post please send it to the USENET discussion groups.

Instructions for the EvolDir are listed at the end of this message.

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Conferences

Avignon France EvolBiol Aug28-31

Program now available here: https://colloque4.inra.fr/petit_pois_2012/Pre-programme
Never been to Avignon? Good news: the 34th “Petit Pois Deridé“ (Ha-pea meeting) will take place next August 28-31, 2012, in Avignon. This a yearly meeting of the French community of evolutionary biologists, population biologists and ecologists. Emphasis is on having students and postdocs present their work and exchange with more senior scientists. The event is organized by the INRA research groups in Avignon and Sophia-Antipolis, and the University of Avignon. Book these dates! (even if you've been to Avignon before)

Online registration is open at http://www.ppd2012.fr (you'll have to create a user account in order to submit abstracts)

Contact us: ppd2012@avignon.inra.fr

Hoping to see you soon, The organizers

vincent.calcagno@sophia.inra.fr

Cambridge EvolInsectInfection Jul17

The Royal Entomological Society one day meeting of the Infection and Immunology Special Interest Group is to be held on the 17th July 2012 at the University of Cambridge.

The meeting will be a small intimate meeting on the evolution, ecology, genetics and immunology of insect-pathogen interactions, held in the spectacular setting of Gonville and Caius College, Cambridge.

Invited speakers are:

-Prof Greg Hurst (University of Liverpool) http://pcwww.liv.ac.uk/~ghurst/people/peoplegreghurst.html
-Prof George Christophides (Imperial College London) http://www3.imperial.ac.uk/people/g.christophides
We are now taking abstracts for talks, and also have limited places for posters.

To register email: b.longdon@ed.ac.uk (including a title and brief abstract if you would like to give a talk/poster).

-Where: Gonville and Caius College, Trinity St, Cambridge, CB2 1TA http://www.cai.cam.ac.uk/ -When: 17th July 2012 9am-5pm -Cost: £10 (payable on the day), which includes lunch and tea/coffee breaks. - Cambridge is easily accessible by train, and is a short train/bus journey from Stansted airport. -Accommodation is available through: http://www.accommodation.cam.ac.uk/-Info/TemporaryAccommodation http://-www.royensoc.co.uk/content/infection-immunology-special-interest-group-17th-july-2012 Ben Longdon <b.longdon@ed.ac.uk>

Cambridge HumanAdaptation Sep28-29

Dear colleagues,

You are warmly invited to take part in a conference on “High Altitude and Cold: Adaptation to the Extremes”. This two-day meeting aims to bring together leading experts in physiology, population genetics and anthropology to discuss advances in our current understanding of high altitude and cold adaptation and the origins of populations living in extreme environments.

The conference will be held at Magdalene College, University of Cambridge, UK, on 28th-29th September 2012.

Registration deadline: June 30, 2012.

Further details, including registration, can be found at: http://mega.bioanth.cam.ac.uk/conf/extreme/ Best wishes,

Toomas Kivisild Jay Stock Tiago Antao Alexia Cardona Christina Eichstaedt Luca Pagani Emma Pomeroy

– Tiago Rodrigues Antao Research Associate Leverhulme Centre for Human Evolutionary Studies Division of Biological Anthropology University of Cambridge CB2 1QH

tiagoantao@gmail.com

Chicago GalaxyCommunity Jul25-27 Update

The 2012 Galaxy Community Conference (GCC2012), being held in Chicago, Illinois, July 25-27, is now 10 weeks away, and several deadlines are approaching.

About the meeting:

GCC2012 is about integrating, analyzing, and sharing the diverse and very large datasets that are now typical in biomedical research. This is an opportunity to share best practices with, and learn from, a large community of researchers and support staff who are facing the challenges of data-intensive biology. Galaxy is an open web-based platform for data intensive biomedical research (http://galaxyproject.org) that is widely used and deployed at research organizations of all sizes and around the world.

Recent Updates:

1) A day of tutorials has been added to the agenda this year. The GCC2012 Training Day has 3 parallel tracks, each featuring four, 90 minute workshops and covering between and 7 and 12 different topics. Please take a few minutes to vote on topics that you would like to see presented: The survey ends this Friday, May 18, so please provide your feedback now. http://-bit.ly/GCC2012TDSurvey 2) The GCC2012 early registration deadline is June 11, which is just 4 weeks away. Registering early saves 36 to 42% on registration costs, and allows you to book discounted conference lodging before it fills up. Register now at http://wiki.g2.bx.psu.edu/Events/GCC2012/Register 3) A list of confirmed speakers and abstracts are now available on the conference web site. This list is not yet finished, but will give you a pretty accurate idea of the range of topics that will be discussed during the meeting. http://wiki.g2.bx.psu.edu/Events/-GCC2012/Program#Confirmed_Speakers Hope to see you in Chicago,

Dave Clements, on behalf of the GCC2012 Organizing Committee

clementsgalaxy@gmail.com

Durham EvolRecombination Jul14-17

Reminder– early bird deadline (May 13) in one week!

The 2012 annual meeting of the American Genetic Association will be held from 14-17 July at the Durham Convention Center in Durham, North Carolina, USA. The conference is entitled “Recombination: Molecular Mechanisms & Evolutionary Consequences”.

“Recombination” affects myriad areas of biology in general and evolution in particular, ranging from proper segregation of chromosomes to advantages associated with sexual reproduction to patterns of DNA sequence variation within and between species to processes of species formation. Come to this exciting conference and meet our delightful presenters (see below) and participants from diverse areas of biology.

We invite contributed posters in ANY area of biology that touches on recombination, and we invite contributed talks on studying the mechanisms of or patterns/ consequences associated with recombination.

Registration and conference information are online (http://www.theaga.org/2012/)

Early bird registration rates end May 13, 2012.

If you would like additional information about these exciting events, please email noor@duke.edu . Hope to see you there!

Distinguished lecture: Brian Charlesworth- University of Edinburgh, UK Talk title: “Background selection and patterns of molecular evolution and variation”

Symposium speakers: Adam Auton- Albert Einstein College of Medicine Justin Blumenstiel- University of Kansas Francesca Cole- Sloan Kettering Greg Coperhaver- University of North Carolina Justin Fay- Washington University (St Louis) Bret Payseur- University of Wisconsin Tom Petes- Duke University Jeff Sekelsky- University of North Carolina Nadia Singh- North Carolina State University John Willis- Duke University

Mohamed A. F. Noor noor@duke.edu Earl D. McLean Professor Tel: 919-613-8156 & Associate Chair Biology Department Lab: 919-613-8193 Box 90338 FAX: 919-660-7293 Duke University Durham, NC 27708 USA http://www.biology.duke.edu/noorlab/ noor@duke.edu

Edinburgh Phylogeny Jun13

The fourth meeting of the Scottish Phylogeny Discussion Group will be at the Royal Botanic Garden Edinburgh on 13th June 2012, 1 PM to 5:30 PM.

Professor Tim Barraclough(Imperial College) will talk on “Evolutionarily significant units of diversity above the species level”

As in the other meetings, the remainder of the programme will comprise contributed presentations. If you would like to contribute a talk, please email Toby Pennington (t.pennington@rbge.ac.uk)

To register please see:

http://biology.st-andrews.ac.uk/cegg/spdg Registration includes free lunch, tea and coffee.

Please register yourselves, and also encourage interested colleagues and group members to do so. People who can’t make it to this particular meeting can still join the discussion group to receive later announcements.

Toby Pennington (PhD) Head, Tropical Diversity Section Royal Botanic Garden Edinburgh 20a Inverleith Row Edinburgh EH3 5LR, UK Tel: (0)131 248 2818 (direct); 0131 552 7171 (switchboard) Fax: (0)131 248 2901 e-mail: t.pennington@rbge.org.uk http://www.rbge.org.uk Toby Pennington <T.Pennington@rbge.ac.uk>

Edinburgh QuantitativeGenet Jun17-22

4th International Conference in Quantitative Genetics, Edinburgh 17-22 June 2012

This is the final reminder about ICQG 2012. We have an exciting programme covering a wide variety of topics aimed at understanding the inheritance of complex traits and applying this knowledge. We now have over 600 delegates registered from over 50 countries. In addition to invited and contributed talks we will have about 400 contributed posters on display. Edinburgh has a great cultural and social scene for delegates wanting a break, and for accompanying persons.

For details of the programme and registration information go to http://www.icqg4.org.uk/ It is not too late to register - we still have space for some more participants.

We look forward to seeing you in Edinburgh next month.

The Organising Committee, ICQG4 Lutz Bunger, DJ de Koning, Chris Haley, Bill Hill (Chair), Mike Kearsey, Loeske Kruuk, Josephine Pemberton and Alan Wright

Loeske Kruuk <Loeske.Kruuk@ed.ac.uk>

Frankfurt MammalianDiversity Sep4-8

Dear colleagues,

Please note this ULTIMATE circular of the annual conference of the German Society of Mammalogy. The DEADLINE to submit your manuscripts is May 28, less than two weeks from now. As you know, this year this international conference will be hosted at the Senckenberg Institute and Natural History Museum in Frankfurt (Main), Germany. PLEASE DO NOT FORGET TO REGISTER! Main organiser is the Conservation Genetics Group, and several other Senckenberg and BIK-F groups are involved as well. DEADLINE FOR ABSTRACTS: MAY 28 !!!

–> http://www.senckenberg.de/dgs2012 <–

The conference theme is "The Past, Present and Future of Mammalian Diversity", and hence all topics in Mammalian Biology are covered in a modern and multidisciplinary atmosphere. There will be three days of conference with talks and poster sessions, divided into the (non-exclusive) topics:

- past (palaeontology, ancient DNA, phylogeny, phylogeography, evolution ...) - present (population structure and distribution, behaviour, physiology, morphology, current policy, other open topics ...) - future (conservation, policy making, predictive modelling, climate change, evolution again ...)

We have invited three plenary speakers to cover and introduce cutting-edge research in each of these groups of topics:

- Michael Hofreiter (http://www.york.ac.uk/biology/research/ecology-evolution/michael-hofreiter/) - Phil Stephens (http://www.dur.ac.uk/philip.stephens/welcome.htm) - Herbert H.T. Prins (http://www.reg.wur.nl/UK/Staff/Prins/)

We are looking forward to a major event this late summer, and hope to welcome participants from a diverse range of topics and backgrounds.

With best regards, on behalf of the organising committee,

Robert

Dr. Robert H.S. Kraus Conservation Genetics Group Senckenberg Research Institute Research Station Gelnhausen Clamecystrasse 12, D-63571 Gelnhausen, Germany tel. 0049-(0)-6051-61954-3130 fax. 0049-(0)-6051-61954-3118 robert.kraus@senckenberg.de www.senckenberg.de "Chance favours a prepared mind"

Senckenberg Gesellschaft für Naturforschung Rechtsfähiger Verein gemäß Â§22 BGB Senckenberganlage 25 60325 Frankfurt Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Michael Türkay, Dr. Johannes Heilmann, Prof. Dr. Pedro Martinez Arbizu, Prof. Dr. Georg Zizka, Prof. Dr. Uwe Fritz Vorsitzender des Präsidiums: Dietmar Schmid Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Robert.Kraus@senckenberg.de

Greensboro NC SocialInsectEvolution Oct5-7

Registration and Application for Travel Grants now Open for the 2012 IUSSI-NAS Meeting in Greensboro, NC

The 2012 Meeting of the North American Section of the IUSSI will be held on October 5-7, 2012 at Haw River State Park, near Greensboro in North Carolina. To extend the great tradition of this quadrennial meeting, we wish to warmly invite all scholars and especially students of social insects to this meeting. Registration and application for a number of competitive grants is now open. Please refer to the conference webpage for further details: http://www.cals.ncsu.edu/entomology/apiculture/IUSSI2012/HOME.html .Hurry! Participation is limited to the first 125 registrants and there will be no extended deadline for grant applications and talk registration... If you would like additional information about this exciting event, please email olav_rueppell@uncg.edu. Hope to see you there!

The organizers (David Tarpy, Ed Vargo, Humberto Boncristiani, Jim Hunt, Juliana Rangel-Posada, Mike Simone-Finstroem, Olav Rueppell, Stan Schneider).

Dr. Olav Rueppell Associate Professor Department of Biology Univ. North Carolina at Greensboro 312 Eberhart Bldg. Greensboro, NC 27403, USA Tel.: (1) 336-256-2591 Fax: (1) 336-334-5839 http://www.uncg.edu/bio/faculty/olav_rueppell/-lab/index.html orueppell@gmail.com

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Halle Germany PlantBreeding NGS Jun20-22

RNASeq Meeting, June 20-22, 2012 in Halle/Saale

First Call for Abstracts and Participation

Meeting on Advances and Challenges of RNA-seq Analysis

Halle (Saale), 20-22 June 2012

The tremendous pace at which sequencing technologies have been developed over the last years has triggered a plethora of new research projects that were unthinkable a decade ago. Examples are the 1000 Genomes Project, the Genome 10K Project, the Human Microbiome Project, or the Plant 1KP Project. Next-generation sequencing technologies have not only led to incredible advances, but also to great challenges, and our goal is to bring together researchers from different fields of science to discuss these topics in a stimulating environment at Martin Luther University Halle-Wittenberg.

We would like to invite abstracts for talks and posters on advances and challenges of RNA sequencing, both experimental and computational, from both users and developers of novel techniques. The meeting will be focused on plant transcriptomics, specifically on flowering time control, but otherwise ranging from small to long RNAs, from non-coding to coding RNAs, from model plants to crop plants. Despite the focus on plant transcriptomics, contributions to advances and challenges in bacterial, fungal, or animal RNA-seq analyses are highly welcome.

Keynote Speakers

- Gunnar Raetsch, Memorial Sloan-Kettering Cancer Center, New York, USA: “Computational Methods for Accurate Transcriptome Reconstruction”

- Peter Stadler, University of Leipzig, Leipzig, Germany: “Hidden Treasures in RNA-seq Data Sets”

- Gane Ka-Shu Wong, University of Alberta, Alberta, Canada: “1KP - An International Consortium Sequencing the Transcriptomes of 1000 Phylogenetically Diverse Plant Species from Angiosperms to Algae”

Key Dates

- Submission of abstracts: May 14, 2012 - Notification of acceptance: May 18, 2012 - Early registration deadline: May 31, 2012 - RNA-seq meeting: June 20-22, 2012

Organizing Committee

- Martina Bluemel, Kiel - Ivo Grosse, Halle - Yvonne Poeschl, Halle - Wolf Zimmermann, Halle

Program Committee

- Ivo Grosse, Halle - Korbinian Schneeberger, Cologne - Dorothee Staiger, Bielefeld - Conny Traenkner, Kiel

Location

Martin Luther University Halle-Wittenberg, Von-Seckendorff-Platz 1, 06120 Halle (Saale), Germany.

Contact

Martina Bluemel Christian Albrechts University Kiel Plant Breeding Institute Am Botanischen Garten 1-9 24118 Kiel, Germany

Phone: +49 (0)431 880 2135 Fax: +49 (0)431 880 2566

Further Information

WWW: http://www.flowercrop.uni-kiel.de/-scientific-workshops/rnaseq-workshop/ Email: m.bluemel(at)plantbreeding.uni-kiel.de

Martina Bluemel

Dr. Martina Blümel SPP 1530: Flowering time control - from natural variation to crop improvement - Administrative Manager - Plant Breeding Institute Christian-Albrechts-Universität zu Kiel Am Botanischen Garten 1-9 D-24118 Kiel Phone: +49-431-8802135 Mail: m.bluemel@plantbreeding.uni-kiel.de

“Bluemel, Martina” <m.bluemel@plantbreeding.uni-kiel.de>

Halle Germany PlantBreeding NGS Jun20-22 CallPosters

Call for Poster Abstracts and Participation

Meeting on Advances and Challenges of RNA-seq Analysis

Halle (Saale), 20-22 June 2012

The tremendous pace at which sequencing technologies have been developed over the last years has triggered a plethora of new research projects that were unthinkable a decade ago. Examples are the 1000 Genomes Project, the Genome 10K Project, the Human Microbiome Project, or the Plant 1KP Project. Next-generation sequencing technologies have not only led to incredible advances, but also to great challenges, and our goal is to bring together researchers from different fields of science to discuss these topics in a stimulating environment at Martin Luther University Halle-Wittenberg.

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- Gane Ka-Shu Wong, University of Alberta, Alberta, Canada:

“1KP - An International Consortium Sequencing the Transcriptomes of 1000 Phylogenetically Diverse Plant Species from Angiosperms to Algae”

Key Dates

- Submission of abstracts for posters: May 28, 2012
- Notification of acceptance for posters: June 4, 2012
- Early registration deadline: May 31, 2012
- RNA-seq meeting: June 20-22, 2012

Organizing Committee

- Martina Bluemel, Kiel
- Ivo Grosse, Halle
- Yvonne Poeschl, Halle
- Wolf Zimmermann, Halle

Program Committee

- Ivo Grosse, Halle
- Korbinian Schneeberger, Cologne
- Dorothee Staiger, Bielefeld
- Conny Traenkner, Kiel

Location

Martin Luther University Halle-Wittenberg, Von-Seckendorff-Platz 1, 06120 Halle (Saale), Germany

Contact

Martina Bluemel

Christian Albrechts University Kiel Plant Breeding Institute Am Botanischen Garten 1-9 24118 Kiel, Germany Phone: +49 (0)431 880 2135 Fax: +49 (0)431 880 2566

Further Information

WWW: http://www.flowercrop.uni-kiel.de/scientific-workshops/rnaseq-workshop/ Email: m.bluemel(at)plantbreeding.uni-kiel.de

Preliminary Program available at: http://www.flowercrop.uni-kiel.de/scientific-workshops/rnaseq-workshop/preliminary-program “Bluemel, Martina” <m.bluemel@plantbreeding.uni-kiel.de>

Lisbon ESEB2013 Aug19-24 CallSymposia

The 14th Congress of the European Society for Evolutionary Biology Lisbon, Portugal, 19-24 August 2013

CALL FOR SUBMISSION OF SYMPOSIUM PROPOSALS

Deadline for the submission of symposium proposal is 15 of July 2012

Symposia typically start with one or two invited speakers (40 min plus 5 for discussion) and are followed by submitted talks (15 min plus 5 for discussion). Symposia take place in one, two or a maximum of three 95-min windows. On special request, symposia can take the form of a discussion round or other more interactive forms of scientific exchange.

A symposium proposal consists of:

1. One organizer (for all communication) and one co-organizer (as a replacement) with contact details. Both are committed to attend the whole meeting. We do not provide financial support for organizing a symposium.

2. Topic: Please provide a title as well as a 5-line short summary.

3. Proposal details: Summarize in max. 1 page why you think this makes a good subject for the ESEB Congress and propose up to 4 possible (alternative) invited speakers (please check beforehand whether these people are available). If feasible, attach a list of possible submitted contributions (name + institution). ESEB will pay the registration fee for the (one or two) invited speakers in symposia. Please indicate whether you can generate financial support for accommodation or travelling of the guest speakers.

4. Time window: Explain why you want to apply for one, two or three 95- min time windows.

5. Submission: Send an email before 15 July 2012 tomail@eseb2013.com. Proposals will be evaluated and selected by the Scientific Committee. We expect to decide on symposia by September. Symposia proposals on overlapping subjects may be requested to fuse.

6. A call for talks submission will be sent out in November 2012. Symposium organizers must be prepared to screen submissions for their symposium (online evaluation system).

Check our webpagewww.eseb2013.com for updates.

Looking forward to your contributions

Yours

Octavio Paulo Chairman

Assistant Professor Computational Biology and Population Genomics Group Centro de Biologia Ambiental Departamento de Biologia Animal Faculdade de Ciências da Universidade de Lisboa P-1749-016 Lisboa Portugal

Tel: 00 351 217500614 direct Tel: 00 351 217500000 ext22359 Fax: 00 351 217500028 url:http://cobig2.fc.ul.pt/ Octavio Paulo <octavio.paulo@fc.ul.pt>

Lisbon ESEB2013 Aug19-24 CallSymposia 2

The 14th Congress of the European Society for Evolutionary Biology Lisbon, Portugal, 19-24 August 2013

CALL FOR SUBMISSION OF SYMPOSIUM PROPOSALS

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Octavio Paulo Chairman

Assistant Professor Computational Biology and Population Genomics Group Centro de Biologia Ambiental Departamento de Biologia Animal Faculdade de Ciências da Universidade de Lisboa P-1749-016 Lisboa Portugal

Tel: 00 351 217500614 direct Tel: 00 351 217500000 ext22359 Fax: 00 351 217500028 url:http://cobig2.fc.ul.pt/ Octavio Paulo <octavio.paulo@fc.ul.pt>

LosAngeles ProtistEvolution Sep6-9

Dear Colleagues,

Please visit the website for the 5th International Conference of Anaerobic Protists - https://sites.google.com/site/2012icap/home - which will be in Los Angeles, California Sept 6-9, 2012 for information about this important and exciting conference.

You will be able to register and submit abstracts (for both talks and poster presentations) between now and July 1. Detailed information about how to do this can be found on the website. Additional information regarding the goals and structure of the meeting, travel and housing, etc. is also available on the website.

Your participation in this meeting is important to make it a success! We hope to see you in LA in September!

Best regards, Patricia Johnson (on behalf of the organizing committee) Professor, UCLA

Robert Hirt - PhD Senior Lecturer Institute for Cell and Molecular Biosciences Catherine Cookson Building (2nd floor, room M2.042A) Framlington Place, Faculty of Medical Sciences, Newcastle University, Newcastle upon Tyne NE2 4HH, UK Tel. 0191 222 6963 (direct) Fax. 0191 222 7424 (central office)

Home and Lab page http://www.ncl.ac.uk/camb/staff/profile/robert.hirt http://research.ncl.ac.uk/microbial_eukaryotes/ Limbs are cherished because they are parts of the body Why then are other people not cherished because they are parts of humanity? Shantiveda

nrph2 <robert.hirt@newcastle.ac.uk>

Lund BehaviourSpeciation Aug18

ESF-symposium: “The role of Behaviour in Non-adaptive and Non-ecological Speciation” August 18 2012 (LUND)

Dear EvolDir-members,

We would like to remind everybody who are interested about a small and informal ESF-funded symposium in August 2012 entitled “The Role of Behaviour in Non-Adaptive and Non-ecological Speciation”, that will take place Saturday August 18 in Lund (Sweden). This symposium is one of several “post-conference symposia” that will take place after the ISBE-meeting (“Behavioural Ecology Congress) August 12 - 17 2012 (also in Lund).

Participation in the ESF-symposium is free of charge, and it is not required that one has participated in the regular ISBE-conference preceeding August 18. Participants have to arrange their own transport and ackomodation in Lund, however. There are three invited plenary speakers (see below), and also room for contributed talks (15 minutes + questions). You can sign up to this symposium and other post-conference symposia through this link (deadline June 15, 2012):

https://docs.google.com/spreadsheet/viewform?formkey=dFZCR0lMRS1BRmwxZ2dEV0Zfb1ZPZmc6MQ#gid=0 Invited plenary speakers:

Prof. Kerry Shaw (Cornell University, USA) Prof. John Wiens (SUNY, Stony Brook, USA) Dr. Rampal S. Etienne (Groningen University, Netherlands)

Here is more information about the symposium:

http://svenssonresearchlaboratory.blogspot.se/2011/07/esflund18aug2012.html Enquiries should be sent to Maren Wellenreuther (maren.wellenreuther@biol.lu.se)

Most welcome!

Erik Svensson

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

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

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

Marseilles EvolutionaryBiol Sep18-21 2

Dear All,

The registration and abstract submission for the 16th Evolutionary Biology Meeting at Marseilles, September 18-21, 2012, are open. Please visit the web site of the meeting http://sites.univ-provence.fr/evol-cgr where you will find all relevant information. The dead line is the 30 of june

The following subjects will be discussed:

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

Pierre

Pierre.Pontarotti@univ-provence.fr

MichiganStateU ArtificialLife13 Jul19-22 DeadlineExt

CALL FOR PARTICIPATION

Artificial Life 13 || Call for Participation

EARLY REGISTRATION DEADLINE EXTENDED UNTIL MAY 28th

The early registration deadline to attend Artificial Life 13 with the reduced registration fees has been extended until midnight, May 28th. Registration at the regular rate may be made at any time thereafter.

Artificial Life 13 The Thirteenth International Conference on the Synthesis and Simulation of Living Systems "Evolution in Action" July 19-22, 2012, Michigan State University East Lansing, Michigan, USA

www.alife13.org/ You are invited to participate to the upcoming Thirteenth International Artificial Life Conference. Please forward this call responsibly.

I. OVERVIEW It is a great pleasure for the BEACON Center for the Study of Evolution in Action at Michigan State University to host the 13th International Artificial Life Conference. Artificial life (ALife) refers to the synthesis and simulation of living systems as these occur in nature and also to possible alternative life forms and concepts that may not have occurred in natural evolution-that is, not only in "life-as-we-know-it", but also "life-as-it-might-be". ALife research may use not only biochemical models, but also computer models and robotics. The Artificial Life conference is held every other year under the auspices of the International Society for Artificial Life (ISAL), alternating with the European Conference on Artificial Life.

This year's major conference theme is "Evolution in Action." Life is shaped by evolutionary processes, and ALife models are a powerful way to investigate and utilize this key characteristic of living systems. We encourage submissions by biologists as well as by computer scientists and engineers, especially interdisciplinary papers that explore the many ways that evolution and artificial life research intersect. Other tracks this year include Behavior & Intelligence, Collective Dynamics, Synthetic Biology, and The Humanities and ALife. See the list of tracks below for examples of topics that may fall under these headings.

II. KEYNOTE SPEAKERS - Steven Benner, Foundation for Applied Molecular Evolution, Synthetic Biology - Oron Catts, University of Western Australia, Biotechnology & Art - Benjamin Kerr, University of Washington, Experimental Evolution - Radhika Nagpal, Harvard University, Self-Organizing Systems - Jack Szostak, 2009 Nobel Laureate in Physiology or Medicine, Massachusetts General Hospital, Evolution in Action

III. IMPORTANT DATES - Conference: 19-22 July 2012

IV. SUBMISSIONS Submissions are now closed.

V. TRACKS - Evolution in Action - Including evolutionary dynamics, simulations of evolution, developmental systems, experimental evolution, viral and bacterial evolution, evolution of drug resistance.

- Behavior & Intelligence - Including animal behavior; evolution of cognition and intelligence; evolutionary robotics; embedded systems.

- Collective Dynamics - Including group selection; evolution and stability of ecosystems; network dynamics; social dynamics; evolution of cooperation and conflict; collective motion and swarming in animals and animats.

- Synthetic Biology - Including synthetic cells, synthetic organisms, biological engineering, artificial genetic systems, artificial chemistry, origin of life, paleogenetics

- The Humanities and ALife - Including art, music, history and philosophy of artificial life.

See the conference web site www.alife13.com for more detailed descriptions of each of the tracks.

VI. LOCATION & LOGISTICS The conference will be held in East Lansing, Michigan, home of Michigan State University (MSU). Sessions will take place at MSU's Kellogg Hotel and Conference Center, located on the Red Cedar River on the edge of campus and within walking distance of downtown East Lansing.

Flights are available directly into Lansing, Michigan's Capital City Airport. Alternatively, one may fly to Detroit and then take a bus (the Michigan Flyer - www.michiganflyer.com) from Detroit Metro Airport to East Lansing.

Accommodations: A block of rooms in the Kellogg Center hotel will be available, as well as some university dormitory rooms. See the conference web page for further information.

VII. ORGANIZING COMMITTEE - Charles Ofria - Organizing Chair - Chris Adami - Program Chair - Adam Brown - Art Advisory Committee Chair - David Bryson - Technology Chair - Erik Goodman - Engineering Advisory Committee Chair - Connie James - Local Logistics Chair - Taylor Kelsaw - Sponsorship Chair - Richard Lenski - Scientific Advisory Committee Chair - Phil McKinley - Workshops & Tutorials Chair - Robert T. Pennock - Publicity & Proceedings Chair - Danielle Whittaker - BEACON Coordination Chair

VIII. HOST INSTITUTION BEACON Center for the Study of Evolution in Action Michigan State University East Lansing, Michigan U.S.A.

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Moscow MolecularPhylogenetics Jul31-Aug4 2

III Moscow conference ≪Molecular Phylogenetics MolPhy-3≫ New School Building, Moscow State University, 31 July - 4 August 2012, Russia

In response to communication with attendees the submission and registration deadlines have been extended for May 31, 2012.

Important dates: May 31, 2012- Registration and abstracts submission deadline June 5, 2012- Abstract acceptance notification date

The primary conference scope is in molecular phylogenetics and systematics, phyloinformatics, evolutionary genomics, problematic of the Tree of Life, applied phylogenetics.

Current invited lecturers:

Simonetta Gribaldo - Department of Microbiology, Institut Pasteur, Paris, France ≪Ancient evolution in the light of most recent genomic data≫

Arndt von Haeseler - Center for Integrative Bioinformatics Vienna (CIBIV), Vienna, Austria ≪One step mutation matrices: fresh view on modeling sequence evolution and some applications≫

Douglas Soltis - Department of Biology, University of Florida, USA ≪Big phylogenetic trees and plant evolution≫

Jim Leebens-Mack - Department of Plant Biology, University of Georgia, USA ≪Phylogenomic analyses across the green plant tree of life≫

Maximilian Telford - Department of Genetics, Evolution and Environment, University College London, UK Lecture title: TBA

Christian Bachem - Department of Plant Sciences, Wageningen University & Research Centre, Wageningen, the Netherlands ≪Comparative analysis of the highly heterozygous potato with the homozygous tomato genome≫

Evgeny M. Zdobnov - Computational Evolutionary Genomics Group, Swiss Institute of Bioinformatics, Geneva, Switzerland Lecture title: TBA

Svetlana A. Burlak - Faculty of Philology (Moscow State University), Institute of Oriental Studies (Russian Academy of Sciences), Moscow, Russia ≪Languages and Evolution≫

Irina Arkhipova - Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, Woods Hole, USA ≪Use of phylogenetic approaches to study horizontal gene transfer and evolutionary history of gene families≫

Alexander Gorbalenya - Faculty of Bioengineering and Bioinformatics (Moscow State University), Leiden University, the Netherlands ≪Viruses - their origin, systematics and evolution≫

The conference will take place in modern media-equipped facilities of the New School Building of Moscow State University. Among the organizers and sponsors are Moscow State University (the Faculty of Biology, Belozersky Institute for Physicochemical Biology, Faculty of Bioengineering and Bioinformatics, Research & Training Center "Evolutionary Genomics and Bioinformatics"), Russian Academy of Sciences (Institute for Information Transmission Problems, Institute of Paleontology), Russian Foundation for Basic Research, Ministry for Education and Science of Russia, Applied Biosystems (Life Technologies).

The conference language is English.

For further information please visit www.en.molphy.ru or e-mail at molphy@molphy.ru.

Sincerely, Organizers of MolPhy-3

roussine@yandex.ru

NMNH Paris EvolAnthro Sep3-5

The final program of the following international meeting is now available and registrations are open!

Revisiting the 'Negrito' Hypothesis, An Inter-Disciplinary Synthesis of the Prehistory of Southeast Asia www.mnhn.fr/mnhn/ecoanthropologie/-paris2012negrito/negrito_index.html What: Anthropology When: September 3-5, 2012 Where: The National Museum of Natural History, Paris, France

The 'negrito' hypothesis was one of the first evolutionary paradigms to emerge from the nascent academic discipline of Anthropology in the late 19th Century. It posits that various indigenous groups throughout island and mainland Southeast Asia have a shared phenotype - defined by short but gracile stature, dark complexion, and tightly curled hair - due to common descent from a putative ancestral population, representing a pre-agricultural substrate of humanity in the region. The meeting to be held in Paris 3-5th September 2012 is designed to revisit the 'negrito' hypothesis within an inter-disciplinary framework involving contributions from Archaeology, Biological Anthropology, Cultural Anthropology, Physical Anthropology, Social Anthropology, Linguistics, and Population Genetics. Methodological approaches will be both synchronic and diachronic, and a comparative approach is actively encouraged. The meeting will present the latest research available and explore where there is a common framework between the different disciplines.

This event will be open for attendance by other interested scholars working in the fields of Anthropology (Social, Cultural and Biological), Archaeology, History, Linguistics, and Population Genetics of Southeast Asia.

More information on the website: www.mnhn.fr/-mnhn/ecoanthropologie/paris2012negrito/-negrito_index.html Franz Manni <manni@mnhn.fr>

Niteroi Brazil ComparativeGenomics Oct17-19

Tenth Annual RECOMB Satellite Workshop on Comparative Genomics

October 17-19, 2012, Niterói, Brazil

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

KEY DATES

Paper submission deadline June 12, 2012

Acceptance notification July 03, 2012

Workshop October 17-19, 2012 - Niterói, Brazil

CONFIRMED KEYNOTE SPEAKERS

- E. Virginia Armbrust (University of Washington, USA)

- Mariangela Hungria da Cunha (Embrapa, Brazil)

- J. Peter Gogarten (University of Connecticut, USA)

- Dario Grattapaglia (Embrapa, Brazil)

- J. Chris Pires (University of Missouri, USA)

THEME AND SCOPE

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

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

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

Specific topics of interest include but are not limited to:

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

CALL FOR PAPERS

Papers should be submitted via the EasyChair system: https://www.easychair.org/conferences/?conf=-3Drecombcg12. Submissions must be received in electronic form by 11:59pm (Samoa time), June 12th, 2012.

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

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

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

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

Address any questions to the program committee chairs: Mathieu Blanchette (blanchem at mcb.mcgill.ca), Marilia D. V. Braga (mdbraga at inmetro.gov.br) and Marie-France Sagot (Marie-France.Sagot at inria.fr).

PROGRAM COMMITTEE

Chairs:

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Ottawa Evolution2012 Jul6-10 deadline

1st Joint Congress on Evolutionary Biology (i.e. 'Evolution2012' and more), July 6-10, 2012 - Ottawa, Canada www.evolution2012.org ***POSTER SUBMISSION CLOSES IN A FEW DAYS (i.e. FRIDAY, MAY. 250 @ midnight UTC/GMT -4 hrs)***

The 1st Joint Congress is a merging of the traditional

'Evolution' meeting (the annual meeting of the American Society of Naturalists, the Society for the Study of Evolution, and the Society of Systematic Biologists) with the annual meeting of the Canadian Society for Ecology and Evolution and the (normally biennial) meeting of the European Society for Evolutionary Biology. Along with a full range of topics in evolutionary biology, with the joint participation of the CSEE and the ASN, we look forward to increased representation of our ecologists.

LATEST NEWS

- Space remains in a number of optional workshops both before ("Communicating Science to Society" and "R for Biodiversity Analysis") and after ("Mathematical modelling in evolutionary ecology") the congress. For more details, see http://www.confersense.ca/Evolution2012/workshops.htm - Detailed information for those giving talks or posters is being posted on the congress website in the next few days. Note: talks will be held (forcefully) to 14 min.

- There are a number of exciting pre- or post-conference tours, including white water rafting, a guided tour of the National Gallery of Canada, and others. see http://www.confersense.ca/Evolution2012/tours.htm for more details

- The congress blog is up and running and will feature all sorts of useful information, including immediate conference updates and twitter tags (http://evolution2012ottawa.com/wordpress/)

- Accommodations remain at the Delta hotel. Book now.

- Travel information and advice on getting to Ottawa, and from the airport to your hotel can be found online, along with travel discounts codes (airline and train). See http://www.confersense.ca/Evolution2012/travel.htm Looking forward to seeing you in July.

Howard Rundle

Howard D. Rundle, Associate Professor Department of Biology, 30 Marie-Curie Priv. University of Ottawa, Ottawa, ON, K1N 6N5, CANADA Ph: +1 613-562-5800 x2835; Fax: +1 613-562-5486 Skype: howarddrundle http://www.science.uottawa.ca/~hrund050 http://www.evolution.uottawa.ca howard.rundle@uottawa.ca

Ottawa iEvoBio Jul10-11 Mentorship

The iEvoBio Mentorship Program pairs undergraduate and graduate students with faculty who have extensive experience in evolution, systematics, biodiversity, mathematics and/or software development to enhance their experience at iEvoBio 2012. Mentors will guide participants in collaborative and networking opportunities throughout the two-day conference.

If you would like to gain the wisdom of your colleagues' experiences by participating in this program, please email the iEvoBio 2012 organizing committee at committee@ievobio.org by June 1, indicating if you have any activities you would like to be included in the mentorship program, or a particular field of interest. You can find more information about the meeting and registration at http://ievobio.org/ . iEvoBio 2012 is sponsored by the US National Evolutionary Synthesis Center (NESCent) and by Biomatters Ltd., in partnership with the Society for the Study of Evolution (SSE) and the Systematic Biologists (SSB).

The iEvoBio 2012 Organizing Committee: Hilmar Lapp, US National Evolutionary Synthesis Center (chair) Robert Beiko, Dalhousie University Nico Cellinese, University of Florida Robert Guralnick, University of Colorado at Boulder Rebecca Kao, Denver Botanic Gardens Ellinor Michel, Natural History Museum, London Nadia Talent, Royal Ontario Museum Andrea Thomer, University of Illinois at Urbana-Champaign

becky.h.kao@gmail.com

Ottawa iEvoBioChallenge

Many trees enter. Fresh analysis ensues. New insights emerge.

As a reminder, the iEvoBio conference is again holding a Challenge competition in 2012, this time on the theme, "Synthesizing Phylogenies." Further information on the nature of challenge entries and how to submit them can be found on the iEvoBio website at http://ievobio.org/challenge.html. Submissions are due by June 25, 2012. Cash prizes will be awarded for first place (USD 1,500) and runner-up entries. The winning entries will be selected by a vote of the iEvoBio meeting participants.

Also, alongside the iEvoBio Challenge, 2012 iEvoBio sponsor Biomatters Ltd is running the Geneious Challenge. The goal of this challenge is to develop a new plugin to Geneious Pro, using the public API, that enables a new and exciting visualization or analysis. The winning entry will receive a $1000 cash prize, and all entrants who submit by the deadline will receive a 12-month subscription license. The deadline for the Geneious Challenge is the same as for the iEvoBio Challenge. See http://ievobio.org/geneious_challenge.html for more information.

More details about the iEvoBio conference and program are available at http://ievobio.org. You can also find continuous updates on the conference's Twitter feed at http://twitter.com/iEvoBio and Google+ page, or subscribe to the low-traffic iEvoBio announcements mailing list at http://groups.google.com/group/-ievobio-announce . iEvoBio 2012 is sponsored by the US National Evolutionary Synthesis Center (NESCent) and by Biomatters Ltd., in partnership with the Society for the Study of Evolution (SSE) and the Systematic Biologists (SSB).

The iEvoBio 2012 Organizing Committee: Hilmar Lapp, US National Evolutionary Synthesis Center (chair) Robert Beiko, Dalhousie University Nico Cellinese, University of Florida Robert Guralnick, University of Colorado at Boulder Rebecca Kao, Denver Botanic Gardens Ellinor Michel, Natural History Museum, London Nadia Talent, Royal Ontario Museum Andrea Thomer, University of Illinois at Urbana-Champaign

hlapp@nescent.org

UCambridge InsectPathogenEvol Jul17

The Royal Entomological Society one day meeting of the Infection and Immunology Special Interest Group is to be held on the 17th July 2012 at the University of Cambridge.

The meeting will be a small intimate meeting on the evolution, ecology, genetics and immunology of insect-pathogen interactions, held in the spectacular setting of Gonville and Caius College, Cambridge.

Invited speakers are:

-Prof Greg Hurst (University of Liverpool) http://-pcwww.liv.ac.uk/~ghurst/people/peoplegreghurst.html -Prof George Christophides (Imperial College London) http://www3.imperial.ac.uk/people/g.christophides We are now taking abstracts for talks, and also have limited places for posters.

To register email: b.longdon@ed.ac.uk (including a title and brief abstract if you would like to give a talk/poster).

-Where: Gonville and Caius College, Trinity St, Cambridge, CB2 1TA http://www.cai.cam.ac.uk/ -When: 17th July 2012 9am-5pm -Cost: £10 (payable on the day), which includes lunch and tea/coffee breaks. - Cambridge is easily accessible by train, and is a short train/bus journey from Stansted airport. -Accommodation is available through: http://www.accommodation.cam.ac.uk/-Info/TemporaryAccommodation http:/-/www.royensoc.co.uk/content/infection-immunology-special-interest-group-17th-july-2012 b.longdon@ed.ac.uk

UCentralFlorida SEEC Mar1-3

2013 Southeastern Ecology and Evolution Conference

University of Central Florida

Call For Abstracts

University of Central Florida will host the 2013 Southeastern Ecology and Evolution Conference and is announcing a call for abstracts for presentations of research. This is a scientific symposium aimed at graduate, post-doctoral, and undergraduate researchers in the fields of ecology, systematics, and evolutionary biology. The conference will be held on the campus of University of Central Florida on March 1st-3rd, 2013.

Abstract submission information:

Researchers interested in presenting posters or 12-minute talks are invited to submit abstracts. The deadline for the early registration and submission of abstracts is Friday, February 1st, 2013. Please submit your abstract along with registration at the SEEC website, found at http://www.seec2013.com . Abstracts should be limited to 150 words, and please include any primary and co-authors. Information about poster and talk requirements is available on the SEEC website. Early registration fees for the meeting are $25.

Please contact Joshua Solomon & Jason Strickland

mailto:SEEC.Host@gmail.com for questions

regarding registration or abstract submission, or general questions

about SEEC.

Or find us at facebook at https://www.facebook.com/-SoutheasternEcologyEvolution . Joshua Solomon

University of Central Florida Department of Biological Science Orlando, Florida 32817 mailto:joshua.a.solomon@knights.ucf.edu?subject=SEEC2013 Work: 203.520.2816

joshua.a.solomon@knights.ucf.edu

UHeidelberg EvolutionStemCells Jul6

COS Symposium "At the Roots of Stemness" - Evolution of regeneration mechanisms and stem cell systems- Heidelberg, Germany, July 6th, 2012

Dear Colleague,

the first annual symposium of the Centre for Organismal Studies (COS) entitled "At the Roots of Stemness" will highlight recent progress in regeneration mechanisms and stem cell function, with a particular focus on evolution.

The symposium will take place at the University of Heidelberg on Friday July 6th, 2012, in the big lecture hall (Grosser Hörsaal), Im Neuenheimer Feld 230, 69120 Germany. We would like to cordially invite you and your colleagues and collaborators to take part in this meeting.

Registration for the symposium, which is free of charge, will be open until June 15th, 2012. Please go to www.cos-hd.de to register; here you will also find the programme and announcement poster, in addition to information on the venue and accommodation.

In case of any questions, please contact us by email:

ildiko.somorjai@cos.uni-heidelberg.de
ute.volbehr@cos.uni-heidelberg.de

We look forward to seeing you in Heidelberg this summer!

Ildiko Somorjai Ute Volbehr

Dr. Ildiko Somorjai, PhD Cantab. Centre for Organismal Studies (COS) University of Heidelberg Im Neuenheimer Feld 230 69120 Heidelberg Germany

phone: (+49) (0)6221 54 52 56 fax: (+49) (0)6221 54 56 78

Ildiko Somorjai <somorjai@cantab.net>

GradStudentPositions

AveiroU GeneticPopStructure

ONE FELLOWSHIP (MASTER DEGREE) FOR MOLECULAR GENETIC ANALYSIS

One application is open for the allocation of one research fellowship (BI for an applicant with a Masters degree), under the project *Roads and mammals: implications on behavior and genetic structure *(PTDC/BIA-BIC/110097/2009) funded by FundaÃ§Ã£o para a Ciência e Tecnologia (FCT) from Portugal.

*1. **Scientific Area -* Biological Sciences

2. Professional experience requirements - Candidates to this fellowship must have a University first degree and Master in Biological Science (or related areas). Successful candidates should have a strong background in genetics, and laboratorial work that fits the plan of the project (see below). Good communication skills, ability to work independently, willingness to conduct intensive and flexible laboratory schedule work are essential.

*3. **Purpose of activity **- *We are seeking for a candidate with responsibility to perform laboratory procedures, such as DNA extraction, amplification, mitochondrial DNA sequencing and microsatellite genotyping to access the population structure of small mammals sampled in roads. The selected candidate will be also charged with statistical analysis of genetic data and scientific manuscript writing. We expect from the selected candidate a full commitment to the tasks involved in this project.

*4. **Place of work -* Aveiro University, Biology Department & CESAM (Portugal).

*5. **Principal contractor* - FundaÃ§Ã£o da Faculdade de Ciências da Universidade de Lisboa (FFCUL).

*6. **Host Institutions* - Centro de Biologia Ambiental /Faculdade de Ciências da Universidade de Lisboa (CBA, Lisbon Portugal) and Estacion Biológica de Doñana (EBD-CSIC, Seville Spain) in collaboration with Aveiro University, Biology Department & CESAM.

*7. ** Duration and conditions of activity*: This research fellowship is for an initial period of three months, scheduled to start in 1 September 2012 on an exclusive basis, in accordance with regulations for Advanced Training of Human Resources of FCT (980 euros/month) (http://alfa.fct.mctes.pt/apoios/bolsas/normasbolsasemprojectosunidades.phtml.en) and the Regulation of Scientific Research Grants from FFCUL. The contract may be renewed for a period of 13 months depending of the performance of the candidate.

*8. **Scientific orientation* - Research will be supervised by Dr. Clara Grilo (CBA/FCUL).

*9. **Documents*: All applications must contain the following documents: Cover letter with full contacts of the applicant and a motivation statement (máx. 1 page), Curriculum Vitae (máx. 3 pages including scores for each degree: graduation and Master) in Portuguese, Spanish or English, and two recommendation letters.

*10. **Applications should be directed by e-mail* to Clara Grilo - E-mail: cbgrilo@fc.ul.pt.

*11. **Opening date and deadline for applications: *The period to submit an application is from 1 June to 30 June 2012*.*

*12. **Criteria for fellowship selection*: The evaluation will comprise two steps: first step - CV evaluation (scores from 1-3 for lab experience, 1-3 for motivation, 1-3 for CV, 1-3 for recommendation letters; second step performance in an interview.

*13. **Jury*: Jury president: Clara Grilo (PhD, CESAM/EBD); effective vogals: José Godoy (PhD, EBD/CSIC), Carlos Fonseca (PhD, CESAM/UA), Rita Gomes Rocha (PhD, CESAM/UA); alternate vogal: Eloy Revilla (PhD, EBD/CSIC).

*14. **Results of the applications *will be sending by email to candidates until 30 July 2012*.*

Clara Grilo

Departamento de Biologia & CESAM Universidade de Aveiro 3810-193 Aveiro, Portugal

Departamento de Biología de la Conservación, Estación Biológica de Doñana (EBD-CSIC) Calle Américo Vespucio s/n, E-41092 Sevilla, España. http://www.ebd.csic.es/carnivoros/personal/grilo Clara Grilo <clarabentesgrilo@gmail.com>

BournemouthU GeneticPedigrees

Fully-funded, full-time PhD studentship (NERC)

Centre for Conservation Ecology & Environmental Sciences

Bournemouth University

**

Genetic pedigrees and individual trait variability: ecological and evolutionary consequences for wild fish populations

Recent advances in genetic data analysis have provided the tools so that evolutionary processes in wild populations can be inferred from molecular data. Molecular based pedigrees can be used to estimate reproductive success of individuals or phenotypes and for quantitative genetic analysis. The resulting information on heritability of ecologically significant life history traits or behaviours is crucial in accurately predicting responses to selection and is therefore a key element of evolutionary models. Here we will use sophisticated maximum-likelihood and Bayesian approaches for parentage analysis (e.g. molecular pedigree reconstruction) to produce field based heritability estimates. Important aspects of population structure such as geographic or behavioural barriers to migration to gene flow between subpopulations and the effective population size, can be inferred from these molecular data and as such provide both a framework for understanding micro-evolutionary processes and key information for the validation of evolutionary models.

In this PhD, we will use a riverine pike /Esox lucius/ population from the River Frome as a model for our predictions. The River Frome is a chalk stream with a total length of approximately 15km where pike are present. Since no freshwater connections exist to other river catchments it constitutes a closed system regarding non-migratory freshwater fish populations. The core investigation area covers approximately 4km of river length (33% of the available pike habitat) including seven discrete spawning sites. Data on growth, diet and sampling location are available for a large proportion of /E. Lucius,/ whose population has been studied on the river since 1976. These data have enabled quantitative measures to be made of population changes in terms of abundance, age structure, mortality, individual growth and diet, but a collection of tissue material also provide the opportunity to obtain genetic data and link them on individual life-history traits, providing an important temporal component for the project.

Candidates will be expected to have a strong ecological and mathematical background, and have a good theoretical and practical understanding of population genetics. Note the research will require an initial period of laboratory work for developing the genetic component of the model where full training will be provided. This is a fully-funded, full time studentship supported by the Natural Environment Research Council. For further details, please contact the supervisory team of Dr R Britton, Prof R Stillman and Prof Rudy Gozlan.

Closing dates for applications: 30^th of May

Starting date: October 2012

Informal Enquiries: To discuss this opportunity further please contact Prof. Rudy Gozlan 01202 966780 rgozlan@bournemouth.ac.uk

Information on how to apply can be found on: http://www.bournemouth.ac.uk/research/graduate_school/apply_phd_studentships.html

Emilie Hardouin <ehardouin@bournemouth.ac.uk>

ClarkU AnnelidEvoDevo

PhD position in evo-devo to study annelid central nervous system development

A PhD student position is available for the fall of 2012 in the Department of Biology at Clark University in Worcester, MA. Support is guaranteed for up to 5 years. Candidates should have a strong interest in developmental biology, nervous system evolution, or spiralian biology. Experience with molecular biology, phylogenetic analysis, or development is preferred.

Clark University offers a friendly and stimulating intellectual environment with equipment for high-resolution, time-lapse imaging and microinjection. The Meyer lab focuses on elucidating the molecular and cellular mechanisms driving central nervous system development in the annelid Capitella teleta. Current projects include the development of methods to visualize neural precursor cells in real time, characterization ventral nerve cord development, and functional analysis of genes involved in neural development. Further information is available at:

http://wordpress.clarku.edu/nmeyer/ Interested applicants should contact Dr. Néva Meyer at nmeyer@clarku.edu

Application information can be found at:

http://www.clarku.edu/departments/biology/phd/-gradapp.cfm Néva P. Meyer, Ph.D. Assistant Professor Clark University Department of Biology 950 Main Street Worcester, MA 01610 508-793-7476

NMeyer@clarku.edu

Dijon France DentalEvolution

Ecole Pratique des Hautes Etudes PhD Section of Life and Earth sciences

Title: Evolutionary novelties and emergence of dental phenotypes in Mammals. Host laboratory: EPHE Paléobiodiversité et évolution - UMR 6282 Biogéosciences

Laboratory address:

UMR 6282 uB/CNRS - Biogéosciences Phone / Fax

6 bd Gabriel, 2100 Dijon, FRANCE +333 80 39 63 47 / +333 80 39 63 87

PhD supervisors:

Names: Montuire Sophie, Couette Sébastien, Navarro Nicolas

Address: UMR 6282 uB/CNRS Biogéosciences, 6 bd Gabriel, 2100 Dijon, FRANCE Téléphone /Fax

+333 80 39 63 47 / +333 80 39 63 87

Emails : sophie.montuire@u-bourgogne.fr, sebastien.couette@u-bourgogne.fr, nicolas.navarro@u-bourgogne.fr

Descriptions and objectives

Background - Mammals display a high dental diversity in terms of number and complexity of teeth. This diversity attests of the influence of several parameters including diet and suggests a mammalian morphospace on which shape changes are possible in every direction. However, morphological changes within lineages seem to be constrained. Developmental processes producing the phenotypic expression of genetic variation are under natural selection. Favouring or limiting some directions of change in the morphospace, these processes will modify the evolutionary capacity on the short and long time scales. These constraints can influence the diversity of a clade (at a macroevolutionay level), forcing the accumulation of new species in one peculiar direction of the morphospace. In the dental raw the eruption of teeth follows an iterative developmental model in which interactions between teeth are controlled and lead to a final dental phenotype. Within teeth themselves, interactions occur between cusps following the same iterations and defining tooth morphology (number, position and shape of cusps). Some recent works showed that small modifications of cusp interactions can imply large modifications at the tooth scale, and for instance the development of new cusps.

Objectives - This subject will focus on two different mammal groups (rodents and primates) at different scales (population, lineages, clades). Complementary approaches will be addressed by both groups. Rodents display a reduced variation of the dental formula but a high diversity of molar form. In primates, the major part of variation occurs on the number of teeth and number of cusps on each tooth rather than on their shape. The main goal of this project is to understand the cusp interactions and their consequences on dental formula and teeth complexity (gains or losses of cusps and teeth). These variations of complexity will be analysed in the historic and evolutionary frameworks of the groups, and of the biotic (size, dietâ) and abiotic parameters.

National and international context- The ≪ EPHE -Paléobiodiversité et évolution ≫ and ≪ UMR uB/CNRS 6282 Biogéosciences ≫ laboratories have national and international recognition for their knowledge and skills in form analysis. The evolution of dental morphology in rodents and especially Arvicolinae is an historic and major topic of the EPHE laboratory since it establishment. These last years, people from the laboratory developed international collaborations on Evo-Devo themes on teeth.

Details:

- The duration of the fellowship is 3 years if accepted by the Doctoral School.

- The position is open until the 13th of june and the oral presentation will take place on the 3rd and 4th of july 2012 in Paris.

- Please contact Sophie Montuire (Sophie.Montuire@u-bourgogne.fr) for informal inquiries or applications (please attach CV and describe motivation).

- More details available on our group website: http://biogeosciences.u-bourgogne.fr/ and http://www.ephe.sorbonne.fr - More details available concerning the application (pratical details and fundings) on http://www.ephe.sorbonne.fr/recherche/-

contrat-doctoral- 2012.html

Pr. Sophie Montuire EPHE & UMR CNRS 6282 Biogéosciences Université de Bourgogne 6 Bld Gabriel 21000 Dijon Tél.: 33. (0)3.80.39.63.47 Fax : 33. (0)3.80.39.63.87 Sophie.Montuire@u-bourgogne.fr http://www.u-bourgogne.fr/BIOGEOSCIENCE/ http://www.ephe.sorbonne.fr Paleontological database http://transtyfipal.u-bourgogne.fr/ Sophie Montuire <sophie.montuire@u-bourgogne.fr>

ETH Zurich AnimalBehvaiourEvol

PhD Position: Quantitative study of dynamical animal social networks

At the Chair of Systems Design, we use methods from complex systems theory to understand the structure and dynamics of social systems, ranging from animal groups to human social networks. One of our areas of interest is the study of evolving social networks, and the link between the formation of social bonds and individual payoff.

We are starting a 3-year project in collaboration with the Institute of Evolutionary Biology at the University of Zurich to study the incentives of social interaction and social bond formation. The project will combine the analysis of a large data set on social interactions and individual fitness in a population of wild house mice with formal models of network formation in economic and social systems. It will also involve experimental manipulation of the social network to study its robustness and adaptivity to structural changes.

We are looking for an enthusiastic PhD candidate to join interdisciplinary research group in charge of this project. Whilst we are looking for people with a quantitative background in order to efficiently conduct data analysis and deal with formal models, the candidate will also interact extensively with researchers from the field of behavioural and evolutionary biology. As such, the candidate is expected to have a keen interest beyond the boundaries of his/her original field.

The candidate will have the opportunity to integrate in a lively team of scientists with various backgrounds (from economics to computer science), and maintain close collaboration with biologists from the partner institution. Occasional help with field work near Zurich may be required. The position requires strong communication skills and fluent English, written and spoken.

We offer excellent working conditions in a motivated team, a competitive salary (according to the ETH Zurich salary scale), and innovative research in close collaboration with leading institutions all over the world.

Applicants are asked to send their curriculum vitae, a list of their publications (if applicable), names of at least two references, and a short overview of their research interests (all in PDF files and in English) to Ms. Rahel Dulik, rdulik@ethz.ch

For specific inquiries, Prof. Frank Schweitzer (fschweitzer@ethz.ch) should be contacted.

The candidate is expected to start in July or August 2012 (flexible starting date). We expect applications at the latest by May 20, 2012. If no suitable candidate is found at this date, the position will be remain open for a second round of interviews at a later date.

Dr. Nicolas Perony, ETH Zurich, Chair of Systems Design, KPL F 32, Kreuzplatz 5, CH-8032 Zurich, Switzerland Tel +41 44 632 84 39, Fax +41 44 632 18 80 http://www.sg.ethz.ch/people/peronyn Nicolas Perony <nperony@ethz.ch>

France SalmonSelection

Hi Evoldir,

We are seeking a postgraduate student for a 3 year PhD (starting in fall 2012) on the effect of balancing selection acting on the (epi)genotype of Atlantic salmon at growth-, immunity- and reproduction-related traits. The project is managed by researchers from the UMR INRA-UPPA ECOBIOP (St Pée/Nivelle, France) and the Genomics and animal health Group at University of Basque Country (Bilbao, Spain).

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

Please send application (CV, letter, name of two referees) to etienne.prevost@st-pee.inra.fr, olivier.lepais@st-pee.inra.fr, cedric.tentelier@univ-pau.fr and begonamarina.jugo@ehu.es before the end of May.

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

cedric.tentelier@univ-pau.fr

GoetheU MolSystematics

The Department of Phylogeny and Systematics (Institute for Ecology, Evolution and Diversity) at Goethe-University Frankfurt am Main, Germany, invites applications for a

PhD position (EG 13 TV-G-U, 50%, ˜ £á 12.000 V 13.000 netto per annum).

The position is limited to three years and will start as soon as possible.

Our group focuses on molecular systematics, phylogenetics and evolution of inverte-brates with a taxonomic focus on molluscs. Recently strong emphasis is laid upon questions relating to the correlation between past climate changes and diversification. We are part of and in close collaboration with and in close collaboration with various researchers of the Biodiversity and Climate Research Centre. We are looking for a highly motivated biologist with a strong research focus in phylogenetics and/or evolutionary biology of invertebrates. An MSc. degree in Biology is required. The successful applicant will work on gastropod phylogeny and niche evo-lution with special emphasis on Pulmonata. Evolutionary questions like the transition from marine to terrestrial habitats shall be addressed. Solid methodological expertise in molecular phylogenetic techniques (including lab work and phylogenetic inference methods) is required. Knowledge of genomics is ad-vantageous. Additional knowledge of the morphology, anatomy and ecology of Gastropoda is beneficial.

Apart from scientific research the successful candidate will be involved in teaching activities of the Department of Phylogeny and Systematics at masters degree as well as in organization tasks within the department.

Please send your applications until June 15th 2012 to Klussmann-Kolb@bio.uni-frankfurt.de. The application should include a CV, a summary of the master thesis, as well as two references of academic supervisors.

Empfehlen Sie GMX DSL Ihren Freunden und Bekannten und wir belohnen Sie mit bis zu 50,- Euro! https://freundschaftswerbung.gmx.de Alexander Weigand <WeigandA@gmx.net>

LMU Munich PopGenetics

University of Munich (LMU), Department of Biology II, Section of Evolutionary Biology

PhD student position: Evidence for balancing selection at immunity genes in Drosophila

We are searching for a highly motivated PhD candidate to work on detecting signatures of natural selection on the genomic scale using next-generation sequencing data. The successful applicant will make use of population genomics data which has become available over the recent years for Drosophila melanogaster (e.g. http://www.dpgp.org) in order to uncover genomic regions that have been affected by natural selection. The focus will lie on genes involved in immune related processes which are thought to be governed by complex modes of selection such as balancing selection. The applicant will use statistical tests based on population genetics theory to distinguish between genomic regions evolving under neutrality and those where selection might have shaped patterns of DNA polymorphism.

The ideal candidate should have a Masters degree (or equivalent) in biology or bioinformatics with a strong background in population genetics and evolution. Since the majority of the project consists of large scale DNA sequence data analysis the candidate should have adequate computer programming and/or scripting skills to handle such kind of data. Additionally, some wet lab work (Sanger sequencing, qRT-PCR) might be required to verify results obtained from sequence analysis.

The research will be carried out in the lab of Prof. Dr. Wolfgang Stephan. The lab is part of the Section of Evolutionary Biology at the LMU Munich which is a strong, interactive group of theoreticians and experimentalists working on both plant and animal systems. We have a very international group and the everyday working language is English. The department is housed in a new, state-of-the-art BioCenter on the University of Munich High-Tech campus. More information is available on the web at: http://evol.bio.lmu.de The position (TV-L 13 65%) is funded by the Deutsche Forschungsgemeinschaft for three years and will be available starting August 2012.

Applicants should send a PDF including a cover letter detailing research experience and motivation for the position, CV, list of publications and contact details of 2-3 referees to:

hutter@bio.lmu.de

Application review will begin June 1st and continue until the position is filled.

The LMU Munich is an equal opportunity employer with an affirmative action program for the handicapped. Applications from women are encouraged.

Dr. Stephan Hutter Department of Biology II University of Munich Grosshaderner Str. 2 82152 Planegg-Martinsried Germany

Stephan Hutter <hutter@zi.biologie.uni-muenchen.de>

RennesU TheoPopGenet

Rennes University, France and the French National Institute for Agricultural research invite applications for a full-funded postgraduate PhD position in

POPULATION GENETICS AND EVOLUTION OF PARTIAL ASEXUALITY: INFERRING AND MODELLING THE IMPACTS OF PARTIAL ASEXUALITY ON POPULATION GENOMICS

At the Joint Research Unit "Institute of Genetic, Environment and Plant Protection".

Application before the 11th June 2012 (12 o'clock, French time). Please contact solenn.stoeckel@rennes.inra.fr and jean-christophe.simon@rennes.inra.fr

http://www.vas.univ-rennes1.fr/en/ Socio-economic and scientific context

The sudden advances of molecular biology in the last thirty years allowed biologists to extensively test, successfully use and improve the conceptual framework of population genetics. Regarding partially asexual species, population genetics allowed biologists to qualitatively identify some sexual or asexual events within populations and to disentangle sexual from asexual lines using empirical criteria. However, because of the lack of adapted theoretical model, biologists cannot compare the observed evolutionary patterns of these species to theoretical referential predictions, as they commonly do to study the ecology and the evolution of sexual species. We cannot content on current methods as they mainly rely on qualitative expertise. We are developing adapted models that take into account for the specific genetic functioning of such species. These models will enable non-biased predictions and reliable biological inference methods from field genetic data.

Assomptions and questions

Questions prompting this project are 1) what are the quantitative effects of partial asexuality on the expected gen-etic/-omic diversity and its structure in metapopulations when those ones undergo selective pressures? and 2) Do the joint effects of the evolutionary forces and this mating mode result in distinctive genomic patterns from which biologists may infer the current and past evolution of such species? The PhD student will answer by completing a population genetics model dedicated to partially asexual organisms so it takes into account for selective processes. This model will allow to study the evolutionary specificities and the genomic patterns left by of such functioning, and to propose some inference methods. Our model without selection has already shown that evolution of partially asexual species diverges from pure sexual and asexual species.

The main steps of the thesis

The work will consist in extending a mathematical model by formalizing the selective processes applied on genotypes. This step will complete the integration of all evolutionary processes in a population genetics model adapted to partially asexual species that has been developed with the appropriate formalism. The model will be included in optimized computation algorithms (coll. Symbiosis team, IRISA, Rennes). The model outputs will be analysed and confronted to simulation results, biological knowledge and experimental data already obtained by the host team, the partners of the ANR (the collaborative grant that fund the PhD expenses) and a scientific network. Then, the PhD student will explore the trends of his quantitative predictions, identify the characteristic effects of partial asexuality on population genetics indices under selection and participate in providing new descriptive indices adapted to such species (Coll. S.Arnaud-Haond, Ifremer, Brest). He will participate in the development of quantitative inference methods to identify forces and effective rates of asexuality under which genomes have evolved. Finally, the PhD student will reinterpret the historical significance of asexuality in the evolutionary histories of varied organisms. According to the student interests, our lab performs global surveys of some partially asexual species of aphids and whole genome functional and evolutionary analyses. If interested, the PhD student will have the opportunity to collaborate to these others works to open up on field, bioinformatics and lab works.

Methodological and technical approaches considered

(~15%) Running and developing mathematical population genetics models (Markov chain, differential equation, diffusion process, network analyses, sensitivity analysis) and simulations. (~15%) Low level parallel computation, optimized compilation, GPGPU. (~70%) Analyses and interpretations of theoretical predictions in population genomics and of already acquired datasets.

Scientific and technical skills required by the candidate

Good knowledge in at least one of those domains and motivated interests to learn the others: a) Mathematical modelling (Markov chain, stochastic differential equation); b) optimized algorithm and

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RobertKochInst Germany ClostridiumGenomics

PhD position - Genome-based molecular epidemiology of Clostridium difficile.

(Robert Koch Institute, Wernigerode, Germany)

Application deadline: 25. May 2012

In the group of Nosocomial Infections we search for a PhD candidate to investigate the short-term evolution and spatial spread of Clostridium difficile through analyses of the pathogen's genomic variability. Among the duties and responsibilites of the candidate will be the sequencing of bacterial genomes by applying second generation technologies, statistical and population genetic analyses of large datasets (>100 bacterial genomes), and additional molecular biological analyses.

Required qualifications are a Master's level university degree in the life sciences, or related, and a strong interest in population genetics and bioinformatics. A good command of English is essential. Bacic programming skills in Python, Perl, or R, and experience with molecular biological methods will be a plus.

The position (13 TVöD, 50%) is funded for three years, and the project should start by mid of 2012.

The Robert Koch Institute is one of the central institutions for health protection in Germany. It serves the Federal Ministry of Health as a central scientific institution in the field of biomedicine. The Institute combines basic research with risk assessment and with political advice. Its most important tasks include protection against infectious diseases and the analysis of the health situation in Germany.

The RKI is committed to equal opportunity for men and women and specifically encourage women to apply. In principle, part-time employment is possible. Severely disabled applicants will be given preference over non-disabled competitors if they possess the same qualification and aptitude.

Please send a cover letter stating the application code "22/12", a statement of your research interests, your CV, and contact details of two references to nuebelu@rki.de.

Dr. Ulrich Nübel Robert-Koch-Institut Burgstr. 37 38855 Wernigerode Germany

Tel. +49-3943-679-338 Fax +49-3943-679-317

"Nübel, Ulrich" <NuebelU@rki.de>

SwanseaU BacterialGenomics

BBSRC-funded Ph.D. studentshipÂin bacterial genomics and evolution (2012-2015)

Research will be conducted under the direct supervision of Dr Samuel K. Sheppard, and based in the Department of Medical Microbiology and Infectious DiseasesÂat the College of Medicine of Swansea University (Wales, United Kingdom).

Project description:

The successful applicant will join a multidisciplinary group focusing on population biology and evolution of bacterial pathogens of public health importance. They will investigate the genetic basis and ecology of niche adaptation in bacteria by explaining the factors involved in generating and maintaining genotypic and phenotypic diversity in pathogenic bacteria such as Campylobacter, E. coli and Staphylococcus. Comparative genomics and functional characterisation approaches will examine the genetic structuring within pathogenic populations and answer fundamental questions about how genetic variation and genome plasticity influence adaptation and the evolution of pathogenicity. They will be responsible for culturing isolates, extracting DNA for genetic characterisation, analysing genomic data and carrying molecular and functional characterisation in the lab.

Requirements:

Enthusiasm and practical experience in microbiology, molecular techniques (PCR, sequencing) and computer based genetic analysis, is necessary but training and support will be provided to strengthen these areas. The successful candidate will be highly motivated, creative, independent and have a good degree in molecular biology, microbiology, bioinformatics, genetics or ecology. Previous experience in a molecular biology laboratory or in bioinformatics research is also strongly desirable. Good English writing and oral skills are essential.

Details:

- The duration of a studentship is 3 years (2012-2015). - The position is open until filled, but a preferred deadline for application is 31st August, to allow for registration to start in the Fall semester. - Salary will be commensurate with regular UK postgraduate stipends, i.e. Â£13,950 (â¬17, 062)*perannum, tax − free. − PleasecontactSamuelSheppard(s.k.sheppard@swansea.ac.uk)forinformalinquiriesorapplications(pleaseattachCVanddescr* *Moredetailsavailableonourgroupwebsite : https : //sites.google.com/site/sheppardlab/GuillaumeMéric*

Guillaume Méric <G.Meric@swansea.ac.uk>

SwanseaU StaphylococcusEvolution

CASE(Industry/Academia)-funded Ph.D. studentshipÂ in Staphylococcus genomics and evolution (2012-2015)

Research will be conducted under the direct supervision of Dr Samuel K. Sheppard, and based in the Department of Medical Microbiology and Infectious DiseasesÂat the College of Medicine of Swansea University (Wales, United Kingdom). Additionaly sampling and research will be conducted in collaboration with an industrial partner co-funding this studentship.

Project description:

The successful applicant will join a multidisciplinary group focusing on population biology and evolution of bacterial pathogens of public health importance. They will investigate the genetic basis and ecology of niche adaptation in Staphylococcus sp. by explaining the factors involved in generating and maintaining genotypic and phenotypic diversity in isolates associated with poultry and human disease. Specifically, we will address questions about the transmission route of pathogenic S. aureus between agricultural and human hosts, and the various evolutionary bottlenecks associated with it. Comparative genomics and functional characterisation approaches will examine the genetic structuring within pathogenic populations and answer fundamental questions about how genetic variation and genome plasticity influence adaptation and the evolution of pathogenicity. They will be responsible for sampling isolates from chicken production sites (in collaboration with an industrial partner), culturing isolates, extracting DNA for genetic characterisation, analysing genomic data and carrying molecular and functional characterisation in the lab.

Requirements:

Enthusiasm and practical experience in microbiology, molecular techniques (PCR, sequencing) and computer based genetic analysis, is necessary but training and support will be provided to strengthen these areas. The successful candidate will be highly motivated, creative, independent and have a good degree in molecular biology, microbiology, bioinformatics, genetics or ecology. Previous experience in a molecular biology laboratory or in bioinformatics research is also strongly desirable. Good English writing and oral skills are essential.

Details:

- The duration of a studentship is 3 years (2012-2015). - The position is open until filled, but a preferred deadline for application is 31st August, to allow for registration to start in the Fall semester. - Salary will be commensurate with regular UK postgraduate stipends, i.e. approx. Â£14,000 (â¬17, 500)*perannum, tax − free. − PleasecontactSamuelSheppard(s.k.sheppard@swansea.ac.uk)forinf* *Moredetailsavailableonourgroupwebsite : https : //sites.google.com/site/sheppardlab/GuillaumeMéric¡G.Meric@swansea.ac.uk¿*

UCoimbra Portugal EvolutionInvasiveWeeds

We are looking for candidates that want to apply for an FCT (Portuguese Foundation for Science and Technology) doctoral fellowship to join us at the Centre for Functional Ecology (cfe.uc.pt) of the Department of Life Sciences of the University of Coimbra (Portugal).

The successful candidate will be expected to develop his/her research within the framework of the European project ReproWeed, which will investigate the creation of reproductive barriers between native and non-native ranges of the invasive weed Centaurea solstitialis. The research involves laboratory and field-based work and involves the interaction with an international network of collaborators, with the possibility to travel to California, Chile, Argentina, Australia, Turkey and Spain.

The candidate should have a good scientific background, with an interest into reproductive and evolutionary ecology of invasive weeds, and willingness to learn genetic molecular techniques. A good knowledge of the English language, experience with molecular techniques and ecological statistics is highly desirable. Candidates should be Portuguese or permanent residents and comply with the conditions to be a candidate for the FCT Doctoral Grants (BD; see previous year conditions at: https://www.fct.pt/apoios/bolsas/regulamento2011.phtml.en).

The doctoral fellowship includes a monthly payment of 980 euros (tax-free), plus an accident insurance and a monthly contribution to the Portuguese Social Security system (full healthcare and retirement, but no unemployment benefits). The project ReproWeed will cover for all research costs, including travels, attendance to conferences, etc. The scholarship is renewable for up to four years, at the end of which the candidate is expected to defend his or her PhD. dissertation thesis.

A call for fellowship applications will be open until June 21, 2012 but contacts should be made before June 15, at 5pm CET. Interested candidates should send a covering letter describing their research interests and experience, a CV, and the contact information for up to three professional referees to Daniel Montesinos (danimontesinos@gmail.com) or Sílvia Castro (scastro@bot.uc.pt). Informal inquiries are welcome.

More informations about the group:

http://www.mendeley.com/profiles/daniel-montesinos/ http://cfe.uc.pt/scastro http://www.uc.pt/en/fctuc/ID/plantecolevol Daniel Montesinos Centro de Ecologia Funcional Universidade de Coimbra Apartado 3046 3001-401 Coimbra, Portugal T: (+351) 239 855 238 (ext. 139) http://cfe.uc.pt/daniel-montesinos http://www.mendeley.com/profiles/daniel-montesinos danimontesinos@gmail.com

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UCologne HymenopteraMolEvol

PhD position - molecular evolution of sex determining genes in social hymenoptera

(University of Cologne, Institute of Genetics)

Application deadline: 20. Mai 2012

* *

We are looking for a highly motivated PhD candidate to study the population dynamic and molecular evolution of sex determining genes in social hymenoptera (honey and bumble bees). Understanding the evolutionary forces and processes that have led to the fascinating (single locus) sex determining system in these bees will contribute to elucidate general principles in evolution. Sex determination in the honey bee /Apis mellifera/ is governed by heterozygosity at a single locus harbouring the /complementary sex determiner/ (/csd/) gene, which arose by gene duplication prior honey bee divergence. Bees heterozygous at /csd/ are females, whereas homozygotes and hemizygotes (haploid individuals) are males. Diploid males occur when /csd/ is homozygous and are lethal in /Apis mellifera/. Rare alleles thus have a selective advantage, are seldom lost by the effect of genetic drift, and are maintained over extended periods of time when compared with neutral polymorphisms.

The ideal candidate should have a Masters degree (or equivalent degree) with a strong background in population genetics, including excellent skills in molecular lab work and major interest in bioinformatics. Genome data from several honey and bumble bees will be available for future research projects. We offer a stimulating and dynamic working environment and excellent research facilities in my recently established independent research group as Heisenberg fellow. Latest publications (PNAS; Nature, PlosBiol) can be found under http://www.ncbi.nlm.nih.gov/pubmed?term=Hasselmann%20Martin . The position (TV-L 13 65%) is funded by the Deutsche Forschungsgemeinschaft for three years.

The University of Cologne is committed to promoting equal-opportunity in employment. Women are particularly encouraged to apply. In case of equal qualification and aptitude, dis-abled persons will be given priority.

Applicants should send a cover letter, C.V., list of publications, a statement outlining past research experience and particular motivation for the position (max. 2 pages), and contact details of 2-3 referees to martin.hasselmann@uni-duesseldorf.de. Please contact me for any further questions and send in your application as a single pdf by 20. Mai 2012 latest. Interviews will start in June. The candidate should start working by mid of 2012.

PD Dr. Martin Hasselmann - Heisenberg fellow - University of Cologne Institute of Genetics Zülpicher Straße 47a, 4th floor

50647 Koeln Germany

Martin Hasselmann <Martin.Hasselmann@uni-duesseldorf.de>

UCopenhagen 2 InvertMarineEvoDevo

Two PhD scholarships in invertebrate morphology: [3]Evolution and development of central organ systems in marine meiofauna[2]

Two 3-year PhD positions are available at the Marine Biological Section, Department of Biology, University of Copenhagen. The positions will be jointly supervised by Katrine Worsaae, University of Copenhagen and Andreas Hejnol, Uni Sars Centre, Norway. Deadline for applications is June 11, 2012. The scholarships will address the origin of central body designs through detailed studies of, microscopic, complex animals of the lesser-studied spiralian lineages. Hereby we seek answers to central questions such as: Was the last common spiralian ancestor relatively large and complex as annelids and mollusks? Or was it microscopic consisting of low number of cells only? How complex and regionalized is the brain of microscopic animals? The PhD projects are expected to provide new scientific insight into the detailed structure, development, and evolution of central characters in selected spiralian meiofaunal taxa. Transcriptomes of these taxa are either in progress or will be generated during the project. The projects will combine the disciplines of advanced microscopy and immunochemistry (histology, TEM, CLSM, 3D reconstructions) with studies of gene expression patterns. Body designs and organ systems of interest could be e.g., the brain, sensory structures, seriality, cell numbers and size, dwarfism, alimentary canal. For further information on the project contact Assoc. Prof. Katrine Worsaae at kworsaae@bio.ku.dk. **Please do not post your application to this address**.

See full announcement and apply online via http://www1.bio.ku.dk/english/about/jobs/ Or at http://www.offentlige-stillinger.dk/sites/cfml/kbhuni/kbhuniVis.cfm?plugin=1 &englishJobs=NO&nJobNo 4560&nLangNo=1

Katrine Worsaae, Assoc. Prof. Marine Biological Section, Dep. of Biology, Univ. of Copenhagen Strandpromenaden 5, DK-3000 Helsingør, Denmark Associate editor, Acta Zoologica Homepage: http://www.bio.ku.dk/staff/kworsaae Katrine Worsaae <kworsaae@bio.ku.dk>

UEdinburgh DiseaseEvolution

A PhD-student position is available at the University of Edinburgh's Centre for Immunity, Infection and Evolution (CIIE) and working closely with partners in other institutions in the UK and Kenya.

The Wellcome Trust-funded Centre for Immunity, Infection and Evolution (CIIE) has become a major centre for interdisciplinary research into infectious disease since its inception in 2008. This thriving Centre is attracting dynamic and enthusiastic researchers, operating at the interface between disciplines (e.g. infection biology, immunology, evolutionary biology, ecology, epidemiology and mathematical modelling) to create new research paradigms to tackle infectious diseases.

CIIE is hosted within the Institute for Immunology and Infection Research (http://www.ed.ac.uk/schools-departments/biology/immunology-infection) and Institute for Evolutionary Biology (http://www.ed.ac.uk/schools-departments/biology/evolutionary-biology), these being part of the 'Edinburgh Infectious Disease' research community, one of the largest groups of infection biologists world-wide.

The PhD opportunity is funded by the Environmental and Social Ecology of Human Infectious Diseases (ESEI) project led by the University of Edinburgh together with nine other institutional partners in the UK and Kenya. This is an interdisciplinary project aiming to understand the mechanisms leading to the emergence of pathogens into urban populations, and their subsequent spread. Further details of the overall research programme are available at http://www.zoonotic- diseases.org/home/research/urbanzoonoses. The PhD will be co-supervised by members of the project consortium, and would involve working closely not only with the specific expertise relevant to the project, but also with economists, public health and veterinary public health practitioners, social scientists, epidemiologists and urban planners. Both projects will involve interacting with policy makers and a formal policy advice process in both the UK and Kenya.

How to apply:By 22nd June 2012, interested individuals who meet the eligibility criteria should send a pdf file " one document " which should include 1) CV (max. of 2 pages including the email and name of two academic referees) and 2) a one page statement of research interests directly to Eric.Fevre@ed.ac.uk, clearly marking "ESEI PhD studentship application" and "Project 2" in the subject line. Shortlisted candidates will be informed about interview dates (likely to be sometime in July).

Note: Due to restrictions imposed by the funding body, these opportunities are only open to those who meet the Medical Research Council eligibility criteria for PhD funding (see http://www.mrc.ac.uk/Fundingopportunities/Applicanthandbook/Studentships/Eligibility/index .htm).

Project 2: "Peri-domestic wildlife in urban Nairobi: ecology and epidemiological role in zoonotic pathogen emergence"

We are seeking a biologist/ecologist, preferably with a relevant Masters level degree, with quantitative skills, and in particular an interest in the epidemiology of pathogen transmission. The student would be registered at the University of Edinburgh, and would also be part of collaborators research groups at the University of Nairobi, the International Livestock Research Institute (both in Nairobi, Kenya) and the University of Liverpool. This studentship would involve extensive periods of time in the field in Kenya.

Urbanized environments in Africa are melting pots of activity and interaction: the wealthy live alongside the poor; livestock live alongside people; human and livestock waste is poorly disposed of near food production areas; formal and informal trading take place in internal and externally connected networks. This degree of mixing and contact creates ecological niches with opportunities for pathogen transmission, and several influential reports (Smolinski et al., 2003; Knobler et al., 2006) have linked urbanization to the risk of emerging infectious diseases (EIDs).

Approximately 60% of human pathogens are zoonotic (Taylor et al., 2001), and approximately 80% of novel pathogens have zoonotic origins (Woolhouse & Gowtage-Sequeria, 2005). Additionally, urbanization is likely to make pathogen emergence more likely, but the actual mechanisms for this happening are poorly understood.

This project would address a set of questions as part of a wider research programme on disease emergence in urban environments. The focus would be on the ecology and role of peri-domestic wildlife species (eg rodents, scavenging birds) on transmission of pathogens between livestock, humans

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UGuelph PopGenetics

University of Guelph - Population Genetics

An M.Sc. position beginning in September 2012 is available in the area of statistical population genetics or population genetic theory.

A student can attain the degree either through the Department of Integrative Biology (www.uoguelph.ca/ib) or the Graduate Program in Bioinformatics (www.bioinf.uoguelph.ca).

Statistical population genetics: The project will involve developing a novel approach to understand protein sequence evolution using multivariate statistical methods that are nonparametric. The approach will be initially applied to proteins involved in calcium signalling, but is a general technique applicable to all types of sequence data. Calcium signalling is an important and broadly used physiological process that occurs in heart, neural and skeletal muscle tissues.

Population genetic theory: Current research in my lab focuses on linking together the coalescent and ancestral graph to quantitative genetic variation. A student can work in this area or an area of their own interest.

In your introductory email, please send a statement of research interests and career goals, a brief CV including an official or unofficial summary of grades and contact information of two references. This information is to be sent to Dr. Cortland Griswold at cgriswol@uoguelph.ca.

The deadline for applications is June 15, 2012.

International students incur higher tuition fees than domestic students and will likely require outside support if they wish to attend the University of Guelph.

Cortland Griswold Assistant Professor Department of Integrative Biology University of Guelph Guelph, ON N1G 2W1 Canada

cgriswol@uoguelph.ca Telephone: 519-824-4120

x56240 http://sites.google.com/site/griswoldlab/
cgriswol@uoguelph.ca

UHawaii Honolulu LandSnailEvolution

Dear Evoldir community,

We have National Science Foundation funding to support two graduate students, one at the MS level and the other at the PhD level to work on systematics, evolution, biogeography and conservation of Hawaiian Land Snails in our lab at the University of Hawaii.

For full details and application instructions please go to http://www.hawaii.edu/cowielab/HLS_GA_notice.htm Kenneth A. Hayes University of Hawaii Pacific Biosciences Research Center Center for Conservation Research and Training 3050 Maile Way, Gilmore 408 Honolulu, HI 96822

khayes@hawaii.edu

UJyvaskyla Finland EvolEcolParasites

A PhD-student position is available at University of Jyväskylä (Department of Biological and Environmental Science), Finland

EVOLUTIONARY ECOLOGY OF CO-INFECTIONS IN PARASITES WITH COMPLEX LIFE CYCLES

Wild hosts are typically infected with a range of parasite species and genotypes of one species at the same time. This has significant implications for parasite-parasite interactions (one factor underlying parasite virulence) and for host's ability to defend itself against infections. These associations may also be subjected to considerable variation depending on the stage of a parasite life cycle. This is particularly true for parasites with complex life cycles that include several consecutive hosts with different conditions for co-infections in each. However, very little is currently known about these interactions in natural host-parasite systems.

This project will explore responses of parasites and their hosts to multiple parasite species and genotype infections, primarily using trematodes of the genus Diplostomum. The aims of the project are to determine (1) the role of antagonistic and facilitative parasite interactions in shaping co-infection dynamics, (2) the role of different types of host responses in determining the outcome of multiple infections, and (3) the influence of spatiotemporal dynamics of host-parasite interactions on patterns of parasite community assembly. Considerable latitude in specific research questions will be given to the student based on his/her personals interests.

Recent related papers:

Karvonen, A., Rellstab, C., Louhi, K.-R., Jokela, J. (2012). Synchronous attack is advantageous - mixed genotype infections lead to higher infection success in trematode parasites. Proceedings of the Royal Society B 279, 171-176.

Rellstab, C., Louhi, K.-R., Karvonen, A., Jokela, J. (2011). Analysis of trematode parasite communities in fish eye lenses by pyrosequencing of naturally pooled DNA. Infection, Genetics and Evolution 11, 1276-1286.

Karvonen, A., Seppälä, O., Valtonen, E.T. (2009). Host immunisation shapes interspecific associations in trematode parasites. Journal of Animal Ecology 78, 945-952.

Seppälä, O., Karvonen, A., Valtonen, E.T., Jokela, J. (2009). Interactions among co-infecting parasite species: a mechanism maintaining genetic variation in parasites? Proceedings of the Royal Society B 276, 691-697.

I invite highly motivated students with a background in evolutionary ecology / parasitology to apply. Starting date: 1st January 2013. For further information contact Dr. Anssi Karvonen (Group leader) anssi.t.karvonen@jyu.fi and visit http://users.jyu.fi/~anskarv/ More information of how to apply etc. can be found at: htpps://www.jyu.fi/science/en/phdstudentpositions < https://www.jyu.fi/science/en/PhD/ph2012 >

If interested, please submit your CV, contact information for two references, and a brief summary of research experience and interests through University of Jyväskylä electronic application system at: www.jyu.fi/science/en/applicationformphdstudents Application deadline is 15th June 2012.

Dr. Anssi Karvonen

anssi.t.karvonen@jyu.fi

Karvonen Anssi <anssi.t.karvonen@jyu.fi>

UKonstanz EvoDevo

PhD position in vertebrate Evo-Devo at the University of Konstanz, Germany

We are looking to recruit a PhD student with an interest in vertebrate Evo-Devo, to examine the molecular basis of jaw development in cichlid fishes. Cichlid fishes are exciting models for studying evolution as they have radiated to produce stunning morphological and behavioural diversity in a relatively recent time frame. Perhaps one of the drivers of this radiation has been innovation in their jaw morphologies. This has enabled them to occupy a broad range of trophic niches, with the ability to ingest diverse diets such as algae, zooplankton and molluscs and even the scales and embryos of other cichlids. It is believed that several unique features of the pharyngeal jaws of cichlids have facilitated this innovation in their trophic morphologies. The goal of this project is to identify the molecular determinants of pharyngeal jaw development that are unique to cichlids as a first step in determining the genetic basis of their trophic diversification.

This project is being conducted within the laboratory of Prof. Axel Meyer, which combines both extensive fish breeding and molecular laboratory facilities. The University of Konstanz is one of GermanyâÃôs Excellence Universities, providing world-class facilities, and is situated in Konstanz, a small, vibrant city on the beautiful shores of Lake Constance. The candidate should have experience in one or more of the following techniques: cloning, QRT-PCR, histology or in situ hybridization.

Please send a statement of your research interests, your CV, the names and contact details of two references and a letter of motivation by 10th June 2012. Applications and any informal enquiries should be directed to Helen Gunter (details below).

Helen Gunter helen.gunter@uni-konstanz.de http://www.evolutionsbiologie.uni-konstanz.de/index.php?section=109 http://www.zukunftskolleg.uni-konstanz.de/personen/fellows/helen-gunter/

Helen Gunter, PhD Postdoctoral Fellow, Zukunftskolleg LS Meyer, Evolutionary Biology Department of Biology University of Konstanz Universitaetsstr. 10 78457 Konstanz

Helen Gunter <Helen.Gunter@uni-konstanz.de>

UQueensland EvoDevo

University of Queensland, Mammalian EvoDevo

Call for applications for a PhD position: EVO-DEVO AND DEVELOPMENTAL BIOMECHANICS OF THE MAMMALIAN SECONDARY JAW JOINT

The Weisbecker Lab at the University of Queensland, Brisbane, Australia, is looking for a motivated PhD student, ideally with a background in either comparative anatomy, palaeontology, developmental biology, or biomechanics/engineering to work on a project on developmental evidence for the processes surrounding the evolution of the mammalian secondary jaw joint.

The origin of the mammalian middle ear was an extreme transformation in the evolution of mammals from reptile-like ancestors. Initially devoted to feeding, the jaw joint of the ancestral reptilian jaw joint was “re-tooled” and miniaturized to form middle ear bones (tympanic ring, hammer, and anvil). This process recapitulates during marsupial mammal development, presenting a great opportunity to infer intermediate stages and functional properties of MME detachment for which fossils are lacking. With research funding provided by the Hermon Slade Foundation, the Weisbecker lab is calling for applications for a PhD project on developing marsupials and monotremes to understand the history of the mammalian middle ear. The use of CT scanning, advanced virtual reconstruction, and virtual biomechanics (FEA) will allow asking whether the growing brain really pulled the MME bones away from the lower jaw, whether marsupials and monotremes really evolved their middle ear independently, and whether the developing marsupial jaw provides insights into the biomechanical functionality of jaw joint intermediates. For further details, visit http://sci-s03.bacs.uq.edu.au/biol/biol-news/may12/feature2.html Acceptance for this PhD is contingent on a successful application for PhD funding. Overseas applications are particularly encouraged, as the School of Biological Sciences at The University of Queensland has made available a number of international PhD scholarships. For further information and conditions of employment, please visit http://www.biology.uq.edu.au/scholarships. Students within Australia can apply for an Australian Postgraduate Award.

Please send expressions of interest, along with a CV, to v.weisbecker@uq.edu.au.

v.weisbecker@uq.edu.au

UWesternSydney EvolutionLifeHistory

PhD Scholarship: Using telomere dynamics to detect a physiological constraint on the pace of life-histories.

The Hawkesbury Institute for the Environment at the University of Western Sydney, Australia, is seeking a PhD candidate to work on a project in the field of physiological and evolutionary ecology. The PhD candidate is anticipated to commence in first semester 2012.

The project broadly seeks to understand the physiological basis of trade-offs in life history ecology and evolution. In particular, it will test the hypothesis that oxidative stress is a cost associated with increased investment in current production relative to future survival. The candidate will design and conduct a series of hypothesis-driven experiments to determine how variation in the pace of key life-history traits affect rates of telomere shortening and other molecular indices of oxidative stress. These experiments will shed light on the potential for individual mice to make physiological adjustments in response to perceived environmental conditions that maximise lifetime fitness but are associated with variation in rates of decline in physiological function.

The student will be advised by Dr Christopher Turbill (Hawkesbury Institute for the Environment) and work in collaboration with Professor Rob Brooks, Director of the Evolution and Ecology Research Centre at the University of New South Wales.

CRITERIA

The successful applicant should: demonstrate excellent academic performance related to the research proposed; hold qualifications and experience equal to an Australian First Class Bachelor Honours degree; be highly motivated to undertake further study at an advanced level; preferably have a background that includes the fields of comparative animal physiology, metabolism and ageing, free radical biology, and the evolution of variation in life history traits. Knowledge and experience of experimental design and statistical data analysis would be an advantage.

International applicants must also demonstrate a high level of proficiency in the English language. Please refer to the University's web site for information about English language requirements at www.uws.edu.au/international/admissions/-english_language_requirement WHAT DOES THE SCHOLARSHIP PROVIDE?

Tax free stipend of $33,728 per annum and a funded place in the doctoral degree. International candidates with a strong track record will receive a fee waiver. Funding is also available for project costs and conference travel.

NEED MORE INFORMATION?

Applicants should discuss their research aspirations and eligibility with Dr Christopher Turbill: c.turbill@uws.edu.au. Contact the Research Training, Policy and Programs Officer to discuss enrolment and scholarships: Ms Natalie McLaughlin: n.mclaughlin@uws.edu.au. To find out more about the Hawkesbury Institute for the Environment: www.uws.edu.au/hie HOW TO APPLY

Submit an application form and CV (including two referees) by the closing date. The application form can be downloaded from the web: www.uws.edu.au/research/-scholarships APPLICATIONS CLOSE: 25 MAY 2012 (Note extended deadline)

C.Turbill@uws.edu.au

UppsalaU FungalSystematics

*PhD-student position available in Systematics, *

at the Department of Organismal Biology, Uppsala University, Sweden.

The overall objective of the PhD project is to improve the understanding of speciation and intraspecific differentiation of ascomycete fungi. Using molecular sequence analysis, we will examine whether differentiation within and between closely related species correlate to spatial or ecological factors, estimate species niche amplitude and dissemination, and study how the morphological variation correlates with the genetic. The project includes work in the field, museum collections and molecular lab, as well as phylogenetic and population genetic sequence analyses and morphological microscopy studies. The student is expected to follow appropriate courses in mycology and systematic theory and practice, including phylogenetics, population genetics, bioinformatics, statistics and taxonomy.**

**

*Use the link below for more information*about the position or contact Åsa Kruys Asa.kruys@ebc.uu.se, tel: +46 18- 471 2770 or Stefan Ekman Stefan.ekman@em.uu.se, tel: +46 18- 471 2821.

http://www.uu.se/jobb/phd-students/-annonsvisning?languageId=1&tarContentId=188085

You are welcome to submit you application no later than June, 15th, 2012.

Åsa Kruys <asa.kruys@ebc.uu.se>

Vienna PopGenetics DeadlineMay15 2

Reminder: call for applications closing on May 15, 2012

New positions are available at *The Vienna Graduate School of Population Genetics* the application deadline is *May 15, 2012*:

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. Applicants with a genuine interest for interdisciplinary PhD education will be preferred.

All information about the about the PhD program, the projects and the application procedure can be found at www.popgen-vienna.at Only full applications (CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by *May 15, 2012* will be considered. Two letters of recommendation need to be sent directly by the referees.

Available topics:

* * + *Inferring selection using Drosophila whole genome sequence data* A whole genome survey of selected sites in African Drosophila melanogaster populations Incorporation of demography in theoretical models

+ *New algorithm and models to analyze population genetic massive parallel sequence data* Phylogenetic sequence assembly of 454 and Illumina reads A fast and efficient implementation of reference assembly

+ *Experimental evolution in Drosophila * + *Evolution of gene expression in Drosophila * + *Gene duplication and relocation: insights into adaptive specialization and sex-specific selection * + *Speciation genomics: mapping of hybrid incompatibilities * + *The nature of differentiation between two closely related species of oak * + *The genetics of two closely related species of Aquilegia * + *Natural variation in transposable element defense systems * + *Functionally important variation in lifespan and other life history traits in natural and experimental evolution populations * + *Mathematical models of spatially varying selection in subdivided populations * + *Statistical methods for detecting selective sweeps using genome-wide data * + *Population genetic estimators from NGS data: assessing the power for methods for genome scans of selection * + *The footprint of adaptive gene introgression after secondary contact *

+ *Probabilistic models for the population genetics of molecular evolution:* *Episodic selection histories and co-evolution * *Population trees and selection *

– 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

Jobs

BaylorCollegeMedicine Statistics

Research positions available for a statistician and a postdoc

The statistical genetics lab at Baylor College Medicine (http://www.bcm.edu/cnrc/mcmcmc/), headed by Dr. Yongtao Guan, is seeking candidates to fill two research positions: a statistician and a postdoc. The research focus of the lab is to develop statistical models and computational methods to address problems in modern genetics. Here are some research projects in the lab: 1) modeling linkage disequilibrium by approximating coalescent process with recombination and the applications in statistical and population genetics; 2) developing novel computational methods for de novo assembly and variants calling; 3) developing statistical methods for causal inference, in particular, efficient sampling schemes for directed acyclic graphs and its application; 4) statistical methods for non-invasive prenatal diagnostic using SNP arrays.

The Guan lab resides in the Children's Nutrition Research Center that is funded by USDA/ARS and Baylor College of Medicine. The center is located at the heart of the Texas Medical Center that consists of 40+ research institutes and hospitals. Here through collaborations, the statistician and postdoc will have the opportunities to work with world leading experts in statistical genetics, epigenetics, medical genetics, and clinicians. The candidates are expected to be motivated and passionate about science and innovation. The postdoc candidate is expected to have demonstrated ability in critical thinking, problem solving and writing. A Ph.D. degree in statistics / applied math / computer science is expected. A Ph.D. in bio-related major will be considered only if the candidate has demonstrated outstanding computational skills. For the statistician position, a Master degree in statistics / applied math / computer science is required. Experience in manipulating large-scale data set is expected. Fluency in C/C++ and Perl/Python is a must. The job title is negotiable and the salary is competitive based on qualifications with minimum annual salary of 50K (both positions come with full benefits). The initial term is two years with possible renew subject to performance and funding availability.

To apply, please send CV and contact information of three references to yongtaog@bcm.edu with headings 'postdoc application' or 'statistician application'. Baylor College of Medicine is an Equal Opportunity, Affirmative Action and Equal Access Employer.

Yongtao Guan, PhD Assistant Professor Baylor College of Medicine Tel: 713-798-0362 http://bcm.edu/cnrc/mcmcmc "Guan, Yongtao" <yongtaog@bcm.edu>

CollegeCharleston ResTech PlantVariation

Research technician at College of Charleston:

A research technician position in plant ecological genetics is available at the College of Charleston. Recent university graduates interested in research experience prior to graduate school or individuals with a master's degree who interested in additional research experience are encouraged to apply. This position requires a bachelor's in biology or related field. Candidates with master's degrees will also be considered. The research project includes field work, greenhouse work, and detailed morphometric analyses to study aboveground and belowground traits and their relationships. We will be investigating natural variation in Europe as well as examination of specific T-DNA insertion mutants. Qualifications include previous experience with greenhouse methods and plant growth, excellent organizational skills, ability to work alone or in groups, self-motivation and independence, and general facility with quantitative data. Spanish language skills are an asset. Valid driver's license and ability to lift large bales of potting mix are required. Duties will include plant care in greenhouse setting, travel to international field sites in Europe required, field experiments at remote field sites, phenotyping root and aboveground traits, data management including entering data into a database, participation in outreach activities, some supervising of undergraduate researchers, general laboratory, greenhouse and computational tasks. Currently available for one year. For additional details and to apply https://-jobs.cofc.edu < https://jobs.cofc.edu/ > Research Assistant Position in Biology. Closing date May 31 or until appropriate candidate identified. Questions regarding the position can be directed to Courtney Murren, murrenc@cofc.edu.

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

DurhamU ComputationalBiol

Professorship/ Readership at Durham University

Position available for a Professor (preferably) or Reader in Computational Biology to be affiliated with the School of Biological and Biomedical Sciences at Durham University, and the Durham Centre for Computational Science

The post will be in the area of computational biology, especially in the analysis and interpretation of genomic data based on next-generation DNA sequencing. This appointment would build on internationally-renowned expertise on gene-environment interactions, functional genomics, evolutionary biology and population genetics/ genomics within the School of Biological and Biomedical Sciences (SBBS). We welcome candidates working in the area of bioinformatics, genome evolution, environmental genomics, population genomics, theoretical evolutionary biology or similar.

The Durham Centre for Computational Science is being created as an interdisciplinary centre of excellence in computational science with world-class facilities and delivering leading research and postgraduate teaching/training.

Durham University is one of the UK's leading Universities with a strong commitment to the highest international levels of excellence in research and education.

The University wishes to appoint a number of world leading Professors to support its strategic growth.

The ideal candidate will be a leading authority in their field, with a strong track record of teaching and research excellence. Successful candidates will be expected to provide leadership, promote interdisciplinarity research and education.

As a leading academic your primary role is within your department, although you will have very considerable freedom to undertake research at the international forefront. This also places obligations on you to take personal responsibility for developing your role, and to show excellence in leadership in working with students, your academic colleagues and the professional support staff. You are expected to engage with students and academic colleagues outside your immediate discipline through membership of a College Senior Common Room.

As a senior member of staff, you will be expected to demonstrate leadership both within our University community and also externally in promoting the interests of the University.

Qualifications & skills required:

PhD in relevant subject area; relevant experience; excellent leadership skills; a commitment to international research excellence, including potential to plan, lead and deliver collaborative projects; a strong, sustained record of published academic output at international/world-leading levels of recognition; demonstrable success in winning external research funding competitively; a proven track record of successful post-graduate supervision; demonstrable ability to engage in research leadership; a record of high achievement in teaching; and an external profile in terms of eg: editorial boards or other equivalent bodies, offering expert legal advice, membership of policy-making bodies or review panels, advisory boards or funding councils.

For more information please contact the chair of the search committee, Prof. Rus Hoelzel (a.r.holezel@dur.ac.uk)

To apply, please complete the application process online at:

http://www.joindurham.com/professorships/-vacancies/view/13 and copy your cover letter, your c.v., and have three letters of reference sent to a.r.holezel@dur.ac.uk.

The deadline for applications is 8 June 2012.

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

EAWAG Switzerland FishConservation

Senior Scientist and Research Group Leader, Ecology and Conservation of River Fish

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is a Swiss-based and internationally networked aquatic research institute within the ETH domain (Swiss Federal Institute of Science and Technology). It is committed to the ecologically, economically and socially responsible management of water resources and aquatic ecosystems.

The Fish Ecology & Evolution Department located in Kastanienbaum (Lucerne) has a vacancy for a Group Leader in Ecology and Conservation of River Fish

Applications are sought from individuals with an excellent research record in river fish ecology, an earned doctorate in a relevant field (e.g., ecology or conservation biology), and an interest in integrating applied research in fish conservation and habitat restoration with the initiation of a strong research program on river fish ecology in Switzerland drawing from evolutionary, ecosystem and community ecology perspectives. This program will benefit from the large diversity of riverine habitats in Switzerland and the planned investment of public funding into the restoration of river habitat over the coming decades. Research that combines field work, data analysis and theory is needed to inform and strengthen the scientific basis for decision making in conservation and management of fish and habitat restoration.

The Center for Ecology, Evolution & Biogeochemistry (http://www.eawag.ch/forschung/cc/ceeb/-index_EN) and the Department of Fish Ecology and Evolution (http://www.eawag.ch/forschung/-fishec/index_EN) at Eawag provide excellent opportunities for collaborative research. The Department is also closely affiliated with the Institute of Ecology & Evolution at the University of Bern through the joint appointment of Prof. Ole Seehausen. The successful candidate should take advantage of this collaborative environment and of Eawag's world-class infrastructure and facilities to develop a strong research program, acquire third party funding to support it, recruit PhD and Masters students, and contribute to Eawag's mandate in teaching and expert consulting. Excellent communication skills in English and skills in team work are essential; an ability to communicate in German is needed for interaction with stakeholders.

Applications must be submitted by 30.06.2012 and should include an application letter describing your interests and their relevance to this position, a CV and list of publications, and the names and contact information for three references. Applications from women are especially welcome. Applications from mid-career and established researchers are encouraged; the level of the appointment will be commensurate with experience. Eawag is committed to promote equal opportunities for men and woman and to support the compatibility of family and work. The earliest starting date for the position is anticipated to be 01.01.2013.

For further information, please contact Prof. Ole Seehausen (ole.seehausen@eawag.ch).

We look forward to receive your application. The quickest way is to apply online. Please click on http://-internet1.refline.ch/673277/0113/++publications++/-1/index.html .This will take you directly to the application form.

Ole Seehausen

Ole.Seehausen@eawag.ch

ErlhamCollege CollectionManager

Classification: Administrative Faculty - Collections Manager Department: Joseph Moore Museum Status: Part-time, no benefits. One-year appointment with merit-based renewal up to five years Salary: Commensurate with experience

The Joseph Moore Museum at Earlham College seeks a part-time Collections Manager to help oversee its zoological, paleontological, geologic and anthropological collections. This position will be supervised by the director of the museum.

About the Joseph Moore Museum The Joseph Moore Museum (JMM) is the regional natural history museum for eastern Indiana. First publicly opened in 1887, the JMM is located in Richmond, Indiana on the campus of Earlham College. Collections include more than 12,000 vertebrate specimens as skins, skeletons, alcohol preps, fossils and subfossils, and ~40,000 invertebrate specimens, including fossil invertebrate type specimens. Many state vouchers for birds and mammals are held. The JMM is a thriving place of undergraduate research using the museum collections and undergraduate training in collections practices. A clean room (ISO-7) for ancient DNA research is currently being established.

Responsibilities - Organization, care and improve the collections, daily; - Manage collections data using a computerized database (Specify 6); - Preparation and conservation of specimens; - Develop and implement an integrated pest management plan (with direction from the Director); - Supervise students and volunteers; - Administer loans and facilitate use of the collections; - Assist with grant-writing to support Museum operations and improvements; - Other duties as assigned.

Collaborative research with students is highly encouraged; independent research may also be supported on a case-by-case basis.

Qualifications - BA/BSc in biology, geology or related field is required; - Experience preparing vertebrate specimens is required; - Must be self-directed and have the ability to work independently. - Must have good manual dexterity, impeccable handwriting and good time-management skills; - Museum experience, integrated pest management knowledge, excellent computer skills (particularly, knowledge of collections databases), and a background in systematics are highly desirable;

More information Potential applicants are encouraged to contact JMM Director Heather Lerner at 765-983-1402 or lernehe@earlham.edu

To Apply: Interested candidates should send letter of application, curriculum vita, and names of three references electronically (as a pdf) to:

leama@earlham.edu

Review of applications will begin immediately.

Appointment will begin September 1, 2012. Earlham College continues to build a community that reflects the gender and racial diversity of the society at large, and, therefore, we are particularly interested in inviting and encouraging applications from African Americans, other ethnic minorities, and women. Earlham also is eager to solicit applications from members of the Religious Society of Friends (Quakers). Earlham is an Affirmative Action/Equal Opportunity Employer.

Heather R. L. Lerner, Ph.D., M.S. Joseph Moore Museum Director Assistant Professor of Biology Earlham College 801 National Road West Richmond IN 47374

Google Voice: 949-GENOMES Email: hlerner@gmail.com http://heatherlerner.com/ hlerner@gmail.com

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LMU Munich EvolInstructor

Instructor (full- or part-time)

The section of evolutionary ecology at the University of Munich (LMU) invites applications for an instructor (full- or part-time) to organize and teach already established bachelor- and master-level courses in ecology, evolution and zoology. The full-time teaching load is 18 contact hours per week during the semesters. Teaching may include:

- Introductory ecology

- Evolutionary ecology - Zoology (basic practical courses) - "Skills" courses (e.g. scientific writing/presentations) for advanced students

Most bachelor courses are taught in German, while master's courses are taught in English, so fluency in both languages is required. The position is available beginning October 1, 2012 and will be paid at the E13 (TVL) level according to the German salary scale. The position is initially available until the end of 2014, and may be extended further.

Although the primary duty is teaching, there is also an opportunity to participate in research projects related to those ongoing in the section of evolutionary ecology. For more information, see: http://sci.bio.lmu.de/-ecology A MSc is required, a PhD in ecology (or in related fields) would be advantageous. Applicants should send a letter of motivation, including teaching experience, a curriculum vitae, and contact information of at least two personal references, preferably as a single .pdf file, to:

Prof. Dr. Wilfried Gabriel

wilfried.gabriel@lmu.de

The application deadline is July 1, 2012.

The LMU-Munich is an equal opportunity employer with an affirmative action program for the handicapped. Applications from women are encouraged.**

wilfriedmgabriel@googlemail.com

LouisianaStateU ResAssoc HIVPhylogenomics

RESEARCH ASSOCIATE OR POSTDOCTORAL RESEARCHER Louisiana State University Department of Biological Sciences

A research associate or postdoctoral researcher position is available in the computational evolutionary biology lab of Jeremy M. Brown. This position is part of a project funded by the National Institute of Justice to further investigate the forensic application of phylogenetic approaches for reconstructing HIV transmission histories. This project will expand upon previous work by utilizing whole-genome sequences and applying more sophisticated statistical phylogenetic approaches. The Brown lab will be collaborating extensively with the Metzker lab at Baylor College of Medicine. Informal inquiries are encouraged and can be directed to jembrown@lsu.edu. More information on the Brown lab is available at http://www.phyleauxgenetics.org/- Responsibilities: This position will be responsible for performing cutting-edge research on phylogenetic analysis of HIV genomes for use in forensics. Responsibilities will include running analyses on high-performance computing resources, writing manuscripts, creating new bioinformatic tools (depending on applicant background), and supervising graduate and undergraduate student workers.

Required Qualifications: Research Associate 4: Master's degree in biology, bioinformatics, computer science, statistics, or related discipline; experience performing phylogenetic analyses. Postdoctoral Researcher: Ph.D. and experience performing phylogenetic analyses.

Additional Qualifications Desired: Experience with Unix and one or more of the following programming languages: C++, Java, Python; experience using high-performance computing resources. An offer of employment is contingent on a satisfactory pre-employment background check.

Application review will begin promptly on June 1, 2012 and continue until a candidate is selected. The position will be available to start as soon as an offer is made and accepted.

Apply online and view a more detailed ad at: www.lsusystemcareers.lsu.edu. Position #012809.

LSU IS AN EQUAL OPPORTUNITY/EQUAL ACCESS EMPLOYER

Quick link ad URL: https://lsusystemcareers.lsu.edu/-applicants/Central?quickFind=3D53795 Jeremy M. Brown Assistant Professor Louisiana State University Dept. of Biological Sciences 202 Life Sciences Building Baton Rouge, LA 70803

(225) 578-1745

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

LundU EvolutionaryPhysiology

Two research positions in Physiology (Lund University, Sweden)

Dear Colleagues,

We would like to announce to positions in Physiology at Lund University: one Lecturer and one Professor at Department of Biology (Lund, Sweden). These positions are intended to focus on Animal Physiology, but are otherwise open, and candidates could focus on the cellular, organs or whole-organismal level. These positions are thus open for orgranismal biologists, ecophysiologists and/or evolutionary physiologists as well as those performing research at lower levels of biological organisation. More information can be found below (follow the links).

Deadline for applications: June 15 2012.

Further information:

Two positions in Animal Physiology, professor and senior lecturer open for application

The Department of Biology has a long tradition on research and education in animal cell biology and physiology. Within the next 4-6 years several of the professors and lecturer will retire. For building a competitive research program and securing the teaching excellence in animal physiology, we are now making two recruitments including a professor (dnr PA 2012/24) and a senior university lecturer (dnr PA 2012/25). It is expected that the successful candidates will actively interact with other research groups at the Department of Biology.

The department has excellent equipment for research in animal physiology including facilities for experiments on model animals, cell culturing, microscopy, electrophysiology and DNA sequencing, and a wind tunnel for animal flight research. A new laboratory for heterologous protein expression will be established during 2012. In addition, Lund University will host MAX IV, the national synchrotron radiation laboratory with excellent possibilities for research in structure biology and dynamic micro-imaging of living cells and organisms.

More information available on the Lund University web (http://www.science.lu.se/o.o.i.s/30640)

Best wishes,

Erik Svensson

Erik Svensson <Erik.Svensson@biol.lu.se>

NewMexicoStateU SequencingLab

LABORATORY COORDINATOR, Genome Sequencing Laboratory

Department of Biology, New Mexico State University

To Apply, go to:

https://jobs.nmsu.edu/applicants/jsp/shared/-frameset/Frameset.jsp?time=3D1336085507767
or

http://jobs.nmsu.edu< http://jobs.nmsu.edu/ > Requisition # 0600440

Qualifications: BS in Biology, Molecular Biology or related field, plus one year of professional (post degree) experience; MS in Biology preferred. Strong background in molecular biology techniques preferably including recombinant cloning, PCR, qPCR, Sanger sequencing and capillary electrophoresis, cDNA construction and normalization, Roche 454 shotgun, amplicon, and transcriptome pyrosequencing. Ability to communicate clearly, both verbally and in writing, with researchers, clientele, and students regarding molecular biology protocols and experimental design relating to ecology and evolution; previous scholarly products (e.g., papers, presentations) and teaching or academic supervisory experience is preferred.

Examples of Duties: Preparation, management, and expansion of NMSU's core Genome Sequencing Laboratory. Daily operation and routine maintenance of a Roche 454 GS FLX+ emPCR pyrosequencer. Successful operation of the instrument requires meticulous adherence to protocols. Additional laboratory duties include the preparation of a wide variety of samples for genomic sequencing, and training/supervising graduate student laboratory assistants. Other duties include project management, record-keeping, accounting, and purchasing reagents/expendables. Must keep abreast of technical advances in genomics in order to advise research clientele in experimental design and seek new applications of genomics technology. Must work collaboratively with team of faculty researchers, bioinformatics specialists, graduate students, and facilities staff.

Benefits Offered: Group medical and hospital insurance, group life insurance, long-term disability insurance, state educational retirement, worker's compensation, sick leave, annual leave and unemployment compensation. Opportunity for educational advancement.

Conditions: Offer of employment is contingent on funding.

All offers of employment, oral and written, are contingent on the University's verification of credentials and other information required by Federal Law, State Law, and NMSU policies/procedures, and may include the completion of a criminal history check.

Applications must include: letter of interest, current resume, and three professional references with names, titles, addresses, daytime phone numbers, and email addresses.

Review of applications will begin 5/15/2012 and will continue until the position is filled. Incomplete application packets will not be considered.

phoude@nmsu.edu

NorthCarolinaStateU 3 EvolBiology

Three Open-Rank Faculty Positions Global Environmental Change and Human Well-Being North Carolina State University Raleigh, NC USA

North Carolina State University is proud to announce its Chancellor's Faculty Excellence Program. Starting in 2012, NC State will hire thirty-eight faculty in twelve research areas or "clusters" to promote interdisciplinary scholarship and the development of innovative curricula in emerging areas of strategic strength.

As part of this university-wide program, the Department of Biology and the Department of Forestry and

Environmental Resources are hiring a cluster of three faculty at any rank to provide leadership for a new initiative in Global Environmental Change and Human Well-Being. We seek leaders in any area of biology under this theme, and encourage applications from those who study global change as it relates to fisheries and aquatic diversity, quantitative ecology, evolutionary biology, or other areas. Successful applicants are expected to have a strong vision for their vibrant and extramurally funded research program, a commitment to leadership in the area of Global Environmental Change, and demonstrated excellence and innovation in graduate education.

This cluster will strengthen and bridge emerging initiatives at NC State including: 1) the Southeast Climate Science Center; 2) the Nature Research Center of the NC Museum of Natural Sciences; and 3) programs in Ecology and Evolutionary Biology. More information on these positions and this initiative can be found at http://www.theglobalchangeforum.org/clusterhire/ We are targeting applicants already holding a position at the level of Assistant Professor or higher (or equivalent), but exceptional postdoctoral fellows also will be considered. To apply for these positions, go to http://-jobs.ncsu.edu/postings/7389 and provide a cover letter, curriculum vitae, and a 1-page vision for Global Environmental Change and Human Well-being, focused on your research program and/or building this programmatic theme at NC State. Confidential inquiries and nominations should be directed to Dr. Damian Shea, Search Chair, d_shea@ncsu.edu, 919-513-3065. Review of applications will begin 15 August 2012 and continue until the positions are filled. We welcome applications from groups of individuals and dual-career couples and will work with candidates to identify suitable employment opportunities for spouses or partners.

NCSU is an AA/EO employer. All qualified applicants will receive consideration for employment without regard to race, color, national origin, religion, sex, age, veteran status or disability. In its commitment to diversity and equity, NC State University seeks applications from women, minorities, and persons with disabilities. NC State welcomes all persons without regard to sexual orientation. ADA Accommodations: please call 919-515-3148.

langerhans@ncsu.edu

NorthCarolinaStateU HoneyBeeEvolution

GRADUATE/POSTGRADUATE RESEARCH POSITIONS IN HONEY BEE GENETICS, NORTH CAROLINA, USA

North Carolina State University (Raleigh, NC) & University of North Carolina (Greensboro, NC)

We are looking for one individual to join our collaborative research team on an established project to study the genetics of honey bee stress resistance, life-history, and lifespan. The team involves Dr. Olav Rueppell (UNC-Greensboro), Dr. David Tarpy (NC State), Dr. Mike Simone-Finstroem, and Dr. Micheline Strand (ARO, Research Triangle Park). We will consider applications for graduate students (PhD level) or postdoctoral researchers.

The project will continue to address genetic and environmental variation in stress resistance and its relation to honey bee health, life history, and life expectancy. The applicant should have molecular research experience, be willing to travel, and be comfortable working with live honey bees. The project is funded for 3 additional years, and salary will depend on qualifications.

Please send inquiries and applications until the 1st of June 2012 to olav_rueppell@uncg.edu. Applications should be electronic and contain a CV, contact information of three professional references, and a short (<1 page) description of why you are interested in joining our team.

Review of applicants will begin immediately and will continue until the position is filled.

Distributed in furtherance of the acts of Congress of May 8 and June 30, 1914. North Carolina State University and North Carolina A&T State University commit themselves to positive action to secure equal opportunity regardless of race, color, creed, national origin, religion, sex, age, or disability. In addition, the two Universities welcome all persons without regard to sexual orientation. Dr. David Tarpy david_tarpy@ncsu.edu, 919.515.1660

Dr. Olav Rueppell Associate Professor Department of Biology Univ. North Carolina at Greensboro 312 Eberhart Bldg. Greensboro, NC 27403, USA Tel.: (1) 336-256-2591 Fax: (1) 336-334-5839 http://www.uncg.edu/bio/faculty/olav_rueppell/-lab/index.html orueppell@gmail.com

OxfordBrookesU Genomics

Reference: 212/17201/BC Faculty of Health and Life Sciences Senior Lecturer in Molecular Biology and Genomics Starting salary: £37,012, rising annually to £45,486

Oxford Brookes University wishes to appoint a Senior Lecturer in Molecular Biology and Genomics.

Candidates with research experience in biomedical science with a significant focus on molecular biology and genomics, including those with interests in the fields of bioinformatics, evo-devo and evolutionary medicine, are encouraged to apply.

There is a great variety of research groups in the Department of Biological and Medical Sciences with which the successful candidate can interact and collaborate: http://bms.brookes.ac.uk/-research=0A=0AFor more information about the position and how to apply see: https://-edm.brookes.ac.uk/hr/hr/vacancies.do;jsessionid=-c1e6752a95fc0c0f3bf80bbf650a8085e413288a5fd58ed809d1[illegible]d7ff105[illegible]MbPyGha[illegible]AmljGr5XDqQL 14220673 Casper Breuker Dpt of Biological and Medical Sciences, Faculty of Health and Life Sciences Oxford Brookes University

cbreuker@brookes.ac.uk

PacificGrove CA GenomicsTech

Marine Genetics/Genomics Technician position: Steve Palumbi's lab at Stanford's marine lab in Pacific Grove, California is looking for a technician to collect data on DNA sequence variation of a wide range of different marine organisms from different habitats. The position is available starting June 1, and applications will be screened starting immediately. See the full description below for details.

Research technician at Stanford University's Hopkins Marine Station, in Pacific Grove, CA. Under the direction of the Principal Investigator the technician will assist with research related to genetic characterization of populations of marine vertebrates and invertebrates in the context of ongoing research into marine conservation and management. Duties include: - Collecting larvae and adult specimens of marine species. This may involve some travel within California and into Oregon and possibly Washington. - Extracting DNA and documenting genetic variation. This will include processing samples in the lab for DNA extraction and sequencing as well as entering, managing, and analyzing the resulting data. This will require the use (or development) of many research skills using a variety of molecular genetic tools. These include, but are not limited to DNA extraction, PCR, gel electrophoresis, and next generation DNA sequencing. - Field monitoring of multiple sites in central California. - Animal care including aquarium maintenance and routine care and feeding of marine species (primarily invertebrates). - Laboratory maintenance including maintaining the lab and taking responsibility for ordering some of the general supplies. There is potential for extension of the technician position to other research projects as well as the possibility of co-authorship of at least one resulting publication. QUALIFICATIONS: The successful applicant will be highly organized, have attention to detail, be able to work as an independent part of a team, have a basic understanding of and facility with standard computer software programs, and have practical experience with a variety of standard molecular tools (for example, DNA extraction, PCR, gel electrophoresis, DNA sequencing, etc). In addition to these basic requirements, we desire an applicant with an interest in marine ecosystems and their ecological functioning. Apply online at: http://recruit.trovix.com/jobhostmaster/-jobhost/ViewJobPostDetails.do?jobPostId=-ghoz2hgq6bf3vfwt336mszrrih&accountId=-de85ad313f8598db1c42b567a3df24a00497ba22&button=&action=viewDetails Thank you for your interest!

Cheryl Butner Research Assistant - Palumbi and Micheli Labs Hopkins Marine Station, Stanford University Pacific Grove, CA, 93950 USA

cbutner@stanford.edu

Paris 6mnth EvolPlasticityHatching

Topic: evolution and plasticity of hatching

We are looking for a Msc student or a research assistant who will participate in an exciting project for a period of six months, and who will be paid a small salary according French regulations. The experiment will take place at the CEREEP-ECOTRON Ile de France research station in Saint-Pierre-les-Nemours, France (http://www.foljuif.ens.fr/). Lodging can be arranged on-site and the experiment is intended to start in September 2012.

We will use the ECOLAB system to investigate effects of several environmental variables on the hatching of annual South-American killifish embryos (genus Austrolebias). The experiment will investigate species differences in a comparative approach, such that we can assess variation in these plastic responses produced by evolution. The ECOLAB is a newly developed research instrument, a climate room where one can change and control many environmental variables with high speed and reliability. We need a team member who will carry out one of the first experiments in this new facility.

The goal of the experiment is to investigate the dependence of a rapid and drastic life history decision -hatching of fish embryos- on evolved species differences and on several environmental variables which vary a lot during a single diurnal cycle. Annual killifish embryos spend several months in an egg bank when temporary fish ponds are dry, but they hatch within few hours when water arrives after heavy rainfall. Hatching is generally facultative and seems to vary between species. However, hatching proportions also depend on the environment, which implies that it might constitute an evolved bet-hedging strategy with plasticity.

For more information please contact Tom Van Dooren, CR1 Researcher, UMR7625 Ecology and Evolution, Paris. vandoore@biologie.ens.fr

vandoore@biologie.ens.fr

PuertoRico FieldAssist RhesusMonkeys

Rhesus monkey research on Cayo Santiago, Puerto Rico.

Hiring Organization:

University of Leipzig and Max Planck Institute for Evolutionary Anthropology, Leipzig (Germany)

Position Description: We are looking for a volunteer to assist on a project examining kin recognition on a semi free-ranging rhesus macaque population on Cayo Santiago, Puerto Rico (USA). The project is being undertaken in the Lab of Prof. Dr. Anja Widdig and Dr. Dana Pfefferle (Leipzig University & Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany; see http://www.eva.mpg.de/pks/index.html) The volunteer will work alongside Dr. Pfefferle (http://www.eva.mpg.de/pks/staff/pfefferle/).

The successful applicant will be expected to work on Cayo Santiago for 5-6 days a week, and may also be required to undertake data entry and/or processing in the later afternoon and early evenings. On Cayo Santiago, the primary task will be to assist carrying out playback experiments. In order to do so, appropriate training will be provided. This position is ideal for graduate students or recent graduates looking to gain experience in fieldwork and data collection.

Qualifications/Experience: Applicants should have a Bachelor in Biology, Ecology, Animal Behavior, Physical Anthropology, Primatology, or a related field. Previous field experiences (preferably in the tropics) and knowledge of Spanish is helpful, but not necessary. In general, carrying out playback experiments can be a protracted and patience challenging task, including many hours of waiting for the correct situation. Thus you must be able to maintain a positive attitude. Applicants also must be in good physical and mental condition; feel comfortable being far away from family and friends; be emotionally mature, energetic, and very patient; have an excellent eye for detail; don't be afraid of approaching monkeys (!); willing to work in a small team setting and follow instructions; be able to maintain a positive and humorous attitude towards challenging and tiring work. Although the work can be demanding and tiring, being close to habituated primates is very rewarding and a great experience.

The language in our team is English. The successful candidate must have medical insurance, a valid IACUC certificate (www.citiprogram.org) and will have to provide medical test in order to be allowed to work on Cayo Santiago (information will be provided after acceptance).

Salary/funding: Initially no support will be provided. However, AFTER SUCCESSFUL COMPLETION of the internship, depending on experience, performance as well as on final costs for housing and travel, the field assistant can get partial compensation.

Costs that have to be expected:

- Round-trip to Puerto Rico (cost varies)

- Transportation from and to the airport (transportation might be arranged privately, otherwise approx. 60 US$/trip)

- Housing (depending whether houses can be shared between 200-500 US$)

- Medical insurance (cost varies, proof needs to be provided)

- Medical tests required to work on Cayo Santiago (costs vary)

- Field clothes and personal expenses

Term of Appointment: >From Mid of September 2012 till end November 2012 (most likely 15th of September - 18th of November).

Application Deadline: Target application date is June 12th 2012, but open until a suitable candidate has been found.

Comments: To apply, candidates should email a brief cover letter outlining their interests, experience, and why they wish to undertake work on the project. They should attach a CV that includes at least contact details of two academic references. If asked, it will be the responsibility of candidates that academic references are send to danapfefferle@gmail.com. All documents should be submitted as one PDF file. Please only send email applications.

Contact Information: Dana Pfefferle

danapfefferle@googlemail.com

SangerInst TreeFamProgrammer

Bioinformatician (http://goo.gl/gyGbf) Salary range £21485 to £28489 per annum dependent on experience. Closing Date: 10th June 2012

A position has become available for an enthusiastic Bioinformatician (or a computer scientist with interest in biology) to join Alex Bateman's group. TreeFam is a key resource for assigning orthology and paralogy relationships within animal genomes. The successful applicant will have the unique opportunity to participate in all aspects of the TreeFam database, bringing new ideas to fruition in a small and dynamic team.

Essential Skills The candidate will have a degree in Computer science/Bioinformatics and detailed knowledge of core computer science concepts (e.g. object oriented design, memory management, algorithm implementation) and practices (e.g. version control, agile development). Excellent software design and development skills with particular experience of programming analysis pipelines are a requirement as is extensive knowledge in the scripting language Perl. The candidate will also have knowledge and experience of UNIX/LINUX to an advanced level.

Ideal Skills It would be an advantage if the candidate has experience of programming with relational databases e.g. MySQL and experience in dealing with large scale data sets (involving dozens of proteomes) using software on computer farms and/or parallel computing. Also knowledge of tools and techniques for phylogenetics would be desired. The ideal candidate should be able to prioritise tasks and deliver to deadlines. Having excellent communication skills both verbal and written for interacting with collaborators and other software designers would also be an advantage.

Other information The Wellcome Trust Sanger Institute leads the world in genomic research, with an expanding scientific programme dedicated to understanding the role of genomes in biological systems. These activities are supported by a large Genome Informatics infrastructure. The Institute also develops and maintains numerous high quality informatics resources. Less experienced scientists who do not meet all the essential requirements will be considered and the salary will reflect their experience, skills and qualification.

Please apply here: http://goo.gl/gyGbf For informal inquiries contact

Dr. Fabian Schreiber TreeFam Project Leader The Wellcome Trust Sanger Institute

e: fs9@sanger.ac.uk t: 01223 494726 w: www.treefam.org/ –

Fabian Schreiber <fs9@sanger.ac.uk>

StandfordU Tech MarineConservation

Technician position in marine ecology and conservation

The Hopkins Marine Station of Stanford University and the Mexican non profit marine conservation organization Comunidad y Biodiversidad (COBI) invite applications for a technician position. The selected candidate will work in the laboratory of Fiorenza Micheli at the Hopkins Marine Station http://micheli.stanford.edu/-index.html and will spend considerable time doing fieldwork in Baja California, México, working on a project investigating oceanographic variability and ecological responses within coastal fishing communities that have committed to marine conservation through marine reserves. The main tasks for this position are to conduct field studies to investigate the efficacy of fully-protected marine reserves to confer resilience to climate variability and recover depleted populations of marine invertebrates http://www.cobi.org.mx/?pag=r-pbc-building-ocean- resilience&idioma=eng. Field activities will involve the design and conduction of underwater ecological monitoring, the deployment and maintenance of oceanographic sensors, and the conduction of ecological experiments using scuba. Laboratory activities will include creation and maintenance of databases, data analyses, processing of samples (e.g., phytoplankton, recruitment collectors) that will be conducted both in the field and at the Hopkins Marine Station of Stanford University. Required qualifications include: a MS in marine sciences or marine ecology; extensive experience in ecological monitoring and field experiments; and willingness to spend extended periods of time at remote field locations. Because of the setting of the field locations, and the international nature of this project, bilingual skills (Spanish and English) are required. All else being equal, preference will be given to candidates that would be able to start as early as July 1, 2012. The position is initially for 12 months, but it could likely be extended to up to four years. Candidates should send via email a letter of interest describing their qualifications relevant to the project and past research experience, their full CVs, and arrange for the names and contact information of two references to both of the following addresses:

Dr. Fiorenza Micheli Professor Hopkins Marine Station Stanford University Oceanview Blvd. Pacific Grove, CA 93950, USA micheli@stanford.edu

Dr. Andrea Sáenz-Arroyo Science Director Comunidad y Biodiversidad A.C. Popocatepetl # 28 Despacho 1 Colonia Hipódromo Condesa México 06100 DF andrea.saenzarroyo@gmail.com

Application deadline is May 25, 2012. Review of applications and interviews will begin immediately after this date and continue until a suitable candidate is found.

Thank you for your interest!

Cheryl Butner Research Assistant - Palumbi and Micheli Labs Hopkins Marine Station, Stanford University Pacific Grove, CA, 93950 USA

cbutner@stanford.edu

UBern FieldAssist Zambia

Wanted: Field assistants for underwater observations

The Behavioural Ecology department of the University Bern, Switzerland (chair: Prof. Michael Taborsky) provides opportunities for assistants to participate in field work in Zambia in autumn 2012.

Project: We study cooperatively breeding, colonial cichlids in Lake Tanganyika, including questions regarding the significance of coloniality, the ecology of dispersal decisions of group members, and habitat-related variation of behaviour and social structure between populations. All work will be done using SCUBA diving down to about 12 meters depth. Detailed behavioural observations are recorded in situ and individuals will be caught and measured as required.

Tasks: Usually there will be 2 dives/day on 6 days /week. Applicants will work independently after a training phase that will also include learning about the social structure and behavioural repertoire of the fish.

Field site: We dive mainly in front of a secluded and very basic lodge located at the lakeshore of Lake Tanganyika in the vicinity of Mpulungu. Limited computer and internet facilities are available. Meals will be provided at the lodge.

Requirements: Applicants must be in good health and physically fit, as the diving is very demanding. Experience with the tropics and with basic conditions without access to the usual amenities of modern life would be advantageous. A PADI (or equivalent) diving certificate and diving experience are required. Experience with behavioural observations would be very useful.

Conditions: Travelling and accommodation costs will be covered, whereas costs for food and personal needs are the responsibility of each team member. Consider at least ca. 7 US$ for food expenses/day). Diving equipment will be provided, but mask, fins, wet-suit (7mm+) need to be brought by each team member. The exact dates of the expedition are not yet determined, but the trip will last from late August until early December. Applicants should be ready to briefly visit the institute in Bern beforehand for the required training in behavioural observations.

Please send applications per e-mail attachment as a single file (.doc or .pdf) to arne.jungwirth@iee.unibe.ch. Applications should include a motivation statement and information about your experience with diving, field work in general, living in the tropics, your background in biology, and an up-to-date CV. Reference letters would be an asset.

arne.jungwirth@iee.unibe.ch

UIllinois LabTech EvolBiol

The Department of Animal Biology/School of Integrative Biology is searching for a full time Visiting Research Specialist to assist with research in Zachary Cheviron's lab. Research in the Cheviron lab focuses on the ecophysiology and evolutionary genetics of adaptation along environmental gradients, and current work is focused primarily on birds and mammals that are distributed across broad elevational gradients in the Andes and the Rocky Mountains. For additional details about ongoing projects, please visit the lab website (http://-web.me.com/zcheviron)

The Visiting Research Specialist will assist principal investigator and graduate students in ongoing research projects by conducting basic molecular biology and physiology lab work. Responsibilities will include nucleic acid extractions, PCR, gel electrophoresis, preparation of libraries for next-gen sequencing, assisting animal care staff with the maintenance of a deer mouse breeding colony, database entry and management, maintaining laboratory supplies/ equipment, ensuring compliance with laboratory safety regulations, and training students. The position will be appointed for one year with the possibility of renewal for up to a total of three years, after which it may be converted to a non-visiting position.

Qualifications:

Required: a Bachelors degree in Biology or a related field and experience with molecular genetic methods (e.g. DNA/RNA extraction, electrophoresis, PCR, sequencing).

Preferred: familiarity with next-gen sequencing, experience with rodent handling and husbandry, experience with respirometry techniques, and an interest in ecological physiology and evolutionary biology.

Salary: Will be determined by experience and qualifications.

Starting Date: July 1, 2012.

Please create your candidate profile at http://-go.illinois.edu/VstResSpecAB and upload a resume, letter of interest, and the names and email addresses for three professional references. For further information, please contact: Dr. Zac Cheviron, cheviron@illinois.edu.

Closing date: For full consideration, all application materials must be submitted by May 15, 2012. Interviews may be conducted before the closing date; however, no hiring decision will be made until after that date.

Illinois is an Affirmative Action /Equal Opportunity Employer and welcomes individuals with diverse backgrounds, experiences, and ideas who embrace and value diversity and inclusivity. (www.inclusiveillinois.illinois.edu)

Zachary Cheviron Assistant Professor Department of Animal Biology School of Integrative Biology University of Illinois @ Urbana-Champaign 433 Morrill Hall Urbana, IL 61801

Phone: 217-244-2787 (office) 217-244-1957 (lab) Website: http://web.me.com/zcheviron cheviron@illinois.edu

UOslo EvolutionaryBiology

Centre for Ecological and Evolutionary Synthesis (CEES), University of Oslo would like to announce the two following positions on EvolDir:

Researcher in evolutionary biology/bioinformatics

http://uio.easycruit.com/vacancy/758275/-64421?iso=no Application date June 8, 2012

Postdoctoral Research Fellow in Marine Ecology

http://uio.easycruit.com/vacancy/756713/-64421?iso=no Application date June 20, 2012

Please contact me if you have any questions regarding the announcements

Best regards,

Torunn Standal Guttormsen Senior Executive Officer University of Oslo Faculty of Mathematics and Natural Sciences P.O. Box 1032, Blindern NO-0315 OSLO NORWAY

Telephone: +47 22 85 42 72 Fax: +47 22 85 63 39 e-mail: t.s.guttormsen@mn.uio.no

Torunn Standal Guttormsen <t.s.guttormsen@mn.uio.no>

UOtago PlantEvolution

PROFESSOR IN BOTANY UNIVERSITY OF OTAGO

The University of Otago is New Zealand's oldest and most research- intensive university, and has an international reputation for excellence in education and research quality.

The University of Otago has the only Department of Botany in New Zealand. It has a long history, being the first Botany Department to be formed in New Zealand, and dates back to 1924. It is a research-active Department, with research strengths in ecology, terrestrial and aquatic environmental physiology, and the study of responses to environmental change.

The University is seeking an outstanding academic for the position of Professor in Botany. The Department of Botany wishes to appoint an academic with an excellent research record in any area related to plant science, and who has the ability to provide outstanding research leadership to the Department of Botany.

Applicants should be capable of establishing an active research programme that will attract external funding in the New Zealand or international research funding environments and be able to develop a proactive research program to attract postdoctoral researchers, PhD and Masters students.

A sustained competence in teaching, assessment and curriculum development would be essential. The successful applicant will be a proven and inspiring teacher who enjoys contact with students and promoting the learning of plant sciences, both within and outside of their research area. The successful applicant will be expected to contribute to curriculum review and course development in the Department of Botany and in relevant Teaching Programmes.

Appointees at the level of Professor must have outstanding leadership qualities. They will be expected to have energy, drive and enthusiasm, and to take a constructive and active role in the academic development and management of the Department, with a view to assuming the Head of Department position in the future.

The successful candidate should also demonstrate sustained outstanding leadership in relation to university service, and in service to relevant external communities which will aid the strategic management of the Department of Botany.

This position presents an exceptional opportunity to contribute strongly to a developing academic environment.

APPLICATION INFORMATION

All applications and enquiries should be directed to:

Dr Kathrin Soehnel, Senior Consultant, Academic Search International Kathrin.Soehnel@academic-search.net

Phone: +64 9 379 6900 Fax: +64 9 379 6901 Address: PO Box 106-976 Auckland City Centre 1143 Auckland, New Zealand

Further information

www.botany.otago.ac.nz www.otago.ac.nz/jobs lindsay.robertson@otago.ac.nz

UPennsylvania LabTech AntEvolution

A full-time Research Lab Technician position is available in the Linksvayer lab in the Department of Biology at the University of Pennsylvania. The research focus is on the evolution and genetic basis of complex social systems, using tiny ants as a model system. A variety of approaches are used, including behavioral observations, functional genomics, and evolutionary genetics.The position involves caring for ant stocks as well as basic lab organization, maintenance, and administration. Furthermore, the position involves assisting with a range of experiments, including manipulating tiny ants, basic molecular genetics, and measuring ant phenotypes.

The successful candidate will have a BA/BS in Biology or a related field, a strong work ethic, positive attitude, excellent communication and organizational skills, some experience with basic molecular biology techniques, and the desire to learn new skills. Experience working with insects is preferred but not required.

Applicants must apply directly through Penn's job posting website, http://www.hr.upenn.edu/-jobs/. Search for the staff position with the reference number 120432589 and apply to the posting through the website. Alternatively, go straight to http://jobs.hr.upenn.edu/applicants/-

Central?quickFind=3D195483 Please contact me directly (tlinks@sas.upenn.edu) with any questions.

Tim Linksvayer Assistant Professor Department of Biology, University of Pennsylvania 225 Leidy Laboratories, 433 South University Avenue Philadelphia PA 19104-6018 tlinks@sas.upenn.edu phone +1 215 573 2657 http://www.bio.upenn.edu/faculty/linksvayer/ tlinksvayer@gmail.com

USFWS WashingtonState FishEvolution

The Abernathy Fish Technology Center (AFTC), Longview, Washington, provides applied fishery research and development capabilities for the U.S. Fish and Wildlife Service (Service) Pacific and Pacific Southwest Regions (CA, ID, NV, OR, WA, and the Pacific Islands). AFTC currently maintains active Applied Research Programs in the fields of Conservation Genetics; Nutrition; Ecological Physiology; and Modeling and Decision Support. The Applied Research Programs assist restoration and recovery efforts by scientific development and evaluation of new methods, concepts, systems, and approaches for use by various Fish and Wildlife Management Offices, Fish Health Centers, National Fish Hatcheries, other programs such as Ecological Services, National Wildlife Refuges, and Law Enforcement, and various external partners such as state and other federal agencies, tribal governments, and non-governmental organizations. For further information about AFTC and our research programs, please see the following web site: http://www.fws.gov/aftc/- The Conservation Genetics Program currently has one open position. For a full position description please see the following at USAJobs.

http://www.usajobs.gov/GetJob/ViewDetails/-312443500 Position/Title: Interdisciplinary Geneticist or Fish Biologist

Responsibilities: Takes the lead in genetic data collection, analysis, and report writing for a variety of projects working with different fish species and genetic analysis methods (e.g. to address questions of population structure, population assignment, and species and sex identification). Provides overall technical coordination and uses genetic methods to estimate the relative reproductive success of hatchery and natural origin Pacific salmon in the wild. Performs statistical analyses and generates graphical representations of study results, and incorporates these data into written reports, scientific publications, and oral presentations.

Qualifications: Master's degree or equivalent work experience. Extensive work experience in: the principles, theories, and techniques of molecular and population genetics in order to determine pedigree relationships based on multi-locus genotypic data; genetic analytical and statistical techniques for determination of parentage, genetic variation within and among populations, population assignment, population structure, and hybrid status; and demonstrated oral and written communications skills.

Salary: $47,448.00 - $74,628.00 /year

Closing Date: May 21, 2012

Contact: USAJOBS at http://www.usajobs.gov. USFWS, Abernathy Fish Technology Center web site: http://www.fws.gov/aftc. Applicants MUST follow the application process described in the vacancy announcement to receive consideration.

Denise Hawkins Regional Geneticist U.S. Fish & Wildlife Service Abernathy Fish Technology Center 1440 Abernathy Creek Rd. Longview, WA, 98632 Phone: (360)425-6072 x339 Fax: (360)636-1855

Denise_Hawkins@fws.gov

UStAndrews Bioinformatics

Dear Evoldir,

Although an evolutionary bioinformatics background is not required, applications from people with such a background are welcome.

Bioinformatician - CD1173

Description

School of Medicine, £30,122 - £35,938 pa, Start: As soon as possible, Fixed-Term for 3 years in the first instance

Details

An exciting opportunity for a Bioinformatician is available at the School of Medicine at St Andrews University. You will join a dynamic and multidisciplinary community and will play a key role in providing specialist support to diverse projects across different research areas. You will contribute to the development of a next generation sequence analysis service to analyse and interpret data from deep sequencing projects. Alongside provision of high quality support, a significant contribution is expected towards the expansion of the service in scope and staffing by increasing the number of users and attracting external funding.

You will have a degree in bio-computing, preferably to PhD level with significant experience in bioinformatics. Advanced scripting and experience in the analysis of genome scale biological datasets, particularly high throughput sequencing data are required. We also envisage a role in the installation/maintenance of bioinformatics applications and provision of advice/training to users. Good communications and management skills together with a clear vision of the advances and progress in the field are essential.

The post will be available immediately for three years in first instance and will be based at the School of Medicine.

Informal enquiries to Dr Silvia Paracchini, e-mail: sp58@st-andrews.ac.uk

Details and application via: https://www.vacancies.st-andrews.ac.uk/welcome.aspx Ref No: CD1173

Closing Date: 27 June 2012

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

UTexasTyler Genomics

ASSISTANT PROFESSOR GENOMICS AND BIOINFORMATICS Department of Biology, The University of Texas at Tyler

Position: Assistant Professor, 9-month, tenure-track. Research and teaching.

Location: Department of Biology, The University of Texas at Tyler, Tyler, TX.

Start date: Negotiable.

Duties and responsibilities: The successful candidate will establish a strong, extramurally-funded research program in genomics and bioinformatics of animals or plants to complement existing departmental strengths in ecology, evolution, and genomics, mentor undergraduate and graduate students, and teach graduate and undergraduate courses in his/her areas of expertise. Participation in departmental, college, and university committees and outreach programs is expected; collaborative research with other faculty and institutions is strongly encouraged.

Qualifications: Required: (i) Ph.D. in genomics and bioinformatics or a closely related field. (ii) Demonstrated research creativity and productivity. (iii) Ability to develop a strong, extramurally-funded research program. (iv) Evidence of effective teaching and other communication skills.

Preferred: Postdoctoral experience and evidence of research productivity is strongly preferred. Teaching experience at undergraduate or graduate levels is desirable.

Available resources: The Department of Biology offers a stimulating intellectual environment and has an excellent reputation in research and teaching. Twelve faculty members undertake research in diverse subdisciplines, including genomics, population genetics, evolution, ecology, and physiology. A new expansion with state-of-the-art research and teaching labs is under construction, and several existing teaching labs are being renovated. A NSF-funded infrastructure grant will provide three large and sophisticated walk-in environmental chambers, and a computer lab will connect UT Tyler to the Texas Advanced Computer Center via a 10 Gb internet connection. For additional information please visit www.uttyler.edu/biology . One of the 15 campuses of the University of Texas System, UT Tyler is a fast-growing university. More than 80 undergraduate and graduate degrees are available from its campuses in Tyler, Longview and Palestine. Tyler is located 90 miles east of Dallas in the scenic Piney Woods area of East Texas. Tyler is the cultural center of East Texas, a region with over one million people, and boasts many amenities such as a science museum, a planetarium, an art museum, a ballet, a symphony orchestra, and a renowned performing arts center.

Applications: Please include (as a single PDF file) a) cover letter; b) detailed curriculum vitae; c) statement of research interests and professional goals, d) statement of teaching interests and philosophy; e) reprints of 3 relevant publications and arrange to have 3 reference letters sent to: Dr. Lance Williams, Chair, Genomics Search Committee, Department of Biology, The University of Texas at Tyler, 3900 University Blvd., Tyler, TX 75799. E-mail: lwilliams@uttyler.edu.

Review of applications will begin July 31, 2012 and continue until a suitable candidate is found. The University of Texas is an Affirmative Action/Equal Opportunity Employer. Women and minorities are strongly encouraged to apply. The successful applicant must be able to demonstrate eligibility to legally work in the

United States. This position is security-sensitive and subject to Texas Education Code Section 51.215 which authorizes employer to obtain criminal history record information. The position is subject to availability of funding.

jbanta@uttyler.edu

UUlm Germany Biodiversity

W3-Professorship - Institute of Experimental Ecology

The University of Ulm, Germany, Faculty of Natural Sciences, invites applications for the position of the

Director (head) of the Institute of Experimental Ecology, full professor (W3) (succeeding Prof. Dr. Elisabeth Kalko)

The successful candidate has excellent scientific standing in the research area of functional biodiversity of animals. Research activities should include modern methods and approaches to topics in biodiversity, such as the relevance of animals as vectors for zoonoses or the role of animals in ecosystem services with relevance to humans. Experience in heading research projects and successful grant application is essential. Establishment of close interdisciplinary networks with Institutes in the Faculty of Natural Sciences, in particular Biology, and the Medical Faculty are expected. In addition, the appointee is expected to take up a leading function in the envisaged research focus EcoHealth Sustainability±.

Teaching expertise should cover a broad spectrum in the area of animal ecology. Current teaching of the Institute focuses on basic courses in zoology and ecology (bachelor and teacher training programs) and on advanced courses in biodiversity/ecology in the bachelor and master programs in biology.

Conditions for appointment are a completed course of studies at a university, pedagogical aptitude, doctorate and additional academic achievements (ì47 LHG).

The University of Ulm is committed to increase the share of women in research and teaching positions and therefore explicitly encourages female candidates to apply.

Ulm University is certified as a family-friendly university and offers a dual career program for partner hiring.

Please send detailed applications with the usual documents

to the Vice-Dean of the Faculty of Natural Sciences Prof. Dr. G^{1}nter Ehret Albert-Einstein-Allee 11 D-89081 Ulm Germany

by 25 June 2012. Please indicate on the envelope the index number 40.

Physically disabled applicants receive favourable consideration when equally qualified.

Link: http://www.uni-ulm.de/en/homepage/-news-details/article/w3-professur-institut-fuer-experimentelle-oekologie.html Dr. Stefan Klose stefan.klose@uni-ulm.de

Institute of Experimental Ecology (Bio III) Ulm University Albert Einstein Allee 11 89069 Ulm, Germany phone +49.731.50.22661 http://www.coronavirus.org Institute of Virology, Bonn University phone +49.228.2400.3875 http://www.virology-bonn.de "Stefan Klose (Ulm Univ - Exp Ecology)" <stefan.klose@uni-ulm.de>

UmeaU EvolutionTheory

See the complete ad at http://www8.umu.se/umu/-aktuellt/arkiv/lediga_tjanster/312-383-12.html Umeå University announces...

Senior Lecturer in Theoretical Ecology

The Department of Ecology and Environmental Science has 150 members from 20 different countries including 50 PhD students and 15 professors (for more information see the department's homepage: http:/-/www.emg.umu.se/english/?languageId=1). Our department offers a unique breadth of research and education in ecology, physical geography, paleolimnology and environmental health.

IceLab (Interdisciplinary Science Laboratory) seeks to constitute a hub of interdisciplinary, theoretical science at Umeå University that gathers researchers looking for new ways of modelling and analyzing systems within a broad spectrum, including life- and social sciences. At present, IceLab is a joint collaboration between the Departments of Ecology and Environmental Science, Mathematics and Mathematical Statistics, and Physics.

In a joint effort, IceLab and the Department of Ecology and Environmental Science are now announcing a position as senior lecturer to carry out research within the area of theoretical and computational ecology defined in a broad sense. Research may include studies of evolutionary processes, population and community dynamics, and/or biogeochemical processes. We are looking for a visionary researcher who is able to develop and scrutinize causal explanations for phenomena driven by dynamical feedbacks under environmental and organismal constraints. The successful candidate is expected to join us in developing the dynamic and international environment at IceLab and to strengthen the scientific interactions between IceLab and the Department of Ecology and Environmental Science. Candidates who link theory with experimental and empirical data are therefore particularly encouraged to apply, but we welcome applications from all candidates with a relevant background. The candidate should be competent to teach undergraduate courses in evolutionary ecology, community and ecosystem ecology, and/or theoretical ecology and modelling.

The applicant should have a PhD, or an equivalent exam, with focus on theoretical modelling of research problems in ecology, evolutionary biology, or a related field. Documented experience of real interdisciplinary collaborations, as well as several years of international post-doc experience, are highly qualifying.

The position as senior lecturer is permanent and its responsibilities include research, teaching, and administration, with a strong emphasis on research during the first four years. The successful applicant is expected to create his/her own research group and to supervise graduate students as well as post-docs. He/she is also expected to attract research grants from external sources of funding and to have a vivid collaboration with scientists at both Umeå University and other universities. In the evaluation, particular emphasis will be given to scientific skills. Pedagogical and administrative skills and the ability to collaborate with other researchers are also considered. Merits and skills will be evaluated in relation to the seniority of the candidate, and we encourage both qualified junior and senior candidates to apply.

Applicants should submit, electronically or in hard-copy form:

- a curriculum vitae (CV), - copies of relevant degree certificates and diploma, - a statement of academic, interdisciplinary, and teaching qualifications, - a publication list, - copies of relevant articles, numbered according to the publication list, - a research plan (maximum 5 pages) with a strong basic science approach that explicitly addresses opportunities for in house collaborations, - a list of 3 references (with contact details).

All documents submitted in hard-copy form should be in three copies, and all electronically submitted material should be in MS Word or PDF format. Note, in order to be considered, applications must include copies of reprints.

For further information concerning the position, please contact Prof. Sebastian Diehl, phone +46-(0)90-786 5738, sebastian.diehl@emg.umu.se and/or Assistant Prof. Martin Rosvall, phone +46-(0)70-239 1973, martin.rosvall@physics.umu.se.

Your complete application, marked with reference number 312-383-12, should be sent to jobb@umu.se (state the reference number as subject) or to the Registrar, Umeå University, SE-901 87 Umeå, Sweden to arrive June 7, 2012 at the latest.

Sebastian Diehl Professor of Ecology Department of Ecology and Environmental Science Umeå University 90187 Umeå, Sweden

sebastian.diehl@emg.umu.se

VolunteerFieldAssistants AustralianCuckoos

Two field assistants for a study on Australian cuckoos and their hosts Sept 2012 - Jan 2013

Two motivated and capable volunteer field assistants are needed for our research project studying the interactions between Australian cuckoos and their hosts in Canberra, Australia. This is an excellent opportunity for recent science graduates to gain valuable, hands-on experience of behavioural and evolutionary research.

Fieldwork will involve:

* assisting with mist-netting of superb fairy-wrens and yellow-rumped thornbills * searching for nests * monitoring nests * assisting with acoustic and video recording * monitoring colour banded birds

The fieldwork requires spending 6-8 hours/day, 5 days/week at the field site. You will be part of a team of researchers and students working on the project. The study site is a nature reserve comprising open eucalypt woodland, and it is 10mins drive from Canberra city centre and the Australian National University. We will provide $1500/month living allowance for food and accommodation.

Ideally, applicants should have some field experience, good observational skills, be physically fit, reliable and able to work independently. Experience monitoring colour banded birds, nest searching or mist-netting would be a great advantage, but is not essential.

For more information, and to apply, please contact Naomi Langmore (naomi.langmore@anu.edu.au). Interested applicants should email a cover letter, a CV and the contact details for two referees (ideally at least one referee who has worked with you in the field) to the address above. Please send your application by 30 June at the latest.

wendy.dimond@anu.edu.au

Other

Alberta Volunteer SquirrelPops

Field Assistants Required Immediately-Columbian ground squirrels

Sheep River Provincial Park, Alberta, Canada

We are looking for 2 volunteers to assist with fieldwork beginning ASAP and continuing until Aug 3, 2012. The project investigates the evolutionary ecology of Columbian ground squirrels. As a member of the study, assistants will be involved with monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals. Fieldwork will involve live-trapping and handling of animals, behavioural observation, radio-telemetry (to locate natal burrows) and assistance with the measurement of physiological (metabolism) traits on free-ranging animals. This is an excellent opportunity to gain experience working with a collaborative research team on a long-term study of a wild mammal.

All fieldwork is carried out in the spectacular Rocky Mountains of southwestern Alberta, Canada, home to some of the most majestic wildlife in North America. We will be staying at the University of Calgary's R.B. Miller research station in Sheep River Provincial Park, Alberta. You will interact with other researchers working with ground squirrels on a diversity of projects in behavioural and population ecology. Additionally, the field station is home to a number of other researchers working on a variety of projects, ranging from insects to large mammals.

Food and accommodation are provided, but you will be required to make your own way to either Calgary or Edmonton. Training will be provided and no experience is necessary, but candidates should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal behaviour. Periods of time will be spent camping and, as such, successful applicants need to enjoy the outdoors, be up-beat, positive, responsible and work well as a member of a team. If you wish to apply for one of these posts then please send a CV with a cover letter and contact details of three references (with e-mail address), by email to Jeff Lane (contact info below). Review of applications will commence immediately and continue until suitable candidates are found.

Contact:

Dr. Jeff Lane

u.columbianus@hotmail.com Department of Biological Sciences

University of Alberta

Edmonton, AB Canada T6G 2E9

u.columbianus@hotmail.com

EvolutionVideo contest

Enter your evolution-themed video for screening at this year's Evolution meeting by June 29th, and you could win $$$ to attend the scientific meeting of your choice.

The first- and second-place winners will receive a travel allowance of up to $1,000 and $500, respectively, for travel expenses to attend any scientific meeting they wish.

This year's application deadline is June 29.

The videos should be 3min or less, and have something to do with ecology or evolution. We had nearly 150 people at last year's event. You don't have to attend the meeting to enter the contest.

Please consider it! More info here: http://filmfestival.nescent.org/how-to-submit/ [1]

About the center: NESCent is a scientific research center that supports cutting-edge, cross-disciplinary research in evolutionary biology. The center offers a range of fellowships for visiting scientists and educators and sponsors numerous scientific meetings each year. Since its beginnings in 2004, NESCent has hosted more than 3,000 visitors from nearly 35 countries. For more information please visit www.nescent.org [2]. [3]

Links:

[1] http://filmfestival.nescent.org/how-to-submit/ [2] http://www.nescent.org [3] http://filmfestival.nescent.org/how-to-submit/ "Robin Smith, Ph.D." <ras10@duke.edu>

Frontiers Biogeography

From evoldir@evol.biology.mcmaster.ca Mon May 21 01:02:27 2012 Return-Path: <evoldir@evol.biology.mcmaster.ca> X-Spam-Checker-Version: SpamAssassin 3.3.1 (2010-03-16) on helix X-Spam-Level: X-Spam-Status: No, score=-100.0 required=5.0 tests=SHORTCIRCUIT, USER_IN_WHITELIST shortcircuit=ham autolearn=disabled version=3.3.1 X-Original-To: brian@helix.biology.mcmaster.ca Delivered-To: brian@helix.biology.mcmaster.ca Received: from pinegw02.uts.mcmaster.ca (pinegw02.UTS.McMaster.CA [130.113.128.25]) by helix.biology.mcmaster.ca (Postfix) with ESMTP id 63B0E84FC0 for <brian@helix.biology.mcmaster.ca>; Mon, 21 May 2012 01:02:27 -0400 (EDT) Received: from Gorash7.UTS.McMaster.CA (Gorash7.UTS.McMaster.CA [130.113.196.61]) by pinegw02.uts.mcmaster.ca (8.14.4/8.14.4) with ESMTP id q4L523IL030693 for <brian@helix.biology.mcmaster.ca>; Mon, 21 May 2012 01:02:05 -0400 Received: from evol.biology.mcmaster.ca (evol.Biology.McMaster.CA [130.113.246.218]) by Gorash7.UTS.McMaster.CA (8.13.7/8.13.7) with ESMTP id q4L51ldC023565 for <brian@helix.mcmaster.ca>; Mon, 21 May 2012 01:01:47 -0400 Received: by evol.biology.mcmaster.ca (Postfix, from userid 10048) id 324A5684F5; Mon, 21 May 2012 01:01:39 -0400 (EDT) To: brian@helix.biology.mcmaster.ca Subject: Err:500-1 Other: Frontiers of Biogeography - IBS Open Access journal, now published by UC eScholarship Reply-To: dawson.mn@gmail.com Message-Id: <20120521050139.324A5684F5@evol.biology.mcmaster.ca> Date: Mon, 21 May 2012 01:01:39 -0400 (EDT) From: evoldir@evol.biology.mcmaster.ca X-PMX-Version-Mac: 5.6.1.2065439, Antispam-Engine: 2.7.2.376379, Antispam-Data: 2012.5.21.45121 X-PerlMx-Spam: Gauge=X, Probability%, Report=' WEBMAIL_REPLYTO_NOT_FROM 0.5, HTML_00_01 0.05, HTML_00_10 0.05, SUPERLONG_LINE 0.05, BODYTEXTP_SIZE_3000_LESS 0, BODY_SIZE_2000_2999 0, BODY_SIZE_5000_LESS 0, BODY_SIZE_7000_LESS 0, NO_REAL_NAME 0, __ANY_URI 0, __CP_URI_IN_BODY 0, __FRAUD_BODY_WEBMAIL 0, __FRAUD_WEBMAIL 0,

__FRAUD_WEBMAIL_REPLYTO 0, __HAS_MSGID 0, __INT_PROD_LOC 0, __MIME_TEXT_ONLY 0, __OEM_PRICE 0, __PHISH_SPEAR_STRUCTURE_1 0, __PHISH_SPEAR_STRUCTURE_2 0, __SANE_MSGID 0, __STOCK_PHRASE_7 0, __TO_NO_NAME 0, __URI_NS ' Status: RO Content-Length: 2807 Lines: 34

Frontiers of Biogeography - Open Access journal

Frontiers of Biogeography is published by the International Biogeography Society (www.biogeography.org) and the University of California's eScholarship system (http://escholarship.org/uc/fb).

Our hybridization of the Society Journal and Open Access publishing models enables Frontiers of Biogeography to provide both exceptionally low publication fees ($200 per article, with waiver or partial-waiver options) and free access to all content for all readers.

Volume 4 issue 1 is now available at http://escholarship.org/uc/search?entity=3Dfb;volume=3D4;issue=3D1 and we encourage you to submit Opinion, Perspective, or Review Articles and Research Letters on the geographical variation of life at all levels of organization. This includes, but is not limited to, studies on temporal and/or evolutionary variation in any component of biodiversity if they have a geographical perspective, as well as studies at more local scales if they have a spatially-explicit component. Papers may study aerial, freshwater, marine, subterranean, or terrestrial biogeography of extant and/or extinct taxa spanning the entire tree of life and all time periods.

A sample of the articles published in Frontiers of Biogeography includes:

Losing time? Incorporating a deeper temporal perspective into modern ecology Felisa A. Smith & Alison G. Boyer (2012) Frontiers of Biogeography v.4 (1) http://escholarship.org/uc/item/3bg6583c Individual variation and weak neutrality as determinants of forest diversity Brian Beckage et al. (2012) Frontiers of Biogeography v.3 (4) http://escholarship.org/uc/item/5xv4k3tr Musings on the Acropolis: terminology for biogeography Samuel M. Scheiner (2011) Frontiers of Biogeography v.3 (2) http://escholarship.org/uc/item/4jr46958

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GenomicResources CallForMeetingProposals

GENOMIC-RESOURCES - Call for Science Meetings - Conference / Workshop 2012

The project GENOMIC-RESOURCES of the European Science Foundation aims to contribute to the education of a new generation of scientists in applying cutting edge approaches to the characterization, economic evaluation, management, exploitation and conservation of Farm Animal Genetic Resources (FAnGR). Target researchers learn and work with novel tools and methods made available by recent advances in molecular technologies, statistical and socio-economic approaches, GIScience and integrated data analysis.

See http://genomic-resources.epfl.ch (and http://www.esf.org/genomic-resources)

For 2012, GENOMIC-RESOURCES invites proposals from potential organisers of a 2 or 3-day **Conference / Workshop** to take place between July and November 2012, addressing the application and development of quantitative methods in measuring and modeling farm animal genetic diversity.

The main theme of the event may be broad in remit and/or address one of the following subtopics: - New methods for prioritizing resource allocation in FAnGR conservation using genetic data, - Population viability assessment, - Incorporating signatures of genomic adaptation in FAnGR conservation schemes, - From data to policy: how best to translate genetic information into management decisions at the national and EU level.

A maximum budget of 15,000 will be available for the organization of the conference/workshop.

Organizers should ask interested speakers to submit a one page abstract for assessment. Keynote speakers should also contribute a one page abstract. All abstracts and presentations of the Workshop should be made available for publication on the GENOMIC-RESOURCES website.

Priority will be given to applicants who come from countries that financially support the programme (Austria, Belgium, Croatia, Finland, Germany, Netherlands, Norway, Sweden, Switzerland, and United Kingdom).

Detailed conditions are described on the following web page: http://genomic-resources.epfl.ch The deadline for submission of Summer School proposals is June 1, 2012, at 17:00 CET. Late or incomplete applications will not be considered.

The GENOMIC-RESOURCES Steering Committee

Murelli Elena <elena.murelli@unicatt.it>

Irwin lab manual

Hello folks (and, hopefully, Rebecca Irwin, herself)!

I'm preparing to teach a laboratory class in Evolution in January and have been searching around for inspiration. There are lots of great ideas out there and one resource that is repeatedly suggested by the interwebs is a lab manual prepared by someone named Rebecca Irwin who worked at the University of Tennessee at Martin (http://www.utm.edu/staff/rirwin/evol.htm). [Please note, I'm almost positive this is not the Rebecca E. Irwin who works at Dartmouth].

Unfortunately, however, all of the links on her class page are dead and the email contact listed on the page doesn't work either. If anyone happens to know Rebecca, could you please forward this request to her? Or, if anyone happens to have a copy of the lab manual, would you consider sharing it with me?

Have a great evening, BEST wishes, Lesley

Lesley Campbell <lesley.g.campbell@ryerson.ca>

Journal Society Coevolution clarification 3

Dear Colleagues,

Since my proposal of a journal coevolution, I have received a number of emails how what should be included as coevolution. I can sense a great deal of inconsistencies and wish to post what I (probably wrongly) thought to be coevolution and co-adaptation.

I. We should first define evolution, adaptation, preadaptation and exaptation before discussing coevolution.

What we need to specify:

1. A species S (e.g., a locust) with n genotypes, represented by a population with genotypes g1, g2, ..., gn.

2. The associated genotypic frequencies Pg1, Pg2, ..., Pgn, represented by the vector Pg.

Evolution happens when Pg changes over time. This can be caused by mutation, selection, drift and may other mechanisms. However, our focus is on selection and its possible outcome, adaptation.

Environmental factors, such as the application of pesticide, can cause dramatic changes in Pg in some insect species. If it eliminates all genetic lineages contained in all populations of a species, then extinction happens.

If the pesticide can reduce g1, g2, ..., gn individuals by a fraction of q1, q2, ..., qn, but the genotypic frequencies rebound to the original values after the pesticide is cleared off, then we see evolution as well as selection in action, but there is no adaptation of the population to the pesticide. We probably should define selection a bit more explicitly. Let F1, F2, ..., Fn be the fitness of genotypes g1, g2, ..., gn, respectively. Whenever an environmental factor can differentially change F1, F2, ..., Fn and consequently Pg1, Pg2, ..., Pgn, that environmental factor is a selection agent and the process of differential change of F1, F2, ..., Fn is selection.

Suppose some individuals in the population happen to have an enzyme (E) that can partially detoxify the pesticide and allow the carriers to propagate their lineages, albeit at a much reduced rate r_new relative to the original r_old. If the enzyme E originated before the application of pesticide, we again see natural selection in action but do not see adaptation.

If, in the presence of the selection agent (i.e., pesticide), some individuals evolved a much more effective E that can completely detoxify the pesticide so that the fitness of the carriers of the enzyme (i.e., the gene encoding the enzyme) increases as a consequence, then we can claim to have observed adaptation (the origin of a new trait or a new trait value beneficial to the carriers in response to a selection agent).

If the new enzyme E can now also detoxifies a nasty compound in a plant and allows the insect species to exploit this previously unavailable food resource, then that is preadaptation which, according to Stephen J. Gould, involves a trait that was selected for a function but later gained a new function beneficial to the carrier.

In contrast to preadaptation, if a trait originated as a neutral trait but subsequently become beneficial in a new environment, then that is exaptation.

All three hypotheses (adaptation, preadaptation and exaptation) are potential explanations for the gain of positive charges in the proteins of the gastric pathogen, Helicobacter pylori, that inhabits the acidic environment in the mammalian stomach. A test of these three hypotheses was reported in an earlier paper of mine (Xia, X. and G. Palidwor. 2005. Genomic Adaptation to Acidic Environment: Evidence from Helicobacter pylori. American Naturalist 166:776-784).

How can adaptation be observed given that we typically cannot observe the ancestral trait, e.g., when we have the current E enzyme but do not have the original E enzyme. How would we know if this enzyme represents adaptation, preadaptation or exaptation? We do this by comparing the species/population to its phylogenetically related lineages. If all phylogenetic lineages, regardless of whether they have been exposed to the pesticide or not, all have an effective detoxifying enzyme, then we have to settle with either preadaptation or exaptation. In contrast, if those phylogenetic lineages that have not been exposed to the pesticide have only a weakly detoxifying E enzyme and only those that are exposed to the pesticide harbour an effective detoxifying E enzyme, then we may infer that the effective detoxifying enzyme may indeed represent an adaptation, evolved in response to the pesticide as a selection agent.

II. Let's now come to coevolution and co-adaptation at the organismal level.

What we need to specify:

1. A minimum of two species, A and B, each represented by a population with n and m genotypes, respectively. That is a1, a2, ..., an for species A, and b1, b2, ..., bm for species B.

2. The associated genotypic frequencies Pa1, Pa2, ..., Pan, and Pb1, Pb2, ..., Pbm, represented by vectors Pa and Pb, respectively.

3. Fitness of each genotype: Fa1, Fa2, ..., Fan, and Fb1, Fb2, ..., Fbm, represented by vectors Fa and Fb, respectively.

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MateChoice JCurrZoo

Dear Colleagues,

The Journal CURRENT ZOOLOGY (ISSN 1674-5507, http://www.currentzoology.org) is preparing one special column (A special column is three to eight papers published along with some regular accepted papers in the same issue), Mate Choice, for the second issue of 2013.

Deadline for abstract submission: Aug. 1 , 2012; Deadline for manuscript submission: Nov. 10,2012;

Title and abstract submissions should be sent to Dr Gil Rosenthal<grosenthal@bio.tamu.edu> and copy to the executive editor, jiazy@ioz.ac.cn . You may send your manuscript now or by the deadline. Manuscripts should be submitted to the special column via ScholarOne ManuscriptsTM http://www.currentzoology.org/newsdetail.asp?id=1283 , or 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 is no publication or processing charge. Please visit the Instructions for Authors before submitting a manuscript (http://www.currentzoology.org/instruct.asp)

Examples of previous and future special columns/issues are listed below.

We look forward to your future submissions.

Sincerely

Zhi-Yun JIA,Ph.D. Executive Editor Current Zoology http://www.currentzoology.org

The published special columns:

Speciation and Sexual Selection: 2012, 58(3), http://www.currentzoology.org/currentissue.asp , Maria SERVEDIO, Department of Biology,University of North Carolina;

Animal Culture: 2012, 58(2), http://www.currentzoology.org/issuedetail.asp?volume=58&number=2&issue_id=525 , guest editors: Alex BENTLEY, University of Bristol, UK;Michael O'BRIEN, University of Missouri,USA;

Animal Social Networks: 2012, 58(2), http://www.currentzoology.org/issuedetail.asp?volume=58&number=2&issue_id=525 , guest editor: Daniel W. FRANKS, University of York, UK;

Aquatic Invasive Species Science: 2011, Vol 57(6), http://www.currentzoology.org/issuedetail.asp?volume=57&number=6&issue_id=522 , guest editor: Gerard van der Velde, Rob S.E.W. Leuven, Radboud University Nijmegen,The Netherland

Animal Ecology and Evolution in Alpine Regions: 2011, Vol 57(6), http://www.currentzoology.org/issuedetail.asp?volume=57&number=6&issue_id=522 , guest editor:Fumin LEI, Institute of Zoology, CAS, China

Effects of Extreme Climate Change on Birds: 2011, Vol 57(3), http://www.currentzoology.org/issuedetail.asp?volume=57&number=3&issue_id=518 , guest editor: A. P. MÃLLER,Université Paris-Sud, France

Avian Metabolic Diversity: 2010, Vol 56(6), http://www.currentzoology.org/issuedetail.asp?volume=56&number=6&issue_id=505 , guest editor: David SWANSON, University of South Dakota,USA

Stress Physiology in Ecology and Evolution: 2010, Vol 56(6), http://www.currentzoology.org/issuedetail.asp?volume=56&number=6&issue_id=505 , guest editor: David COSTANTINI, University of Glasgow, UK

Chemical Sense and Communication: 2010, Vol 56(6), http://www.currentzoology.org/issuedetail.asp?volume=56&number=6&issue_id=505 , guest editor: Liquan Huang, Gary Beauchamp,Monell Chemical Senses Center, USA

Upcoming special columns for 2012:

Evolution of Mimicry: 4th issue, David Pfennig, Department of Biology,University of North Carolina,University of North Carolina;

Invertebrate Personality: 4th issue, Claudio CARERE, Università degli Studi della Tuscia, Italy;Jennifer Mather, Behaviour and Evolution Research Group, University of Lethbridge,Canada

Ecological Speciation: 5th issue, Jenny Boughman, Michigan State University,USA

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NESCent Call For Proposals

POSTDOCTORAL FELLOWSHIPS IN EVOLUTIONARY BIOLOGY AND RELATED FIELDS

We are now accepting proposals for Postdoctoral Fellowships at The National Evolutionary Synthesis Center (NESCent). We are looking to support innovative approaches to outstanding problems in evolutionary science. Proposals in any area of evolutionary science are welcome, but proposals in the following areas are of particular interest: Evolutionary Medicine, Synthetic Biology and Origins of Life, Evolution and the Social Sciences, and K-12 Minority Education in Evolution. Proposals are due July 10 for two-year Fellowships that will begin no later than January 2013; we anticipate that award decisions will be made by first week of October. For more information, please see our website at https://www.nescent.org/science/proposals.php . CALL FOR PROPOSALS - SABBATICAL SCHOLARS, WORKING GROUPS AND CATALYSIS MEETINGS

Proposals for Sabbaticals, Working Groups and Catalysis Meetings are now being accepted at The National Evolutionary Synthesis Center (NESCent). We are looking to support innovative approaches to outstanding problems in evolutionary science. In particular, proposals that have a clear interdisciplinary focus, or involve evolutionary concepts in non-traditional disciplines, are strongly encouraged, as are proposals that demonstrate international participation and a mix of senior and emerging researchers, including graduate students. Proposals are accepted twice a year, with deadlines on July 10 and December 1. Proposals in any area of evolutionary science are welcome, but proposals in Evolution and the Social Sciences and K-12 Minority Education in Evolution are also being considered for the July 10 deadline (Proposals in one of these two areas must include $B!H(BTargeted Initiative$B!I(B in proposal title; see also http://www.nescent.org/news/newsdetail.php?id=225 and https://www.nescent.org/news/newsdetail.php?id=229). Proposals for Sabbaticals may be for up to a full year. We also accept proposals for short-term visits (2 weeks to 3 months; deadlines on January 1, April 1, July 1 and September 1). For more information, please see our website at https://www.nescent.org/science/proposals.php . GRADUATE FELLOWSHIPS IN EVOLUTIONARY SCIENCE AND RELATED FIELDS

NESCent is now including graduate training in its portfolio, by offering one-semester fellowships for graduate students to pursue research with a NESCent sabbatical scholar, a NESCent postdoctoral scholar, or a NESCent Working Group. Deadlines are January 1 (for a fall semester fellowship) and July 1 (for a spring semester fellowship). For more information, please see our website at https://www.nescent.org/science/proposals.php . Craig R. McClain, Ph.D.

Assistant Director of Science National Evolutionary

Synthesis Center 2024 W. Main St. Suite A200 Box 104403 Durham, NC 27705

919-668-4590

cmcclain@nescent.org

Associate Editor for Journal of Biogeography: http://www.wiley.com/bw/journal.asp?ref=0305-0270 Deep-Sea News: http://deepseanews.com/ National Evolutionary Synthesis Center: http://www.nescent.org/ Research Homepage: http://craigmcclain.com/ McClain Craig <cmcclain@nescent.org>

PCR machines

Dear all,

our last PCR machine broke down a few weeks ago and we are now at a standstill. Does any of you have a PCR machine (and any other basic equipment) that they can freely pass on to our lab in Uganda (Makerere University) so that we can continue training our students and conducting research? Thanks a lot.

Best wishes Charles

Charles Masembe (BVM, MSc., PhD), Senior Lecturer (Molecular Genetics & Evolution), Makerere University, College of Natural Sciences School of Biological Sciences Department of Biology Box 7062, KAMPALA, Uganda Skype: cmasembe10 Phone +256712455987

Charles Masembe <cmasembe@muienr.mak.ac.ug>

PCR machines thanks

Dear all, Thank you very much to all of those who took time and responded to our plea. We have got several positive responses to the above. Thank you very much. Best wishes Charles

Charles Masembe (BVM, MSc., PhD), Senior Lecturer (Molecular Genetics & Evolution) Makerere University College of Natural Sciences School of Bio-Sciences Department of Biological Sciences Box 7062, KAMPALA, Uganda Skype: cmasembe10 +256712455987

cmasembe@muienr.mak.ac.ug

Phyloseminar DavidPollock May30

Next talk on http://phyloseminar.org/ : “Adaptation, coevolution, and convergence in the context of protein thermodynamics” David Pollock (University of Colorado School of Medicine)

Interactions within and between proteins are a fundamentally important part of how they evolve and adapt. We have been considering how and why proteins adapt, coevolve, and converge, and working to understand these concepts in the context of protein thermostability and function. We will expand from the previous talk of our collaborator, Dr. Goldstein, and discuss how and why coevolution is and should be detected, and how thermostability affects reconstruction of ancestral functions. Further, we will discuss our work on adaptive redesign in mitochondrial proteins, perhaps the largest known case of an adaptive burst in multiple metabolic proteins. The convergence between ancestral snakes and ancestral acrodont lizards is also perhaps the largest known case of adaptive convergence. We will consider what these examples tell us about the theory of how proteins appear to evolve in the context of nearly neutral versus cases of adaptive change. Further, we will discuss the impact on understanding phylogenetic relationships, and we will also discuss a unified theory of nearly neutral and adaptive evolution in the context of structure and function.

West Coast USA: 10:00 (10:00 AM) on Wednesday, May 30 East Coast USA: 13:00 (01:00 PM) on Wednesday, May 30 UK: 18:00 (06:00 PM) on Wednesday, May 30 France: 19:00 (07:00 PM) on Wednesday, May 30 Japan: 02:00 (02:00 AM) on Thursday, May 31 New Zealand: 05:00 (05:00 AM) on Thursday, May 31

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

Rennes France EcolEvol ResearchOpportunties

Dear all

This is to inform you about the opportunity to develop research with me and my collaborators at Rennes, using existing extensive data sets, well studied field settings and my support to put together a proposal for one of the multiple French/European/outside funding opportunities. I will below present (i) some of the data or field settings exploitable; (ii) a very incomplete list of possible research questions to be developed and for which databases or field setting would be available; (iii) the research environment at Rennes and Rennes per se; (iv) a list of different funding opportunities from the Rennes/French/European side - but you may have many others from your own locality/country/continent; (v) a list of my recent publications showing (hopefully) the competences in the field.

Please do not hesitate to transmit or contact me if interested.

Best regards

Andreas Prinzing

(i) DATA and FIELD SETTINGS potentially available (data are in part assembled from freely available sources and any publication project will of course need to acknowledge these sources, many other data are available via/due to internal or external collaboration and any publication project will of course need to find the agreement of, and involve, these collaborators)

- descriptions of tens of thousands of local plant species communities

- niche requirements of most plant species from field measurements for an entire region (Netherlands)

- dated phylogeny of all Angiosperm plant species of an entire regional species pool resolved to at least genus level (Netherlands; > 500 genera)

- dozens of functional traits of many to all plant species of an entire regional pool (Central Eruope)

- composition of arthropod communities (oribatid mites, heteroptera, coleoptera, galls, lepidoptera, miners, parasitoid groups) of canopy trees, linked to measurements of soil biota (mycorrhiza and their activity, invertebrates, microbial biomass) and of biotic and abiotic environmental factors on the same trees, as well as the composition of the ambient forest canopy, notably the phylogenetic distance of the neighbours.

- the trees from which many of the above data stem

- descendents of plants whose ancestors grew in different community neighbourhoods, and morphological and biochemical characterizations

- community compositions of plants, their ant mutualists, their services and the role of cheaters along environmental disturbance gradients

(ii) Possible QUESTIONS to be developed with the data or field settings already available in my group. For some of them, projects are already written and can serve as a basis for proposal writing. Of course many other questions would be equally interesting and possible to develop, and again partly even with available data.***:

- Microevolution on macroevolutionary islands: accelerated evolution of colonizers on phylogenetically isolated host trees?

- Leaving its ancestral niche to respond to environmental change: a problem of recruitment limitation?

- Does phylogenetic heritage of different vegetation types control decomposer assembly and decomposition?

- Does phylogenetic heritage of different vegetation types control productivity?

- Is niche conservatism a blessing under environmental change due increased evolution of hybrids? Is it a blessing due to improved nutrient cycling in communities composed of closely related species?

- How does plant neighbourhood influence plant traits?

- What are the steps involved in the expression of local adaptation?

- How does patch age and patch isolation control community assembly in the canopy?

- What is the role of phenotypic integration for the response to environmental change?

(iii) The host lab here is the UNITE MIXTE DE RECHERCHE (UMR) ECOBIO - ECOSYSTEMES , BIODIVERSITE , EVOLUTION, co-funded by University of Rennes 1 and Centre National de la Recherche Scientifique, is a large institution with several dozen CNRS-researchers, docents and professors, plus technical staff. See http://ecobio.univ-rennes1.fr/. Ecobio was ranked A in the national evaluation of research institutions. Ecobio has particular expertise in Integrative Ecology, such as: mechanisms of speciation, life history evolution, and adaptation, expertise at the interface between macroevolution and macroecology, expertise in ecophysiology, landscape ecology and behavioral ecology, environmental genomics (very strong), community assembly and plant/herbivore interactions. Among others, Ecobio has given itself a Research Axis on “Species communities: assembly rules, evolutionary diversification, ecosystem functioning” (animated by A. Prinzing). Several further research institutions in ecology and evolutionary biology exist at Rennes.

Note that we are well equipped with analytical labs, servers etc. and to some degree technical personnel and have space and do not charge for this

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Software Phylogenetics for Pi

Dear EvolDir,

We are happy to announce LVB 2.31 for Raspberry Pi. Download it here:

http://biology.st-andrews.ac.uk/cegg/lvb.aspx LVB reconstructs phylogeny from a nucleotide multiple alignment using parsimony, with a heuristic search based on simulated annealing.

The Raspberry Pi is a low cost ARM computer that runs GNU/Linux. For information on the Raspberry Pi see:

http://www.raspberrypi.org LVB is also available for Mac OS X and as C source code.

Best wishes,

Daniel

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

db60@st-andrews.ac.uk

SouthAfrica Volunteers SmallMammalEvolution

3 volunteers needed from July / August to November / December 2012

as field assistants for the project:

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

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

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

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

Work of field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers will participate in a project on personality traits of striped mice, doing behavioral tests at the research station and in the field. Volunteers are also expected to help with maintenance of the research station (water pump, solar power, etc.).

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

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

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

When and how long: At the moment we are looking for 2-3 volunteers starting in July / August 2012. Volunteers are expected to stay at least three months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to carsten.schradin@ieu.uzh.ch.

More information under

http://stripedmouse.com/site1_3_5.htm

http://www.ieu.uzh.ch/research/behaviour/-endocrinology.html

Contact via e-mail: carsten.schradin@ieu.uzh.ch

Dr. Carsten Schradin Research Assistant, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel: +41 -(0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

Working as a field assistant in Goegap Nature Reserve

A report by Romy Höppli, student at the University of Zurich, who staid in Goegap June to August 2008

Blue skies without a single cloud for six weeks rocky mountains with little vegetation yellow, orange and pink fields of flowers in whatever direction you look small mammals, lizards and birds in our front yard and Mountain Zebras, Springbok and Ostrich right next door...

This was my time at the Succulent Karoo Research Station in Goegap Nature Reserve in South Africa! During six weeks from the beginning of July until the middle of August I've been living here, studying mice, experiencing nature like never before and being part of a small community where there was always something to laugh and joke about!

After arriving in Goegap, right the next morning my scientific adventure in South Africa began: Setting and checking traps, nest observations and radio-tracking were our daily routine. While I got bitten by the mice quite often in the beginning and my right middle finger was scarred all over, I

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UExeter Masters Scholarships

Biosciences in the College of Life and Environmental Sciences at the University of Exeter UK is delighted to offer a number of Masters Distinction Awards, covering the full cost of tuition-fees, to top performing students who accept a place to study on any taught Masters programme within the College, enrolling in 2012.

Eligible programmes with an evolutionary focus in Biosciences are:

MSc Bioinformatics MSc Bioinformatics and Systems Biology MSc Evolutionary and Behavioural Ecology

Please note that these awards may not be held in conjunction with any others. Summary Application deadline: 11th May 2012 Value: Full tuition fees Duration of award: for 1 year Contact: Ruth Tyrer r.tyrer@exeter.ac.uk

How to apply:

To be eligible for a College of Life and Environmental Sciences Masters Distinction Award you must hold an offer of a place to study on one of the eligible taught Masters programmes, commencing in 2012.

Once you have received the offer of a place, please complete and submit the Masters Distinction Award application form including the following details:

academic qualification additional academic achievements career ambitions non-academic achievements details of the difference the award would make to you.

All completed forms received from eligible students by 11 May 2012 will be considered.

Prof DJ Hosken Chair in Evolutionary Biology Director, Centre for Ecology & Conservation Biosciences, College of Life & Environmental Sciences University of Exeter, Cornwall Campus Tremough, Penryn, TR10 9EZ UK

d.j.hosken@exeter.ac.uk 01326 371843 http://-biosciences.exeter.ac.uk/staff/index.php?web_id=-david_hosken DJ Hosken <D.J.Hosken@exeter.ac.uk>

UndergradMentors Evolution2012

Undergraduate Diversity at Evolution 2012: call for additional mentors

“UndergraduateDiversity at Evolution 2012” seeks volunteers (graduate students,postdocs, and faculty members) to serve as mentors to 18 participants. Mentors meet with pairs of students andattend a half day of talks with them, introduce them to colleagues, help them network,and generally make the meetings a welcoming place for them. Although costs are not covered for mentors,it is a rewarding experience. Please contact Rich Kliman(rmkliman@cedarcrest.edu) if you are interested in serving as a mentor. Thanks!

rmkliman@cedarcrest.edu

genosat

GenoSat: NGS Microsatellites Library Full Service.

Based on high throughput sequencing, the technique is validated on 160 different libraries, sequenced by Genoscreen. From 1 Î¼g of genomic DNA, this technology produces a minimum of 8000 raw sequences, 2000 sequences presenting microsatellites motives and 100 primers pairs fraiming microsatellites motives in a record time of 2 months. For more information and offers don’t hesitate to have a look on our website www.genoscreen.com or please feel free to send an email to frederic.antigny@genoscreen.com

Sincerely,

Frédéric Antigny, MSc, MBA

Business Developer

GENOSCREEN Campus Pasteur 1 rue du Professeur Calmette 59000 Lille, FRANCE Cell.:+33 (0) 652 614 790 Tel: +33 (0) 320 877 708 Tel: +33 (0) 320 877 153 (Accueil/Welcome Desk) Fax : +33 (0) 320 877 264 www.genoscreen.com

PostDocs

ArizonaStateU ComputationalGenomics

Multiple postdoctoral fellow positions are available in the Biodesign Institute at Arizona State University in the group of Computational Genomics and Evolutionary Medicine (CGEM).

We are: A young dynamic group studies the nascent and fancy field of genomics and evolutionary medicine. The research of CGEM group focuses on three areas: (1) Integrative Network Biology. We integrate multiscale (genotype, genetic and epigenetic) data from large cohort studies to reconstruct the human disease maps, and identify genetic mechanisms of obesity, diabetes, and cancer. (2) Cancer genomics. We use next-generation sequencing techniques to sequence single-cell human cancer tissues, and model the evolution of cancer progression. (3) Evolutionary Medicine. We use phylogenetic and evolutionary methods to predict novel therapeutic targets of complex human diseases. Finally, group members are also highly encouraged to develop their own research projects.

You are: For postdoc positions, a candidate with PhD or MD/PhD degree with trainings from both biology/biomedicine and quantitative computation (e.g. computational biology, genetics, evolutionary biology, computer sciences, etc.). Experience in large-scale data analysis is required and knowledge of biological networks is a plus. You should be energetic, self-motivated with good oral and written communication skills.

How to: Qualified candidates are invited to email a letter of motivation, CV, and contact information for 3 references to Dr. Zhi Wang (appl2cgem@gmail.com). A generous salary and benefits will be provided. The positions will start on August 15, 2012 or after.

appl2cgem@gmail.com

Austin Texas EvolutionaryGenetics of Cancer

Evolutionary Genetics of Glioblastoma Multiformae

The Center for Computational Neuroscience at NeuroTexas Institute at St. David's HealthCare seeks a highly motivated individual to study the evolutionary genetics and genomics of glioblastoma multiformae (GBM). Of particular interest, is the development of evolutionary-genomic models suitable for studying the genetic variation in GBM or the dynamics of mutations within growing tumors. Also of interest is the development of bioinformatic approaches for studying the variation observed in DNA/RNA sequence data obtained from GBM tumors.

NeuroTexas Institute (NTI) is a highly multidisciplinary clinical, research and educational institute affiliated with St. David's HealthCare in Austin, TX. The Institute enjoys an open and highly productive relationship with the adjacent University of Texas at Austin. NTI leads the Austin Brain Tumor Repository, which collects GBM specimens from our patients in a manner suitable for genomics projects.

The two-year position is available immediately. Candidates must have completed their PhDs in computational biology, computer science, mathematics or physics, and have at least three years of post-doctoral research experience. Ideal candidates will be familiar with evolutionary theory and modeling, DNA/RNA next-generation sequence analysis and bioinformatics, and systems biological approaches. Previous knowledge and experience with cancer genomics and modeling is an additional plus.

Please submit a letter of intent, curriculum vitae and the names and addresses of two references to:

Dr. Matthew C. Cowperthwaite Center for Computational Neuroscience NeuroTexas Institute at St. David's HealthCare 1015 East 32nd Street, Suite 404 Austin, Texas 78705

Matthew.Cowperthwaite@stdavids.com

Barcelona Chordate EvoDevo Genomics

BARCELONA POST-DOC: FELLOWSHIP APPLICATIONS in Chordate Fuctional Evo- Devo and Genomics

University of Barcelona Department of Genetics

Our new group on the field of Functional Evo-Devo and Genomics on Chordates is looking for candidates to apply for forthcoming post-doc FELLOWSHIP from Spanish and European funding programs (see below).

Candidates need to have a competitive CV to successfully apply for the fellowship. Experience in Molecular Genetics, Transgenesis and Developmental Biology, and (or) Background in Bioinformatics, and Comparative Genomics will be positively considered.

Our main research interest is to understand the impact of gene losses on the evolutionary diversification of mechanisms of development in chordates. Our work focuses on comparative approaches between vertebrates (zebrafish), urochordates and cephalochordates. Our main subject of study is Oikopleura dioica, a new emergent urochordate model within our own phylum, with the smallest metazoan genome size known so far, and with an outstanding amount of gene losses (Denoeud et al., Science, 2010).

Interested candidates, please send a brief letter of interest and a CV in ONE single pdf file to Cristian Cañestro (canestro@ub.edu)

Interested candidates for future POST- or PRE-DOCTORAL applications, please feel free to contact too. For an outline of our group's research: http://www.ub.edu/genetica/evo-devoen/canestro.htm http://www.uoneuro.uoregon.edu/ ˜ cristian/Canestro.html Forthcoming Postdoctoral calls: European Programs: IEF and IIF Marie Curie (open calls - deadline 16-8-2012) http://ec.europa.eu/research/participants/portal/page/people EMBO (open call - deadline 15-8-2012) http://ec.europa.eu/research/participants/portal/page/people Spanish Programs: Juan de la Cierva (not opened yet) http://www.idi.mineco.gob.es/portal/site/MICINN/ Beatriu de Pinós (not opened yet) http://www10.gencat.cat/agaur_web/AppJava/english/a_beques.jsp?categoria=3Dpostdoctorals oikocris@gmail.com

BrownU PlantPhylogenomics

The Edwards lab at Brown University is looking for a post-doctoral research associate to join our ongoing efforts focused on the evolution of succulence and alternative photosynthetic syndromes in the Caryophyllales. The postdoc will take the lead in the molecular/phylogenomic aspects of the project. We are currently building molecular phylogenies with traditional, whole chloroplast-genome and transcriptome approaches, and she/he will be responsible for generating and analyzing all of these data types. She/he will also take responsibility for general oversight of the molecular lab. While some goals are quite firm (e.g., improved phylogenies for several clades of Caryophyllales), there will be plenty of opportunity to develop other projects based on the postdoc's own interests- this will be actively encouraged.

The successful candidate will be a highly motivated, careful scientist and a team player, with a genuine love of plants and their remarkable evolutionary history. She/he will have a proven track record in project design, data collection, analysis, and publication. Previous lab experience with library prep/analysis of next-gen sequencing, a familiarity with large datasets, and good computing and analytical skills are also important qualities. Contingent upon funding, there may be exciting field work opportunities as well, so experience with (and enthusiasm for) plant collecting is an added bonus (though not essential).

The position start date is flexible and could potentially begin in September 2012; ideally the position will start no later than December 2012. The initial appointment will be for one year, with extension dependent on performance and funding. To apply, please send a letter describing research interests, a current CV, and contact information for three references to Erika Edwards (erika_edwards@brown.edu). Applications will be reviewed starting immediately and accepted until the position is filled. Brown University is an EEO/AA employer.

Erika J. Edwards Department of Ecology and Evolutionary Biology Brown University 80 Waterman St Box G-W Providence, RI 02912

office: 401.863.2081 lab: 401.863.6275 fax: 401.863.2166

lab website: http://www.brown.edu/Research/Edwards_Lab/index.php erika_edwards@brown.edu

BrownU PopulationGenetics

Postdoctoral Positions, Brown University

Funding for two postdoctoral fellows is available in Sohini Ramachandran's lab at Brown University.ÂÂThe lab uses mathematical and computational approaches to study human population genetics; for more information about recent projects in the group see http://www.brown.edu/Research/Ramachandran_Lab/. The group is affiliated with Ecology and Evolutionary Biology and Brown's Center for Computational Molecular

Biology.ÂÂAs a result, we interact with and collaborate with research groups at Brown in evolutionary genetics, the Division of Applied Mathematics, and Department of Computer Science.

Project details for successful candidates are flexible. Current projects in the lab focus on the evolutionary history of mutations associated with leukemia, comparing X-chromosomal and autosomal differentiation among human populations, and the inference of human evolutionary history from population genomic data.ÂÂApplicants must have a background in theoretical population genetics with experience analyzing genome-wide data, or a quantitative background (e.g., statistics, computer science) and a desire to do research in genetics and evolutionary biology.

Informal inquiries as well as applications (consisting of a CV, copies of relevant publications, and contact information for at least two references) should be emailed to sramachandran[at]brown.edu.

Starting dates are negotiable, and could begin as early as July 2012.

Sohini Ramachandran Assistant Professor Ecology and Evolutionary Biology Center for Computational Molecular Biology Box GâW, Providence, RI 02912 Office:ÂÂ(401) 863â9701 sramachandran@brown.edu

sohinir@gmail.com

CSIRO ComputBiol

OCE Postdoctoral Fellow - Com. Biol.

* Positive real-world IMPACT * Reputation for excellence * Offering outstanding career development and professional support

The Position:

Enzymes are crucial components of the agricultural, medical, and industrial biotechnologies, and they play a critical role in protein biochemistry research conducted at CSIRO Ecosystem Sciences (CES). Wild-type enzymes sourced from nature are often found not to be fit for intended purposes, requiring significant modifications by modern protein engineering technologies before being incorporated into commercial processes and products. These technologies are already powerful, but their successful application is often stymied by the problem of unpredictable negative intramolecular epistasis.

The Bioinformatics & Phylogenomics team at CES, led by Lars Jermiin, is leading a collaboration (with Colin Scott and John Oakeshott (CES) and Dan Tawfik (Weizmann Institute of Science, Israel)) aimed at developing novel computational methods to predict patterns of intramolecular interactions reliably in enzymes of interest, which would significantly improve our ability to rationally redesign enzymes. In this context, CSIRO is offering an exciting opportunity for a three-year OCE Postdoctoral Fellowship in computational biology within the Bioinformatics & Phylogenomics team.

In this position, you will have primary responsibility for the development of a theoretical framework for the analysis of intramolecular epistasis and the implementation and evaluation of computational methods to exploit semi-automatically the vast amounts of sequence data already available to identify residues within enzymes that may have co-evolved.

CSIRO offers all postdoctoral fellows a development plan, tailored to your experience and interests, to further your career in science. Part of the plan includes formal and on-the-job training, with mentoring also an option. You will have access to CSIRO's extensive research facilities as well as the opportunity to collaborate with postdoctoral and research scientists in other CSIRO Divisions.

Specifically you will:

* Develop, implement, and test methods to measure and predict intramolecular epistasis in proteins. * Apply the computational methods in research on protein structure- function relationships. * Participate in the identification of further opportunities arising from research and initiate new lines of research. * Assist in the planning and preparation of research proposals and carry out investigations.

Location: Black Mountain, Canberra, Australia Salary: $75K - $82K plus up to 15.4% superannuation Ref no: ACT12/00960 Tenure: 3 year term appointment

To be successful you will have:

* A PhD, or will shortly satisfy the requirements for this degree, in Computational Biology or related field (e.g., Molecular Evolution, Bioinformatics, or Biostatistics), with no more than three years of relevant postdoctoral experience. * Research experience in relevant areas of Computational Science and software development (e.g., C++, C, Java). * Experience in identifying, developing and/or pursuing novel research approaches

About CSIRO: Australia is founding its future on science and innovation. Its national science agency, CSIRO is a powerhouse of ideas, technologies and skills for building prosperity, growth, health and sustainability. It serves governments, industries, business and communities across the nation. Find out more! www.csiro.au About CSIRO Ecosystem Sciences: CSIRO Ecosystem Sciences is a globally significant centre for sustainability science. It brings together many of CSIRO's ecologists, social scientists, agricultural scientists, environmental biotechnologists, systems experts and urban scientists. It applies a multidisciplinary scientific approach to help ensure the sustainability of Australia's agricultural and forestry systems, built environments, biodiversity, and rural and urban communities and industries.

To find out more, go to www.csiro.au/Organisation-Structure/Divisions/Ecosystem-Sciences.aspx Find out more! For further information and instructions on how to lodge your application, please visit our website at CSIRO Careers http://csiro.nga.net.au/cp/index.cfm, choose "Job Search" and insert Reference Number ACT12/00960 where indicated.

Katie.Wise@csiro.au

CSIRO MolecularPhylogeny

CSIRO Advertisement

The Bioinformatics & Phylogenomics team at CES, led by Dr Lars Jermiin, is driving the development of phylogenetic methods that go well beyond what current phylogenetic methods are capable of doing in terms of modelling molecular evolution accurately and efficiently. In this context, CSIRO is offering an exciting opportunity for a 3-year Postdoctoral Fellowship in molecular phylogenetics within the Bioinformatics & Phylogenomics team.

Specifically you will:

* Develop, implement, and test molecular phylogenetic software * Apply phylogenetic software in research on genomic/transcriptomic data. * Participate in the identification of further opportunities arising from research and initiate new lines of research. * Under broad supervision, assist in the planning and preparation of research proposals and carry out investigations requiring originality, creativity, and innovation. * Present results in a meaningful format and write scientific papers for publication.

Location: Canberra, Australia Salary: $75K-$82K + up to 15.4% superannuation Tenure: 3 year term Ref No: ACT12/00962

To be successful you will have:

* A PhD, or will shortly satisfy the requirements for this degree, in Molecular Phylogenetics or related field (e.g., Bioinformatics, Statistics, Molecular Evolution, or Computational Science), with no more than three years of relevant postdoctoral experience * Research experience in relevant areas of software development (e.g., using C++, C, Java, MPI, or OpenMP). * Experience in identifying, developing and/or pursuing novel research approaches. * Evidence of strong oral and written communication skills, including the ability to publish results of research in scientific journals and to present the research at national or international meetings.

About CSIRO: Australia is founding its future on science and innovation. Its national science agency, Commonwealth Scientific and Industrial Research Organisation (CSIRO), is a powerhouse of ideas, technologies and skills for building prosperity, growth, health and sustainability. It serves governments, industries, business and communities.

About CSIRO Ecosystem Sciences: CSIRO Ecosystem Sciences is a globally significant centre for sustainability science. It brings together many of CSIRO's ecologists, social scientists, agricultural scientists, environmental biotechnologists, systems experts and urban scientists. It applies a multidisciplinary scientific approach to help ensure the sustainability of Australia's agricultural and forestry systems, built environments, biodiversity, and rural and urban communities and industries.

To find out more, go to: www.csiro.au/Organisation-Structure/Divisions/Ecosystem- Sciences.aspx

For further information and to apply online for the position of Postdoctoral Fellowship: Molecular Phylogeny: Optimizing the fit of phylogenetic estimates please visit our website at CSIRO CAREERS http://csiro.nga.net.au/cp/index.cfm, choose "Jobs Search" and insert Reference Number ACT12/00962 where indicated.

Applications close: 11.30pm on 4 June 2012.

RecruitmentTeam-ACT@csiro.au

CSIRO SoilMicrobeEvolution

Postdoctoral Fellow - Soil Microbial Ecology and Evolution

* Real world impact * Collaboration opportunity * Ground-breaking research using new technologies

The Position: Opportunity for Post-doctoral fellow, with strong experimental and molecular experience, to take part in ground-breaking research into the ecology and evolution of Australian soil microbial communities. You will be part of an exciting new initiative, The Biomes of Australian Soil Environments project, focused on conducting a comprehensive audit of soil microbial communities in Australian landscapes and analysis of their structure, diversity, function and evolutionary relationships.

The Biomes of Australian soil Environments is a collaborative project between CSIRO and Bioplatforms Australia, DEC WA, Vic DPI and SEWPaC aimed at quantifying the diversity and structure of soil microbial communities across the Australian continent and understanding their evolution in relation to environment. A key component of this effort will be to characterise and quantify the influence of abiotic and biotic environment, space and time on the evolution of soil microbial communities. Techniques for the molecular description of microbial communities will be utilised to link community structure and function to key bio-geochemical processes in soil.

CSIRO offers all Post-doctoral fellows a development plan, tailored to your experience and interests, to further your career in science. Part of the plan includes formal and on the job training with mentoring also an option. You will have access to CSIRO's extensive research facilities as well as the opportunity to collaborate with post-doctoral and research scientists in other CSIRO Divisions.

As part of the team you will:

* Undertake genomics-based experimental and/or observational field and laboratory research activities in soil microbial ecology and evolution * Pursue new ideas, theoretical perspectives and approaches through networking with scientific colleagues across a range of disciplines. * Write scientific papers for publication. * Communicate results through presentations at meetings and conferences.

About CSIRO: Australia is founding its future on science and innovation. Its national science agency, CSIRO is a powerhouse of ideas, technologies and skills for building prosperity, growth, health and sustainability. It serves governments, industries, business and communities across the nation. Find out more! www.csiro.au . Find out more! For further information and instructions on how to lodge your application, please visit our website at CSIRO Careers http://csiro.nga.net.au/cp/index.cfm, choose "Job Search" and insert Reference Number ACT12/00187 where indicated.

Kind Regards, Katie Wise Recruitment Consultant CSIRO Human Resources Phone: +61262464045 Katie.wise@csiro.au | RecruitmentteamACT@CSIRO.au | www.csiro.au RecruitmentTeamACT@csiro.au

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CSIRO Brisbane PlantInvasions

OCE Postdoctoral Fellowship 2012 - Ecogenomics and Plant Invasions

* An esteemed early career research fellowship * Work in an innovative and dedicated team of researchers in Ecology * Join CSIRO - Australia's premier science & technology research organisation - and make a difference

The Position: CSIRO Ecosystem Sciences is offering a prestigious OCE (Office of the Chief Executive) Postdoctoral Fellowship in the area of plant invasion ecology. The Postdoctoral Fellow will apply ecogenomic approaches to determine why several of Australia's worst environmental weeds are undergoing dieback. The project will involve testing likely hypotheses using a combination of theory, field survey, experimental work and ecogenomics. The application of next generation sequencing technologies and ecogenomics will be particularly critical given the complexity of soil-associated microbial flora and the need to comprehensively document endophytic communities and their interactions. The Postdoctoral Fellow will be part of a high-performing, collaborative group of researchers producing high impact science in the ecology and management of invasive plants, evolutionary ecology of plant-soil microbe interactions, plant pathology and metagenomics.

Location: Queensland EcoSciences Precinct, Dutton Park, Brisbane Salary: AUD75K - AUD82K per annum plus up to 15.4% superannuation Tenure: 3 year term Ref No.: Q12/00946

Requirements of the successful candidate will include: * PhD (or will shortly satisfy requirements for PhD) in a relevant field such as plant community ecology, soil biology or the evolutionary ecology of host-microbe interactions; * Demonstrated experience in ecogenomics and bioinformatics, or plant-fungal interactions, and good knowledge of/ familiarity with the other of these; * Excellent interpersonal, written and oral communication skills, including an ability to publish in high quality journals and present research at national/international conferences.

For further information and to apply online for the position of OCE Postdoctoral Fellowship 2012 - Ecogenomics and Plant Invasions please visit our website at http://csiro.nga.net.au/ choose "Jobs Search" and insert Reference Number Q12/00946 where indicated.

Applications close 7 June 2012.

Amy.E.Wilson@csiro.au

Canberra InvasiveGenePopulationGenomics

The Position: Opportunity for a Post-Doctoral researcher to use genome-wide approaches to study population connectivity and gene flow in globally distributed and highly mobile insect species. The project will focus on two of the most destructive global caterpillar pests, the cotton bollworm (Helicoverpa armigera) and the tropical armyworm (Spodoptera litura), with the aim of determining the degree to which neighbouring countries are important as sources of genes of ecological interest in Australia. These are, in particular, genes significant for pesticide resistance, host use, and mobility. This information will benefit agricultural industries worldwide.

In this position, you will have primary responsibility for developing and implementing a population genomics study that uses genome, transcriptome and resequencing data to examine population structure, and identify adaptation signatures in regional populations of these emerging non-model species. Developing the appropriate bioinformatic and biostatistical approaches will be a significant part of the work, as well as the opportunity to collaborate with international partners and contribute to empirical studies.

As part of the CSIRO Ecosystem Sciences team, you will visit leading scientists in the field and be trained to use state-of-the-art technology. You will also have a development plan tailored to your experience and interests, to further your career in science. There is access to CSIRO's extensive Library services and facilities as well as the opportunity to collaborate with post-doctoral and research scientists in other CSIRO Divisions.

Specifically you will:

* Undertake research on the population and comparative genomics and transcriptomics in species of Helicoverpa and Spodoptera, with a focus on genes significant for pesticide resistance, host use, and mobility * Participate in the identification of further opportunities arising from research and initiate new lines of research * Assist in the planning and preparation of research proposals and carry out investigations requiring originality, creativity and innovation * Publish and present results to national and international audiences

Location: Black Mountain, Canberra Salary: AU$75K - $82K per annum plus up to 15.4% superannuation Ref no: ACT12/00784 Tenure: 3 year term

To be successful you will have:

* Completed, or will shortly complete, the requirements for a PhD degree in a relevant scientific discipline with not more than 3 years of relevant Postdoctoral experience. * Experience in genome bioinformatics using next-generation sequence technologies and in quantitative population / evolutionary genetics * Ability to publish in scientific journals and present research at conferences * Experience cooperating and collaborate with others to achieve objectives

About CSIRO: Australia is founding its future on science and innovation. Its national science agency, CSIRO is a powerhouse of ideas, technologies and skills for building prosperity, growth, health and sustainability. It serves governments, industries, business and communities across the nation. Find out more! www.csiro.au Applications close 31st May 2012 Find out more! For further information and instructions on how to lodge your application, please visit our website at CSIRO Careers http://csiro.nga.net.au/cp/-index.cfm, choose "Job Search" and insert Reference Number above where indicated.

Kind Regards, Katie Wise Recruitment Consultant CSIRO Human Resources Phone: +61 2 62464045 Katie.wise@csiro.au | Recruitmentteam-ACT@CSIRO.au | www.csiro.au Katie.Wise@csiro.au

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CornellU ComputationalGenomics

Dr. Adam Boyko's laboratory at Cornell University is focused on studying the rapid evolution and diversification of dogs and genetic basis of complex traits and disease. We seek a skilled, motivated postdoctoral researcher in computational genomics to address evolutionary and medical genetics questions using high-throughput genomic datasets. The fellow can expect to be part of cutting-edge studies involving analysis of high-throughput array data, whole-genome next-generation sequencing, and RNA-seq focused on both evolutionary and medical genetics. The position is highly collaborative, involving significant interaction with geneticists, biologists, and clinicians, with ample opportunities for developing independent research projects.

Qualifications: The applicant should have a Ph.D. in biology, computer science, or related field, and a strong background in computational genomics. Applicants should have computer programming experience, should be proficient in statistical analysis (e.g. R), and have research experience in next-generation sequencing and/or genotyping array analysis.

To apply, send a CV, cover letter, statement of research interest and contact information for 3 references to Adam Boyko at boyko@cornell.edu.

arboyko@gmail.com

HarvardUniv FungalNetworkArchitectures

POSTDOCTORAL FELLOW

FUNGAL NETWORK ARCHITECTURES

Pringle Laboratory and Brenner Group Harvard University, Cambridge, MA, USA

We are looking for a full-time postdoctoral fellow to partner with us in research on the biology and physics of fungal networks. The fellowship is funded by the Human Frontiers in Science Program. Experiments aim to understand how fluid flows within indeterminate, modular organisms enable foraging. Fungi can easily reach several square meters in size. Despite lacking a central coordination center (a brain), individuals are able to reshape their morphology in response to local cues, including food sources. How are local signals integrated across a network, and coordinated to mount a global response? Applicants must be genuinely fascinated by basic research. Brenner is an applied mathematician and the Pringle laboratory focuses on the evolution and ecology of fungi. We are housed at Harvard University in Cambridge, MA, a vibrant intellectual community near myriad cultural resources. The fellow will work collaboratively with Professors Brenner and Pringle, and physicist and post-doctoral fellow Karen Alim, to grow fungi, manipulate networks using drugs and physical stimuli, and implement a range of image-processing and analysis tools. A collaboration with Mark Fricker (Plant Biology, Oxford University) will start this Fall. This position requires an independent, organized, and motivated individual with demonstrated skills and experience in experimental techniques involving slime molds and fungi. Biologists interested in quantitative approaches to biological problems are strongly encouraged to apply. Above all, we are looking for someone who is personable, motivated and enthusiastic about working in a group environment.

Information about the Brenner group can be found at http://www.seas.harvard.edu/brenner/Home.html. Information about the Pringle laboratory can be found at http://www.oeb.harvard.edu/faculty/pringle/ . Informal inquiries can be directed to either Michael Brenner (brenner@seas.harvard.edu) or Anne Pringle (pringle@oeb.harvard.edu).

Formal applications should be made to the administration, by emailing Nikki Hughes (nhughes@fasmail.harvard.edu). Please send a letter describing your research interests and experience, a C.V., and contact information for three references.

Applications will be reviewed beginning July 1, 2012 and will be accepted until the position is filled.

Harvard University is an equal opportunity, affirmative action, non-smoking workplace.

cbaker@oeb.harvard.edu

Liverpool MosquitoEvolutionaryGenetics

Salary: £31,020 - £33,884 Vector Group Full-Time, Fixed-Term 12 month appointment

The Liverpool School of Tropical Medicine (LSTM) is an international centre of excellence and our researchers have access to the most up to date, cutting edge technology, making us world leaders in our field.

We are looking for an individual to join Dr Martin Donnelly's laboratory within LSTM's Vector Group. The laboratory uses population genomic, transcriptomic and evolutionary genetic approaches to investigate the evolution of insecticide resistance in the malaria vector Anopheles gambiae. You will be responsible for designing and implementing studies to identify variants associated with insecticide resistance phenotypes and working with a number of malaria control programmes to investigate the impacts of insecticide resistance on malaria epidemiology. You will be expected to travel to sub-Saharan Africa and India to conduct collaborative research.

Possessing a PhD in Biology, you will be an ambitious and self motivated researcher with a strong background in evolutionary genetics and molecular biology. Previous experience working with insect vectors and/ or in malaria endemic countries is highly desirable but is not essential.

You will have very strong analytical skills and have the ability to identify problems and suggest viable solutions when necessary. Computer literacy, time management and organisational skills are also essential to the role, as is the ability to work both collaboratively and independently across a multi-disciplinary research team.

Recent publications from the laboratory may be found at http://www.lstmliverpool.ac.uk/research/academic-groups/staff-profiles/martin-donnelly Additional details may be found at http://www.lstmliverpool.ac.uk/-working-with-us/human-resources/current-vacancies/-ref-619 If you are interested in applying, please return your completed Application Form, Personal Details Form and Equal Opportunities Monitoring Form together with a copy of your CV, stating vacancy reference number (619), via email to Lstmjobs@liverpool.ac.uk, or by post to HR, Liverpool School of Tropical Medicine, Pembroke Place, Liverpool L3 5QA.

Informal enquiries may be directed to Dr Martin Donnelly (m.j.donnelly@liv.ac.uk).

Closing Date: Monday 11th June 2012 (12pm Midday)

M.J.Donnelly@liverpool.ac.uk

London EvolutionInsectCognition

Interested in doing postdoctoral work in London, on the evolution and ecology of sensory, behavioural or cognitive abilities of insects and other animals?

Applications currently invited for Marie-Curie postdoctoral fellowships (deadline for full applications to the European Commission: August 16).

Please email your CV asap to L Chittka at l.chittka@qmul.ac.uk to discuss possibilities.

Lars Chittka, PhD, MSc Director, Research Centre for Psychology Professor in Sensory& Behavioural Ecology School of Biological& Chemical Sciences Fogg Building Queen Mary College University of London Mile End Road London E1 4NS UK

Email: l.chittka@qmul.ac.uk Tel: *44 (0) 20 7882 7485 Fax: *44 (0) 20 7882 7732 http://-chittkalab.sbcs.qmul.ac.uk/ Room 2.03

Lars Chittka <l.chittka@qmul.ac.uk>

LouisianaStateU HIVPhylogenomics

RESEARCH ASSOCIATE OR POSTDOCTORAL RESEARCHER Louisiana State University Department of Biological Sciences

A research associate or postdoctoral researcher position is available in the computational evolutionary biology lab of Jeremy M. Brown. This position is part of a project funded by the National Institute of Justice to further investigate the forensic application of phylogenetic approaches for reconstructing HIV transmission histories. This project will expand upon previous work by utilizing whole-genome sequences and applying more sophisticated statistical phylogenetic approaches. The Brown lab will be collaborating extensively with the Metzker lab at Baylor College of Medicine. Informal inquiries are encouraged and can be directed to jembrown@lsu.edu. More information on the Brown lab is available at http://www.phyleauxgenetics.org/- Responsibilities: This position will be responsible for performing cutting-edge research on phylogenetic analysis of HIV genomes for use in forensics. Responsibilities will include running analyses on high-performance computing resources, writing manuscripts, creating new bioinformatic tools (depending on applicant background), and supervising graduate and undergraduate student workers.

Required Qualifications: Research Associate 4: Master's degree in biology, bioinformatics, computer science, statistics, or related discipline; experience performing phylogenetic analyses. Postdoctoral Researcher: Ph.D. and experience performing phylogenetic analyses.

Additional Qualifications Desired: Experience with Unix and one or more of the following programming languages: C++, Java, Python; experience using high-performance computing resources. An offer of employment is contingent on a satisfactory pre-employment background check.

Application review will begin promptly on June 1, 2012 and continue until a candidate is selected. The position will be available to start as soon as an offer is made and accepted.

Apply online and view a more detailed ad at: www.lsusystemcareers.lsu.edu. Position #012809.

LSU IS AN EQUAL OPPORTUNITY/EQUAL ACCESS EMPLOYER

Quick link ad URL: https://lsusystemcareers.lsu.edu/-applicants/Central?quickFind=3D53795 Jeremy M. Brown Assistant Professor Louisiana State University Dept. of Biological Sciences 202 Life Sciences Building Baton Rouge, LA 70803

(225) 578-1745

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

MPI Marburg FungalBiodiversity

Post doc position Max Planck Marburg Evolutionary Genomics

Post doc position in the Max Planck Research Group in Fungal Biodiversity A one-year postdoctoral position is available in the field of molecular evolution and computational biology in the newly established Max Planck Research Group in Fungal Biodiversity headed by Dr. Eva H. Stukenbrock. Our team is part of the Max Planck Institute of Terrestrial Microbiology in Marburg, Germany (http://www.mpi-marburg.mpg.de).

Background We study speciation and host specialization processes in fungal plant pathogens in an evolutionary and ecological context. A main goal of our research is to understand the underlying molecular mechanism of species divergence and adaptive processes in host-pathogen systems. We integrate functional and experimental approaches with high throughput sequence data and bioinformatics to study the functional and evolutionary biology of closely related pathogen species, which have evolved and specialized to different hosts and environments. Our model system is a group of closely related grass pathogens including the prominent wheat pathogen Mycosphaerella graminicola. To contrast evolutionary processes in different ecosystems we have compared population genomic data from M. graminicola and closely related species infecting non-cultivated hosts in natural grasslands. In the lab, we validate and characterize candidate genes emerging from our evolutionary predictions. For this we have developed genetic tools and functional assays to study the role of candidate genes in host specialization or speciation.

Objectives This post doctoral project focuses on the evolution of gene regulation, and its implication in host specialization and speciation. The selected post doc candidate will be in charge of analyzing a large transcriptome dataset including RNAseq data from different combinations of host and pathogen species. Research perspectives are open, and the post doc candidate will be largely involved in the design of all experiments and analyses, providing they relate to host specialization and speciation.

Prerequisites The post doctoral candidate will ideally: ? Have a PhD in evolutionary biology with expertise in bioinformatics and genomics. ? Be proficient in statistical computing, including experience with R and analysis of large data sets in a linux environment. ? Have basic programming / scripting skills (Bash, Perl, Python, or similar).

Contact Application should be sent to Eva H. Stukenbrock (eva.stukenbrock@mpi-marburg.mpg.de) before June 1st. The position will however remain open until filled. The application should include a short CV with statement of research interests, together with a cover letter including names and contact information of two references.

“Eva H. Stukenbrock” <eva.stukenbrock@mpi-marburg.mpg.de>

MonashU DengueEvolution

Postdoc in dengue vector competence

We are seeking a talented and enthusiastic Postdoctoral Researcher to work in the laboratories of Professor Scott O’Neill and Dr Elizabeth McGraw. We study the interaction between insects and bacteria with particular applications in control of insect transmitted disease (www.eliminatedengue.com). We run a vibrant team of research associates, PhD students and postdoctoral fellows housed in all new research facilities at Monash University located in Melbourne, Australia. You will be responsible for carrying out your own research, collaborating with other members of the team and mentoring more junior staff. Specific research activities will involve developing projects around the interaction between the symbiotic bacterium, *Wolbachia*, and dengue virus in mosquitoes, with a particular focus on vector competence. Applicants must have skills in virology. Entomology skills are an added benefit.

Details of position: 24 month fixed term-appointment, $72,756-82,209 AUD per annum commensurate with experience.

Enquiries,

Dr. Elizabeth McGraw

beth.mcgraw@monash.edu

Closing date for submission of CVs - May 22nd, 2012.

francesca.frentiu@monash.edu

NCStateU BiolComplexity

NC State University Distinguished Postdoctoral Fellow in Biological Complexity

North Carolina State University is embarking on a new university-wide interdisciplinary initiative in biological complexity encompassing systems genetics, behavioral neurogenetics and neurogenomics, genome-environment interactions, ecological genetics, systems ecology, climate change, computational biology and bioinformatics.

Associated with the new initiative in biological complexity is a distinguished postdoctoral fellowship program. Applicants are expected to be near completion of a terminal doctorate degree, have a strong research record with evidence of exceptional scholarship, and embrace interdisciplinary research. Fellows will receive competitive stipends and independent research funds to initiate an innovative research program with guidance from a multidisciplinary mentoring committee in areas covered by the initiative in biological complexity.

To apply for a fellowship, go to jobs.ncsu.edu, search jobs, and enter position number 100730 under keywords. Provide a cover letter, curriculum vitae, a three-sentence statement of the most significant scientific problem(s) to be addressed in the near future, and statements of research interests. Three letters of recommendation should be sent to trudy_mackay@ncsu.edu. Review of applications will begin immediately, and continue until the position is filled.

NCSU is an AA/EO employer. All qualified applicants will receive consideration for employment without regard to race, color, national origin, religion, sex, age, veteran status or disability. In its commitment to diversity and equity, NC State University seeks applications from women, minorities, and persons with disabilities. NC State welcomes all persons without regard to sexual orientation. ADA Accommodations: please call 919-515-5727.

Trudy F. C. Mackay, PhD, FRS William Neal Reynolds and Distinguished University Professor of Genetics Department of Genetics North Carolina State University Campus Box 7614 Raleigh, NC 27695-7614 Tel: 919-515-5810 Fax: 919-515-3355 Email: trudy_mackay@ncsu.edu

Trudy Mackay <trudy_mackay@ncsu.edu>

NHM London EvolutionSnakeVision

Postdoctoral Research Assistant: The Evolution of Snake Vision Salary: Â£27,339 per annum plus benefits Contract: 3 year Fixed Term Appointment Closing date: 5 June 2012

The Natural History Museum is one of the worldÂ^{1}s leading museums, internationally recognised for its dual role as a centre of excellence in scientific research and as a leader in the presentation of natural history through exhibitions, public programmes, publications and the web.

We seek to appoint a postdoctoral Research Assistant (PDRA) to work on a Leverhulme Trust funded project on the evolution of snake vision. The project will use primarily molecular evolutionary biology techniques (complemented with microspectrophotometry Â' MSP - and electron microscopy Â' EM) to investigate aspects of the vision of snakes in order to shed light on broader questions in vertebrate visual evolution. The molecular biology work will focus on opsins, but will also include other components of phototransduction.

This is a collaborative project between the Natural History Museum, London (Dr David Gower), the University of Bristol (Prof. Julian Partridge), and the University of Western Australia (Prof David Hunt, Dr Nathan Hart).

The PDRA will work with the collaborating PIs and lab technicians. They will work on both wet lab and analytical molecular evolutionary biology and take a substantial role in academic and public dissemination of results. The selected candidate will be proficient in practical molecular biology and be able to implement techniques including mRNA extraction, cDNA synthesis, PCR, qPCR, RACE, PCR primer design, cloning, and tissue culture. They will be familiar with phylogenetic analysis of molecular data and the handling of genomic data. The ideal candidate will have experience of vision biology or similar GPCR-mediated transduction cascades, some experience of MSP, EM and vertebrate biology, and of scientific public engagement. Start date July 2012.

For a full job description and to apply online please visit the Natural History Museum website: www.nhm.ac.uk/jobs

Dr David Gower Department of Zoology The Natural History Museum London SW7 5BD UK

d.gower@nhm.ac.uk Tel: +44 (0)20 79425080 Fax: +44 (0)20 79425054

David Gower <d.gower@nhm.ac.uk>

PennState EvolutionDisease

A Bill and Melinda Gates Foundation funded postdoctoral position ins available with Matthew Ferrari's group (http://www.cidd.psu.edu/people/mjf283) at the Center for Infectious Disease Dynamics at Penn State. The lab studies the spatial and temporal dynamics of vaccine-preventable, childhood infections. We are seeking a post-doctoral researcher to participate in collaboration with national and international agencies to understand the persistence of measles in Southeast Asia and sub-Saharan Africa and evaluate strategies for novel vaccination programs to facilitate measles elimination goals. A Ph.D. in Quantitative Ecology, Population Biology, Applied Mathematics, Statistics or an equivalent area is required. Experience with computational analysis of time series data is highly desirable. Candidates should demonstrate a track record of publication; have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team. Candidates with a multidisciplinary background, spanning the life sciences, social sciences and computer sciences, are especially encouraged to apply. The Center for Infectious Disease Dynamics (www.cidd.psu.edu) brings together theoreticians and empirical scientists in a wide variety of disciplines to collaborate and innovate in the area of infectious disease research. In September 2011, several CIDD research groups (including ours) will move into Penn States new Millennium Science Complex, a building that has been designed around shared open spaces to facilitate frequent interactions among graduate students, postdoctoral researchers, and faculty working across all levels of biological complexity and methodological approaches to the study of infectious disease dynamics. Interested applicants should submit a CV, a one[page letter explicitly describing professional qualifications for this position, and contact information of three references to Matthew Ferrari (mferrari@psu.edu). Review of applications will begin immediately, and continue until the position is filled. Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

Matthew Ferrari <matthewferrari@me.com>

PennState EvolutionParasiteInfection

A postdoctoral position is available with Matthew Ferrari's group (http://www.cidd.psu.edu/people/mjf283) and Isabella Cattadori's group (http://www.cidd.psu.edu/people/imc3) at the Center for Infectious Disease Dynamics at Penn State. We are seeking a post-doctoral researcher to work on a collaborative project with the Cattadori Lab studying the consequence of within-host immuno-dynamics of parasite co-infection on population-scale transmission. This project offers an exceptional opportunity to combine quantitative analysis and modeling methods with an experimental lab system and long-term field monitoring of host-parasite dynamics. A Ph.D. in Quantitative Ecology, Population Biology, Applied Mathematics, Statistics or an equivalent area is required. Experience with computational analysis of time series data is highly desirable. Candidates should demonstrate a track record of publication; have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team. Candidates with a multidisciplinary background, spanning the life sciences, social sciences and computer sciences, are especially encouraged to apply. The Center for Infectious Disease Dynamics (www.cidd.psu.edu) brings together theoreticians and empirical scientists in a wide variety of disciplines to collaborate and innovate in the area of infectious disease research. Many of the CIDD research groups (including ours) have recently moved into Penn States new Millennium Science Complex, a building that has been designed around shared open spaces to facilitate frequent interactions among graduate students, postdoctoral researchers, and faculty working across all levels of biological complexity and methodological approaches to the study of infectious disease dynamics. Interested applicants should submit a CV, a one-page letter explicitly describing professional qualifications for this position, and contact information of three references to Matthew Ferrari (mferrari@psu.edu). Review of applications will begin immediately, and continue until the position is filled. Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

Matthew Ferrari <matthewferrari@me.com>

Prague ProtistGenomics

Postdoctoral position in protist genomics (Prague, Czech Republic) - PrF06

Postdoctoral position is available at the newly established institute BIOCEV at the suburb of Prague (Czech Republic). The post doctoral worker will join the team of Vladimir Hampl (https://web.natur.cuni.cz/~vlada/lab/) that is focused on the evolution of protists and their organelles. The team is currently running or preparing to launch several transcriptome, plastid genome and nuclear genome projects on various protists from the groups of Euglenida and Preaxostyla. These protists are interesting for example for their anaerobic or facultatively anaerobic life styles, absence of observable sexual reproduction, and massive reduction of mitochondria in Preaxostyla or evolution of secondary plastids in Euglenida. There are no published nuclear genomes from these groups.

The main task of the postdoctoral worker will be to establish and maintain an annotation pipeline for the transcriptomic and genomic data and to coordinate work on selected genome projects. Mandatory part of the contract will be teaching a specialised course depending on the interest and expertise of the worker (e.g. genome annotation, phylogenetics, or genomics).

The contract may start any time after the 1st of July 2012 and it finishes on the 30th of June 2015. The salary is 40 000 CZK (~2000 USD) per month. The contract contains also funds for travelling and consumables.

Ideal candidate is an interdisciplinary person, either a keen bioinformatician/genomicist skilled in programming that is interested in microbes, genomics and evolution or a protistologist with experiences in bioinformatics, genomics and programming. The candidate must fulfil the mandatory criterion of minimum 5 publications or sum of IF more than 7. The candidate has to be the first or corresponding author of at least 2 publications.

If you are interested, please send your motivation letter, CV and list of publications directly to Vladimir Hampl (vlada@natur.cuni.cz).

Vladimir Hampl <vladimir.hampl@natur.cuni.cz>

SmithCollege MicrobesTreeOfLife

Postdoctoral Position: OpenTree – Interpreting the position and impact of microorganisms on the tree of life

Smith College invites applications for a full-time postdoctoral research position focusing on reconstructing the tree of life, with emphasis on the placement of microbial lineages. The initial appointment is for one year, with the possibility of extending for additional years. The position will be housed in Professor Laura Katz's laboratory in the Department of Biological Sciences (http://www.science.smith.edu/departments/Biology/lkatz/Research.htm).

The postdoc will interact with collaborators at 10 institutions through the Open Tree of Life project (http://opentreeoflife.wordpress.com/). An ideal candidate will: 1) be a productive researcher with interests in phylogenetics and phylogenomics of microorganisms; 2) have experience in bioinformatics, including managing and manipulating large data sets; 3) have excellent communication and interpersonal skills; and 4) be interested in collaborating with students in the laboratory.

To apply, submit application at https://jobs.smith.edu/postings/2729 with cover letter, c.v., a statement of research interests, representative publications, and the names and contact information of three references. Review of applications will begin June 1, 2012.

Smith College is a member of the Five College Consortium with Amherst, Hampshire, and Mount Holyoke Colleges and the University of Massachusetts Amherst. Smith College is an equal opportunity employer encouraging excellence through diversity.

lkatz@smith.edu

SyracuseU EvolutionaryGenomics

POST-DOCTORAL POSITIONS IN EVOLUTIONARY GENOMICS AT SYRACUSE UNIVERISTY

Applications are invited for postdoctoral research positions in the laboratory of Steve Dorus at Syracuse University. My lab is interested in evolutionary genetics and the role sexual selection plays in genome evolution. Much of our current research focuses on integrating proteomic, transcriptomic and chromatin immunoprecipitation (CHiP) approaches to obtain systems level insights into the evolutionary genomics of sperm development and function. Our experimental work has historically focused on sperm proteomics and genomics in Drosophila and mammals, including various mouse and non-human primate species. We have now expanded our studies to avian taxa, where we are studying the functional capacities of seminal fluid proteins, and to lepidoptera to better understand the evolutionary genetics underlying sperm heteromorphism. Ultimately, we are interested in understanding the interplay between evolutionary conservation and adaptation associated with sexual reproduction through the molecular characterization of male reproductive systems across a diverse range of taxa.

We encourage applications from highly motivated and independent candidates with strong backgrounds in evolutionary genetics, genomics, bioinformatics and/or reproductive biology. Postdocs in the lab can expect to be involved in a variety of research projects and are encouraged to bring their scientific interest to bear on the direction of the research. Most research in the lab will involve both wet lab and computational approaches, including the generation and analysis of proteomic, transcriptomic and genome-wide chromatin maps. Competitive applicants are expected to have relevant experimental and analytic training.

Environment: The Department of Biology at SU is located in the recently constructed Life Science Center, which includes modern lab and computational facilities. The Department has a strong concentration in ecology and evolutionary research, including sexual selection and the genetics of adaptation. SU benefits from a close association with SUNY Upstate Medical University, which has a large faculty devoted to clinical research as well as next-generation sequencing, proteomics and microarray facilities.

Additional information: Please visit our lab website (http://doruslab.syr.edu) or contact me directly (sdorus@syr.edu) to discuss research options in greater detail.

How to apply: Email your application to sdorus@syr.edu as a single pdf file containing your CV with publications, contact details of two referees, and a letter describing your research interests and why you would be an exceptional candidate. Priority will be given to applications received by July 15th, 2012.

Salary: A competitive salary commensurate with experience and full benefits is guaranteed for one year with subsequent years renewable depending on performance.

Steve Dorus Associate Professor Department of Biology Syracuse University 107 College Place Syracuse, NY 13244

email: sdorus@syr.edu lab website: http://doruslab.syr.edu sdorus@syr.edu

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UAmsterdam MothSexPheromone

In collaboration with Max Planck Institute for Chemical Ecology (Jena, Germany) and North Carolina State University (Raleigh, USA), the Institute for Biodiversity and Ecosystem Dynamics (IBED, University of Amsterdam) has started a research project that combines evolutionary biology with molecular and chemical ecology. It aims to identify the gene(s) underlying sex pheromone variation in the noctuid moth /Heliothis subflexa/. This project has a vacancy for a

Postdoc molecular / evolutionary biology

1,0 fte (38 hours/week)

In /H. subflexa/, one group of sex pheromone components, the acetates, emitted by the female, plays a crucial isolating role in preventing interspecific matings to males of the closely related /H. virescens, /in which females do not produce acetates and males are repelled by them. We previously found intraspecific variation in the acetates in /H. subflexa/: females in Eastern North America contain significantly more acetates than females in Western Mexico. Recently, we found the persistence of this intraspecific variation in laboratory-reared strains, and identified one major QTL, explaining 40% of the variance in acetate amounts. We homologized this intraspecific QTL to our previously identified interspecific QTL using Restriction Associated DNA (RAD) tags.We found that the major intraspecific QTL overlaps with one of the two major interspecific QTL.

This project will be a unique opportunity to identify the gene(s) involved in intra- and interspecific variation in moth sexual communication. Even though premating isolation is hypothesized to be a major driving force in speciation, its genetic basis is poorly known, and identifying genes will greatly help to understand how moth sexual communication may evolve. Since we identified the genomic location, as well as candidate genes, and we have introgressed lines available, this project has great potential.

Requirements

We are looking for a molecular biologist with an evolutionary background. The ideal candidate is highly motivated and has a strong interest in molecular ecology and evolution. Molecular skills are required and extensive experience is preferred. At the start of the project the candidate will need to collect larvae from North Carolina and Western Mexico. The candidate is also willing to work in the three different labs involved, even though the basis will be in Amsterdam.

Further information

More information can be obtained from: Dr. Astrid Groot, A.T.Groot@uva.nl, tel. ++31 20 525 5400

Appointment

The appointment starting a.s.a.p. will be on a temporary basis for a period of one year with the intention to extend with one year. The salary is in accordance with the university regulations for academic personnel (Collective Labour Agreement Dutch Universities) and will range from EUR 2,379 up to a maximum of EUR 3,755 gross per month (scale 10). The salary of experienced candidates that are able to perform moreindependently will range up to a maximum of EUR 4,374 (scale 11). The annual salary will be increased by 8 % holiday allowance and 8.3 % end-of-year bonus.

Job application

Applications should include a cover letter, a curriculum vitae, a one-page description of research interests, and contact information (including e-mail and phone number) of two referees. All application materials should be submitted as a single pdf to application-science@uva.nl with a CC to A.T.Groot@uva.nl

Evaluation of applications will begin at June 25, 2012 and continue until the position is filled.

Links

http://www.science.uva.nl/ibed http://-home.medewerker.uva.nl/a.t.groot Astrid Groot <A.T.Groot@uva.nl>

UAutonomaBarcelona 2 Bioinfo Genomics

POSTDOCS IN BIOINFORMATICS, GENOMICS AND EVOLUTION

Two postdoctoral positions are available to work on the project entitled “Evolutionary and functional analysis of polymorphic inversions in the human genome” funded through an ERC Starting Grant from the European Research Council. This project aims to determine the impact of inversions in the human genome at multiple levels by combining methods of different disciplines, such as next-generation genomic analysis, bioinformatics, population genetics, and molecular evolution. Successful candidates will form part of a young, dynamic, and interdisciplinary research team located at the Institut de Biotecnologia i de Biomedicina (IBB) of the Universitat Autònoma de Barcelona (UAB).

The IBB is a multidisciplinary and international research institute located at the beautiful UAB campus, which has been selected Campus of International Excellence in biomedicine. It is located in Bellaterra, a small residential town just 20 km away from Barcelona and with great public transportation connections.

Available positions: We are seeking highly motivated and talented individuals with a PhD degree and research experience in the following relevant fields:

1. Postdoc with experience in bioinformatic analysis of DNA sequences. This person will be responsible of the study of the functional consequences of inversions by taking advantage of all the available information in the human genome (annotation, expression levels, etc).

2. Postdoc with experience in molecular evolution and population genetics. The work will consist in the study of the effect of inversions on nucleotide variation patterns in humans and test the role of natural selection in their maintenance.

Conditions: Salaries will be very competitive according to profile and experience of candidates. Duration of contracts will range from 1 to 2 years.

Starting date: All positions are available from July 2012.

Application: Send a CV and a one-paragraph summary of previous research experience to Mario Cáceres (mcaceres@icrea.cat).

Application deadline: Please send application as soon as possible, preferably before May 31st 2012. After that applications will be accepted until positions are filled.

Additional information: Comparative and Functional Genomics group: http://grupsderecerca.uab.cat/-cacereslab/ Mario Cáceres, PhD ICREA Research Professor Institut de Biotecnologia i de Biomedicina Universitat Autònoma de Barcelona 08193 Bellaterra, Spain

Phone: +34 93 581 2805 Fax: +34 93 581 2011 E-mail: mcaceres@icrea.cat http://grupsderecerca.uab.cat/-cacereslab/ mcaceres@icrea.cat

UBrest MarineEvolution

LabexMER, a newly created consortium of French Universities and Institutions (laboratoires d'excellence) is enthusiastically inviting applications for an *international chair in Evolutionary Marine Ecology*. This chair aims to promote research on both the evolutionary influences on ecological processes and on the ecological influences on evolutionary processes, using both theoretical and experimental approaches.

The person entitled to the chair will have to bring expertise in the following scientific set of issues:

1. The links between the evolutionary and ecological processes for a better understanding of the mechanisms which drive the dynamics of the functional biodiversity. 2. The effects of the planetary changes on the organisms, the populations and the communities (especially in terms of acclimation, adaptation, ...).

In particular, we'd like to develop in the future metagenomics of phytoplancton, bacteria to characterize the changes in biodiversity driven by the environment, and for other specific topics (eg, microbiome of molluscs, microflora on macroalgae), and on ecological experimental processes (biotic interactions and evolution, trangenerational approaches, epigenetic phenomenon..).

Most of these subjects could be included in the topics developed in both axes 6 and 2 of the LaberMER.

The chair is set up for a duration of three years. It is awarded with a grant of*200,000 EUR/year. *

*Keywords : *Evolutionary Ecology, theoretical modeling, Functional Biodiversity, Biogeochemistry, Plasticity, Acclimatation, Adaptation

*Applications must be sent no later than June 15th, 2012 *

Apply now : http://www.labexmer.eu/-international-fellowships For more information you can contact : Philippe.Pondaven@univ-brest.fr or Christine.paillard@univ-brest.fr or Cedric.Bacher@ifremer.fr or Olivier.Aumont@ird.fr

labexmer

Christine Paillard Thème "Interactions hôtes-pathogènes" Laboratoire des Sciences de l'Environnement Marin UMR CNRS 6539 Institut Universitaire Europeen de la Mer, Technopole Brest-Iroise Place Copernic 29280 PLOUZANE, France Domestic calls: telephone: 02 98 49 86 50 fax: 02 98 49 86 45 International calls: phone: 33 2 98 49 86 50 fax: 33 2 98 49 86 45

E-mail:paillard@univ-brest.fr http://www.univ-brest.fr/IUEM/UMR6539/ Christine Paillard <Christine.Paillard@univ-brest.fr>

UBritishColumbia ForestPathogen PopGenomics

Population genomics of forest pathogens Department of Forest Sciences and Conservation University of British Columbia, Vancouver, Canada Supervisors: Richard Hamelin and Kermit Ritland

A post-doctoral fellowship is available in the area of population and evolutionary genomics of forest fungal pathogens. We are resequencing whole genomes of several isolates of a Pucciniales, an Oomycete, and a Dothydeomycetes species. All three species are invasive and currently causing considerable damage to native forest trees. The major objective of this position is to (1) identify patterns of SNP variation and perform tests of neutrality, (2) identify and study the evolution of genes involved with pathogenicity, (3) infer migrational and sexual history of these pathogens, and (4) develop new approaches for using whole genome scans to infer migrational processes. Applicants should have the appropriate computational or statistical skills, and should have a penchant for developing new approaches. No background in mycology is needed. To apply, submit a CV, a cover letter and names and contact information of three referees to Kermit Ritland (kermit.ritland@ubc.ca). The start date can be immediate or by September 2012 at the latest. The duration can be up to 2 years. This project is funded by Genome BC, Genome Canada, and the Canadian Forest Service.

"Ritland, Kermit" <kermit.ritland@ubc.ca>

UCDavis EvolutionaryGenomics

Postdoctoral researcher: Ecological/evolutionary genomics of non-model plants (UC Davis). We seek a postdoctoral researcher to join a collaborative, international project on the ecological and genomic diversification of two lineages of plants in the Cape Floristic Region of South Africa. Genus Protea and genus Pelargonium contain hundreds of species packed into the super-diverse fynbos and succulent karroo biomes. These lineages have radiated in an aridifying climate over the past 10+ MY, occupying new ecological space and rapidly diversifying in morphology and function. The project group^{1}s members have previously studied geographic distributions and functional trait variation in these plants. In this project, funded by NSF^{1}s Dimensions of Biodiversity program, we are using next-generation sequencing and genomic data analysis to link functional traits of species and populations in these groups to genetic variation. We are especially interested in how traits and genes have evolved along gradients in aridity and nutrient limitation. (http://darwin.eeb.uconn.edu/-wiki/index.php/Parallel_Evolutionary_radiation
s_in_Protea_and_Pelargonium_in_the_Greater_Cape_Floristic_Region)

In the first year of the project, we established a common garden in Cape Town containing families from many populations of two focal species. The initial focus of this postdoctoral research project will be to use transcriptome sequences from these common garden plants to associate genetic variation with plant trait expression and source environments. Beyond this initial analysis, the postdoctoral researcher will be encouraged to pursue their own interests within the larger project framework. Topics include but are not limited to phylogenetic trait evolution, phylogeography, and adaptation to drought and nutrient deficient soils.

This position will be based in Andrew Latimer^{1}s lab in the Department of Plant Sciences and Graduate Group in Ecology at the University of California Davis (http://www.plantsciences.ucdavis.edu/-faculty/latimer/index.htm). We have a strong community of plant genomics researchers on campus and encourage development of collaborations. There will also be opportunities to visit the labs of collaborating investigators at the University of Connecticut, Australian National University and/or Cape Town. The postdoctoral researcher will participate in and supervise lab work, but will focus on data analysis, statistical method development and paper writing.

Requirements: Ph.D. in Genetics, Ecology & Evolutionary Biology, Bioinformatics, or closely related field. Experience in producing, analyzing and interpreting genomic data. Enthusiasm for collaborating with an interdisciplinary research group that includes ecologists, systematists, population geneticists, and plant scientists. Skill in mentoring graduate and undergraduate students.

Start date: September 2012 (flexible). Position is available for three years, pending reappointment each year. Please apply by email to amlatimer@ucdavis.edu. In your application include: a cover letter explaining why you are interested in this position and what approaches or projects you would like to pursue within it, your CV, names and contact information for three references, and one of your papers.

Salary: UC Davis postdoc scale starts at $39,264 (new PhD), increases with experience.

amlatimer@ucdavis.edu

UChicago computational genomics

Postdoctoral positions are available in the laboratory of Jonathan Pritchard at the University of Chicago (http://pritch.bsd.uchicago.edu).

We are searching for computational biologists interested in either (1) evolution of gene regulation within and between species, or (2) applications of population genetics to study population history and natural selection.

The current main focus of the lab is on computational analysis and modeling of how genetic variation drives differences in gene regulation within and between species. This work is in close collaboration with Yoav Gilad's lab. It involves extensive data collection using a wide variety of modern genomics techniques, as well as development of statistical methods and applied data analysis.

Other areas of interest in the lab include data analysis and modeling of natural selection, inference of population history and structure, and the genetics of complex traits. Most projects in the lab include both data analysis and development of new statistical/computational methods or occasionally theoretical models.

We seek applicants who are creative, energetic, and can work independently. We operate a relatively small but intense lab. The goal is that everyone should have the resources and support that they need to be successful, and our past lab members have an outstanding record of going on to successful scientific careers.

Our lab shares physical space and joint group meetings with the groups led by Matthew Stephens and Molly Przeworski, and we also interact extensively with the wet lab groups of Yoav Gilad and Anna Di Rienzo, as well as other outstanding groups on campus in genomics and evolutionary biology. This provides an extremely stimulating and interactive training environment.

Applicants should have strong computational or statistical skills, and a strong interest in biological applications. A background in genomics or population genetics would be an advantage. There may be some flexibility as to the research area and organism of study, provided that the project falls within the general areas of interest of the lab. Note that for experimentalists, there may be a possibility of a joint position between the Pritchard and Yoav Gilad labs.

To apply for a postdoc position please send a CV to J. Pritchard (pritch at uchicago.edu) and include information describing current research and contact details for three references.

pritch@uchicago.edu

UHongKong Phylogenomics

Postdoc opportunity in phylogenomics at The University of Hong Kong

The Plant Systematics & Phylogenetics lab at The University of Hong Kong is seeking a highly motivated postdoctoral fellow to join our research team. Our group has successfully adopted a holistic approach to the study of the early-divergent angiosperm family Annonaceae, with on-going research that integrates classical morphology-based systematics, molecular phylogenetics, historical biogeography and evolutionary pollination ecology. We are now seeking a researcher to spearhead research using whole-chloroplast genome data generated using next-generation sequencing. Further details of the proposed research project are available from Richard Saunders (saunders@hku.hk).

The post will be for 3 years, with a highly competitive salary. The successful candidate is expected to integrate with other postdocs and postgraduate students in the lab, providing academic advice and mentoring. The appointee should have a solid publication record with evidence of project design, data collection and analysis. Previous experience with next-generation sequencing data assembly, handling of large-scale datasets, and expertise in bioinformatics is desirable.

The start date is negotiable, although the appointee must be in place by February 2013. To apply, please write to Richard Saunders (saunders@hku.hk) describing research interests, a current CV, and contact information for three academic referees. Applications will be reviewed starting immediately and accepted until the position is filled.

Professor Richard M.K. Saunders School of Biological Sciences The University of Hong Kong Pokfulam Road Hong Kong

Email: saunders@hku.hk Lab website: http://web.hku.hk/~saunders/rmks.htm dthomas <dthomas@hku.hk>

ULausanne PolyploidEvolution

Postdoc in plant molecular evolution, University of Lausanne The Pannell lab at the University of Lausanne, Switzerland, is seeking to appoint a postdoctoral research associate with an interest in molecular evolution and comparative genomics. The project will principally involve the comparative analysis of polyploidy across several related species in the plant genus Mercurialis annua, with a particular focus on the implications of polyploidy and hybridization for the evolution of sexual systems and incipient sex chromosomes. The genome and several transcriptomes of diploid M. annua have recently been sequenced, and a draft assembly of the genome will soon be completed. Funding will be available for further large-scale sequencing across the genus. We are especially interested in testing hypotheses about the evolution of sex determination in a context where separate sexes have evolved and been lost more than once.

The successful candidate will have a PhD or equivalent, be highly motivated, and have experience (and publications) in molecular and genome evolution and phylogenomics. Skills in both the generation and the analysis of sequence data to test evolutionary hypotheses are essential. A background and interest in polyploidy and/or sex-chromosome evolution would be an advantage. There will be plenty of scope for the postdoc to develop his/her own research ideas compatible with the current goals of the lab.

Current research in the Pannell lab is directed towards understanding the evolution of plant sexual systems, using a number of study systems and employing approaches that range from bioinformatics through ecological and population genetics to evolutionary ecology. Research in molecular evolution and bioinformatics in Lausanne is currently strong, offering scope for collaborations among researchers across a number of departments. Lausanne, situated on the northern shore of Lake Geneva, has a lively cultural life and is surrounded by spectacular mountain environments.

Informal enquiries can be sent to John Pannell (john.pannell@unil.ch). Formal applications should also be sent to John Pannell, and should include a letter of motivation, a detailed CV, and the names of referees and should. Full consideration will be given to all applications received by the 22nd June. The postdoc would ideally be able to start in September or October, 2012, but the starting date is flexible.

John Pannell Department of Ecology and Evolution Biophore Building University of Lausanne CH-1015 Lausanne Switzerland

Phone: + 41 (0) 21 692 4170 Fax: + 41 (0) 21 692 4265 web: http://www.unil.ch/dee/page86963_en.html
John Pannell <John.Pannell@unil.ch>

UMiami DolphinPopGenetics

The Cooperative Institute for Marine and Atmospheric Studies (CIMAS) of the University of Miami invites applicants for a Postdoctoral Associate position in Marine Biology and Fisheries. This position is situated at the NOAA Fisheries Southeast Fisheries Science Center Protected Resources and Biodiversity Division located in Lafayette, LA.

We seek a postdoctoral researcher to join our group and oversee a project on genetic population structure of bottlenose dolphins in the Gulf of Mexico. The incumbent will be involved in planning and overseeing bottlenose dolphin biopsy field sampling and will also be responsible for collection and analysis of genetic data.

Applicants must have a Ph.D. in Molecular Biology, Biology or related field and experience in DNA sequencing and microsatellite genotyping methodologies, and the computer skills necessary for analysis of population structure and diversity from genetic data. In addition, the applicant should have some field experience with small-boat surveys for marine mammals.

Apply on line at: www.miami.edu/careers, position# 044826. Curriculum Vitae and the contact information for 3 people who can provide letters of recommendation are required.

The University of Miami offers competitive salaries and a comprehensive benefits package including medical and dental benefits, tuition remission, vacation, paid holidays and much more. The University of Miami is an Equal Opportunity/Affirmative Action Employer.

patricia.rosel@noaa.gov

UMontana Evolutionary Genomics

Postdoctoral Research Associate V Evolutionary Genomics, University of Montana

A postdoctoral position in mammalian evolutionary genomics is available in the laboratory of Jeffrey Good at the University of Montana, Missoula. The position is part of an NIH-funded collaborative project to determine the genetic basis of male reproductive variance using mouse models. The position involves using diverse high-throughput genomic approaches to study the molecular evolution of male reproduction between closely related species of mice. The successful candidate will demonstrate a strong background in molecular biology, evolution, comparative genomics, and bioinformatics. A Ph.D. in biology or a related field is required. Candidates with previous experience collecting genomic data, working with experimental rodent systems, and/or mammalian reproductive biology are strongly encouraged to apply.

The Good lab is based in the Division of Biological

Sciences at the University of Montana. The University of Montana is home to a diverse and highly interactive collection of faculty with expertise in ecology, evolution, genetics, genomics, physiology, and behavior. Missoula is a great western college town with an exceptional quality of life and unrivaled access to the scenic beauty of western Montana. For further information on this position and our research please visit the Good Lab website (http://good-lab.dbs.umt.edu/Good_Lab/Home.html) or email Jeffrey Good directly at jeffrey.good@mso.umt.edu.

To apply, please visit http://umjobs.silkroad.com and click the job title for this position under Openings (tracking code 408-254). Candidates must apply online, and will be asked to upload the following application materials: a cover letter describing your research interests and qualifications, a CV, and the names and contact information for three references. Applications must be received by May 25 to assure full consideration, however, the position will remain open until filled. The initial appointment is for one year but is renewable for up to three years. The position is available immediately but the start date will be flexible contingent on the needs of the preferred candidate.

ADA/EOE/AA/Veteran's Preference Employer

Jeffrey M. Good, Ph.D.

Assistant Professor Division of Biological Sciences The University of Montana 32 Campus Drive, HS104 Missoula MT 59812 Phone: 406-243-5771 Fax: 406-243-4184 Website: http://good-lab.dbs.umt.edu/ Jeffrey Good <jeffrey.good@mso.umt.edu>

UNottingham EvolutionMicrobeSignalling

A new Post Doc position in the UK. Its about the testing the "Evolution of Signalling" using microbes.

Details are here:

http://www.stevediggle.com/#/opportunities/4544178712 Many thanks!

Steve

Dr Steve Diggle Royal Society University Research Fellow School of Molecular Medical Sciences Room B86, Centre for Biomolecular Sciences University Park University of Nottingham Nottingham, NG7 2RD, U.K. Tel: +44(0)115 846 7949 Web: http://www.stevediggle.com; http://www.unusual-suspects.org

Steve Diggle <Steve.Diggle@nottingham.ac.uk>

UOttawa PlantAnimalInteractions

Postdoc position in Evolutionary Ecology - Sargent Lab, Department of Biology, University of Ottawa (www. http://mysite.science.uottawa.ca/rsargent/)

I am seeking a highly motivated postdoctoral fellow with a keen interest in the evolutionary ecology of plant animal interactions (esp. plant-herbivore or plant-pollinator). The selected individual will have a PhD (having defended by the position start date) and a strong publication record in this field.

Good communication and interpersonal skills, a strong work ethic, and the ability to think creatively and critically are also assets.

The position is for two years and comes with a competitive salary. The start date is flexible, although, I would prefer to fill the position by September, 2012.

Applications should include a cover letter, a curriculum vitae, a short (~1 page) description of research interests, and the names and contact information (including e-mail) of two referees. All application materials should be submitted via email, as a single pdf, to Risa Sargent (rsargent@uottawa.ca), to whom queries may also be addressed. Evaluation of applications will begin immediately and continue until the position is filled.

Located at the confluence of English and French Canada, Ottawa is a rich and vibrant G8 national capital of approximately 1 million inhabitants (http://www.ottawatourism.ca). The city offers a wide range of cultural activities in the visual and performing arts, as well as easy access to green spaces and wilderness. The University of Ottawa is located next to the historic Rideau Canal, steps from Parliament and within easy access to a wide range of research facilities of interest to evolutionary biologists including the Canadian Museum of Nature, the National Wildlife Research Center, Health Canada, and Environment Canada. Carleton University is only a few km away and research ties between the two Biology Departments are strong.

The Department of Biology has an active group of evolutionary biologists with diverse interests (http://www.evolution.uottawa.ca). Ottawa is also playing host to the first joint meeting of the SSE, ASN, SSB, ESEB, and CSEE in July of 2012 (www.evolution2012.org).

Dr. Risa Sargent Assistant Professor Department of Biology University of Ottawa 30 Marie-Curie (160 Gendron) Ottawa, Ontario, K1N 6N5, CANADA http://www.science.uottawa.ca/ ~ rsargent/ Skype name: risasargent Phone: (613)562-5800 x6840 Fax: (613) 562-5486

rsargent@uottawa.ca

UOxford PopGenetics

Postdoctoral Research Scientist in Statistical, Population, or Human Genetics (up to 3 positions available)

The Wellcome Trust Centre for Human Genetics, Roosevelt Drive, Headington, Oxford, OX3 7BN

Grade 8: £37,012 - £44,166 with a discretionary range to £48,246 per annum. Applications where not all the set criteria are met will be considered, and if appointed, will be at the appropriate salary range of Grade 7: £29,249 to £35,938 per annum, with amended duties and responsibilities.

Applications are invited for up to three Postdoctoral Research Scientists in Statistical Genetics to join the research group of Prof Peter Donnelly FRS, the Centre Director.

Successful applicants will work in one or more of the following areas, although there will not necessarily be one appointment in each area: 1) The development and application of statistical methods for genomic sequence data in health and disease, 2) Analysis of genomic sequence from bacterial isolates or 3) mammalian recombination.

Applicants should have a PhD in statistics or quantitative genetics, or equivalent experience and either: direct research experience and success in one of the three research areas outlined above; or an excellent working understanding of modern statistical methods and the potential to apply them within the statistical genetics context with the ability to lead and assist in the development of novel methods in that context. They will have the ability to handle and analyse short-read sequence data, and good computational skills and experience of low-level programming language such as C or C++. As they will be managing the day-to-day running of the research project, good organisation and communication skills are essential.

Applications are welcomed from candidates with very strong statistical backgrounds who have not yet worked in genetics but are enthusiastic about doing so, as well as from researchers already working in statistical genetics and related areas.

The positions are available for up to three years in the first instance and are funded by the Wellcome Trust. To apply for this role and for further details, including a job description and person specification, please click on the link below: https://www.recruit.ox.ac.uk/pls/hrisliverecruit/erq_jobspec_version_4.jobspec?p_id=102750 Only applications received before 12:00, midday on Monday 21st May 2012 can be considered. Applicants will be required to upload a CV and supporting statement as part of your online application, please quote reference 102750 in all correspondence.

donnelly@well.ox.ac.uk

USouthDakota LotusEvolution

POSTDOCTORAL FELLOW

POSTDOCTORAL FELLOW TO WORK ON EVOLUTION OF LOTUS ON CALIFORNIA$B!G(BS CHANNEL ISLANDS AND ON CONSERVATION GENETICS OF ISLAND ENDEMIC PLANTS A NSF-funded post-doctoral position is available in the laboratory of Kaius Helenurm in the Department of Biology at The University of South Dakota. This position would involve working on (a) the dispersal and differentiation of endemic species of California$B!G(Bs Channel Islands, and (b) the conservation genetics of endemic plants of San Clemente Island, CA. I am looking for a colleague who would be involved in data collection, field work, and contribute intellectually to the future development of this island system.

The ideal candidate would be a recent Ph.D. with a strong background in population genetics and molecular techniques. The start date is flexible, but the position is available immediately. Applications will be considered until the position is filled.

Please apply via e-mail to Kaius Helenurm (helenurm@usd.edu), and include: (1) a brief cover letter describing your research interests and qualifications, (2) a full CV, (3) your preferred start date, (4) contact information (email, phone number) of three references, and (5) pdf$B!G(Bs of up to three representative publications. Please include $B!H(Bpostdoctoral application$B!I(B in the subject line of the e-mail. Informal inquiries are welcome.

Kaius Helenurm Professor and Chair of Biology Department of Biology The University of South Dakota

Email: helenurm@usd.edu

Website: http://people.usd.edu/~helenurm/Home.html Kaius Helenurm <Kaius.Helenurm@usd.edu>

USouthernCalifornia ComputationalBiol

Position: Postdoctoral Researcher Employer: University of Southern California, Keck School of Medicine

Description: A funded Postdoctoral Researcher position is available at the Laboratory for Computational and High-Throughput Genomics, Department of Preventive Medicine, University of Southern California Keck School of Medicine.

The focus for this position is on computational data analysis based on high-throughput DNA sequencing data and computational method development in the following potential areas:

Medical genomics

Disease genomics

Cancer genomics

Population genetics

Chromatin structure and gene regulation

Qualified individuals may also conduct experimental work with focus on genetics, genomics and DNA sequencing. See below for a list of relevant publications.

Requirements: We are looking for a motivated, self-driven individual with a strong background in any of the following areas:

Genetics

Genomics

Computation

Probability and statistics

Prior experience in any areas related to genomics is a strong plus. Experimental experience in molecular biology is a plus. Strong publication record is a must.

To apply: Send your CV along with links or copies of your publications, thesis, working papers, or other relevant scientific work to Anton Valouev (valouev@usc.edu). Please include names and contact information of three references.

Anton Valouev, Ph.D. Assistant Professor Division of Bioinformatics Department of Preventive Medicine University of Southern California Keck School of Medicine

1450 Biggy Str., NRT2509K Los Angeles, CA phone: (323) 442-7941

Relevant publications:

Valouev A, Johnson SM, Boyd S, Smith CL, Fire AZ, Sidow A, “Determinants of nucleosome organization in primary human cells” Nature, 2011

Peng J, Valouev A, Swigut T, Zhang J, Zhao Y, Sidow A, Wysocka J, “Jarid2/Jumonji coordinates control of PRC2 enzymatic activity and target gene occupancy in pluripotent cells” Cell, Dec 2009

Valouev* A, Johnson* DS, Sundquist A, Medina C, Anton E, Batzoglou S, Myers RM, Sidow A, “Genome-Â’âwide analysis of transcription factor binding sites based on ChIP-Â’â Seq data”, Nature Methods, Sep 2008

Valouev A, Schwartz DC, Zhou S, Waterman MS, “An algorithm for assembly of ordered restriction maps from single DNA molecules”, PNAS, Oct 2006

Anton Valouev <valouev@usc.edu>

UUtah HerbivoreGutGenomics

Postdoctoral Fellowship Metagenomics of the Herbivore Microbiome

The Dearing lab at the University of Utah invites applications for a postdoctoral fellow to participate in a collaborative study to understand the gut microbiome of mammalian herbivores with respect to detoxification of plant defensive compounds. Our preliminary data suggest that microbiome in the foregut of woodrats is critical for ingesting dietary toxins, that biodiversity is important in this process and that previous exposure to toxins shapes the microbiome.

For more information on previous research, see

http://biologylabs.utah.edu/dearing/2011/Research/-

Detox_Plant.html http://biologylabs.utah.edu/-dearing/2011/Publications/Kohl_2011_Symbiosis.pdf
The ideal candidate will have a strong interest and experience in microbial ecology and metagenomics preferably in the gut systems. Basic bioinformatic and molecular skills are required; more extensive experience is preferred. Field work for animal collection is possible. The candidate should have at least one first authored publication in press. The Dearing lab provides a strong training and career development environment for candidates interested in academic positions.

Applications will be reviewed as they are received through June 15, 2012. The anticipated start date is no later than September 1, 2012 although August 1, 2012 is preferred. Please send a C.V., statement of research experience and interests that includes career goals (1-2 pgs), pdfs of papers, and contact information (emails and phone numbers) for at least 3 professional references to Dr. Denise Dearing, denise.dearing@utah.edu; please put $B!H(BMicrobiome Postdoctoral Applicant$B!I(B in the Subject Line.

Denise Dearing, Ph.D Professor, Department of Biology Associate Dean, College of Science University of Utah Salt Lake City, UT 84112

Phone: 801-585-1298 Fax: 801-581-2174

http://biologylabs.utah.edu/dearing/-2011/Index_New.html Denise Dearing <dearing.denise@gmail.com>

UVigo Spain Phylogenomics

Postdoctoral positions in Phylogenomics University of Vigo, Spain

Two postdoctoral positions are available to work on phylogenomic methodology and applications under a project funded by the European Research Council (ERC) in David Posada's lab at the University of Vigo, Spain (http://darwin.uvigo.es). Initial appointments will be made for one year, with possible extension. Gross annual salary including benefits will be around 24-30 kEuros, commensurate with experience. Starting date should be as soon as possible.

Candidates should have a doctoral degree in Biology, Computer Science, Statistics or Mathematics. Excellent bioinformatic skills and prior experience with phylogenomics are essential. Strong communication and teamwork abilities are fundamental. Familiarity with parallel and distributed computing environments is convenient. Advanced statistical skills would be a plus.

Please send a letter of interest, C.V., and the names and contact details of two referees to David Posada at dposada@uvigo.es, indicating “postdoc phylogenomics” in the subject of the email. Questions and requests for more information should be directed at the same address. Review of applications will begin immediately, and continue until the positions are filled.

David Posada University of Vigo 36310 Vigo, Spain +34 986 812038 dposada@uvigo.es http://darwin.uvigo.es David Posada <dposada@uvigo.es>

WashingtonDC MarineMammalSystematics

Announcement of Opportunity for NMFS/NMNH Marine Mammal Post-Doc

http://nrc58.nas.edu/RAPLab10/Opportunity/-Opportunity.aspx?LabCode=26&ROPCD=-260352&RONum=B7721 Location National Marine Fisheries Service, NEFSC/National Systematics Laboratory

RO# Location

26.03.52.B7721 Washington, DC 20235

Advisers Name E-mail Phone

Vecchione, Michael vecchiom@si.edu 202.633.1751

Description NOAA's National Marine Fisheries Service (NMFS) has statutory obligations to protect marine mammals within its Extended Economic Zone and beyond. Such protection requires thorough understanding of the natural history of the various groups, such as cetaceans, pinnipeds, and sirenians, including all levels of evolutionary relationships. The marine-mammal collection of over 11,000 specimens at the Smithsonian Institution's National Museum of Natural History (NMNH) is a result of long-term collaboration between NMNH and NMFS and is one of the best in the world. The diversity of this collection allows broadly-based research on comparative morphology of systematic characters. The large number of specimens of many species permits analyses of variability among individuals, sexes, life-history stages. and geographic areas. Furthermore, the museum's Laboratory for Analytical Biology, located at the Museum Support Center, provides the capability for state-of-the-art analyses for molecular systematics. We expect that the Associate will work with the National Collection at NMNH using combined morphological and molecular methods to investigate questions of importance to NMFS. Possible general directions for the research include (1) examination of taxonomic problems of complex groups of species and their populations, (2) phylogenetic and biogeographic investigations using molecular techniques in combination with morphological characters from specimens in museum collections, and (3) comparative studies examining evolution of life-history characteristics or biogeography.

Keywords: Evolution; Biodiversity; Biogeography; Life history; Taxonomy; Classifications; Eligibility Citizenship: Open to U.S. citizens, permanent residents and non-U.S. citizens Level: Open to Regular and Senior applicants

"Helgen, Kristofer" <HELGENK@si.edu>

WorkshopsCourses

Arizona LepidopteraSystematics Aug11-20

The 2012 Lepidoptera Course will be held at the SW Research Station in the heart of the Chirichahua Mts. of SE Arizona (about 2 hours from Tucson) on 11-20 August. This setting is one of the highest areas of lepidoptera biodiversity in the US. The focus of the course is to train serious amateurs, citizen-scientists, and academic professor in lepidoptera identification, classification, and biology.

The staff for the 2012 course includes: -Deane Bowers, U of Colorado -Jason Dombroskie, Cornell University -Lee Dyer, U of Nevada, Reno -Paul Goldstein, USNM -Hugh McGuinness -Jim Miller, AMNH -Ray Nagle, U of Arizona -Chris Schmidt, CNC -Dave Wagner, U of Connecticut. -Bruce Walsh, U of Arizona

Course fees (which includes room and board) is $1070 for students (and course alumni) and $1170 for non-students. Application deadline is 11 June 2012. Further details, and a link to the application form, can be found at www.lepcourse.org. You can also see photos and comments from students in the 2011 course at their facebook site, "2011 Lep Course, SWRS SEAZ". For any questions, contact Bruce Walsh, jbwalsh@u.arizona.edu

Bruce Walsh <jbwalsh@u.arizona.edu>

Barcelona Diversity Jul2-6

Dear colleagues,

We are pleased to announce a workshop on the measurement of diversity - from managing the genetic diversity of farm animals to quantifying the biodiversity of ecosystems. This forms part of a five-week event at the Centre de Recerca Matemàtica, Barcelona on "The Mathematics of Biodiversity", with the one week workshop/exploratory conference taking up the middle week from the 2nd to the 6th July, 2012.

The two weeks before the workshop will focus on understanding the problems faced in the various fields, identifying how these problems overlap between research domains, and understanding what solutions already exist in different areas. The workshop itself will focus on communicating identified problems and potential solutions between all of the participants. The final two weeks will focus on the development of (potentially novel) solutions to the problems that have been previously identified.

We welcome experienced researchers, both pure and applied, in these fields to the workshop as well as people new to the area and with related problems and interests, and we encourage people to stay for longer than the single week of the workshop if they wish to develop their interests further. We are also taking offers of contributed talks - if you would like to give one, please contact us as soon as possible.

Our current list of speakers is:

Benjamin Allen John Baez Michael Bonsall Anne Chao Christina Cobbold Glenn De'ath Elizabeth Gillet Hans-Rolf Gregorius Lou Jost Tom Leinster Alison Mather Louise Matthews Hans Metz Sandrine Pavoine Richard Reeve Carlo Ricotta William Sherwin Mike Stear John Woolliams

More details are available at http://www.crm.cat/CBIO and grants for attendance expenses are available at http://www.crm.cat/en/Activities/Pages/ActivityDescriptions/Grant-Biodiversity.aspx - the official deadline is Saturday 12th May. If you want to apply but think you will miss the deadline (or have already missed it), all is not lost: let us know at the addresses below.

Best wishes,

Richard Reeve and Tom Leinster

on behalf of the scientific committee: Benjamin Allen, Silvia Cuadrado, Tom Leinster, Richard Reeve, John Woolliams

Scientific enquiries: Richard.Reeve@glasgow.ac.uk or Tom.Leinster@glasgow.ac.uk Administrative enquiries: NPortet@crm.cat (Ms Neus Portet)

Dr Richard Reeve | Research Fellow

Boyd Orr Centre for Population and Ecosystem Health Institute of Biodiversity, Animal Health and Comparative Medicine College of Medical, Veterinary and Life Sciences University of Glasgow | Glasgow | G12 8QQ

Tel +44 141 330 6638 Web http://www.gla.ac.uk/boydorr/people/byname/richardreeve Administrateur@esf.org

Basel MicrobiotaEvolution Sep12-14

Just a reminder that the WORKSHOP DEADLINE (for the tutorial) IS APPROACHING!!!

The Organizing Committee would like to invite you to attend a 3-day international workshop on the "Evolution and Ecology of Host-Associated Microbiota" to be held at the Zoological Institute, University of Basel, Switzerland on September 12- 14, 2012. The major aim of this workshop is to provide a synthesis of the emerging evolutionary and ecological patterns governing the complex interactions of host-microbiota across different biological systems. We have invited leaders in the field of host-associated microbiota and microbial ecology to share their insights on the evolutionary and ecological principles that shape bacterial community structure and host-microbiota interactions.

This workshop is intended for undergraduate students, graduate students, postdoctoral researchers and early career investigators (100 slots available) who wanted to be exposed to the evolutionary and ecological concepts and bioinformatics tools being applied on the study of host-associated microbiota systems and microbial ecology. Together with the lecture, a hands-on tutorial (bioinformatic tools and approaches encompassing microbial ecology, comparative genomics, molecular evolution) will be provided on the analysis of complex sequence data sets derived from next-generation sequencing.

Thanks to the generous funding from ProDoc of the Swiss National Science Foundation and the University of Basel, we are only charging a minimal fee of CHF 150 for registration (includes 3 lunches, 1 social dinner, 2 social mixers and snacks during the entire workshop) or CHF 250 (+ tutorial on the analysis of next-generation sequences; 50 slots available). We also have arranged for a number of rooms around Basel ranging from youth hostel dormitories (CHF 32-79/ day) to 3-star hotels (CHF 160- 250/ day). Moreover, Basel/Mulhouse Airport is a hub for Easyjet, a budget airline in Europe. Application deadline for the tutorial is May 30 and for the lecture series is June 30, 2012. More information can be found at this website: http://evolution.unibas.ch/ebert/microbiota/index.htm Please direct any questions to the organizing committee: Marilou Sison-Mangus (m.sison@unibas.ch), Samuel Pichon (samuel.pichon@unibas.ch) and Dieter Ebert (dieter.ebert@unibas.ch)

Confirmed Speakers:

Bioinformatics and Computational Tools

1. KNIGHT, Rob (University of Colorado Boulder, USA) - computational tools for understanding the evolution of microbiota through time and space

2. CAPORASO Greg (Northern Arizona University, USA) - QIIME (Quantitative Insights Into Microbial Ecology) and microbiota dynamics

3. HUSON, Daniel (University of Tubingen, DE) - MEGAN (MetaGenome ANalyzer) and phylogenetic networks

4. QI Weihong (ETH Zürich, CH) - Trends and applications of next- generation sequencing technologies

Microbial Diversity and Symbiosis

5. DUBILIER Nicole (Max Plank Institute, Bremen, DE) - Symbioses of bacteria and hydrothermal vent organisms

6. BRUNE, Andreas (Max Plank Institute, Marburg, DE) - Insect gut microbiology and symbiosis

7. EBERT Dieter (University of Basel, CH) - Daphnia parasites and microbiota

Microbiota Dynamics and Evolution

8. GILBERT Jack (University of Chicago, USA) - Microbial community dynamics and function

9. JANSSON, Janet (LNL, DOE-JGI, USA)- bacterial diversity in the environment

10. LEE Carol Eunmi (University of Wisconsin-Madison, USA) - Copepod microbiota and invasion success

11. Van der MEER Jan (University of Lausanne, CH) - Genetic adaptation and evolution of bacteria in the environment

Genomics of Health- and Nutrition-Associated Microorganisms

12. SVANBORG Catharina (University of Lund, SE) - Host imprints on human-associated bacterial genomes

13. VORHOLT Julia (ETH Zürich, CH) - Physiology of plant-associated microbes (metaproteomics)

Bacteria- host interactions and evolution

14. ROSENBERG Eugene and ZILBER-ROSENBERG, Ilana (University of Tel Aviv, IL) - Coral microbial communities and the hologenome theory

15. POULSEN, Michael (University of Copenhagen, DK) - Multiple interactions between symbionts and host

16. HENTSCHEL, Ute (University of Würzburg, DE) - Mechanisms of interactions between sponges and their microbial communities

Marilou P. Sison-Mangus, PhD Postdoctoral Researcher Evolutionary Biology, Zoology Institute University of Basel Vesalgasse 1, 4051 Basel Switzerland

Tel no: 061 267 03 72

m.sison@unibas.ch

CzechRepublic SpeciationResearch Aug28-30

Summer school on Current methods on speciation research, which will be held on 28-30th August 2012 in Czech Republic.

The web page of this school is on this adress. http://www.pruhonice2012.iach.cz/ RNDr. Radka Reifová, Ph.D. Tel.: +420 221 95 1872 E-mail: radka.reifova@natur.cuni.cz Web: http://web.natur.cuni.cz/ ˜ radkas/ Katedra zoologie Univerzita Karlova v Praze Pøírodovìdecká fakulta Vinièná 7, 128 43 Praha 2

Department of Zoology Charles University in Prague Faculty of Science Vinièná 7, 128 43 Praha 2

Radka Reifová <radka.reifova@natur.cuni.cz>

Edinburgh StatisticalGenetics Jun

European Institute in Statistical Genetics 13-15 June and 25-29 June 2012

The European Institute in Statistical Genetics will run in Edinburgh in June 2012, on either side of the 4th International Conference on Quantitative Genetics 2012. This is a series of short courses on a range of methods of statistical analysis of modern genetic data, taught by leading academics in the field. Courses are available in the following topics: 1. Genomic Prediction:

Ben Hayes 2. Genetics of Competition: Peter Bijma and Bill Muir 3. Advanced R for Genetic Analysis: Thomas Lumley and Ken Rice 4. Population Genetic Data Analysis: Jérome Goudet and Bruce Weir 5. Gene Expression Profiling: Greg Gibson and John Storey 6. Mixed Models in Quantitative Genetics: Bill Muir and Bruce Walsh 7. MCMC for Genetics: Eric Anderson and Matthew Stephens 8. Plant and Animal Association Mapping: Peter Bradbury and Michel Georges 9. Inference of Relationships and Relatedness: Eric Anderson and Elizabeth Thompson

* Early-bird registration for the EISG closes on Friday 18 May: http://www.eisg2012.org.uk/ Registration is also still open for the 4th International Conference on Quantitative Genetics 2012 (17-22 June 2012), which contains a diverse and stimulating programme covering state-of-the-art results on the genetics of complex traits. For more details, see http://www.icqg2012.org.uk/ Prof. Loeske Kruuk Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh Edinburgh, EH9 3JT, UK Tel. 0131 650 5515 http://wildevolution.biology.ed.ac.uk/lkruuk Loeske Kruuk <Loeske.Kruuk@ed.ac.uk>

Munich ProteinEvol Jul27-29 reminder

Dear colleagues,

this is just a reminder that the deadline for registration and abstract submission for our workshop on protein evolution and related topics is approaching: *May 18!* /*We kindly invite you to register and submit your abstract.*/

The key dates: The workshop taking place at the University of Munich from July 27th till July 29th, 2012. Registration fee will now be 50EUR. Information on the workshop can be found on our website: http://ieb.uni-muenster.de/protein-evolution-workshop-2012 The workshop comprises four main topics: (1) Evolution of new proteins Keynote speakers: Dr. Mar Albà (Universitat Pompeu Fabra (UPF), Spain) Dr. Florian Hollfelder (University of Cambridge, UK) Dr. David Karlin (University of Oxford, UK) (2) Protein Modelling Keynote speakers: Dr. David Liberles (University of Wyoming, USA) Dr. Markus Porto (University Cologne, Germany) (3) Systems Biology Keynote speakers: Dr. Balázs Papp (Biological Research Center of the Hungarian Academy of Sciences, Hungary) Dr. Orkun Soyer (University of Exeter, UK) Prof.Erich Bornberg-Bauer (The Westfalian Wilhelms University of Münster, Germany) (4) Evolutionary and Functional Genomics Keynote speakers: Prof. Tal Pupko (Tel Aviv University, Israel) Dr. Simon Whelan (University of Manchester, UK)

For each main session, we invited 2-3 international scientists who will present their work in 45min talks. Short oral contributions will be selected from submitted poster abstracts. Overall, we aim for around 50 participants. This meeting provides an opportunity for experts to share their knowledge, present new results, and forge new networks to develop new ideas in the field of protein evolution.

I would also like to ask for your assistance in forwarding the information to your colleagues who may be interested in joining the meeting.

With kind regards,

Sonja Grath

Dr. Sonja Grath Westfalian Wilhelms University Evolutionary Bioinformatics Institute for Evolution and Biodiversity Huefferstrasse 1, D-48149 Muenster, Germany http://ieb.uni-muenster.de/bioinf/people/Sonja-Grath.html s.grath@uni-muenster.de

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Munich ProteinEvolution Jul27-29 AbstractExt

Dear colleagues,

as we still have some slots left for oral presentation (15min), we decided to extend the submission deadline for our workshop on protein evolution and related topics in Munich to:*June 15.*

We kindly invite you to register and submit your abstract (workshop2012@wwu.de).

The key dates: The workshop taking place at the University of Munich from July 27th till July 29th, 2012. Registration fee will be 50EUR. Information on the workshop can be found on our website: http://ieb.uni-muenster.de/protein-evolution-workshop-2012 The workshop comprises four main topics: (1) Evolution of new proteins Keynote speakers: Dr. Mar Albà (Universitat Pompeu Fabra (UPF), Spain) Dr. Florian Hollfelder (University of Cambridge, UK) Dr. David Karlin (University of Oxford, UK) (2) Protein Modelling Keynote speakers: Dr. David Liberles (University of Wyoming, USA) Dr. Markus Porto (University Cologne, Germany) (3) Systems Biology Keynote speakers: Dr. Balázs Papp (Biological Research Center of the Hungarian Academy of Sciences, Hungary) Dr. Orkun Soyer (University of Exeter, UK) Prof.Erich Bornberg-Bauer (The Westfalian Wilhelms University of Münster, Germany) (4) Evolutionary and Functional Genomics Keynote speakers: Prof. Tal Pupko (Tel Aviv University, Israel) Dr. Simon Whelan (University of Manchester, UK)

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I would also like to ask for your assistance in forwarding the information to your colleagues who may be interested in joining the meeting.

Do not hesitate to contact me in case you have any further question.

With kind regards,

Sonja Grath

– Dr. Sonja Grath Westfalian Wilhelms University Evolutionary Bioinformatics Institute for Evolution and Biodiversity Huefferstrasse 1, D-48149 Muenster, Germany http://ieb.uni-muenster.de/bioinf/people/Sonja-Grath.html s.grath@uni-muenster.de

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Ottawa RforBiodiversity Evolution2012 Jul6

Canadian Society for Ecology & Evolution (CSEE) Graduate Student Workshop

“R for Biodiversity Analysis”

Friday, July 6, 1 -5 pm, University of Ottawa This is the afternoon before the opening reception of the 1st Joint Congress on Evolutionary Biology (i.e. Evolution2012); www.evolution2012.org Instructor: Steve Kembel (University of Oregon) Register here! http://-evo2012-r-biodiversity.eventbrite.com/ Fee: $45

For more information contact: evo2012.workshop@gmail.com

Workshop Summary: An introduction to the use of the R statistical computing environment for analysis of biodiversity data. This workshop will provide a brief introduction to R, an overview of resources for ecological and evolutionary analysis in R, and give participants hands-on experience using R to analyze the evolution of species traits and the taxonomic, functional, and phylogenetic diversity of ecological communities. Please bring your laptop to this workshop.

*You must be a member of the CSEE to register for this event. For CSEE membership please see: http://-www.ecoevo.ca/en/membership.htm Sponsored by the Canadian Institute of Ecology & Evolution (CIEE) and the Canadian Society for Ecology & Evolution (CSEE)

Howard D. Rundle, Associate Professor Department of Biology, 30 Marie-Curie Priv. University of Ottawa, Ottawa, ON, K1N 6N5, CANADA Ph: +1 613-562-5800 x2835; Fax: +1 613-562-5486 Skype: howarddrundle http://www.science.uottawa.ca/~hrund050 http://-www.evolution.uottawa.ca howard.rundle@uottawa.ca

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Ottawa ScienceCommunication

Along side the main Evolution 2012 conference, numerous other satellite workshop < http://-www.confersense.ca/Evolution2012/workshops.htm > will taking place. Of these include the Communicating Science to Society< http://-evo2012commsciencetosociety.eventbrite.com/ > workshop, sponsored by the Canadian Society for Ecology and Evolution< http://www.ecoevo.ca/en/-index.htm > .

< http://evolution2012ottawa.com/wordpress/wp-content/uploads/2012/04/media-workshop.jpg >

Whether you need to learn the basics or fine tune the dark art of science communication, this half day workshop is for you. Come for insider advice from a group of North Americas top science communicators. The session will open with evolutionary ecologist Tom Sherratt talking about his experience with the media and why he does it. The panellists will introduce an area of journalism and discuss their experiences with interviewing researchers. Then the panel discussion will expand on some of the challenges scientists face and the practical communication solutions. Finally a break-out session will allow for an interactive round table letting participants choose a topic of particular interest (how to give an interview, how to pitch a science book to a publisher, 101 for scientists using social media). The workshop will conclude with a networking session between fellow science communicators and the panellists. By the end, delegates can expect to have built a strategy as to how to effectively approach and handle different media opportunities (such as TV, radio, print & social media) and also leave with a handout of useful tips.

Speakers:

- *Carl Zimmer* (NYT columnist & author of A Planet of Viruses < http://carlzimmer.com/books/-aplanetofviruses/index.html > and many other best sellers) - *Penny Park* (Producer of CBCs Quirks & Quarks and Discovery Channels The Daily Planet. Now Executive Director of the Science Media Centre of Canada < http://www.sciencemediacentre.ca/smc/ >) - *Elizabeth Howell* *Ottawa Business* *Journal*, freelance science journalist and* *social media expert - *Tim Lougheed* Freelance science journalist - *Tom Sherratt *Evolutionary ecologist, Carleton University

There are limited spaces for the science communication workshop so register now: http://-evo2012commsciencetosociety.eventbrite.com/ cell # : 613 255 5149 lab # : 613 520 2600 extn 3866

http://websterswildshots.com http://-www.carleton.ca/ ˜ sherratt Richard Webster <richard.j.webster@googlemail.com>

Seattle StatGenetics Jul9-Aug10

Summer Institutes in Seattle

The Department of Biostatistics is conducting Summer Institutes in Seattle: Statistical Genetics: July 9-27. Statistics and Modeling in Infectious Diseases: July 9-25. Biostatistics, emphasizing Clinical Trials: August 6-10.

Details at the “Summer Institutes” tab on http://-www.biostat.washington.edu Bruce Weir

Bruce Weir <bsweir@u.washington.edu>

UOttawa MathematicalModelling Jul11

American Society of Naturalists Graduate Student Workshop

Mathematical Modelling in Evolutionary Ecology

July 11, 9 am 12 noon, University of Ottawa

Workshop Leader: Hanna Kokko (The Australian National University)

Register here! http://-evo2012mathmodelecoevo.eventbrite.com/ Everything you wanted to know about modelling but were afraid to ask! Still time to sign up!

The aim is to improve students’ ability to digest theoretical papers and give some initial guidance to wannabe modelers.

For more information contact: evo2012.workshop@gmail.com

Workshop Summary:

To most young students of evolutionary biology it comes as a surprise that the field is quite mathematically oriented. Understanding evolution requires a firm grasp of its theoretical foundation, and making statements about specific cases may require developing new models. With mathematical modeling, it is impossible to bring people from novice to expert level in one half-day workshop, but improved scientific literacy regarding theoretical work is a reasonable goal. With this goal in mind, this workshop -dissects’ examples from recent theoretical work. The aim is to improve students’ ability to digest theoretical papers beyond the often encountered attitude “I’ll read the introduction and the discussion only, and will trust whatever is in between”, and give some initial guidance to wannabe modellers.

Please bring your laptop to this workshop.

*You must be a member of the American Society of Naturalists to register for this event

For ASN membership please see: http://-www.asnamnat.org/beamember This event is sponsored by the American Society of Naturalists.

mark.mcpeek@dartmouth.edu

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.