EvolDir

January 1, 2008

Month in Review

Forward

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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Barcelona MetazoanEvolution Oct24-25

Dear colleagues,

We are pleased to announce the "ICREA Conference on the Origin and Early Evolution of Metazoans" to be held in Barcelona, Spain, 24th-25th October 2008.

The conference will bring together internationally renowned experts from a diversity of disciplines, including systematics, paleontology, evo-devo, and phylogenomics. Please visit the homepage at http://www.originmetazoa.com for further information and feel free to distribute this announcement to colleagues and suitable lists.

Best regards,

Iï¿½aki Ruiz-Trillo, Pere Martinez and Andrew J. Roger http://www.originmetazoa.com inaki.ruiz@icrea.es

Dublin ClimateChangeSystematics Sep1-3

Climate Change and Systematics Conference, 1 - 3 September 2008, Trinity College Dublin, Dublin, Ireland. First Announcement and call for research papers on aspects of the interaction between Climate Change and Systematics. The conference will deal with this topic under three headings as follows: 1. Climate Change and Speciation/ extinction: 2. Climate Change and Biogeography: 3. Climate Change: documenting and conserving biodiversity. To obtain further information and register for the conference please see http://www.tcd.ie/Botany/Conference.php' – Dr Trevor Hodkinson Department of Botany School of Natural Sciences University of Dublin, Trinity College D2, Ireland

Phone: 353-1-8961128 Fax: 353-1-8961147 Email: trevor.hodkinson@tcd.ie

hodkinst@tcd.ie

Hungary AnimalCooperation Jan17-20 2

CONFLICT AND COOPERATION IN ANIMAL SOCIETIES Workshop in Debrecen, Hungary; 17-20 January 2008

IMPORTANT UPDATE:

The workshop's web site < http://vocs.unideb.hu/cooperation > is up. Here you can register and find information.

We are organising a Training Workshop to understand various aspects of cooperation and conflict in animals. Topics will include theoretical modeling, comparative evolutionary analyses, physiology and genetics.

The Workshop will be in Debrecen, Eastern Hungary 17-20 January 2008. We target postgraduate students and young post-docs in Europe, although attendance will be open to everyone. The Workshop will be hold under the aegis of a multi-partner EU-funded coordination-action project, INCORE. The venue will be hosted by University of Debrecen http://www.unideb.hu/ Invited speakers will include Professor John M McNamara (University of Bristol), Professor Rob Freckelton (University of Sheffield), Professor Mike Siva-Jothy (University of Sheffield), Professor Michael Taborsky (University of Berne), Dr Istvan Karsai (East Tennessee University), Dr Lajos Rozsa (Natural History Museum Budapest), Dr Berhard Voelkl (University of Strasbourg) and Professor Tamas Szekely (University of Bath).

Postgraduate students and post-docs are encouraged to give a 15 min talk followed by 5 min discussion.

For students registered at an Eastern/Central European institution, partial financial support will be available from INCORE. For further information and to register please contact Miklos Ban banm@vocs.unideb.hu

Best regards,

Zoltan Barta Peter Laszlo Pap Tamas Szekely zbarta@delfin.unideb.hu peterlpap@gmail.com T.Szekely@bath.ac.uk

Peter Laszlo Pap <peterlpap@gmail.com>

Marseilles EvolutionaryBiology Sep24-26

12th Evolutionary Biology Meeting 2008 at Marseilles will take place the September 24-26

The following subjects will be discussed: - Evolutionary biology concepts and modelisations for biological annotation; - Biodiversity and Systematics; - Comparative genomics and post-genomics (at all taxonomic levels); - Functional phylogeny; - Environment and biological evolution; - Origin of Life and exobiology. - Non-adaptative versus adaptative evolution

The early registrations start the First January

more informations http://www.up.univ-mrs.fr/evolcgr/ best regards Pierre Pontarotti

Pierre.Pontarotti@univ-provence.fr

Milwaukee PlantPollinatorEvolution Aug2-3

CONFERENCE ON THE ECOLOGY AND EVOLUTION OF PLANT-POLLINATOR INTERACTIONS

A two-day conference on the Ecology and Evolution of Plant-Pollinator Interactions will be held on August 2-3, 2008, immediately prior to the Ecological Society of America Meeting in Milwaukee, Wisconsin, USA.

The goal of this conference is to highlight the most exciting recent advances in community and evolutionary pollination biology, and foster interaction among pollination biologists. We aim to encourage a unified framework to the study of community and evolutionary approaches, and to draw attention to largely unexplored questions at the intersection of these disciplines. This two-day conference will feature 23 speakers from five continents, as well as a poster session.

Conference speakers and topics have been selected to complement, rather than repeat, the major themes covered at the 2007 International Pollinator Symposium. The 30 minute symposium presentations will be scheduled throughout the day on Saturday, August 2 and Sunday, August 3. To promote interaction between symposium speakers and participants, there are planned breaks with time for discussion as well as a two-hour poster session and reception on the evening of Saturday, August 2. The poster session will provide an outstanding opportunity for pollination ecologists at all levels to share ideas. We encourage all conference attendees to present a poster. Note that individuals presenting a talk or poster in this Pollination Conference are also welcome to present a contributed paper or poster (even the same poster) at the Ecological Society of America meeting.

REGISTRATION: Individuals planning to attend the Pollination Conference must register online at the ESA website: http://www.esa.org/milwaukee/ Registration will open in early April, 2008 and must be completed by June 2, 2008. There are two registration options:

a) If you plan to attend BOTH the Pollination Conference and the Main ESA meeting, you should pay the ESA annual meeting fee (approx. $ 140 for student members; $ 285 for regular members) PLUS the Pollination Conference fee of $ 50.

b) If you plan to attend the Pollination Conference, but will NOT be attending the Main ESA meeting, you should pay the "ESA one-event registration fee" of $ 45 PLUS the Pollination Conference Fee of $ 50. Note that the total cost of registration for this option would be $95.

POSTER PRESENTATION: All participants in the Pollination Conference are encouraged to present posters. Poster titles should be submitted to Jeff Karron by June 2, 2008 at: karron@uwm.edu. In the subject line of the email, list "pollination ecology poster". Due to space limitations, we will only be able to accommodate 150 posters. Titles will be accepted on a first-come first-served basis. Note that poster presenters do not register their posters for the Pollination Conference on the ESA website; they can only do so by emailing Jeff Karron.

POSTER DIMENSIONS: Poster boards are approximately 2.4 m wide x 1.2 m tall (8 x 4 feet). Please design your poster to be at least 5 cm (2 inch) smaller on each margin.

HOUSING: ESA has reserved a limited number of hotel rooms and dorm rooms for Friday and Saturday evenings. See the ESA housing link for more information.

ESA MEETINGS: We encourage participants to stay throughout the week and attend the ESA annual meeting (August 3-8) that follows the Pollination Conference. Participants in the Pollination Conference can present a talk and/or poster at the ESA meeting as well. Titles of talks and posters for the ESA meeting should be submitted online between December 17, 2007 and February 28, 2008. The link for the ESA meeting page is: http://www.esa.org/milwaukee/ CONTACT: If you have questions about this Pollination Conference, please contact Jeff Karron (karron@uwm.edu), Randy Mitchell (rjm2@uakron.edu), or Rebecca Irwin (Rebecca.Irwin@Dartmouth.edu).

CONFERENCE WEBSITE: http://www3.uakron.edu/biology/pollination/ The Pollination Conference is being generously supported by the Ecological Society of America.

Rebecca.E.Irwin@Dartmouth.EDU Rebecca.E.Irwin@Dartmouth.EDU

Nairobi Kenya MEEGID IX Oct30-Nov1

MEEGID IX Congress in Nairobi, Kenya, 30th October-1st November 2008

Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases

Co-organized by the Institut de Recherche pour le Dï¿½veloppement in France and the Centers for Disease Control in Atlanta. Hosted by ICIPE. Other co-organizers: KEMRI, ILRI, CDC Kenya, the University of Nairobi, CNRS, CIRAD and the French Embassy in Nairobi.

The major event in genetics and evolution of infectious diseases. Just one year before Darwin's bicentennial. Don't miss it!

Topics: genetics, genomics, proteomics, population biology, mathematical modeling, and bioinformatics. Papers can report on the host, the pathogen (viruses, parasitic protozoa, helminths, fungal organisms, and prions), or the vector for vector-borne diseases. Papers considering co-evolution phenomena are particularly encouraged. All infectious models can be considered, including those of veterinary or agronomical relevance. Special emphasis will be given to health problems of particular interest to Africa and the Indian Ocean: AIDS, malaria, tuberculosis, sleeping sickness, ebola, chikungunya, cattle and crop pathogens.

Abstracts and main papers to be published in a special issue of Infection, Genetics and Evolution (http://www.elsevier.com/locate/meegid).

Keynote speakers:

Morris Agaba (International Livestock Research Institute, Nairobi, kenya): QTL Mapping and Epidemiology of Transmissible Diseases. Francisco J. Ayala (Dept Ecology and Evolution, UC Irvine, California): (i) Evolution of malaria; (ii) Darwin's Revolution Koussay Dellagi (Centre for Research and Surveillance of Emerging Diseases in the Indian Ocean): Chikungunya epidemics. Appolinaire Djikeng (J. Craig Venter Institute, Rockville, Maryland, USA): Viral genomics. Wendy Gibson (University of Bristol, UK): Epidemiology and evolution of human African trypanosomiasis. Martine Peeters (IRD Montpellier, France): HIV epidemiology and molecular evolution. Michel Tibayrenc (IRD, Bangkok, Thailand): Integrated evolutionary epidemiology: where are we now? Sarah Tishkoff, (Pennsylvania State University): Human genetic diversity and transmission of infectious diseases.

Abstract submission deadline: 30th July 2008.

Contact: Michel Tibayrenc, IRD Representative Office, French Embassy, 29, Thanon Sathorn Tai, Bangkok 10120, Thailand; Michel.Tibayrenc@ird.fr; http://www.th.ird.fr See updated information at http://www.th.ird.fr//site_meegid/menu.htm Michel.Tibayrenc@ird.fr

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Neuhausen Germany PlantAnimalSexEvol Sep10-14

Workshop: Analogies in the evolution of gender expression and sexual strategies in plants and animals (Germany, 2008) September 10-14, 2008 (including arrival and departure days)

Application deadline: January 31st, 2008

Current research on the evolution of reproductive strategies and gender expression still tends to proceed almost independently between botanists and zoologists. Yet, the evolutionary processes involved are often complementary, indicating that linkage of ideas between both fields would be highly beneficial. This cross-disciplinary workshop therefore addresses the analogies in reproductive evolution between plants and animals (with a focus on hermaphrodite mating systems). The meeting brings together empiricists and theoreticians from both disciplines. Major topics to be covered include phylogenetic patterns of gender expression and their transitions, the role of mate competition in shaping sexual strategies, and the role of selfing/outcrossing/mixed mating systems.

*Application In your e-mail application, please provide the following information:

1. Full affiliation and contact details: _________

2. Preliminary title for your workshop contribution, as well as the preferred type of presentation (oral or poster): ___________

3. In order to facilitate the potentially necessary selection of participants, please also outline the topics to be addressed in your contribution in a 2-3 sentence statement: _______

4. Would you require partial travel refund: Yes/No (If yes, your expected total travel costs: _________)

*Venue Sparkassen-Akademie Neuhausen (Germany), a conference hotel easily reached from Stuttgart International Airport. Accommodation is on site.

*Meeting style Workshop with max. 60 participants, facilitating discussion of current research highlights, joint project applications and future research collaborations.

*Funding The workshop is generously supported by the Volkswagen foundation, enabling us to offer free bed & breakfast, no conference fees and an option for partial travel refunds.

*Costs Local costs to be covered by all attendants include meals (lunch, dinner) and beverages.

*Type of contributions The number of oral contributions is restricted to 30. Oral presentations must meet the scope of the workshop by presenting broader perspectives relevant to the evolution of reproductive strategies in plants and/or animals. Poster presentations are possible, as is participation in the meeting without any formal contribution.

We are looking forward to receiving your application emails.

With kind regards

Nils Anthes & Nico K. Michiels

Tentatively confirmed speakers include... G. Bernasconi, P. Crowley, L. Harder, P. Jarne, J. Jokkela, P. Klinkhamer, A. Lankinen, P.L. Munday, J. Pannell, M. Schilthuizen, R. Warner, S. Weeks,...

Generously funded by Volkswagen Foundation

Nils Anthes, PhD Zoological Institute Animal Evolutionary Ecology Eberhard Karls-Universität Tübingen Auf der Morgenstelle 28 72076 Tübingen, Germany Tel: ++49-(0)7071-29 74617 Fax: ++49-(0)7071-29 5634 E-Mail: Nils.Anthes@uni-tuebingen.de

http://www.uni-tuebingen.de/evoeco/ Nils.Anthes@uni-tuebingen.de Nils.Anthes@uni-tuebingen.de

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NHM London MolluscSpeciation Apr25

Advance announcement

A ONE DAY SYMPOSIUM “SPECIATION IN MOL-

LUSCS”

Friday, 25th April 2008, starting 10.30 am

Venue: Natural History Museum, London, UK

The Malacological Society of London announces a one day symposium “Speciation in Molluscs” to coincide with the Annual General Meeting of the Society. Talks will be given by invited international speakers at the forefront of this field.

Speakers are:

Ellinor Michel (NHM, London): [3]Gastropod endemism in African freshwaters; traits, time and topography[2] Emilio Rolán-Alvarez (University of Vigo, Spain): “Ecological speciation of Littorina saxatilis in Galicia” Chris Meyer (Smithsonian Institute, USA): Dispersal and speciation in the big pond. Menno Schilthuizen (Naturalis, Leiden) : [3]Evolution on a block of rock; snail speciation on tropical limestone karst[2] Jon Todd (NHM, London): [3]Patterns from the fourth dimension of a marine snail radiation[2] Angus Davison (University of Nottingham, UK): [3]Speciation and gene flow between Japanese snails of contrasting ecology and opposite chirality[2]

This meeting will be of interest to evolutionary biologists, malacologists, students, post-doctoral researchers and researchers.

Registration is FREE and includes a wine reception to follow the meeting. Please let us know if you wish to attend and if you wish to bring a poster. Send applications by e-mail to Suzanne Williams (S.williams@nhm.ac.uk). AGM business will be discussed during the lunch break.

Dr Suzanne Williams Zoology Dept Natural History Museum Cromwell Rd London SW7 5BD United Kingdom Tel: + 44 (0) 207 942 5351 (office) 5774 (lab) Fax: +44 (0) 207 942 5867

Suzanne Williams <s.williams@nhm.ac.uk>

Ottawa FishEvolution Aug17-21

The Genetics Section of the American Fisheries Society is soliciting speakers and titles for consideration for presentations in a symposium “Contributions of genetic principles and technology to sustainable fisheries: concepts, challenges, and case studies”, to be held at 138th Annual Meeting of the American Fisheries Society in Ottawa, Canada, August 17-21, 2008. Symposium proposals must be submitted by January 11, 2008. Presenters’ abstracts will be due February 29, 2008. Accordingly, we would like to receive the names and tentative titles of speakers who would be interested in contributing to this symposium by January 8, 2008. For further information regarding the symposium and contacts for submission of titles, please contact symposium conveners Chris Wilson (Chris.Wilson@nrdpfc.ca) or Kim Scribner (scribne3@msu.edu).

Symposium outline: Populations of most fish species are increasingly impacted by stressors that alter demographic characteristics, distribution, and the features of the environments they inhabit and have adapted to. Genetic theory and technology have become essential components of management programs to understand and overcome stressors that threaten sustainable fisheries. This symposium will develop several conceptual issues for fisheries professionals from a genetics perspective that affect the long-term viability of fish populations. Sections will focus on policy issues, concepts and theory, and empirical data in each of several topical areas. Subject areas will include (1) population delineation and distinctiveness of populations and identification of distinct population segments for management and conservation planning, (2) means of quantifying population-specific levels of exploitation based on estimates of contributions of multiple source populations to mixed-stock and inter-jurisdictional fisheries, (3) response of fisheries to anthropogenic and abiotic stressors such as climate change, (4) consequences of the loss of adaptive variation in heritable phenotypic, behavioral, and physiological traits due to environmental change and to exploitation, and (5) sustainability of populations when natural recruitment is supplemented by stocking. Presentations will present conceptual and empirical analyses highlighting the comparative fitness of wild, stocked, and introgressed fish, potential detrimental effects of inbreeding and outbreeding depression, and (6) empirical applications of molecular genetic data to elucidate aspects of species behavior, reproductive success, and general ecology. Topics will also help inform restoration and rehabilitation efforts for depressed fisheries.

scribne3@msu.edu scribne3@msu.edu

Paris PopulationGeneticStructure Aug24-29

Dear colleagues,

It is a pleasure to announce that the 10th European Multicolloquium of Parasitology (EMOP X) will take place in Paris the 24th 29th of August 2008. There are 15 scheduled symposia. The 11th symposium, entitled "Population Genetic Structure & Molecular Epidemiology" will be organised by Michel Tibayrenc and me. We invite you to register for EMOP X and submit oral communications for one of the four sessions of this symposium.

Symposium XI (T. De Meeis, M. Tibayrenc): Population Genetic Structure & Molecular Epidemiology.

Session 1: Population genetics of parasitic and fungal diseases, invited keynote address by Tatiana Giraud, ESE, Paris Sud, Orsay, France.

Session 2: Population genetics of vectors, invited keynote address by Karen McCoy, GEMI, IRD Montpellier, France.

Session 3: Co-structures of hosts, parasites and vectors, invited keynote address by Charles Criscione, SFBR, San Antonio Texas, and Department of Biology, A&M University, College Station, Texas, USA.

Session 4: Impact of clonality on population genetics, invited keynote address by Franck Prugnolle, GEMI, IRD, Montpellier, France.

There is room for at least 16 open presentations (10 mn + 5 mn), some of which may be converted into open keynote communications (15 mn + 5 mn).

Registration forms will soon be available on EMOP X website at http://www.emop10.eu/index.php?option=3Dcom_frontpage&Itemid=3D1. You can however already send your talk proposal and abstract to me (demeeus@mpl.ird.fr) so that Michel and I can optimise the organisation of the symposium.

We hope to see you in Paris in August

Best regards

Thierry and Michel

Thierry de Meeis Genetique et Evolution des Maladies Infectieuses UMR CNRS/IRD 2724, UR IRD 165 Equipe: Structures Genetiques et Adaptation dans les Systimes Symbiotiques (SGASS) Centre IRD de Montpellier 911 Avenue Agropolis, B.P. 64501 34394 Montpellier Cedex 5, France.

Tel: +33 (0)467 41 63 10 Secretariat: +33 (0)467 41 61 97 Fax: +33 (0)467 41 62 99 http://-gemi.mpl.ird.fr/SiteSGASS/EntrySGASS.html Site web du groupe "Tiques et maladies e tiques" http:/-/gemi.mpl.ird.fr/SiteSGASS/GroupeTiqueREID/-GroupeTiqueREID.html thierry.demeeus@mpl.ird.fr

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SouthAustralia MathEvolBiology Mar25-30

We are pleased to announce the Adelaide Conference on Mathematical Evolutionary Biology, the first of an annual series that will take place within Blanche Cave, Naracoorte Caves, South Australia. This 5 day meeting is designed to bring together mathematicians and biologists from around Australia and internationally, in an informal collaborative atmosphere limited to just 50 seats. The meeting is closely modelled on the very successful New Zealand Phylogenetics meeting series, which has resulted in the development of a very strong biomathematics community in New Zealand. Four of the leading members of the New Zealand group will help lead and direct the Naracoorte meeting, facilitating communication between these fields which currently have little interaction within Australia.

The organisers cordially invite to you to attend this conference and registration is now open. Students are encouraged to attend and please get your registration in early to guarantee a seat due to the very limited space.

Important Notes Registration deadline: by no later than March 3rd, 2008. Accommodation: a few local hotel/motels have been earmarked especially for this conference, offering negotiated discount rates. Refer to the conference website for details. Please ensure you book accommodation early to safeguard a place to stay at Naracoorte. Conference updates: Our website will be the main source of information with email traffic kept to a minimum. Web updates will be posted regularly at < http://www.adelaide.edu.au/acad/events/ >http://www.adelaide.edu.au/acad/events/ . –

Prof. Alan Cooper ARC Federation Fellow Director, Australian Centre for Ancient DNA

Email: alan.cooper@adelaide.edu.au Ph: 61-8 -8303-5950/3952 Fax: 61-8-8303 4364

http://www.adelaide.edu.au/acad/ Mailing Address: Darling Building University of Adelaide North Terrace Campus South Australia 5005 Australia

alan.cooper@adelaide.edu.au

UMontpellier HumanBehaviour and Evolution Apr2-4

EHBE

European Human Behaviour and Evolution Conference

2-4 April 2008

University of Montpellier

< http://www.ehbe08.com/ >www.ehbe08.com

EXTENDED DEADLINE: Monday 17 December 2007

Call for papers: We are pleased to announce our third annual conference. As last year our aim is to create a multidisciplinary European forum in which researchers applying evolutionary theory to the behavioural sciences can meet and exchange ideas. To this end we are soliciting abstracts for paper presentations.

This is to be a pre-read conference. Those accepted to present will be expected to produce a full paper version of their presentation by the end of February 2008.

We look forward to hearing from you.

EHBE Steering Committee Rebecca Sear (London School of Economics) Tom Dickins (University of East London) David Lawson (University College London) Kevin Laland (St Andrews University)

< http://www.ehbes.com/ >www.ehbes.com

Charlotte Faurie & Michel Raymond Conference organizers European Human Behaviour and Evolution Conference (EHBE 2008) < http://www.ehbes.com/- >www.ehbes.com

Institut des Sciences de l'Evolution (CNRS UMR 5554) Universite Montpellier II - CC 065 Place Eugene Bataillon F-34095 Montpellier cedex 05 TEL: +33 (0)467 144 632 FAX: +33 (0)467 143 622

ehbe08@univ-montp2.fr

USheffield EvolutionaryGeneticsGroup Apr1-3

This is an early announcement of the:- ECOLOGICAL GENETICS GROUP MEETING 2008 In 2008 the Ecological Genetics Group (EGG) will be holding its 52nd annual meeting which will be at the University of Sheffield, England, between the 1st-3rd April. EGG is an informal group of scientists; academics, researchers and graduate students, whose interests include the genetics of evolution and ecology, population genetics & biology, biogeography and evolutionary adaptation, biosystematics, conservation, molecular ecology and phylogeography. For further information go to:- http://www.britishecologicalsociety.org/-articles/groups/genetics/ Talks, discussion topics and posters are welcomed from students giving their first presentation, to senior academics presenting completed work. Offers of papers and poster presentations are welcome and should be sent to Raj Whitlock at:- r.whitlock@sheffield.ac.uk

The invited speaker in 2008 is Professor Loren Reiseberg from the USA, who has received awards for his pioneering research into the evolution of new species and use of a wide range of theoretical and experimental approaches from classical cross-breeding to genomic mapping. Current work includes the evolutionary forces underlying phenotypic diversification. As at all EGG meetings, there will be an afternoon field visit to a local site of ecological and conservation interest. In 2008 this will be to Cressbrookdale, part of the Derbyshire Dales National Nature Reserve, to see the early flowering species and talk about management of the site.

Student support for this meeting is available from the Bitish Ecological Society. Application forms can be downloaded from the BES website and should be sent to the BES at least two weeks before the meeting takes place. For further information visit:- http://www.britishecologicalsociety.org/-articles/grants/attendmeetings/ Student support may also be available from the Genetics Society. For further information go to:- http://www.genetics.org.uk/-sectional_interest_grant The Botanical Society of the British Isles (BSBI) will also give bursaries, but they will be restricted to EU Botany students.

Barbara Jones <b.jones@ccw.gov.uk>

VenturaCA MolEvol GordonResConf Feb3-8

Hi All,

I just wanted to alert you all to the Molecular Evolution Gordon Research Conference to be held in sunny Ventura CA, February 3-8, 2008. http://www.grc.org/programs.aspx?year=2008&program=molecevo < http://www.grc.org/programs.aspx?year=2008&program=molecevo >

We've got a great slate of speakers with varies interests and expertise. This program will broadly address how microevolutionary changes can result in macroevolution. We'll cover evolutionary changes from viruses to organ development.

Registration slots are filling fast, so don't be left in the rain in February! Billie Swalla University of Washington

* Microevolution of Development (Norman Johnson / Eric Haag / Hope Hollocher) * Evolvability (Günter Wagner / Lilach Hadany / Suzannah Rutherford / Susan Rosenberg) * Phylogenomics (Laura Katz / Monica Medina / John Huelsenbeck) * Molecular Evolution of Body Axes (Mike Levine / Elaine Seaver / Mark Martindale / John Gerhart) * Positive and Negative Selection on Noncoding DNA (Peter Andolfatto / Manolis Dermitzakis) * Exploring Adaptive Landscapes (Ben Kerr / Antony Dean / Dan Weinrich / Christina Burch) * Molecular Basis of Heart Evolution (Doug Crawford / Brad Davidson / Jose Xavier-Neto) * Computational and Statistical Advances (Sudhir Kumar / David Haussler / Carlos Bustamante / Lindell Bromham) * Measuring Evolutionary Timescales (Bret Payseur / Asher Cutter / Joanna Mountain)

"Weinreich, Daniel" <Daniel_Weinreich@brown.edu>

YaleU Evolution in Disease Feb21 Apr17

The Yale Symposia on Evolution in Health and Disease will take place on February 21st and April 17th in the Mary S. Harkness Auditorium of the Yale School of Medicine. You may view the program and register at www.yale.edu/evomedsymposia Please also call this to the attention of colleagues in medical schools.

stephen.stearns@yale.edu stephen.stearns@yale.edu

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ClemsonU EvoDevo 10
DrexelU SymbiosisEvolution 11
EmoryU EvolutionaryBiology 11
ETH Zurich HostParasite 12
GhentU PlantComparativeGenomics 12
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LouisianaStateU BioimagingFungalEvolution 13
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PortlandStateU EvolutionaryBiology 14
SAfrica InvasiveSpeciesEvolution 15
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Trondheim QuantEvolutionaryGenet 16
UAkron PlantEvolution 17
UAlaska EvolutionaryBiology 17
UAlaska InvasiveSpecies 18
UArizona TheoPopGenet 18
UBergen 2 FishEvolution 19
UCaliforniaLosAngeles EvolutionaryBiol 19
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UtahStateU ConservationGenetics 27
UTexasAustin CichlidFishEvolution 28
UToronto EvolutionaryGenetics 28
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CarletonU Evolution of Sex

Graduate Positions - Evolution of Sex

Carleton University, Department of Biology

Root Gorelick seeks new graduate students (primarily PhD, but also MSc) to study the evolutionary origin of eukaryotic sex. We are focusing on organisms that only have sex with themselves, e.g. pedestrian self-fertilisation, complete automixis, and restitutional automixis. This work is largely theoretical, but not exclusively so as we are also planning to conduct MSAP (methylation-sensitive amplification polymorphism). Students interested in the social or philosophical question of whether self-sex counts as sex should also contact me.

Interested students should send a cv, summary of research experience and interests, contact details of two referees, approximate GPA, and information on whether you are a Canadian citizen or permanent resident. See Carleton University's Biology website for information on the graduate program (www.carleton.ca/biology/prospect/graduate/index.html < http://www.carleton.ca/biology/prospect/graduate/index.html >). Carleton University is located in the lovely city of Ottawa.

E-mail: Root_Gorelick@caleton.ca <mailto:Root_Gorelick@caleton.ca>

Web: www.carleton.ca/~rgorelic < http://www.carleton.ca/~rgorelic >

Voice: 613-520-2600 ext. 1586

Fax: 613-520-3539

Root_Gorelick@carleton.ca

ClemsonU EvoDevo

Graduate Opportunities in Evolutionary Developmental Biology at Clemson University

Graduate Assistantships (M.Sc., $15,000 or Ph.D., $18,000 for 12 months) are available in the labs of Drs. Susan Chapman and Brad Hersh at Clemson University in the areas of evolutionary developmental biology. Prospective candidates should have strong academic records and some research experience in laboratory bench work is preferred. Motivation, self-discipline, creativity, and good interpersonal skills are essential.

Chapman and her students want to understand the molecular mechanisms required for middle ear induction and patterning. Avians have a primary jaw articulation, while mammals have a secondary jaw articulation that has given rise to the incus and malleus, which together with the stapes form the three ossicles of the middle ear. The single columella in birds is the functional equivalent of the three mammalian ossicles, but developmental equivalent of the stapes. We are focused on identifying the required molecular signals and tissues from which they derive in birds, with the long term goal of testing these in mammals for translational human health benefits. (http://www.clemson.edu/biosci/faculty/chapman/index.htm)

Hersh and his students study the development and evolution of animal shapes, especially insect wings. Current research focuses on two projects studying the evolution and development of Drosophila: (1) The regulation of gene expression in the Drosophila wing and hindwing by the Hox protein Ultrabithorax; (2) the identification of genes involved in divergence of male-specific morphologies within the melanogaster subgroup. (http://www.clemson.edu/biosci/faculty/bhersh/index.htm)

Clemson University (http://www.clemson.edu/) offers a stimulating environment and excellent resources for cell and developmental biologists through the Biological Sciences department (http://www.clemson.edu/biosci). The Cell and Developmental Biology emphasis area in the Biological Sciences graduate program (http://www.clemson.edu/biosci/graduate) brings together faculty from across the campus and the Greenville Hospital System Oncology Research Institute (http://www.ghs.org/335/) in nearby Greenville, South Carolina. Students may apply through the Graduate School (http://www.grad.clemson.edu/Admission.php) by January 15, 2008 for admission in Fall of 2008.

For more information contact: Susan C. Chapman, Ph.D. Assistant Professor Department of Biological Sciences 132 Long Hall Clemson University Clemson, SC 29634 schapm2@clemson.edu http://-www.clemson.edu/biosci/faculty/chapman/index.htm Bradley M. Hersh, Ph.D. Assistant Professor Department of Biological Sciences 132 Long Hall Clemson University Clemson, SC 29634 bhersh@clemson.edu http:/-/www.clemson.edu/biosci/faculty/bhersh/index.htm Margaret Ptacek <mptacek@CLEMSON.EDU>

DrexelU SymbiosisEvolution

I am currently seeking Ph.D students to study symbiosis between insects and microbes, in the Department of Bioscience & Biotechnology at Drexel University.

My current research focuses on 1) the ecology and evolution of ants and their microbes, 2) insect-Wolbachia interactions, and 3) patterns of microbial diversity across the insects. Students would be expected to develop a dissertation project that relates to one of these areas, using molecular and experimental techniques to address ecological and evolutionary questions about symbiosis.

Prior laboratory experience is required, and skills in microscopy and standard techniques of molecular biology are preferred. Applicants should have a broad biological background, with coursework in the fields of molecular biology, genetics, ecology, and evolution.

To apply, please visit the Drexel graduate admissions website:

http://www.drexel.edu/em/apply/coas/ And for specifics on academic requirements, visit:

http://www.drexel.edu/em/apply/coas/p_bio.html Please note that applications are due by January 1.

Feel free to contact me with any inquiries at Jacob.A.Russell@drexel.edu. You can find out more about my research at:

http://www.drexel.edu/coas/bioscience/Russell.html . Dr. Jacob A. Russell

Assistant Professor Department of Bioscience & Biotechnology Drexel University 3141 Chestnut St. Philadelphia, PA 19104

Jacob Russell <jar337@drexel.edu>

EmoryU EvolutionaryBiology

Graduate Student Positions Available in the Program in Population Biology, Ecology and Evolution (PBEE) at Emory University

http://www.biomed.emory.edu/PROGRAM_SITES/-PBEE/ We would like to announce the availability of graduate student positions at Emory University in the graduate program in Population Biology, Ecology, and Evolution (PBEE). Founded in 1994, the PBEE program now includes 32 faculty and 21 graduate students. PBEE faculty include members from the Departments of Biology, Human Genetics, Anthropology, Environmental Studies, and Psychology, the Yerkes Primate Center, the Rollins School of Public Health, and the CDC. Areas of emphasis and expertise include: the ecology and evolution of infectious diseases and molecular evolution and functional genomics. Our students receive a support package that includes a tuition scholarship, health insurance, and stipend ($24,500 for 2007-2008). Emory University and the PBEE program also offer pre-doctoral training fellowships; exceptional applicants are nominated for such awards based on their application materials.

The PBEE graduate program provides the multidisciplinary training required for a successful research and/or teaching career. All students take four core classes spanning the fields of population biology, ecology, and evolution, as well as more specialized courses offered by our diverse faculty. Weekly seminars, journal clubs, and PBEE functions help make us a cohesive group. Emory is located in the vibrant town of Atlanta, GA, a wooded, cosmopolitan, and progressive city known as the capital of the southeast U.S. The Emory campus is 15 minutes from downtown Atlanta and even closer to charming pedestrian neighborhoods like Virginia Highlands, Little Five Points, and downtown Decatur.

The application deadline is January 3. PBEE is part of the Graduate Division of Biological and Biomedical Sciences, and applications are made through the Division. For more information and application materials contact the Division directly (toll free phone: 800.727.6028, phone: 404.727.2545, email: gdbbs@emory.edu, web: www.biomed.emory.edu).

For more information or to answer questions about the PBEE program, visit our website: http://-

www.biomed.emory.edu/PROGRAM_SITES/PBEE/, or contact our recruiting chair directly:

Dr. Todd Schlenke Assistant Professor Department of Biology Emory University tschlen@emory.edu 404-727-0817

tschlen@emory.edu tschlen@emory.edu

ETH Zurich HostParasite

ETH Zürich, Institute of Integrative Biology (IBZ)

The Experimental Ecology Group (Paul Schmid-Hempel) is seeking to fill a new

Ph.D. Position

(Genomics and diversity of host defences)

to work on questions of host-parasite interactions using Bombus spp. and their parasites (protozoa, viruses, bacteria) as the study system. The ecological framework for this study is the relationship of host diversity to the prevalence and diversity of pathogens in natural populations of various Bombus species, with the goal to eventually understand the co-evolutionary dynamics of host-parasite interactions in general. Important elements will be the genetics of immune defences and the respective variation in natural populations. The project will involve field sampling and genetic typing with molecular tools. We will integrate this advance with existing and currently developed genomic databases for B. terrestris to establish relationships and test ideas. The biology and ecology of the species is well known and it is readily accessible in the field and in the lab. In the project, the genomics approach will be integrated into the ecology and evolution of populations to test some major concepts of ecological theory and host-parasite coevolution. Although the prime motivation are questions of basic importance, the project is embedded in a larger set of studies conducted at ETH addressing the significance of ecological and genetic variation in natural systems with respect to disease, climatic change and environmental degradation.

The ideal candidate is one who would like to work with and be fascinated by both this combined approach and the bumblebee system. They should have interests in and see the possibilities at the crossroads of ecology, genetics and evolution. An advantageous background is in any of the relevant fields, such as evolutionary ecology, population genetics or genomics / bioinformatics. Salary and other conditions are in accordance with local regulations. The normal duration of a PhD at ETH is 3 years. Special conditions for acceptance into the PhD program of ETH may apply; a degree equivalent to a M.Sc. is required. Preferred starting date is spring 2008. Please send applications, with CV, names of referees, and short statement of your interests in this position to Prof. Paul Schmid- Hempel, preferably by email (psh@env.ethz.ch). Screening of applications will start 25 January 2008 or until post is filled. For more information, you may check our web page (www.eco.ethz.ch).

Prof. Paul Schmid-Hempel Institute of Integrative Biology (IBZ) Experimental Ecology ETH-Zentrum CHN, K11 CH-8092 Zurich

ph: +41 (0)44 633 6048 / 6033 fax: +41 (0)44 632 1271 psh@env.ethz.ch www.eco.ethz.ch paul.schmid-hempel@env.ethz.ch paul.schmid-hempel@env.ethz.ch

GhentU PlantComparativeGenomics

Dear all,

Our Research Group “Bioinformatics and Evolutionary Genomics” of the Department of Plant Systems Biology at VIB/Ghent University is currently looking for 2 excellent PhD students to work on different topics such as plant comparative genomics, gene and genome duplications, and plants systems biology.

For more information and full job descriptions, please visit: http://bioinformatics.psb.ugent.be/ Yves Van de Peer

– Yves Van de Peer, PhD.

Professor in Bioinformatics and Genome Biology Group Leader Bioinformatics and Evolutionary Genomics VIB Department of Plant Systems Biology, UGent Ghent University Technologiepark 927 B-9052 Ghent Belgium

Phone: +32 (0)9 331 3807 Cell Phone: +32 (0)476 560 091 Fax: +32 (0)9 331 3809 email: yves.vandepeer@psb.ugent.be

http://bioinformatics.psb.ugent.be/
yves.vandepeer@psb.ugent.be

Leipzig HumanOrigins

We invite applications for the Leipzig School of Human Origins, a joint graduate program of the University of Leipzig (Germany) and the Max Planck Institute for Evolutionary Anthropology.

This program provides interdisciplinary training and research opportunities for university graduates who wish to work towards a PhD in anthropology, biology, evolutionary genetics, primatology, paleoanthropology and related fields.

Prospective graduate students will specialize in one of the following directions:

- Comparative and Molecular Primatology

- Evolutionary and Functional Genomics, Ancient DNA, Molecular Anthropology and Genome Bioinformatics

- Human Paleontology, Prehistoric Archaeology and Archaeological Science

Graduate students will be accepted to one of these areas but will have the opportunity to take part in courses and seminars in all of them.

The language of the school is English. Leipzig is a highly livable city in the center of Europe (http://www.leipzig.de).

For project and application details see http://www.leipzig-school.eva.mpg.de or contact us by e-mail at leipzig-school@eva.mpg.de, phone +49 (0) 341 3550-0 or fax+49 (0)341 3550-119.

The closing date for applications is January 31, 2008.

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Sandra Jacob Max Planck Institute for Evolutionary Anthropology / The Leipzig School of Human Origins (Ph.D. Programme) Deutscher Platz 6, 04103 Leipzig, GERMANY phone: ++49 (0) 341 3550-122; fax: ++49 (0) 341 3550-119 http://www.eva.mpg.de/ http://www.leipzig-school.eva.mpg.de/

Sandra Jacob <jacob@eva.mpg.de>

LouisianaStateU BioimagingFungalEvolution

Bioimaging Position V Fungal Evolution Assembling the Fungal Tree of Life (www.aftol.org)

We seek Ph.D. level scientists or M.S. research associates to participate in an exciting multi-investigator project to resolve the origins of major fungal lineages using genomic and morphological data (for a description of the “Assembling the Fungal Tree of Life” project see www.aftol.org).

Two positions in fungal comparative biology/structural evolution using state of the art bioimaging technologies is available at the Department of Biological Sciences, Louisiana State University and at the Department of Plant Biology, University of Minnesota. The person will work closely with other labs to expand the AFTOL structural database (http://aftol.umn.edu), and s/he should have interests in comparative biology/structural evolution and phylogenetic analysis, and some molecular work is a possibility. Previous experience with cryofixation and transmission electron microscopy is desirable; working with a diversity of fungal organisms also is desirable but not required. The appointment period is 2-4 years. If interested, please send a cover letter, vita, and names of references (contact Meredith Blackwell, <mblackwell@lsu.edu>) or David McLaughlin <davem@umn.edu>).

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Department of Biological Sciences Louisiana State University Baton Rouge, Louisiana 70803 (USA) Dept: 225 578-2601 (messages) Lab : 225 578-8551 Fax : 225 578-2597 E-mail: mblackwell@lsu.edu Web site: http://lsb380.plbio.lsu.edu/Home.html Meredith Blackwell <mblackwell@lsu.edu>

MasseyU PlantDomestication

Doctoral Studentship, Massey University

A 3-year PhD studentship is available at the Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand to start in early 2008 (starting date is flexible).

The successful candidate will join a team studying the early phases of crop domestication by examining endemic New Zealand plant species cultivated by Maori. The PhD student will study one of the four species our team is investigating by developing and scoring AFLP and microsatellite DNA markers in order to determine the number of times the species has been brought into cultivation and how domestication has reduced genetic diversity in cultivated populations. Traditional Maori oral histories regarding the origins of specific populations will also be sought and combined with the genetic data to explore pre-European Maori settlement routes and mobility.

We are looking for a student with an MSc or equivalent in biological sciences. Experience in molecular laboratory techniques such as PCR, sequencing and molecular marker development is preferable and a willingness to engage with Maori iwi is also desirable.

More information about the Allan Wilson Centre for Molecular Ecology and Evolution, one New Zealand^{1}s Centres of Research Excellence (CoREs), is available at http://awcmee.massey.ac.nz/ . Interested candidates should contact Dr Lara Shepherd (lara.shepherd@vuw.ac.nz) or Prof. Peter Lockhart (p.j.lockhart@massey.ac.nz) for more information. Applications close on February 10 2008.

Lara.Shepherd@vuw.ac.nz Lara.Shepherd@vuw.ac.nz

MaxPlanckBerlin ComputationalBiol

Dear colleague,

the International Max Planck Research School for Computational Biology and Scientific Computing,

a joint graduate program of the Freie Universitaet Berlin and the Max Planck Institute for Molecular Genetics, Berlin, invites applications for a PhD program.

The PhD program is designed as a 3-year program starting in autumn 2008 and is open for international students.

The closing date for applications is February 24, 2008.

We would be grateful if you could communicate the announcement to interested students. A poster can be downloaded from

http://www.imprs-cbsc.mpg.de/download/-poster2008.pdf For further details and the application procedure, please visit

http://www.imprs-cbsc.mpg.de Thanks for your efforts,

the IMPRS-CBSC team

International Max Planck Research School for Computational Biology and Scientific Computing (IMPRS-CBSC) Contact: Hannes Luz Max Planck Institute for Molecular Genetics | Tel: +49 30 8413 - 1154 Computational Molecular Biology | Fax: +49 30 8413 - 1152 Ihnestrasse 73 | Email: luz@molgen.mpg.de D-14195 Berlin, Germany | www.imprs-cbsc.mpg.de hannes luz <luz@molgen.mpg.de>

PortlandStateU EvolutionaryBiology

The Department of Biology at Portland State University is seeking graduate students to join our research group in ecology and evolutionary biology. Our faculty have active and interrelated research programs spanning all levels of biological organization, including behavior, physiology, population biology, conservation, genetics, systematics, and genomics. Research in this area is complemented by departmental strengths in microbiology, vertebrate biology, botany, and the biology of extremophile organisms.

Portland State University is located in downtown Portland and is the largest university in Oregon. The location provides the benefits of a livable, culturally rich urban center and easy access to the natural diversity of the Cascades, Columbia River Gorge, and the Oregon Coast. The University has a diverse and motivated student body and is committed to sustainability and community outreach. Research facilities in the Department include the Vertebrate Biology Museum, Herbarium, Aquatic Vertebrate Facility, and a brand new, 5000 sq. ft. Greenhouse facility.

Please visit our website (www.biology.pdx.edu) for more information about the Department, faculty, graduate studies, and to submit an online application. For full consideration for fall 2008 admission, applications must be complete by Feb. 15, 2008.

Faculty with research interests in ecology and evolutionary biology include:

Mike Bartlett micb@pdx.edu archaeal transcription mechanism and evolution http://www.biology.pdx.edu/people/bartlett/index.php Brad Buckley bbuckley@pdx.edu marine environmental genomics, ecophysiology, thermal stress

Mitch Cruzan cruzan@pdx.edu plant ecological genetics, invasive species, hybridization http://web.pdx.edu/ ˜ cruzan/ Debbie Duffield duffieldd@pdx.edu population genetics, conservation biology, marine mammals http://www.biology.pdx.edu/faculty/duffield/duffield.html Sarah Eppley eppley@pdx.edu plant population ecology, breeding system evolution http://www.biology.pdx.edu/people/eppley/ Suzanne Estes estess@pdx.edu genetics of adaptation, mutational effects http://www.biology.pdx.edu/faculty/estes/main.html Mark Fishbein mfish@pdx.edu plant systematics, pollination ecology, hybridization http://web.pdx.edu/˜mfish Susan Masta smasta@pdx.edu genome evolution, speciation, arachnid evolution http://web.pdx.edu/ ˜ smasta Michael Murphy murphym@pdx.edu population ecology, behavior, vertebrate ecology, avian mating systems http://www.biology.pdx.edu/faculty/murphy/murphy.html Jason Podrabsky jpod@pdx.edu developmental and evolutionary physiology, desert fishes, life history, functional genomics http://killifish.pdx.edu Radu Popa rpopa@pdx.edu microbial ecology, biogeochemistry, origin of life

Anna-Louise Reysenbach reysenbacha@pdx.edu ecology and diversity of thermophiles http://airlab.pdx.edu Todd Rosenstiel rosensti@pdx.edu biosphere-atmosphere interactions, plant ecophysiology, global change http://www.biology.pdx.edu Ken Stedman kstedman@pdx.edu Ecology and Evolution of Extremophile Viruses http://web.pdx.edu/˜kstedman Luis A. Ruedas ruedas@pdx.edu animal systematics, evolution and biogeography, community ecology, conservation biology http://www.biology.pdx.edu/faculty/ruedas/ruedas.html –Mark Fishbein

mfish@pdx.edu mfish@pdx.edu

SAfrica InvasiveSpeciesEvolution

Postgraduate Bursaries in Ecological Genetics of Invasive Species Several opportunities at Honours, MSc and PhD level at the Centre for Invasion Biology, Stellenbosch University

Please note: these bursaries are only for South Africans

The C*I*B is a dynamic, internationally leading agency which undertakes research to reduce the rate and impacts of biological invasions. We are looking for several postgraduate students interested in ecological genetics and molecular ecology, to form part of a major 5 year collaborative project with the Working for Water Programme and the University of Adelaide / Herbarium of South Australia.

Project details: The projects form part of a broader project to improve our understanding and management of alien plant invasions using molecular techniques. Component 1 focuses on what is essentially a phylogeographic study of Australian plants invasive in South Africa (more than 20 species of wattles and hakeas). We want to understand how, why, and from where exactly plants were introduced. This information is of direct applied benefit to classical biological control efforts. But, by also comparing levels of genetic diversity; analysing species for admixture and hybridization; studying for evidence of local adaptation; and potentially exploring epigenetic differences; we will address one of the most exciting and topical questions in biology: how quickly can species evolve under new selection pressures? In the second component we will extend the analysis to include insect and fungi introduced for classical biological control. Finally, in component 3, we want to combine mathematical models and ecological studies with analyses of gene flow to understand dispersal distances and invasion pathways of major invasive alien species in South Africa. We have a quite a bit of flexibility in the projects, and expect that the students would focus on issues or groups that interested them and, after preliminary analysis, would identify additional research questions.

Requirements: Hons: excellent marks at undergraduate level * a keen interest in molecular ecology * excellent communication skills (speaking, reading, writing) in English and sound mathematical literacy * ability to work independently and take initiative * an interest of some of the main issues in conservation * ability to work within a team * willingness to work extended hours when required * knowledge of basic laboratory etiquette * willingness to travel overseas for training. MSc (in addition to the above): experience in working in a molecular lab PhD (in addition to the above): evidence of producing work published or publishable in international journals * presentations given at national and/or international meetings.

Recommendations: Experience in working with microsatellite markers * experience of working with and analysing population genetic data * experience of ecological field-work * papers published in international journals * an interest in botany, ecology and/or social history.

Closing date: We are currently looking for students to start in the 2008 academic year, but enthusiastic candidates with out-standing academic records may apply at any time of the year (except honours students who must start beginning of February).

Enquiries: Dr John Wilson, jrwilson@sun.ac.za

More information about the DST-NRFCentre for Invasion Biology can be found at http://www.sun.ac.za/cib jrwilson@sun.ac.za jrwilson@sun.ac.za

TowsonU AntDiversity

Towson University Ant Diversity of the Guiana Shield

Seeking masters-level graduate students to participate in on-going studies of ant diversity of the Guiana Shield region of South America. This project is a collaborative effort between Dr. John LaPollas lab at Towson University and the Smithsonian Institutions Ant Lab under Dr. Ted Schultz. Students would be enrolled at Towson University, and will have opportunities to interact with scientists and staff at the National Museum of Natural History in Washington, DC. The museum is only about an hours drive from the University. Projects may range from biodiversity analyses and surveys to systematics and evolutionary biology. Depending on the project there is also the possibility of fieldwork in South America. Potential students should be enthusiastic, capable of working independently and completely committed to a graduate education. Interested students should contact Dr. John LaPolla at jlapolla@towson.edu. Deadlines are: March 15 for the following Fall semester October 15 for the following Spring semester

For further information about the Towson University Biology Graduate Program see: http://wwwnew.towson.edu/biologicalsciences/-graduate_program.html John S. LaPolla, Ph.D. Assistant Professor of Biology Department of Biological Sciences Towson University 8000 York Road Towson, MD 21252-0001 phone: 410-704-3121

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

Trondheim QuantEvolutionaryGenet

PhD fellowship in quantitative evolutionary genetics/statistics

A PhD fellowship in quantitative evolutionary genetics/statistics is available at NTNU. Depending on qualifications and interests of prospective students, the fellowship is suitable for candidates seeking a PhD in either mathematics (statistics/biomodelling) or in biology. The fellowship is for up to four years including 25% teaching duties.

The PhD-fellow will work on a theoretical project focusing on mathematical, quantitative genetic, evolutionary models for the effects of escaped farmed salmon of genetic variability and fitness of populations of wild Atlantic salmon. The main areas of research will be multitrait evolution, intrusion histories and alternative demographic-evolutionary equilibria, parameter estimation, stochastic simulation of explicit genetic models, and models for the loss of genetic variation in the farmed-wild population system. The project, financed by the Norwegian Research Council, is a collaboration between the Dept. of Mathematical Sciences, NTNU, and researchers at NINA, Akvaforsk and Imperial Collage, London. The fellowship is also linked to the Centre for Conservation Biology, NTNU (http://-www.bio.ntnu.no/ccb/).

We are looking for candidates with a background in theoretical evolutionary genetics, statistics and mathematical modelling. In addition, some programming experience is necessary. Candidates must have completed a masters degree in statistics, biology or equivalent before employment can take place, and must fulfill the requirements for doctoral studies at NTNU, see http:/-/www.ime.ntnu.no/english/research/phd Further inquiries about the position may be directed to Associate Professor Jarle Tufto, jarle.tufto@math.ntnu.no

PhD fellows are placed in salary code 1017, which currently corresponds to a yearly gross income of NOK 325 600 (pay scale level 43). From this 2 % will be deducted for mandatory membership in the National Pension Fund.

The appointment will be made in accordance with current regulations with supplementary rules for research fellowship appointments in universities and polytechnics. Applicants must agree to participate in organized doctoral study programs within the period of the appointment. The successful applicant must agree to the conditions laid down for public employees.

Candidates will be required to enroll in a PhD program within the period of employment, and must sign a contract regulating the starting date and duration of employment as well as the mandatory work.

According to Norwegian policies, the government workforce should, as closely as possible, reflect the diversity of the population at large. It is therefore a goal of NTNU, as a government institution, to have a workforce which is balanced with respect to age and gender, and to recruit persons of immigrant background. Persons of immigrant background are encouraged to apply. NTNU also wishes to increase the number of women on its workforce, and women are specifically encouraged to apply.

The application must include information about education, exams and earlier experience. Certified copies of certificates and diplomas must be enclosed. Relevant scientific works should be submitted in triplicate. Joint works will be taken into account. In cases where it is difficult to determine the applicants contribution, a short note of explanation should be supplied.

Applications should be sent to: Faculty of Information Technology, Mathematics and Electrical Engineering Norwegian University of Science and Technology (NTNU) NO-7491 Trondheim, Norway

Deadline: January 21st, 2008. Applications should be marked: IME 092/2007.

Jarle Tufto, Dept. of Mathematical Sci., NTNU, 7491 Trondheim, Norway. http://www.math.ntnu.no/~jarlet +47 73591888 (phone) / 73593524 (fax)

Jarle Tufto <jarle.tufto@math.ntnu.no>

UAkron PlantEvolution

The Plant Sciences faculty at the University of Akron are seeking M.S.- and Ph.D.-level students interested in pursuing research topics in the plant sciences. Research areas broadly encompass ecology, evolution, genetics, and cell biology, such as interspecific interactions (e.g., plant-fungal, plant-pollinator), plant systematics, plant ecology at multiple levels, and cell biology of algae.

For a list of the plant sciences faculty, please see http://www.uakron.edu/colleges/artsci/depts/biology/plantreadinggroup.ph p. Please contact the particular faculty member of interest. Depending on the research area, summer support may also be available. Application materials are available at: http://www.uakron.edu/colleges/artsci/depts/biology/ Dr. Randall J. Mitchell Integrated Biosciences Program Department of Biology The University of Akron Akron OH, 44325-3908 330-972-5122, Fax 330-972-8445 rjm2@uakron.edu www.uakron.edu/biology/mitchell "Mitchell,Randall J" <rjm2@uakron.edu>

UAlaska EvolutionaryBiology

Graduate Fellowships in Ecology and Evolution, University of Alaska

The University of Alaska (UA) will be offering up to eight 1-2 year graduate fellowships for high-quality incoming students conducting research in the general areas of biogeography,landscape & spatial genetics, plant-microbial interactions, ecology & genetics of invasive species, and the influence of species interactions on range expansions. Fellowships include a stipend of approximately $21,000/year plus health insurance and a tuition waiver. This fellowship program is part of a broader Alaska EPSCoR initiative to fund integrative science entitled "Resilience and Vulnerability in a Rapidly Changing North: The Integration of Physical, Biological and Social Processes." This program aims to fund integrative science concerning socio-ecological sustainability in the rapidly transforming northern regions.

The state of Alaska offers unparalleled beauty and untouched landscapes, as well as unique research opportunities. Research at UA includes topics such as adaptations to our extreme climate, plant-mycorrhizal biology, invasive species biology, climate change, how interactions among species influence community composition, the unique evolutionary history of organisms influenced by glacial cycles and migrations from both North America and Asia, and the interactions between ecosystems and the people living in them.

UA offers both Masters and PhD programs. Biology programs at all three UA campuses (Fairbanks, Anchorage and Juneau) offer the potential to interact closely with dedicated faculty and motivated peers. For more information on faculty and their research interests please see www.alaska.edu/epscor/bio.grad.postdoc.08-09.html To be considered for a fellowship, students should contact UA faculty member(s) to discuss potential research, apply for graduate school at the appropriate UA institution, and apply for the fellowship with this application: www.alaska.edu/epscor/awards/EPSCoR-2008-09-grad.app.doc .The project summary noted in the application is at: www.alaska.edu/epscor/AK-EPSCoR-Project-Summary.pdf . The deadline to apply to the graduate school and for these fellowships is February 1, 2008. A copy of all materials should be sent to your faculty sponsor.

Deadlines: Application to graduate school and the fellowship: February 1, 2008. Decisions will be made by late February.

Matt Olson <matt.olson@uaf.edu>

UAlaska InvasiveSpecies

Graduate Fellowships in Ecology and Evolution, University of Alaska

The University of Alaska (UA) will be offering up to eight 1 year graduate fellowships for highquality incoming students conducting research in the general areas of biogeography, landscape & spatial genetics, plant microbial interactions, ecology & genetics of invasive species, and the influence of species interactions on range expansions. Fellowships include a stipend of approximately $21,000/year plus health insurance and a tuition waiver. This fellowship program is part of a broader Alaska EPSCoR initiative to fund integrative science entitled “Resilience and Vulnerability in a Rapidly Changing North: The Integration of Physical, Biological and Social Processes.” This program aims to fund integrative science concerning socioecological sustainability in the rapidly transforming northern regions.

The state of Alaska offers unparalleled beauty and untouched landscapes, as well as unique research opportunities. Research at UA includes topics such as adaptations to our extreme climate, plantmycorrhizal biology, invasive species biology, climate change, how interactions among species influence community composition, the unique evolutionary history of organisms influenced by glacial cycles and migrations from both North America and Asia, and the interactions between ecosystems and the people living in them. UA offers both Masters and PhD programs. Biology programs at all three UA campuses (Fairbanks, Anchorage and Juneau) offer the potential to interact closely with dedicated faculty and motivated peers. For more information on faculty and their research interests please see www.alaska.edu/-epscor/bio.grad.postdoc.0809.html To be considered for a fellowship, students should contact UA faculty member(s) to discuss potential research, apply for graduate school at the appropriate UA institution, and apply for the fellowship with this application: www.alaska.edu/epscor/awards/-EPSCoRgrad.app.doc. The project summary noted in the application is at: www.alaska.edu/epscor/-AKProjectSummary.pdf. The deadline to apply to the graduate school and for these fellowships is February 1, 2008. A copy of all materials should be sent to your faculty sponsor.

Deadlines: Application to graduate school and the fellowship: February 1, 2008. Decisions will be made by late February.

Matt Olson <matt.olson@uaf.edu>

UArizona TheoPopGenet

I am actively recruiting theory-oriented students to join my group in Ecology & Evolutionary Biology at the University of Arizona to work on

1- theoretical population genetics of evolvability.

2- bioinformatics of evolvability using the yeast prion PSI as a model system of evolutionary capacitance to make and test predictions using comparative yeast genomics.

3- in silico evolution of gene regulatory networks, using resampled parameters from yeast.

More information on these research directions and on our research group is at www.eebweb.arizona.edu/-faculty/masel Our group is currently well-funded, so I anticipate being able to offer research assistantships once a student is done with their other rotations in the department.

To apply, write back both to me at masel@u.arizona and apply for a PhD following the instructions at www.eebweb.arizona.edu/grad_info/applying.htm My apologies for the lateness of this posting: the departmental deadline is officially December 8 and is almost here. I fully expect that applications that are a couple of days late will still be considered.

More mathematically inclined students can also join my research group through graduate programs in Applied Math or in Statistics rather than in EEB.

Joanna Masel

UBergen 2 FishEvolution

2 PhD positions are available in research group “Evolutionary Fisheries Ecology” (EvoFish) at the Department of Biology, University of Bergen, Norway. The positions are for 4 years, with the start preferably early in 2008. One position is for the experimentally inclined, the other one is flexible (data analyses, modelling, ...). For more information on these new positions, see http://bio.uib.no/evofish/ Best wishes, Mikko Heino

EvoFish - Evolutionary Fisheries Ecology University of Bergen Institute of Marine Research

Department of Biology Population Genetics and Ecology Box 7800, N-5020 Bergen, Norway tel. +47-55584544 http://bio.uib.no/evofish/ fax +47-55584450

“Heino, Mikko” <mikko.heino@imr.no>

UCaliforniaLosAngeles EvolutionaryBiol

Graduate Positions: UCLA Ecology & Evolutionary Biology

GRADUATE STUDENT POSITIONS IN ECOLOGY & EVOLUTIONARY BIOLOGY University of California Los Angeles Department of Ecology & Evolutionary Biology

The graduate program in Ecology and Evolutionary Biology at UCLA invites applications from prospective Ph.D. and Masters students. Graduate students in our department conduct research all over the world on a wide range of organisms and have full access to the outstanding facilities and resources that the University of California offers. Generous 5-year support packages are provided to all incoming PhD students.

Areas of specialization within the department include behavioral ecology, conservation biology, ecology, evolutionary biology, marine biology, paleobiology, plant biology, physiological ecology, and tropical biology.

Our department includes 25 regular faculty with a broad range of research interests and expertise:

Priyanga Amarasekare Daniel Blumstein Clifford Brunk Donald Buth Peggy Fong Arthur Gibson Malcolm Gordon Patricia Gowaty Greg Grether Stephen Hubbell Henry Hespenheide David Jacobs Glen MacDonald Peter Narins Peter Nonacs John Novembre Philip Rundel Lawren Sack Rebecca Shipe Thomas Smith Victoria Sork Charles Taylor Blaire Van Valkenburgh Robert Wayne Cheryl Ann Zimmer Richard Zimmer

For a complete list of faculty and their research interests, see our website at http://www.eeb.ucla.edu/-faculty.php The official application deadline for fall 2008 admission is Dec 15, 2008, but applications received by Dec 31, 2007 will still be given full consideration. To apply, go to: http://www.eeb.ucla.edu/-grad_onlineappl.php –

Dr. Gregory F. Grether Associate Professor and Vice Chair of Graduate Studies University of California Department of Ecology and Evolutionary Biology 621 Charles E. Young Drive South Los Angeles, CA 90095-1606 USA

(310) 794-9769 (310) 206-3987 or 9184 (fax)

Website: http://www.eeb.ucla.edu/Faculty/Grether/-research.htm Greg Grether <ggrether@ucla.edu>

UFZ Halle 2 PlantEvolutionaryEcol

TWO PHD POSITIONS IN PLANT EVOLUTIONARY ECOLOGY

are available at the Helmholtz Centre for Environmental Research - UFZ, Department of Community Ecology, in Halle, Germany, starting in March 2008.

The two students will be involved in innovative research on the evolutionary consequences of environmental change, carried out within the framework of the Biodiversity Exploratories (www.biodiversity-exploratories.de). They will study the impact of landuse on the genetics & evolution of grassland plants in two complementary projects:

STUDENT 1 will mainly work in the field of population genetics. S/he will use molecular markers to study the relationship between species diversity and genetic diversity, and to test the hypothesis that this relationship depends on a balance between gene flow/drift and colonisation/extinction processes. The student will also carry out pollination experiments in the field. (Contact: Dr. Walter Durka, walter.durka@ufz.de)

STUDENT 2 will work in the field of quantitative genetics. S/he will use a combination of field studies and common garden experiments to examine how land use affects quantitative genetic diversity of plant traits, their heritability, and the strength and direction of natural selection acting upon them. (Contacts: Dr. Harald Auge, harald.auge@ufz.de and Dr. Oliver Bossdorf, oliver.bossdorf@ufz.de)

Both projects will be done on the same set of grassland species. The two PhD students will closely interact. The Biodiversity Exploratories are a large collaborative ecological research initiative, funded by the German Science Foundation, that will allow the students to get in contact with many other excellent ecologists.

We are looking for ambitious students with a keen interest in ecology and evolution. They must have a University degree (MSc or similar) and a driving licence, and they should be fluent in English. Previous experience in population genetics (Student 1), ecological experiments and statistics (Student 2) is a plus but not a requirement. Part of the work will be carried out in the beautiful landscapes of the three Exploratories sites (Schwäbische Alb, Hainich, Schorfheide) where the students must be able to conduct independent and thorough field work.

The positions are for 3 years. They are subject to the final funding decision by the DFG. The primary place of work will be Halle. Salary will be according to the civil service level TvöD-O 13/2. The PhD students will have the opportunity to participate in the newly established Graduate School HIGRADE (http://www.ufz.de/index.php?en=11429). Women are explicitly encouraged to apply to increase their share in science and research.

The Helmholtz Centre for Environmental Research – UFZ (http://www.ufz.de) is the largest public research centre in Germany entirely devoted to the study of environmental problems, with a particular strength in ecological sciences. Halle is a medium-sized city 150 km SW of Berlin with a rich cultural life and a low cost of living.

Please send a short application by email to Walter Durka or Harald Auge, and your complete application (cover letter, curriculum vitae, references) under code 136/2007 to the Personnel department of the Helmholtz Centre for Environmental Research, PO Box 500136, D-04318 Leipzig, Germany, or by email to martin.schroeder@ufz.de. Closing date for applications is 31.01.2008.

The job offer can also be found here: http://www.ufz.de/index.php?en=11426 . Oliver Bossdorf <oliver.bossdorf@ufz.de>

– Dr. Oliver Bossdorf Department of Community Ecology Helmholtz Centre for Environmental Research - UFZ Theodor-Lieser-Str. 4 D-06120 Halle, Germany Phone +49 345 5585-305 (Fax -329) oliver.bossdorf@ufz.de http://www.ufz.de/index.php?en=815 Oliver Bossdorf <oliver.bossdorf@ufz.de>

UGeorgia InvasiveSpecies

PHD STUDENT FELLOWSHIPS ECOLOGICAL GENETICS OF INVASIVE SPECIES

UNIVERSITY OF GEORGIA

Graduate Student Fellowships are available starting in Fall 2008 to study the ecological genetics of invasive species, including plant pathogens. Fellowships offer a highly competitive stipend as well as funds for research and travel.

The University of Georgia has received a Partnerships for International Research and Education (PIRE) grant from the National Science Foundation to support research on the genetics and ecology of invasive plant and pathogen species exchanged between the southeastern US and China, Taiwan and Hong Kong. Successful applicants will develop research projects that will study the population genetics, ecology and/or demography of invasive species that are native to the southeastern US and to China. A significant proportion of each student's research project must be conducted in China in collaboration with Chinese research scientists. Students will receive training in Chinese language and culture as well as appropriate biology courses.

Students can work with any senior personnel on the UGA-PIRE program (see list below and at http://www.genetics.uga.edu/pire/people_senior_US.html). Students should contact a prospective major adviser directly and apply through that department. For additional information concerning the application process, interested students should refer to our website (http://www.genetics.uga.edu/pire/).

Questions? Contact Dr. Rodney Mauricio, UGA-PIRE Program Director, via email (mauricio@uga.edu).

Current List of Senior Personnel on the UGA PIRE:

Michael Arnold (Department of Genetics, University of Georgia) Jeff Bennetzen (Department of Genetics, University of Georgia) John Burke (Department of Plant Biology, University of Georgia) Donald Champagne (Department of Entomology, University of Georgia) Shu-Mei Chang (Department of Plant Biology, University of Georgia) G. Keith Douce (Department of Entomology, University of Georgia, Tifton) John Drake (Odum School of Ecology, University of Georgia) Qinfeng Guo (Research Ecologist, USDA-Southern Research Station) James Hamrick (Department of Plant Biology, University of Georgia) Paul Hendrix (Professor of Ecology, University of Georgia) Lissa Leege (Department of Biology, Georgia Southern University) John Maerz (Department of Forestry and Natural Resources, University of Georgia) Rodney Mauricio (Department of Genetics, University of Georgia) Richard Meagher (Department of Genetics, University of Georgia) Karin Myhre (Department of Comparative Literature, University of Georgia) Andrew Paterson (Departments of Crop and Soil Sciences, Plant Biology, and Genetics, University of Georgia) Harald Scherm (Department of Plant Pathology, University of Georgia) William Vencill (Department of Crop and Soil Sciences, University of Georgia) Ronald Walcott (Department of Plant Pathology, University of Georgia) John Wares (Assistant Professor of Genetics, University of Georgia) Susan Wessler (Department of Plant Biology, University of Georgia) Lorne Wolfe (Department of Biology, Georgia Southern University)

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Rodney Mauricio, Ph.D. Department of Genetics Phone: (706) 542-1417 University of Georgia FAX: (706) 542-3910 Athens, GA 30602-7223 e-mail: mauricio@uga.edu

Lab Web Page: http://www.genetics.uga.edu/mauriciolab PIRE Grant Web Page: http://www.genetics.uga.edu/pire Evolution at UGA: http://www.genetics.uga.edu/evolution mauricio@uga.edu

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UHedmark Norway AppliedEvolution

Call for three PhD candidates to work with an international network

Our research group is involved in an international collaboration. As part of this collaborative network, three 100% positions as a PhD student in applied evolution are available at Hedmark University College, Faculty of Forestry and Wildlife Management at Evenstad in Norway from April 1.2008 to March 31.2011. We accept applications from any qualified person. Whoever is appointed will be based at our Faculty at Evenstad in Norway, but will be formally tied to a university in our team that is accredited to give PhDs (e.g., Oslo, Trondheim).

The position is attached to the scientific project “Extinction mechanisms in small populations: Linking theory, experiments and observational studies in a comparative setting”. The project is financed by the Research Council of Norway and Hedmark University College. In the project Hedmark University College collaborates with scientists from the universities in Oslo (Nils Chr. Stenseth), Trondheim (Bernt-Erik Sï¿½ther), Tromsï¿½ (Rolf A. Ims), Paris (Jean-Franï¿½ois Le Galliard), Jyvï¿½skylï¿½ (Hannu Ylï¿½nen), London (E-J Milner Gulland) and Aberdeen (Xavier Lambin).

The project aims at linking population biological theory to applied evolutionary questions of population extinction using experimental and observational studies of several small rodent populations. This comparative approach between experimental and observational studies, between species varying in ways that may essentially affect population dynamics, and between different localities will contribute fundamentally to generalize our understanding of the processes underlying extinction processes. In total we will appoint 3 PhD-students who will work as a team in this project. The main focus for each PhD student will be: 1) Studies on experimental populations; 2) Studies on natural populations; and 3) Population viability modeling.

Application deadline 10 december 2007.

http://jf.legalliard.free.fr/docs/PhDNorway.pdf Questions about the position or work environment can be directed to Harry P. Andreassen, tlf. +47 62 43 08 52 / +47 92 83 12 02, or e-mail: harry.andreassen@hihm.no. Applications should be made to Hedmark University College. The application and CV should be marked with the reference number (see below) and submitted electronically on the college website: www.hihm.no/stillingledig, or on e-mail directly to harry.andreassen@hihm.no.

– Dr. Jean-Franï¿½ois Le Galliard

CNRS - UMR 7625 Fonctionnement et ï¿½volution des systemes ï¿½cologiques Universitï¿½ Pierre et Marie Curie 7 Quai St Bernard 75005 Paris France

Office : +33.1.44.27.26.68 Fax : +33.1 44 27.35.16 http://jf.legalliard.free.fr/ galliard@biologie.ens.fr

UIllinois 2 HymenopteraSystematics

2 Graduate Research Assistantships Available ï¿½ Parasitoid Hymenoptera Systematics, University of Illinois

Two graduate student research assistantships are available in the Department of Entomology at the University of Illinois, Urbana-Champaign. Each of the assistantships is associated with NSF-funded research on braconid parasitoid wasps in the laboratory of Dr. James Whitfield (http://www.life.uiuc.edu/whitfield). Successful candidates will be expected to apply for admission to the Department of Entomology (information on admission can be found on the Departmentï¿½s website: http://www.life.uiuc.edu/entomology/index.html). The Department of Entomology has recently been ranked #1 nationally among Entomology graduate programs, and the students will join a leading laboratory in insect molecular systematics with close ties to other top insect systematics labs both on campus and at the Illinois Natural History Survey.

Molecular systematics of the hyperdiverse genus /Heterospilus/

Funded by NSF DEB 0717365, this 4-year project encompasses a multigene molecular phylogeny of the speciose braconid wasp genus /Heterospilus/. Under the direction of Dr. Whitfield, the student will extract, amplify and sequence each of 3 genes from roughly 200 species of wasp, and conduct molecular phylogenetic analyses to test monophyly of the genus worldwide, and to explore relationships within the genus, especially for the neotropical fauna. Parallel to this work, collaborator Paul Marsh (http://www.life.uiuc.edu/whitfield/Paul_Marsh.html) and a postdoctoral associate (position currently being advertised) will conduct a taxonomic revision of the genus, and produce online interactive identification keys to the 200+ species in Costa Rica. Some experience in insect systematics, molecular phylogenetics and/or phylogenetic analysis methods is highly desirable for the graduate student part of the project. The position is available as soon as Summer 2008. Application should be at the Ph. D. level.

Braconid caterpillar parasitoids in the eastern Andes of Ecuador

Funded by NSF DEB 0717402, this long-term project (http://www.tulane.edu/ ˜ ldyer/lsacat/ecuador/index.htm) seeks to characterize the fauna of caterpillars and their parasitoids in montane wet forest on the eastern slope of the Andes at Yanayacu Biological Station (http://www.yanayacu.org/). The graduate student will help train parataxonomists in Ecuador, help sort and identify parasitoids reared from the caterpillars, and conduct taxonomic research on a group of braconid parasitoids that are recovered by the project. Considerable interaction with other collaborating taxonomists and ecologists is expected. Strong interest in and some experience with insect descriptive taxonomy and tropical biology are highly desirable. Knowledge of conversational Spanish desirable but not essential. Fieldwork in montane Ecuador can be physically demanding. This position is available as soon as January 2008. Current funding is for two years but renewal expected. Applications at either the M. S. or Ph. D. levels accepted.

Interested candidates should submit the following (preferably by email) to Dr. James Whitfield (jwhitfie@life.uiuc.edu):

1) A letter stating why you want to apply for the position, and why you think you would be the best person for this research. Please also include a broader perspective on your career and graduate school objectives.

2) A current curriculum vitae, including any previous research projects you have been involved with, honors, awards, publications and presentations, and your overall GPA.

3) A list of relevant field, laboratory and analytical techniques with which you have experience.

4) Names and contact information (email, phone, address) for at least 3 people who can supply reference letters.

We will begin assessing applications during late December, and will notify top candidates shortly thereafter, in time to complete applications to the department graduate program.

jwhitfie@life.uiuc.edu

UJyvasky MimicryEvolution

Open PhD position

Centre of Excellence in Evolutionary Research, Department of Biological and Environmental Sciences at the

University of Jyväskylä invites applications for a doctoral student position in the field of evolution of warning signals and mimicry. The planned work includes both field and laboratory work on three trophic level interactions between plants, insects and their enemies. The model species is an Arctiid moth Parasemia plantaginis. We are looking for an individual with a master's degree or equivalent, who is highly self-motivated and can work both independently and in a team. A successful candidate for this position will have background in ecology and evolutionary ecology. The work will be conducted in collaboration with chemists, chemical ecologists and geneticists. Thus, we encourage candidates with good communication skills to apply. The assignment will begin in the early 2008 (start date is flexible) and end in the end of 2011. Experience on population genetics and quantitative genetics is considered an asset! The working language will be English.

An overview of our past and current research can be found at http://users.jyu.fi/˜mappes/aposematism/ The salary will start on level 2 of the demands level chart for teaching and research personnel in the salary system of Finnish universities, and the job specific component of the salary will thus be EUR 1 678 per month. In addition, the appointee will be paid a salary component based on personal work performance.

The application should include: 1) A complete CV 2) Publication list (if available) 3) A scanned academic transcript (list of grades in university courses) 4) A statement of research interests and motivation for applying this position not exceeding two pages 5) Two references

Applications should be addressed to Professor Johanna Mappes mappes@bytl.jyu.fi by e-mail to arrive no later than 31th December 2007. More information about Finland, University of Jyväskylä, and Department of Biological and Environmental Sciences can be found at http://www.jkl.fi/lang/ (city) and http://www.jyu.fi/ (university).

Johanna Mappes <mappes@bytl.jyu.fi>

UKentucky PopulationGenetics

I am seeking graduate students at either the M.S or Ph.D. level to join my new lab at the University of Kentucky starting in the Fall of 2008. My research draws on the disciplines of population genetics, phylogenetics, and phylogeography to study the evolution of geographic genetic variation and the processes of speciation. This research has developed around two main systems: (1) North American salamanders, with a focus on the speciation and diversification of ambystomatid tiger salamanders, and (2) Madagascar's mammals, with a focus on speciation in lemurs. While these are spectacular ad cool systems to study, students in my lab will have the freedom to develop research projects of their choosing, provided the research fits within the general scope of the lab. Funding for students will be available through a combination of research and teaching assistantships.

Interested students should contact me via email (dww8@duke.edu) or phone (919-613-8727).

Dave Weisrock

Department of Biology Duke University Box 90338 Durham, NC 27708 Ph: 919-613-8727

dww8@duke.edu

UKonstanz FishEvolution

PhD thesis in MHC evolution and parasite-host interaction

A Ph.D. studentship (E13TV-L/2) in fish ecology and evolution is available from January 2008 in the group of Jasminca Behrmann-Godel at the Limnological Institute of the University of Konstanz.

The thesis will focus on parasite-host interactions and investigate local and seasonal differences in the parasite community of Eurasian perch and ruffe and its relation to individual immune Parameters (MHC alleles). The planned work includes field and laboratory work such as catch and preparation of fish for parasite assessment and molecular genetics work (fragment analysis and sequencing). The thesis will be financed within the SFB 454 (BLittoral of Lake Constance (http://www.uni-konstanz.de/sfb454/) and cooperation with other working groups within the SFB 454 is planned and desired.

The lab of Jasminca Behrmann-Godel studies ecology and evolution using fish as model species. Ongoing projects range from behavioural experiments on MHC triggered mate choice, kin and population recognition to molecular evolution of MHC genes in fish and phylogeography of the Lake Constance region. A description of our research can be found at http://www.uni-konstanz.de/fish-ecology/ A successful candidate will have a strong background in evolutionary biology. Experience in parasitology is advantageous. We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and can work independently.

Closing date for applications: December 20, 2007

Curriculum Vitae, a letter of application highlighting recent relevant experience, and the names, addresses and e-mail addresses of at least two referees should be sent as a single pdf file to:

Contact address: Jasminca.Behrmann@uni-konstanz.de

Jasminca Behrmann-Godel Limnological Institute University of Konstanz 78457 Konstanz Germany

Jasminca Behrmann-Godel <Jasminca.Behrmann@uni-konstanz.de>

ULaval FishMicrobeCoevolution

I am currently seeking a Ph.D student to characterize the evolution of the relationship between farmed fish (Salvelinus fontinalis, Salmonidae) and their associated microbial community (skin, water). This research will be performed in the Department of Biology at Laval University (Québec, Canada).

This research will focus on 1) the impact of opportunistic diseases on the microbial diversity pattern. 2) fish-microbes interactions, and 3) Identify and test potential probiotics. The student will use molecular and experimental techniques to address fundamental ecological and evolutionary questions about the relationship between microbial communities and fish.

Prior laboratory experience is required, and skills in microbiology and standard techniques of molecular biology are preferred. Applicants should have a broad biological background, with coursework in the fields of molecular biology, genetics, ecology, and evolution.

The position is for 3 years, starting in January 2008.

Feel free to contact me with any inquiries at nicolas.derome@bio.ulaval.ca <mailto:nicolas.derome@bio.ulaval.ca>

Interested students should send me by email a cv, summary of research experience and interests, contact details of two referees.

Nicolas Derome, Professeur adjoint Chaire de recherche du Canada en Génomique et Conservation des Ressources Aquatiques

Département de Biologie Pavillon Charles-Eugène Marchand Université Laval Quebec QC G1V0A6 Canada

Téléphone : 1 (418) 656-7726

Télécopie : 1 (418) 656-2043 Courriel : nicolas.derome@bio.ulaval.ca

Internet : http://www.bio.ulaval.ca/no_cache/-departement/professeurs/fiche_des_professeurs/-professeur/11/240/ http://www2.bio.ulaval.ca/-louisbernatchez/laboderome_fr.htm

Nicolas Derome <Nicolas.Derome@bio.ulaval.ca>

UMassBoston MarineMolecEvol

A Graduate Fellowship (Ph.D.) is available in the lab of Dr. Ron Etter at the University of Massachusetts in Boston in the area of molecular evolution in deep-sea organisms starting in September 2008. I am looking for a highly motivated graduate student to work on a NSF funded project exploring evolution in the deep sea. We are using molecular genetic tools to address questions on a) the geographic and bathymetric scales of population differentiation and speciation, b) the nature and scale of isolating barriers, c) the role of evolution in creating geographic and bathymetric variation in biodiversity and d) the colonization and radiations within the deep Atlantic. The fellowship has an annual stipend of $20,000 for the duration of the project.

Candidates should have a strong undergraduate background in biology, with course work in molecular genetics and evolutionary biology. Prior research experience with molecular techniques is desirable.

Information on our graduate program can be found at http://www.bio.umb.edu/ More information on work in my lab can be found at http://www.bio.umb.edu/-facstaff/faculty_Etter.html If you are interested in pursuing a PhD addressing questions along these lines please contact me at ron.etter@umb.edu or apply to our graduate program.

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Ron J. Etter Professor Biology Department University of Massachusetts 100 Morrissey Blvd Boston, MA 02125 Voice 617-287-6613 FAX 617-287-6650 email ron.etter@umb.edu

UMiami EvolutionaryBiology

GRADUATE OPPORTUNITIES IN BIOLOGY

The Department of Biology at the University of Miami (UM) recently welcomed seven new research faculty and two new researchers as core facility managers. Here we announce the availability of support for new graduate students starting Fall 2008. The University of Miami is southern Floridas gateway to the tropics and Latin America. Our diverse international community, with research foci ranging from Evolution and Ecology through to Development and Neuroscience, interacts with both the medical and marine campuses and exploits resources such as the Everglades, the Fairchild Botanic Garden and the Organization for Tropical Studies.

Graduate students admitted to the PhD program are guaranteed stipend support and tuition waiver.

The following faculty are seeking graduate students:

Akira Chiba V The Chiba lab studies the cell biology of neurons. The lab uses the fruit fly nervous system as a model and employs multi-disciplinary approaches including molecular imaging and transgenic technologies. See: http://www.chibalab.org Julia Dallman - The Dallman lab uses zebrafish as a model system for studying the development of neuronal circuits that underlie swimming. Recently isolated zebrafish mutants present experimental systems to understand how alterations in single genes can disrupt behavior. See: http://www.bio.miami.edu/Fac/Dallman.html Michael S. Gaines V The Gaines lab applies population genetic and molecular approaches to conservation issues such as the effects of habitat fragmentation on small mammals. See: http://www.bio.miami.edu/Fac/Gaines.html Carol C. Horvitz V The Horvitz lab studies population dynamics of tropical plants in variable environments, working at the interface of empirical and theoretical ecology. New mathematical tools are developed and applied to issues concerning the evolutionary ecology of invasive species, plant/animal interactions, and lifespan. See: http://www.bio.miami.edu/Fac/Horvitz.html David P. Janos V The Janos lab investigates mycorrhizal symbioses including the physiological, ecological, and evolutionary costs versus benefits of mycorrhizas of different types; the effects of mycorrhizas on plant competition; and mycorrhizas as determinants of plant community composition. See: http://www.bio.miami.edu/Fac/Janos.html John Lu - The Lu lab is interested in sensory neurobiology with a primary focus on comparative studies of the auditory systems of vertebrates. Previous research involved study of the fish auditory system from the ear to the CNS at cellular, systems, and organismal levels using anatomical, neurophysiological, and behavioral approaches. Current research emphasizes development of auditory function and toxic effects on auditory development using the zebrafish as a model system. See http://www.bio.miami.edu/Fac/Lu.html Matthew D. Potts V The Potts lab investigates the dynamics of coupled human-natural systems for the purpose of developing optimal spatial management regimes. Focal study areas include the sustainable management of tropical forests and the control of vector-borne diseases in urban environments. See: http://www.matthewdpotts.com William A. Searcy V The Searcy lab works on all aspects of avian behavioral ecology, and especially on animal communication using bird song as a model system. See://www.bio.miami.edu/searcylab/index.htm Isaac Skromne V The Skromne lab studies the developmental and evolutionary basis of segment formation and patterning of the vertebrate central nervous system and paraxial mesoderm (spinal column), using the zebrafish and chicken embryo as model organisms. See: http://www.bio.miami.edu/Fac/Skromne.html Kathleen Sullivan Sealey - The Sullivan Sealey lab focuses on the processes that control movement of fresh water, nutrients and other pollutants across the land-sea interface in small tropical island systems. Research includes modeling of fresh water and pollutant flux with the resulting alterations in fish habitat availability and fish species assemblages. See: http://www.bio.miami.edu/Fac/Sealey.html Kathryn W. Tosney - The Tosney lab combines molecular interventions with time lapse digital recordings in cell culture to discover mechanisms crucial to axonal growth and guidance. Current studies examine the regulation and functions of a new cell organelle we recently discovered. See:

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UMontana ConservationGenetics

Master's Degree Project in Wildlife Disease Ecology and Conservation Genetics

Division of Biological Sciences, University of Montana, Missoula, MT

Seeking a Master's Degree Student: A Master's degree project is available on a new NSF-funded project at the interface of disease ecology, population genetics, and ecological immunology. The study focuses on immunologically-mediated interactions between gastrointestinal nematodes and bovine tuberculosis in African buffalo. Specifically, the project will use a combination of field and captive studies, mathematical modeling, and comparative analysis to examine individual-level patterns of co-infection, population dynamics of both parasites, and implications of co-infection for cross-population and cross-species patterns of disease. The Master's student would be isolating DNA and sequencing disease related genes (e.g., MHC) from African buffalo. The preferred applicant will have expertise conducting PCR, primer design and DNA sequencing, as well excellent communication, writing, and organizational skills. The student should be enthusiastic about wildlife genetics, work well independently, and be fully dedicated to graduate school. There is some possibility of visiting the study site in Africa and a collaborating laboratory in Portugal. The position would begin September 1, 2008, and requires application to the graduate school program in Organismal Biology and Ecology (OBE) in the Division of Biological Sciences at the University of Montana. To apply, please contact Dr. Gordon Luikart and Dr. Vanessa Ezenwa (gordon.luikart@mso.umt.edu <mailto:gordon.luikart@mso.umt.edu>). Applications should include a letter of interest and CV. Review of applications will begin December 20, 2007 and continue until the position is filled.

gordon.luikart@mso.umt.edu

UMontana EvolutionaryGenet

Graduate Position: UMontana, Evolutionary Genetics

I have an opening for a Ph.D. student interested in research on genome divergence, adaptation, and speciation in plants, using the genus Mimulus (monkeyflowers) as a model system. The specific area of research is flexible, so this is an ideal opportunity for a motivated student seeking to develop independent research into the genetic mechanisms of evolutionary change. Active research areas in my lab include mating system evolution, hybrid incompatibilities and other species barriers, local adaptation, meiotic drive and chromosomal evolution, and pollen competition/pollen-style coevolution (for more about these projects in the Fishman Lab see http://dbs.umt.edu/research%5Flabs/-fishmanlab/). Mimulus is an emerging model system for evolutionary/ecological genetics, with tremendous biological diversity, excellent genomics resources (permanent mapping populations, genome sequence, markers, and linkage/physical maps), and an interactive community of researchers (http://openwetware . org/wiki/Mimulus_Community).

This position is part of an NSF-funded project in the lab of Lila Fishman in the Organismal Biology and Ecology Program in the Division of Biological Sciences at the University of Montana. It includes research and travel support and two years of Research Assistantship (plus Teaching Assistantships for 2-3 additional years). If interested, please reply to Lila Fishman (lila.fishman@mso.umt.edu) with a statement of interest and attached CV. The official application deadline for the OBE graduate program is Jan. 10th, but this position will remain open until filled (i.e, contact me even if you might miss the formal deadline - the admissions decisions won't be made until early February). More information on the Organismal Biology and Ecology Program at the University of Montana and the formal program application process can be found at http://dbs.umt.edu/gradprogram/-graduate_studies.htm . Lila Fishman Assistant Professor and Director of the UM Herbarium Division of Biological Sciences University of Montana Missoula, MT 59802

Phone:406-243-5166 Fax: 406-243-4184

lila.fishman@mso.umt.edu lila.fishman@mso.umt.edu

UNebraska EvolutionaryBiol

Graduate positions in Ecology, Evolution, and Behavior University of Nebraska

The Ecology, Evolution, and Behavior section of the School of Biological Sciences is seeking highly motivated students to join our graduate program. The EEB group is especially strong in the areas of theoretical ecology, behavioral ecology, life-history evolution, evolutionary physiology, and evolutionary genetics.

We offer generous graduate student support, an extremely collegial and interactive environment for doing science, excellent biotech and computational facilities, and access to the Cedar Point Biological Station. For more information about the department, see: http://www.biosci.unl.edu/ . For a listing of faculty in the Ecology, Evolution, and Behavior Graduate Group, see: http://www.biosci.unl.edu/grad/EEBGREG.shtml For a listing of faculty in the Genetics and Bioinformatics Group, see: http://www.biosci.unl.edu/grad/GeneticsGREG.shtml Interested students are encouraged to contact faculty directly with a letter of interest and CV. Deadline for applications is 15 December. For more information, see: http://www.biosci.unl.edu/grad/ProspectiveStudents.shtml Jay F. Storz School of Biological Sciences University of Nebraska Lincoln, NE 68588 Phone: 402/472-1114 E-mail: jstorz2@unl.edu

http://www.biosci.unl.edu/faculty/Storz/index.html
Jay F Storz <jstorz2@unlnotes.unl.edu>

USouthDakota SexualSelection

Graduate Research in Behavioral Evolution of Stalk-Eyed Flies

I have an opening for a Ph. D. graduate student interested in research on the performance and fitness consequences of elaborate secondary sexual characters in insects using stalk-eyed flies as a model. Stalk-eyed flies provide the ideal model system to test for costs and tradeoffs related to male ornamentation. All species in this extraordinary family display exaggerated head morphology, with eyes and antennae displaced at the end of long stalks, and interspecific variation in eye span can be more than ten-fold. Furthermore, all available evidence indicates that eye stalks are critical sexual signals used in both male-male competition and female choice. This study will examine the effects of elongated eye stalks on flight performance and survivorship of stalk-eyed flies to assess whether these effects run counter to the effects of sexual selection. The position is part of an NSF-funded CAREER project in the laboratory of John Swallow (http://www.usd.edu/~jswallow/index.html), Biology Department, University of South Dakota. Opportunities exist to develop a PhD research program that cover a variety of related issues (flight performance, flight energetics, predation avoidance) but I am particularly interested in finding someone to be involved in a series of mesocosm predation studies. Support will be a combination of Teaching and Research Assistantships. If interested please contact John Swallow (jswallow@usd.edu) Associate Professor, Department of Biology, University of South Dakota, Vermillion, SD 57069, USA. Information regarding our graduate program and the application process can be found at the following web site: http://usd.edu/biol/graduateprogram.cfm "Swallow, John G." <John.Swallow@usd.edu>

UtahStateU ConservationGenetics

Graduate Fellowships Available: Conservation Genetics

Wildland Resources Department, Utah State University, Logan, Utah

Our laboratory is seeking graduate students to participate in the following projects: 1) Genetic variation in aspen (Populus tremuloides)(MS or PhD) 2) Landscape genetic connectivity and chronic wasting disease transmission risk in mule deer populations of Utah and Colorado (MS or PhD) 3) Conservation of spotted frog (Rana luteiventris) populations in Utah (MS)

The applicant should have experience with PCR-based techniques, be highly organized and meticulous in the laboratory, have excellent communication skills, and be fully dedicated to graduate school. The student will work with a skilled laboratory team and will be affiliated with the Wildland Resources Department at Utah State University as well as with the USU Ecology Center. Preferred start date is early summer 2008 or Fall 2008.

For more information about the projects please contact: Dr. Karen Mock (karen.mock@usu.edu).

For details on the fellowship program, as well as application instructions, please see: http://www.cnr.usu.edu/files/uploads/quinney-phd_brochure%202008-2009.pdf or http://www.cnr.usu.edu/files/uploads/quinney_masters_brochure_2008-2009.pdf For additional information about the Ecology Center please see: http://www.usu.edu/ecology/ For additional information about the USU Department of Wildland Resources please see: http://www.cnr.usu.edu/wild/ prvs=karen.mock836d090@usu.edu prvs=karen.mock836d090@usu.edu

UTexasAustin CichlidFishEvolution

GRADUATE FELLOWSHIP AT THE UNIVERSITY OF TEXAS AT AUSTIN

A Graduate Fellowship is available beginning September 2008 for beginning students in the Ecology, Evolution & Behavior (EEB) graduate program at the University of Texas at Austin to conduct graduate research in the laboratory of Dr. Hans Hofmann. The Hofmann laboratory studies the neural and molecular basis of social behavior and its evolution in cichlid fishes from Lake Tanganyika, Africa. Detailed information and recent publications can be found at our website (http://cichlid.biosci.utexas.edu/). Areas of particular interest for this fellowship include, but are not limited to, the molecular basis of pairbonding and its evolution within the Ectodini, a Tanganyikan clade with at least four independent transitions from polygamy to monogamy within the past ~1 million years. This fellowship will be part of an exciting research program that integrates ecological, behavioral, neurobiological, endocrinological and genomic approaches to dissect complex behaviors. The Hofmann laboratory is located in newly renovated space and includes a 1200 sq ft state-of-the-art fish facility specifically designed for maintaining and breeding a range of cichlid species. The lab is also associated with the Institute for Cellular & Molecular Biology, the Institute for Neuroscience and the Brackenridge Field Laboratory, which offer a cutting edge research infrastructure. The University of Texas at Austin EEB program is consistently ranked among the best and offers a world-class academic environment and intellectual interactions with dozens of researchers from throughout the UT Austin community. The city of Austin and surrounding region (Texas Hill Country) is one of the most livable metropolitan areas in the US and boasts a multitude of cultural and outdoor activities.

The Graduate Fellowship aims at increasing student diversity, very broadly defined, and provides an annual stipend of US $24,000 plus health insurance and tuition allowance. Continuing funding is available through research and teaching assistantships as well as University fellowships. Interested applicants are U.S. citizens or Permanent Residents with a Bachelor's Degree in biological sciences and have an interest in approaching animal behavior and evolution with molecular biology/genomics techniques in both field and laboratory-based behavioral experiments. Interested applicants are encouraged to contact Dr. Hans Hofmann via email at hans@mail.utexas.edu as soon as possible. For information regarding the Graduate Program in Ecology, Evolution & Behavior (EEB) and admission requirements see our website (< http://www.biosci.utexas.edu/graduate/eeb/ > http://www.biosci.utexas.edu/graduate/eeb/) or contact the Graduate Coordinator, Sandy Monahan at s.monahan@mail.utexas.edu .

Michael Kidd, Ph.D. Postdoctoral Researcher Section of Integrative Biology University of Texas at Austin 1 University Station #C0930 Austin, TX 78712

Phone 512-475-7318 FAX 512-471-3878 http://hcgs.unh.edu/Staff/KiddM/Kidd%20Research-Main.html Michael Kidd <mckidd@earthlink.net>

UToronto EvolutionaryGenetics

GRADUATE STUDENT POSITIONS IN EVOLUTIONARY & ECOLOGICAL GENETICS University of Toronto, Department of Ecology & Evolutionary Biology http://www.eeb.utoronto.ca We are pleased to announce graduate student positions in EVOLUTIONARY AND ECOLOGICAL GENETICS in the newly formed Department of Ecology and Evolutionary Biology (EEB) at the University of Toronto (St. George campus). EEB is home to over 20 outstanding scientists in the fields of ecology and evolution. Research in evolutionary and ecological genetics is one of the strengths of EEB, comprised of an innovative community of faculty and students studying topical problems in population genetics, molecular evolution, quantitative genetics, experimental evolution, and comparative genomics. Faculty research uses both non-model systems and the classic model organisms, A. thaliana, C. elegans, and D. melanogaster. Recent faculty hires are currently recruiting graduate students, with positions available in the labs of:

Aneil Agrawal (http://labs.eeb.utoronto.ca/agrawal/) Belinda Chang (http://labs.eeb.utoronto.ca/chang/) Asher Cutter (http://labs.eeb.utoronto.ca/cutter/) John Stinchcombe (http://www.botany.utoronto.ca/ResearchLabs/StinchcombeLab/) Stephen Wright (http://www.eeb.utoronto.ca/people/faculty/wright)

and many others (http://www.eeb.utoronto.ca/people/faculty)

The graduate program in EEB provides training for students toward both M.Sc. and Ph.D. degrees and promotes excellence in research. The EEB department is located on the St. George campus of the University of Toronto in downtown Toronto, Ontario. Toronto is a vibrant, multicultural city on the shore of Lake Ontario, and is home to rich cultural options in the arts, music and film, ethnic cuisine, and a high quality of life.

Interested students should contact faculty with a brief cover letter and curriculum vitae indicating their academic background and research interests and file an application with the department. Additional information about faculty research programs and graduate studies, as well as application instructions, is available on the EEB website (http://www.eeb.utoronto.ca/graduate). We welcome strong applicants from any country, but particularly encourage Canadian citizens with NSERC predoctoral fellowships and US citizens with NSF predoctoral fellowships, both of which can be supported at the University of Toronto. The deadline for new applicants in EEB is January 15, 2008.

jstinchc@gmail.com

UWindsor EvolGeneticsInvadingSpecies

University of Windsor, Ontario. Great Lakes Institute for Environmental Research (GLIER)

Graduate Position V Evolutionary genetics of invading species. One MSc position is available beginning September 2008. The project involves analysis of hierarchical genetic structure of invasive tunicates at different spatial scales and aims to i) characterize spatial and temporal patterns of genetic structure during the establishment and subsequent spread of invasive tunicates; ii) identify potential sources and vectors of invasions; and iii) address taxonomic problems related to color morphospecies. Ideal candidates will have prior experience with molecular genetics techniques (e.g. DNA sequencing) but students without prior experience will be considered provided they are interested in using molecular markers to understand species invasions. Priority will be given to Canadian candidates, however exceptional international students with good work ethic and the ability to work well in a collaborative research atmosphere will be considered.

Interested students should send their CV, a brief statement of research interest, and a list of 3 references to:

Dr. Melania Cristescu Great Lakes Institute for Environmental Research University of Windsor Windsor, Ontario Canada N9B3P4

Phone: 519-253-3000 x 3763 Email: mcris@uwindsor.ca

Melania E. Cristescu Assistant Professor University of Windsor Great Lakes Institute for Environmental Research 401 Sunset Ave Windsor Ontario Canada N9B 3P4

Phone: (519) 253-3000 Ext. 3763 FAX: (519) 971-3616 E-Mail: mcris@uwindsor.ca http://cronus.uwindsor.ca/users/m/mcris/main.nsf mcris@uwindsor.ca

UZurich EvolutionaryBiolHybrids

PHD-POSITION IN EVOLUTIONARY BIOLOGY Zoological Institute, Univ. Zurich, Switzerland

The successful candidate is expected to participate in (and further develop) a research project on the

Evolutionary Potential of Pure Hybrid Frog Populations (Rana esculenta)

The focus will be on demography, phylogeny, gene-environment interactions larval development and cytological mechanisms of gametogenesis. The project will combine comparative field studies (mostly to be conducted in south-eastern Europe), molecular and cytological analyses in the lab and experiments on larval development under semi-natural conditions.

Applicants should have some knowledge in at least one of the following areas: population ecology, behavioural ecology, evolution or population genetics. Familiarity with field work on amphibians, microsatellite analysis, cytological techniques, experimental design and/or statistics will be advantageous. Possession of a driving licence and good knowledge of the English language are mandatory.

The position is available from March 1, 2008 for a period of three years. Salaries are paid according to Kanton Zurich standards. If you are interested, please send your application with curriculum vitae, list of publications, summary of research interests and two letters of reference by January 15, 2008 to

Prof. Dr. Heinz-Ulrich Reyer Zoological Institute, Univ. of Zurich Winterthurerstrasse 190, CH-8057

Zurich, Switzerland Tel: ++41 (1) 635 49 80 Fax: ++41 (1) 635 68 21 e-mail: uli.reyer@zool.uzh.ch

Detailed information on the Zoological Institute, present research projects in ecology and publications is available under: www.zool.uzh.ch/Research/-Ecology_en.html Uli Reyer <uli.reyer@zool.uzh.ch>

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AustralianNatlU ForestPopulationGenetics

Please Direct enquiries to Bill Foley:

Australian National University - College of Science School of Botany and Zoology Research Fellow, Plant Molecular Biologist (Ecological Interactions) Fixed Term - 2 years Academic Level A or B

Salary Package: $61,179 - $81,135 pa plus 17% super

Reference No.: FS4475

We are seeking an enthusiastic plant molecular biologist to work on the genetic basis of herbivore defence in Australian Myrtaceae. The project uses a combination of approaches in molecular and population genetics together with chemical ecology, to understand variation in ecologically significant traits in forest trees. The successful applicant will have a strong record in plant molecular biology and an ability to apply these skills to ecological questions.

Further particulars, including selection criteria, are available from: Madeleine Haag, phone 02 6125 5866, e-mail madeleine.haag@anu.edu.au or http://info.anu.edu.au/hr/Jobs/Academic_Positions/-_PDF/FS4475.pdf . If you wish to discuss the position after obtaining the selection documentation, please contact: Prof. William Foley, phone 02 6125 2535, e-mail william.foley@anu.edu.au.

Information for applicants http://info.anu.edu.au/hr/-Jobs/How_To_Apply/index.asp . Job Application Cover sheet - http://info.anu.edu.au/policies/_DHR/-Forms/HR86.asp . Closing Date: 21 December 2007

Rose Andrew Postdoctoral Fellow Department of Botany University of British Columbia 3529-6270 University Blvd Vancouver, B.C. V6T 1Z4 Canada

Phone: 604-827-4425 Fax: 604-822-6089 roseandr@interchange.ubc.ca

roselorien@gmail.com

DalhousieU MicrobialMolEvol

DALHOUSIE UNIVERSITY

DEPARTMENT OF BIOCHEMISTRY & MOLECULAR BIOLOGY

ASSISTANT PROFESSOR POSITION

The Department of Biochemistry & Molecular Biology invites applications for a probationary tenure-track position at the rank of Assistant Professor to begin July 1, 2008. The ideal candidate will have expertise in molecular biology or biochemistry with a research emphasis on microbial molecular evolution and/or comparative genomics. Specific research areas of interest include, but are not limited to: molecular biology and evolution of organelles, microbial genome structure and function, biochemical/cellular diversity in prokaryotes and eukaryotes. The candidate must have a research track record that will be highly competitive in attracting external research funding. The successful candidate will join an internationally recognized group of researchers at Dalhousie working on microbial molecular evolution, comparative genomics, bioinformatics and biodiversity. The candidate will have the opportunity to mentor undergraduate honors and graduate students as well as postdoctoral fellows, and be expected to teach undergraduate and graduate courses in molecular biology/biochemistry consistent with her/his background and interest.

The ability to collaborate across disciplines is encouraged. The Department is closely affiliated with the recently established Program in Integrated Microbial Biodiversity (IMB) of the Canadian Institute for Advanced Research (CIFAR) and with a newly created interdisciplinary Centre in Comparative Genomics and Evolutionary Bioinformatics (CGEB) at Dalhousie University. The successful applicant will be nominated as a Scholar in the CIFAR IMB program (information on this program can be found at www.ciar.ca). More details about the research activities of the Department of Biochemistry and Molecular Biology and the Faculty of Medicine can be found on our web sites: www.biochem.dal.ca and www.medicine.dal.ca . Applicants must have a Ph.D., at least 2 years of postdoctoral experience and a strong publication record. Please submit curriculum vitae, reprints of several recent publications, one- to two-page statements outlining teaching and research plans, and arrange for three references to be sent under separate cover to:

Dr. D.M. Byers Head, Department of Biochemistry & Molecular Biology Faculty of Medicine Sir Charles Tupper Medical Building Dalhousie University Halifax, NS B3H 1X5.

Closing date for receipt of applications is March 31, 2008. The Academic Planning and Appointments Committee will commence reviewing applications in March.

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority.

Dalhousie University is an Employment Equity/Affirmative Action employer. The University encourages applications from qualified Aboriginal people, persons with a disability, racially visible persons and women.

– Andrew J. Roger Associate Professor, Fellow CIAR Program in Evolutionary Biology Dept. of Biochemistry and Molecular Biology, Dalhousie University Rm 8B1, 5850 College St., Halifax, N.S. B3H 1X5 Canada tel:902-494-2620 (office) tel:902-494-2881 (lab) fax:902-494-1355 lab webpage: http://rogerlab.biochem.dal.ca Andrew.Roger@Dal.Ca

Halle Germany BeeEvolution

*** 2 PhD POSITIONS: IMMUNITY / DISEASE RESISTANCE OF BUMBLEBEES ***

Both positions (provided funding) are available in the Molecular Ecology Research Group of the Institute for Biology at the Martin-Luther-University Halle-Wittenberg, in Halle (Saale), Germany (http://www2.biologie.uni-halle.de/zool/mol_ecol/index.html).

Project will be in one or more of the following areas:

Position 1: gene expression studies related to parasite infection in bumblebees

Position 2: QTL mapping of disease / parasite resistance genes in bumblebees

It is expected, that both candidates are closely cooperating with each other as well as with experimental groups of Profs. R.F.A. Moritz (Molecular Ecology, Halle) and P. Schmid- Hempel (Experimental Ecology, Zurich).

The candidate must have a Masters degree or equivalent in the relevant field and should be able to work well both as a member of the group and individually. Prior laboratory experience is required, and skills in handling and maintaining social insect colonies as well as statistical analyses are preferred. Applicants should have a broad biological background, with special emphasis in the fields of evolution, ecology and genetics. Although English is the working language in the lab some basic knowledge of German might be helpful.

To apply, please send an application letter including your research interests, a c.v., and contact details for two or three references by e-mail to lattorff(at)zoologie.uni-halle.de. Please also contact this address if you require further information regarding the research group and/or project.

Both positions will be open until filled, but for full consideration, apply by January 31, 2008. Positions are for three years according to the national TVL salary scale (about 1400 EUR apx 2000 USD). Preferred starting date: early 2008.

Halle hosts many excellent scientific institutions such as Helmholtz Centre for Environmetal Research (UFZ), 3 Max-Planck Institutes and the Leibnitz Institute for Plant Biochemistry (IPB). Halle is the largest city of Saxony-Anhalt with a good infrastructure, hosting two universities. Due to the high number of students Halle has a rich choice of social, cultural and sporting facilities (see www.halle.de).

Dr. Michael Lattorff Institute of Biology, Molecular Ecology Martin-Luther-University Halle-Wittenberg Hoher Weg 4 06099 Halle (Saale) Germany phone. +49-345-5526389 fax. +49-345-5527264 email. lattorff(at)zoologie.uni-halle.de www. http://www.biologie.uni-halle.de/zool/mol_ecol/ lattorff@zoologie.uni-halle.de lattorff@zoologie.uni-halle.de

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Inra France 75 EvolutionaryBiology 11 Postdocs

Dear Sir ,

We are pleased to inform you that INRA is recruiting 75 Research Scientists. INRA is a state-funded organisation. Permanent personnel are civil servants recruited through open competitions.

For these open competitions, the Institute is recruiting in several fields of research like genomic, genetics, nutrition, human and animal food, microbiology, virology, behavioural sciences, ecology, agronomy, biotechnical sciences, modelling, farming systems and breeding, statistics, human and social sciences???

Applications will be available from December 21, 2007 to February 28, 2008.

All useful information to apply (jobs??? profiles, guides for applicants) will be available on Inra???s Web site from December 21, 2007: www.international.inra.fr (see ???Join us???)

Direct link to Web page: http://www.international.inra.fr/join_us/positions/research_scientist_positions/1st_and_2nd_class_junior_sc ientist_open_competitions

For further details, please e-mail to: concours_chercheurs@paris.inra.fr _ _ _ _ _

INRA is recruiting as well 11 post-doctoral fellows.

These young researchers are selected, irrespective of nationality, on the basis of a coherent scientific and professional project to work as part of INRA???s research teams. The recipients are recruited on a two-year contract with a gross monthly salary of 2150???.

These post-doctoral positions are proposed in the following fields of research: - Environment and rural space - Food and human nutrition - Agricultural products and process engineering - Generic research - Innovative and sustainable agricultural systems

Deadline for submitting applications: February 4, 2008

All information on INRA???s web site:

http://www.international.inra.fr/join_us/positions/post_doctoral_positions/annual_campaign For any question concerning post-doctoral positions, you can send an email to the following address: post-doctorant@paris.inra.fr

Thank you for your help. Sincerely.

Fabienne Giroux

INRA ??? DRH Service recrutement et mobilit?? 147, rue de l'Universit?? 75338 PARIS cedex 07 Tel : 01-42-75-90-77 Fax : 01-42-75-90-39

Fabienne Giroux <Fabienne.Giroux@paris.inra.fr>

Manilla RiceInsectRelationships

Responsibilities

Specific responsibilities are to:

. Contribute to developing rice varieties with sustainable insect resistance traits through the understanding of insect/plant relationships of key pests,

. Develop strategies to integrate plant resistance with natural biological control and crop management practices to enhance sustainable pest management.

Qualifications

Candidates should have a PhD in biological sciences with a minimum of 2 years postdoctoral experience and a good publication record. Relevant experience includes any of the following areas: insect host plant resistance, insect/plant interactions, evolutionary biology, or chemical ecology. A background in molecular techniques, host plant resistance deployment, and/or Integrated Pest Management (IPM) is preferred.

IRRI

The International Rice Research Institute (IRRI) is seeking an Entomologist to be a member of its internationally recruited staff. The position will be based in the Institute's Crop and Environmental Sciences Division, with an initial appointment of 3 years and renewable for subsequent multi-year contracts. Renewal is subject to satisfactory performance and availability of funding. IRRI, supported by the Consultative Group on International Agricultural Research (www.cgiar.org), is a nonprofit, autonomous organization engaged in research and training on rice-related technology. Interested candidates can learn more about IRRI and its activities by visiting www.irri.org . IRRI's mission is to reduce poverty and hunger, improve the health of rice farmers and consumers, and ensure environmental sustainability through collaborative research, partnerships, and strengthening of national agricultural and extension systems. Insect pests continue to be a major threat to global rice production. IRRI addresses the insect problems at both plant-crop and ecosystem levels. The successful candidate is expected to focus on plant resistance to insect pests in the context of sustainable pest management strategies. The main geographic emphasis will be on intensive rice-based cropping systems in Asia. The candidate will work in a multidisciplinary research team involving geneticists, plant breeders, agronomists, plant nutritionists, crop physiologists, and social scientists.

Perquisites and IRRI environment

IRRI, located at Los Baños, 70 kilometers south of Manila, Philippines, offers salary and perquisites that are internationally competitive including support for education of children, car and housing at reasonable rental rates, and medical and retirement benefits. IRRI provides a gender-sensitive environment and welcomes women applicants. Citizens of developing countries, particularly rice-producing countries, are encouraged to apply. The Institute is committed to assisting families in making personal and, to the extent possible, professional adjustments to the local environment. IRRI has an accredited international school (pre-K to grade 5) and, excellent preparatory schools for younger children are available locally.

Applications

Please submit your application online at www.irri.org/-jobs/adda.asp or send (preferably via e-mail) a comprehensive curriculum vitae and names and email addresses of three referees to:

Ms. Selene M. Ocampo

Officer-HR Coordination

International Rice Research Institute

DAPO Box 7777,

Metro Manila, Philippines

Tel: (63-2) 891-1292/580-5600

Fax: (63-2) 580-5699

Email: IRRIRecruitment@cgiar.org

Applications will be accepted until 31 December 2007 or until a suitable candidate is found.

Interviews of short-listed applicants will commence in February 2008 and the successful candidate expected to report before June 2008. Only short-listed candidates will be notified.

fred_gould@ncsu.edu fred_gould@ncsu.edu

Newport Oregon LabManager ShellfishPopGenetics

Evoldir-

I have a vacancy for a LABORATORY MANAGER in my USDA lab studying shellfish genetics. The position is best suited for someone with a Masters degree or equivalent experience who is familiar with a wide range of molecular genetics techniques (DNA and RNA extraction, PCR, reverse transcription, quantitative real time PCR, microsatellite markers, AFLP markers, RFLP markers, gel electrophoresis, DNA cloning and sequencing); equipment (ABI 3730XL sequencer, ABI 7500 RT-PCR, Biomek FX pipetting robot, gel image analysis etc.); and data management and analysis methods. Duties include conducting research under the supervision of the PI (me); working closely with and training graduate students, postdocs, and technicians; performing routine maintenance and calibrations on lab equipment; and maintaining stocks and inventories of reagents, buffers, etc. In addition, there is occaisonal field work.

The research in the lab focuses on basic and applied genetics in cultured shellfish species - mainly oysters and geoduck clams. We use a variety of approaches such as traditional quantitative genetics, QTL mapping, various gene expression and transcriptome assays, population genetics using neutral and non-neutral markers, and parentage analysis. We also work closely with the Molluscan Broodstock Program, a selective breeding program for genetic improvement of cultured oyster stocks and also work on native oyster conservation genetics in Washington, Oregon, and California populations of the Olympia oyster.

The position in located at the Hatfield Marine Science Center in Newport, Oregon which is about 1 hour west of Corvallis on Yaquina Bay. Newport is a small but vibrant coastal community with a mixed economy based on tourism, fishing, and scientific research. It rains a lot in the winter.

This is permanent position with the federal government, and as such is only open to US citizens by law. Ideally, the chosen candidate would be seeking a long-term situation. Applications must be directed to personnel specialists in Washington DC. Complete information on how to apply is available at:

http://jobsearch.usajobs.gov/getjob.asp?JobID=-3D66305957 Best-

Mark D. Camara USDA/ARS Shellfish Genetics OSU - Hatfield Marine Science Center 2030 SE Marine Science Dr. Newport, OR 97365

Office: 541-867-0296 Fax: 541-867-0138 Mailto: Mark.Camara@oregonstate.edu

Mark.Camara@oregonstate.edu

Newport Oregon LabManager ShellfishPopGenetics 2

Sorry for the re-posting. The hyperlink in the original post announcing the LAB MANAGER position with the USDA Shellfish Genetics Lab in Newport, Oregon was corrupted by the insertion of a line break. The link below is a shortened version that should work better.

http://jobsearch.usajobs.gov/getjob.asp?JobID=-66305957 Mark D. Camara USDA/ARS Shellfish Genetics OSU - Hatfield Marine Science Center 2030 SE Marine Science Dr. Newport, OR 97365

Office: 541-867-0296 Fax: 541-867-0138 Mailto: Mark.Camara@oregonstate.edu

Mark Camara <Mark.Camara@charter.net>

OregonStateU ResAssist PopGenetics

Hi, I'm looking for someone to join my lab to work on a variety of projects including salmon fitness studies and parasite evolutionary genetics. Labwork involves mainly microsatellite genotyping, sequencing, and some cloning and possible cDNA work. Good computer skills are essential. Someone with bioinformatics or sequence analysis skills would be great. Below is the official job ad. My current technician is leaving end of March, so I'd like someone who can either start before then, or who can come work for a week or two with her before she leaves. Feel free to contact me for more info. Mike

Faculty Research Assistant (lab technician, molecular biology), Dept. Zoology, Oregon State University. Appointee will conduct population genetics research in Michael Blouin's lab. Responsibilities include basic molecular biology procedures, database management, working with students, and ordering and managing supplies. Required qualifications include database management skills and basic RNA and DNA molecular biology skills such as nucleic acid extractions, PCR, and working with cDNA or DNA libraries. Preferred qualifications include experience with bioinformatics or population/evolutionary genetics. This is a full-time, 12-month fixed-term position with renewal at the discretion of the supervisor. To review posting and apply, go to http://oregonstate.edu/jobs. Closing Date: 01/04/08. Preferred start date by 03/01/08. Feel free to contact Michael Blouin for further info. OSU is an AA/EOE.

– Michael Blouin Dept. Zoology, Oregon State University Corvallis, OR 97331-2914 http://oregonstate.edu/-

˜blouinm/ Tel: 541-737-2362 Fax: 541-737-0501

blouinm@science.oregonstate.edu
blouinm@science.oregonstate.edu

Perth MolecularEvolution

Dear EvolDir Members,

We are seeking a marine molecular evolutionist to join our team of marine biologists, physicists, and ecologists. You will have substantial postdoctoral experience in population genetics, microsatellite analysis, DNA sequencing and spatial genetic analysis, preferably in marine systems. You will appreciate the role of hydrodynamic ocean processes in structuring marine populations and know how to infer this relationship from observed patterns of genetic population structure. You will wish to work not only on describing aspects of the marine environment, but also on approaches that will assist state managers to assess current patterns of evolutionary connectivity at large spatial scales and to manage marine ecosystems and resources sustainably. You will be committed to quality research that has practical benefit. You will have a commitment to teamwork and multidisciplinary research.

The oceanscape genetics research will focus on the use of genetics to understand the role of large-scale oceanographic processes in dispersal and population structure in marine organisms in Western Australia (WA). Two projects will be involved: population structure of the spangled emperor fish within Ningaloo reef and more broadly in the north west of WA, and stock structure in the iconic WA fish, dhufish. The coast of WA is dominated by the southward-flowing Leeuwin Current and associated eddies and wind-driven currents. Molecular genetics is a powerful tool for describing population structure at many scales and for inferring the intergenerational mean effect of dispersal and demography throughout a species range. The molecular evolutionist will describe and interpret these patterns as part of a team that includes hydrodynamic modellers, oceanographers, marine evolutionists and geneticists, forming part of the Western Australian Marine Science Institute (WAMSI) that is observing, identifying and describing the important elements and processes which structure the marine environment. The research aims to provide WA agencies with a scientific basis for managing coastal marine systems and applying ecosystem-based fisheries management. The successful applicant will be expected to participate in the design and interpretation of data collection, and may participate in field programs.

For more information and to apply, visit https://recruitment.csiro.au/asp/Job_Details.asp?RefNo=-3D2007%2F1407 Regards,

Phillip England PhD Research Group Leader Genomics & Taxonomy CSIRO Marine & Atmospheric Research Castray Esplanade, Hobart TAS 7000 GPO Box 1538 Hobart TAS 7001 03 6232 5116 :: 0419090811 mob.

phillip.england@csiro.au

Regards, Phillip

Phillip England PhD Research Group Leader Genomics & Taxonomy CSIRO Marine & Atmospheric Research Castray Esplanade, Hobart TAS 7000 GPO Box 1538 Hobart TAS 7001 03 6232 5116 :: 0419090811 mob.

phillip.england@csiro.au phillip.england@csiro.au

SouthAfrica FieldAssist PlantSpeciation

Field Assistant-South Africa

One field assistant is needed to assist with a project studying plant speciation and evolution in the Cape Floristic Region of South Africa. The position is for 3-5 months starting February 1, 2008, with flexibility in both start and end dates.

The assistant will help collect and process specimens, measure plant morphological and physiological data in the field, and enter data. They will also help to establish experimental gardens in the field and in Cape Town.

A successful applicant will have completed or be on track for a BA or BS in biology. Satisfactory completion of at least one class in plant biology and one in evolution is mandatory. Applicants need to be able to walk long distances (10k) in often hot conditions and they should be able to live and work with others in close quarters. A valid passport is also required.

The position covers airfare, room, and board. There is a possibility for a small stipend, depending on the budget.

To apply: send a cover letter explaining your interest in this position, a CV, and the names and contact information of two references to Rachel Prunier <rachel.prunier@uconn.edu>

rachel.prunier@huskymail.uconn.edu
rachel.prunier@huskymail.uconn.edu

StGirons France Volunteer DispersalEvolution

Volunteer Opportunity

We are looking for volunteers on a project examining the evolution of dispersal and sociality. The themes of this work are centered on the evolution of sociality (cooperation), condition-dependent dispersal, and metapopulation dynamics. This project seeks to experimentally manipulate parameters of dispersal behavior and social aggregations to understand trade-offs and key determinants of the evolution of these behaviors. The project is lab based, using Tetrahymena thermophila, a unicellular ciliated protist, as a model organism. Our recent work has shown genetic variation in dispersal and cooperative behavior among clonal lines and has investigated some elements of condition-dependent dispersal (information use, dispersal phenotypes). Future work will examine evolutionary processes affecting dispersal and the stability of social strategies that build on these findings. Volunteers are expected to participate in maintenance of cultures, experimental manipulations, and the best candidates will also be capable of helping to plan experiments and process data.

This project is run in Dr. Jean Cloberts lab and students will work with both Dr. Clobert and Dr. Alexis Chaine. The lab is situated in the foothills of the French Pyrenees Mountains at a CNRS field station (Moulis / Saint Girons). Students will be provided with housing but will be expected to cover their other expenses. Work is ongoing and volunteers can begin at a negotiated date. Duration of work is flexible, and while volunteers are expected to commit to a minimum of 4 weeks, priority will be given to those who can commit to longer periods.

For more information, please contact Alexis Chaine at alexis.chaine@ecoex-moulis.cnrs.fr

Station d'Ecologie Expérimentale du CNRS (USR 2936) Laboratoire Evolution et Diversité Biologique

09200 Moulis

France

Alexis Chaine <alexis.chaine@EcoEx-Moulis.cnrs.fr>

StirlingU 3 EvolutionaryBiologists

As part of our ongoing programme of expansion (including the recent appointment of four evolutionary biologists) we now seek three new Lecturers within the School of Biological and Environmental Sciences (one at Senior Lecturer, two at Lecturer level). The successful applicants will be expected to develop dynamic research programmes and contribute to undergraduate/postgraduate teaching. The School currently consists of three research clusters (Evolutionary Ecology and Conservation, Environmental and Ecological Processes and Geoarchaeology and Environmental History). We welcome internationally excellent applications in any area of biological and environmental sciences. Two of the posts are to be permanent, the third (Lecturer) will be a fixed term 4 year post in the first instance.

Informal enquiries to: Professor Dave Goulson, Head of School. Tel: +44 (0)1786 467759, email: Dave.Goulson@stir.ac.uk. Information about the School can be found on our web site http://-www.sbes.stir.ac.uk Further particulars are available from HR Services, University of Stirling, Stirling, FK9 4LA, Tel: 01786 466155, E-mail hr-services@stir.ac.uk

Application forms, a covering letter and a CV together with the names and addresses of three referees should be returned no later than the closing date.

Closing date: 25 January 2008 at 12 noon The School of Biological & Environmental Sciences at the University of Stirling has three posts available. Lecturer (Fixed term 4 years), Salary £27,466 - £40,335 (Ref: 13625) Lecturer (Permanent), Salary £27,466 - £40,335 (Ref: 13642) Senior Lecturer (Permanent), Salary £41,545 - 48,161 (Ref: 13068)

The advert will appear in the next issue of Nature.

Dr Andre Gilburn Evolution Ecology and Conservation Research Cluster School of Biological and Environmental Sciences University of Stirling Stirling Scotland FK9 4LA

andre.gilburn@stir.ac.uk andre.gilburn@stir.ac.uk

StPetersburg Florida FishConsGenetics

Position Title: Associate Research Scientist (Genetics)

Agency/location: Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, St. Petersburg, Florida.

Institute Website: http://research.myfwc.com Responsibilities: Design and implement genetic research studies for marine sport fish. Procure and process specimens using established molecular genetics techniques. Conduct genetic and statistical analyses of resultant data. Produce or assist in the production of reports and manuscripts as needed. Train technical staff in the laboratory procedures/techniques.

Qualifications: Master's or Ph.D. degree. Knowledge of the technical skills for molecular biology and ecological genetics, particularly automated DNA sequencing and microsatellite genotyping. Familiarity with the application of these data to fisheries management and conservation genetics. Ability to produce technical reports and develop manuscripts.

Salary: $46,685 with an excellent benefits package (State of Florida FTE Career Service Position). Continually funded position; not-term limited.

Closing date: until filled

Contact: Send cover letter, c.v., relevant publications, and contact information for three references to mike.tringali@myfwc.com with “Associate Research Scientist” in the subject line.

Michael D. Tringali, Ph.D. Research Scientist Florida Fish & Wildlife Conservation Commission Fish & Wildlife Research Institute 100 Eighth Avenue SE, St. Petersburg, FL 33701 tel: 727-896-8626(x3116) or 727-235-4331 FAX: 727-823-0166 EMail: mike.tringali@myfwc.com Institute Website: http://research.myfwc.com

“Tringali, Mike” <Mike.Tringali@MyFWC.com>

UAarhus EvolutionaryEcol

FACULTY OF SCIENCE

DEPARTMENT OF BIOLOGICAL SCIENCES

Associate Professor in Evolutionary Ecology

A position as Associate Professor in Evolutionary Ecology is available at the Department of Biological Sciences, Section for Ecology and Genetics, from June 1, 2008.

The candidate is expected to become part of a research group at the Section for Ecology and Genetics, seeking to integrate empirical and theoretical approaches to tackle problems within evolutionary ecology. The candidate should have a strong international research profile and be willing and able to cooperate across borders of research fields, and he/she is expected to be experienced in the use of molecular techniques on evolutionary genetic problems.

Furthermore, the applicant should document teaching and tutoring qualifications at all levels (BSc, MSc, PhD).

Applications must be in English and include a curriculum vitae, a complete list of publications, a statement of future research plans and information about research activities, teaching qualifications and management experience, all in 4 copies (see http://www.nat.au.dk/default.asp?id=7838&la=UK < http://www.nat.au.dk/default.asp?id=7838&la=UK > for the recommended level of detail). If the applicant wants other material to be considered in the evaluation (publications and other documentation of research and teaching qualifications, as well as management experience) such material must be clearly specified and must either be enclosed in hardcopy (3 copies) or must be available electronically.

The Faculty refers to the Ministerial Order No. 170 of 17.03.2005 ((http://www.au.dk/da/21-05.htm) on the appointment of teaching and research staff at the universities under the Ministry of Science, Technology and Innovation.

Salary depends on seniority as agreed between the Danish Ministry of Finance and the Confederation of Professional Unions.

Applications should be addressed to The Faculty of Science, University of Aarhus, Ny Munkegade, Building 1520, DK-8000 Aarhus C, Denmark, and marked 212/5-210.

The deadline for receipt of all applications is February 1, 2007, at 12,00 noon.

For more information contact Professor Volker Loeschcke (phone: +45 8942 3268; E-mail:

volker.loeschcke@biology.au.dk, or the head of the department Dr. J©rgen Bundgaard, Head of Department of Biological Sciences, Build. 1540, Ny Munkegade, 8000 Aarhus C., Denmark; phone: +45 8942 3266; E-mail: biojb@biology.au.dk <mailto:biojb@biology.au.dk>

/The University of Aarhus has 34,000 students, 10,000 staff, and a turnover of DKK 4.5 billion. The University consists of nine main areas: six faculties (Humanities, Health Sciences, Social Sciences, Theology, Science and Agricultural Sciences), two schools (the Aarhus School of Business and the Danish School of Education), and the National Environmental Research Institute. The Universitys activities are based at more than 20 locations all over Denmark./

Volker Loeschcke <volker.loeschcke@biology.au.dk>

UCaliforniaBerkeley PlantPaleobiologyEvolution

THE UNIVERSITY OF CALIFORNIA, BERKELEY

Department of Integrative Biology

Faculty Position in Plant Paleobiology and Evolution

Position ID #714

The Department of Integrative Biology at the University of California, Berkeley, is soliciting applications for a tenure-track position (Assistant Professor) in Plant Paleobiology and Evolution. We seek a colleague to join a department with a strong interdisciplinary emphasis and who will develop a vigorous, independent research and teaching program in the area of plant paleobiology. Applicants should have a Ph.D. or equivalent advanced degree and an exceptional research record in: the evolution and ecology of past plant communities or ecosystems, the evolution of vascular plant lineages in deep time, and/or long-term plant response to environmental change using paleontological and neontological data. The position entails teaching both lower and upper level courses in plant evolution/paleobotany, with an emphasis on structure and function, phylogeny, paleoecology, and/or historical biogeography. An academic curatorship in the UC Museum of Paleontology is associated with this appointment; the successful candidate will be encouraged to promote the use of the museums' extensive holdings, supervise student research, work with museum staff to pursue opportunities for collection improvement and growth, and participate in UCMP and the Berkeley Natural History Museums activities and events. For more information, see: http://-/ib.berkeley.edu .

Application packages should include a CV with a bibliography of published work, a description of research accomplishments and objectives, a statement of teaching interests, and selected reprints. Three letters of reference should be sent separately by the recommender.

Both applications and letters of reference should be submitted electronically via: http://ib.berkeley.edu/-admin/jobs/paleobiojob.php or via email to: PlantPaleobiology@gmail.com. If electronic submission is not possible, materials may be sent by regular mail to:

Plant-Paleobiology Search Committee Department of Integrative Biology 3060 Valley Life Sciences Building University of California Berkeley, CA 94720-3140 USA

Applications and supporting letters must be received electronically or postmarked by February 29, 2008. Review of application will begin March 10, 2008.

Applicants should refer their reviewers to the UC Berkeley Statement of Confidentiality at http://-apo.chance.berkeley.edu/evalltr.html . The University of California is an Equal Opportunity/Affirmative Action Employer.

"Chelsea D. Specht" <cdspecht@nature.berkeley.edu>

UCambridge InvasiveSpeciesModelling

Microsoft Research Fellowship

The Governing Body of Peterhouse, in partnership with Microsoft Research, intends to elect a Research Fellow in the area of Computational Sciences as applied to computational evolution. The Research Fellow, either man or woman, will enter upon their tenure on 1st January 2008 or as soon as possible thereafter.

Candidates must, by 1st January 2008, have had at least one year and no more than three years of post-doctoral experience. Career breaks such as maternity leave, national service and voluntary service overseas can be discounted, but teaching experience and/or time spent in industry since the award of the Ph.D. should be included in the total amount of post-doctoral experience. Candidature will be restricted to graduates of, or those studying at, universities in Europe.

Candidates should have strong expertise in scientific computing. This involves not only some solid basis in computer science but also some strong knowledge in computational evolution. Candidates should be able to drive their own research and work in a team when required. The successful candidate will be provided with research facilities in the University Department of Genetics, and will collaborate with the teams there and in Microsoft research studying invasive species.

Candidates should obtain an application form from the College Secretary (or download it, see below). They will be asked to name two or three referees who know their work and to request them to write to the Master of Peterhouse a letter supporting their candidature. The completed application form and the letters from referees must reach the Master by 14th December 2007.

The Selection Committee for the Fellowship will draw up a short list of candidates who may be invited to submit dissertations or other written work. Some of these candidates will subsequently be invited for interview.

The annual remuneration for the Research Fellow will be £21,500, with an annual research allowance of up to £1,085. The Research Fellow will be asked to sign a standard agreement with Microsoft Research.

Stipends will be subject to deductions in consideration of emoluments from other sources. Emoluments from other industrial sponsors will not be permitted. The Research Fellow will be expected to engage in full-time research, but may be permitted to teach for up to six hours a week and will be paid for this. Rooms in College with service will be provided free of charge for the Research Fellow. All Research Fellows are allowed seven free meals a week at the Common Table. There is an entertainment allowance in kind.

The initial tenure is for two years, with the possibility of extension, subject to the availability of funding and a satisfactory review of performance at the end of the second year.

All correspondence should be directed to the Colelge Secretary, Peterhouse, Cambridge, CB2 1RD, England, (tel: 01223 338202; email: pat.grassick@pet.cam.ac.uk).

ALL ENQUIRIES SHOULD BE CLEARLY MARKED 'MICROSOFT RFC'.

http://www.pet.cam.ac.uk/vacancies/ms-research-fellowship.html Many thanks,

Remy Ware

– Miss R. L. Ware Research Fellow Peterhouse Cambridge CB2 1RD (+44)1223 742980 Evolutionary Genetics Group Department of Genetics University of Cambridge (+44)1223 276190

"R.L. Ware" <rlw29@cam.ac.uk>

UCambridge PopulationGenetics

Hi

I would like to place a job ad for a pop/stat/quant geneticist to work on infectious disease pathogens and their hosts in the Wellcome Tropical Research Centres in Kenya, Vietnam, Thailand and The Gambia.

The adverts for came be found at the links below with a closing date of 25th January

http://www.admin.ox.ac.uk/ps/oao/arrs/arrs1509j.shtml http://www.admin.ox.ac.uk/ps/oao/arrs/arrs1508j.shtml http://www.admin.ox.ac.uk/ps/oao/arrs/arrs1507j.shtml Thanks a lot

margaret Mackinnon

Dr. Margaret Mackinnon

Department of Pathology KEMRI-Wellcome Collaborative Programme, Coast University of Cambridge PO Box 230 Tennis Court Rd. Kilifi Cambridge CB2 1QP Kenya UK

mjm88@cam.ac.uk mmackinnon@kilifi.kemri-wellcome.org Tel: + 44 (0)1223 764518 + 254 41 522535 Ext 228 Fax: + 44 (0)1223 333346 + 254 41 522390

Margaret Mackinnon <mmackinnon@kilifi.kemri-wellcome.org>

UMichigan EvolutionaryPhysiology

Functional Organismal Biology of Fishes, Reptiles or Amphibians University of Michigan

The Department of Ecology and Evolutionary Biology solicits applications for a tenure-track Assistant Professor, university-year appointment, in functional organismal biology of ectothermic vertebrates. We seek outstanding individuals whose research involves innovative approaches to studying ectotherm form and function in an evolutionary and/or ecological context, including such fields as evolutionary physiology, physiological ecology, evolutionary or functional morphology, and/or biomechanics. The successful candidate will have complete access to the outstanding collections of the University of Michigan Museum of Zoology and, as appropriate and desired, could have an affiliation with the Museum. Teaching responsibilities may include courses in physiology or anatomy and areas of specialized research interest. For further information, see www.eeb.lsa.umich.edu and www.ummz.lsa.umich.edu. Women and minorities are encouraged to apply. The University is supportive of the needs of dual-career couples.

To apply, send a curriculum vitae, statements of current and future research plans and of teaching philosophy and experience, evidence of teaching excellence, and copies of publications, as well as arrange to have three reference letters sent to the address below or e-mailed to janesull@umich.edu.

Chair, Functional Biology Search Committee Department of Ecology and Evolutionary Biology University of Michigan, 830 N. University, Room 2019W Kraus Ann Arbor, MI 48109-1048

Review of applications will begin on January 5, 2007 and continue until the position is filled. The University of Michigan is an equal opportunity, affirmative action employer.

Jane A. Sullivan Department Secretary Ecology and Evolutionary Biology University of Michigan Kraus Natural Science Building 830 N. University Room 2019 ph. (734) 615-4917 fx. (734) 763-0544

“Sullivan, Jane” <janesull@umich.edu>

UNebraska ViralEvolution

Tenure Track position Viral Evolution UNIVERSITY of NEBRASKA

Tenure track Assistant Professor in the area of viral evolution at the University of Nebraska Center for Virology and the School of Biological Sciences. Candidates will be expected to develop a nationally recognized research program emphasizing viral evolution. Specific area of research open; appropriate examples of research interests include evolutionary genetics examining virus adaptation, comparative genomics of viral genomes and molecular epidemiology of emerging viral diseases. Candidates will be expected to develop an undergraduate course in the area of the evolution of infectious diseases and participate in graduate teaching in viral evolution. Review of applications will begin on December 10, 2007 (letters of recommendation may follow at a later date). A Ph.D. and post-doctoral experience in related area is required.

Start date Fall 2008. The position will remain open until a suitable candidate is selected. UNL is committed to a pluralistic campus community through Affirmative Action and Equal Opportunity, and is responsive to the needs of dual career couples. We assure responsible accommodation under the Americans with Disabilities Act; for assistance contact Dr. Alan Kamil at 402-472-6676.

To apply log on to http://employment.unl.edu requisition #070860 and complete the Faculty/Administrative information Form and attach CV, cover letter, statement of research interests and teaching interests and philosophy; representative publications; names, addresses and phone numbers of three references. Arrange for three letters of reference to be sent to Dr. Alan Kamil, School of Biological Sciences, University of Nebraska-Lincoln, 348 Manter Hall, Lincoln, NE 68588-0118. Review of applications will continue until the position is filled or the search is closed.

Jay F. Storz School of Biological Sciences University of Nebraska Lincoln, NE 68588 Phone: 402/472-1114 E-mail: jstorz2@unl.edu

http://www.biosci.unl.edu/faculty/Storz/index.html
Jay F Storz <jstorz2@unlnotes.unl.edu>

UTexas Austin ResTech EvolutionaryVirology

Position available for a research technician at the University of Texas at Austin. The successful applicant will work as a member of a brand-new research team engaged in exciting and challenging research at the interface of evolutionary biology and virology. The position is open as early as January. For more information on the lab: http://www.people.cornell.edu/pages/mrd6/-sara/ Applicants should apply through the UT site below.

http://utdirect.utexas.edu/pnjobs/index.WBX Enter 07-11-30-01-4222 in upper left hand corner

Sara Sawyer <ssawyer@fhcrc.org>

UWashington StatisticalGenetics

* *The Department of Biostatistics at the University of Washington wishes to fill one or more full-time (100% FTE) faculty positions in the regular or research track at the Assistant Professor, Associate Professor, or Professor level in statistical genetics/proteomics. The appointees will be able to interact with an unusually strong group of faculty and students in statistical genomics, proteomics, and the interdisciplinary Public Health Genetics Program, all of which involve faculty members from several departments and schools at the University of Washington and the Fred Hutchinson Cancer Research Center. A joint appointment with Genome Sciences is a possibility for suitable candidates. Tenure-track positions include 50% tenure combined with 50% funding secured through the participation in and direction of research. All faculty positions are 12-month and all Biostatistics faculty are eligible to apply for departmental funds for career development. University of Washington faculty engage in teaching, research, and service.

Ph.D. required in Biostatistics, Statistics, or related field. The UW is a recipient of the 2006 Alfred P. Sloan Award for Faculty Career Flexibility and is committed to supporting the work-life balance of its faculty.

Applications will be accepted until position is filled. Submit letter of interest, curriculum vitae, & four signed, original letters of reference by January 15, 2008 to:

StatGen Search, Department of Biostatistics, Box 357232, University of Washington, Seattle, WA 98195-7232

The University of Washington is an affirmative action, equal opportunity employer. The University is building a culturally diverse faculty and staff and strongly encourages applications from women, minorities, individuals with disabilities and covered veterans.

Bruce Weir <bsweir@u.washington.edu>

YorkU EvolutionaryGenetics 2

NOTE: JOB DEADLINE HAS BEEN EXTENDED TO January 15, 2008

Position Rank: Full Time Tenure Stream - Assistant Professor Discipline/Field: Evolutionary Genetics/Genomics Home Faculty: Science and Engineering Home Department/Area/Division: Biology Affiliation/Union: YUFA Position Start Date: July 1, 2008

The Department of Biology invites applications for a tenure-track appointment at the Assistant Professor level in the area of Evolutionary Genetics/Genomics to commence July 1, 2008. Of particular interest are individuals whose proposed research programs complement and extend existing research activities in this area in the department. The successful candidate will have a Ph.D., postdoctoral experience, an outstanding research record, and will be expected to develop strong, externally funded research programs. The successful candidate must be eligible for prompt appointment to the Faculty of Graduate Studies.

All York University appointments are subject to budgetary approval.

York University is an Affirmative Action Employer. The Affirmative Action Program can be found on York's website at www.yorku.ca/acadjobs or a copy can be obtained by calling the affirmative action office at 416-736-5713. All qualified candidates are encouraged to apply; however, Canadian citizens and Permanent Residents will be given priority.

Applicants should forward (as hard copy only) a curriculum vitae, an outline of their research plans, a statement of teaching interests and experience, and single copies of three publications. Please also arrange to have three signed letters of reference to:

Dr. Hilliker, Search Committee (Evolutionary Genetics/Genomics) Department of Biology, Rm 247 Farquharson Building York University, 4700 Keele St., Toronto, Ontario M3J 1P3

The deadline for receipt of applications has been extended to January 15, 2008.

shore@yorku.ca shore@yorku.ca

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Automated DNA extractor

Our laboratory is looking into purchasing an automated DNA extractor for extracting DNA predominantly from whole blood. The two units we are considering are the Qiacube from Qiagen and the Maxwell 16 from Promega. Does anyone have any experience with either of these machines?

Thanks Rita

rspathis@gmail.com

Diversity project

Dear Colleagues,

For the fourth consecutive year, we will be running The Diversity Project, an NSF funded research opportunity at for under-represented minority undergraduate students . In collaboration between Boston University, Old Dominion University and Duke University, students will integrate hands-on field research in the Coral Triangle with cutting edge genetic research. The project will explore the origins marine biodiversity in the Coral Triangle in an effort to improve conservation of this remarkable ecosystems. Students are fully funded for both living and travel expenses. Visit http://people.bu.edu/-pbarber/Intro.htm for more information and on-line application.

This research opportunity has been a remarkable personal and professional experience for the students who have participated. Please encourage any students whom you believe would benefit from such an experience to apply. Applications are due January 15, 2008. For further information, please contact Dr. Paul Barber (pbarber@bu.edu). We look forward to hearing from you.

Sincerely, Paul Barber – Dr. Paul H. Barber Boston University Boston University Marine Program 5 Cummington St. Boston, MA 02215 617-358-4589 office 617-358-4590 lab 617-353-6340 FAX pbarber@bu.edu http://people.bu.edu/pbarber/ Paul Barber <pbarber@bu.edu>

F statistic sample size

I want to look at parasites in a number of separate hosts to check for non-random breeding within hosts. Obviously there will be differences in genotypes between hosts (Fst) and non-random mating would show up as a significant Fis value. The problem is what sample size would I need to detect a given value of Fis? It looks like most people avoid the issue of sample size or power calculations when doing F statistics. The best recent one I could come up with is

N. Patterson, A. L. Price, and D. Reich. Population structure and eigenanalysis. Plos Genetics 2 (12):2074-2093, 2006.

They present calculations for Fst between two populations and state that the minimum Fst that can be reasonable detected is 1/sqrt(nm) where n is no of individuals and m is no. of molecular markers. Would it be outrageous to extrapolate this to Fis so that, for example, examining parasites from 100 animals would have power to detect a minimum Fis of 1/sqrt(100)=0.1?

Thanks in advance, Ian

Ian Hastings Liverpool School of Tropical Medicine Liverpool L3 5QA tel 0151 705 3183 (office) or 0151 705 3147 (Dept. Secretary)

hastings@liverpool.ac.uk

Intelligent design movie

Just a quick note about a new movie, “Expelled” being released in February. Ben Stein is the host and it appears to focus on a pro-Intelligent Design platform as a form of free-speech.

The trailer and information can be found at http://www.expelledthemovie.com/playground.php . Shala Hankison

hankison@gmail.com

Isopod SingleCopyNuclearGenes for phylogenies

Dear members of the evoldir

SINGLE COPY nuclear genes for plylogenesis in isopods(slower rate than 12s, 16s and COI)

my laboratory used to study mostly mitochondrial genes.But we decided to study this time nuclear genes. is there a SINGLE COPY nuclear gene with slower evolutionary rate than 12s , 16s, and COI which i could used in order to study the phylogenesis of isopods (genus:Ligidium).Due to economical and technical reasons we dont use cloning methods, so if this gene exist in 2 copies it would be difficult only by using the gel extraction method to purify the appropriate band, cause this technique (gel extraction) has never met with success.

I have just decided to study the gene EF-1a in the genus Ligidium(Isopods) does anybody knows if in isopods EF-1a exist as a single copy??? or if there 2 copies of that gene (one pseudogene 400 b.p. and another one with an intron at 700 b.p.) as it has been proved in other arthropods??

your help is essential for my master completion im looking forward for your answers

Hara Dova

<xntova@upatras.gr>

MacOSX PopGenet software answers

Dear all,

First of all thanks a lot for the responses I had to my question about user-friendly population genetics programs that run in Mac OSX. Unfortunately, there doesn’t seem to exist such a programme with a graphical interface, which I find curious given that Macs used to be more user-friendly than Windows. Here I post the answsers I have had.

Cheers,

Ramiro

1) What about running DnaSP/DAMBE/etc. on Windows (with bootcamp or Parallels) on the Mac instead?

2) Given your post on the Evoldir, I cannot help but plug my own software, GenoDive. However, it does not handle sequences, but it does handle most other types of genetic markers and can perform several different analyses with them, among which AMOVA’s. Anyway, as far as I can tell myself it is very user friendly, and may be useful to you for some other purposes. The current version can be downloaded from my website: http://www.bentleydrummer.nl/software. Please keep in mind that it is a beta version, so there may still be some bugs.

3) The package of software written by Kevin Thornton and Eli Stahl (molpopgen) is excellent and very flexible. This package is written in C++, and it was relatively painless to compile on my Mac (which runs OSX Tiger). In particular, the ’analysis’ package can do most of the

analyses that DnaSP can do.

4) I saw your post of Evoldir. There is nothing that I am aware of in terms of software with a graphical interface. On Intel-based macs, you can run DNAsp through one of the many windows emulators available (Parallels, VMware, etc.). Alternatively, I have written several software packages of command-line applications which are portable across many Unix systems, and work fine on OS X. http://www.molpopgen.org
5) Kevin Thornton has a set of applications (MKtest, compute, polydNdS) for this sort of thing that work well on Mac OSX; they are available at molpopgen.org. They are not as user-friendly as DnaSP - you have to run them from the terminal, and you will need to compile them from C++ source code (after downloading and installing libraries - instructions are on the website too).

6) You could try GenAlEx6 or Genepop 4.0.

7) You can use Jeffrey Townsend's SeqPop that runs command-line on the terminal: http://www.yale.edu/townsend/software.html A similar option is Kevin Thornton's collection of command-line programs that use his libsequence library: http://molpopgen.org/software/lseqsoftware.html A nice Java program is Fu & Li's NeutralityTest: http://www.hgc.sph.uth.tmc.edu/neutrality_test It implements a variety of tests, like Fu's, Fu & Li's, Tajima's, Fay & Wu's, MK, HKA, LWL, Suzuki-Gojobori.

There a way to run Windows programs without installing Windows per se. The application is called WINE and exists for Linux. It was recently ported to OSX. There is the DarWINE project, but the current version is for PowerPC (PPC) architecture, not Intel-based Macs. This requires getting your hands dirty and installing libraries, compiling, etc. A company called CodeWeavers (http://www.codeweavers.com/products/cxmac) are selling CrossOver for the Mac and Linux, so as to run Windows applications seemlessly. The academic price is $42 and DnaSP runs just fine.

If you have long sequences, like genomic data, the DnaSP crew has written VariScan: http://www.ub.es/softevol/variscan If you're interested in simulations and test statistics, Sebas Ramos-Onsins from the Univ. of Barcelona has written mlSimCoal (based on Hudson's famous ms program): http://www.ub.es/softevol/mlcoalsim Peter Andolfatto from UCSD has a few programs like that at http://www-biology.ucsd.edu/labs/andolfatto/Programs.html 8) Have you tried Arlequin (lgb.unige.ch/arlequin/)? Although I haven't used the Mac version, they do have one and it does alot of tests, including neutrality. Once you get your dataset into the proper format (GenePop on the web can do this for you), which is a pain, it's fairly user friendly.

Dr. Ramiro Morales-Hojas Molecular Evolution Lab IBMC Rua do Campo Alegre 823 Porto 4150-180 Portugal

e-mail: rmhojas@ibmc.up.pt

rmhojas@ibmc.up.pt

MammalianMarkersDatabase OrthoMaM

Dear Evoldir members,

We have constructed and released a database of Orthologous Mammalian Markers (OrthoMaM) that might be useful for people interested in placental mammal phylogenetics and phylogenomics.

Briefly, the EnsEMBL database was used to determine a set of orthologous genes from 12 available complete mammalian genomes (human, chimp, macaque, mouse, rat, rabbit, cow, dog, armadillo, elephant, tenrec, and opossum). More than 3,000 exons of length > 400 bp have been selected as targets for possible amplification and sequencing in additional taxa. A bioinformatic pipeline has been developed to provide evolutionary descriptors (base composition, maximum likelihood model parameters, relative evolutionary rate, variability among codon positions) for these candidate markers in order to assess their potential phylogenetic utility. The resulting OrthoMaM (Orthologous Mammalian Markers) database can be queried and alignments can be downloaded through a dedicated web interface:

http://kimura.univ-montp2.fr/orthomam We expect the OrthoMaM database to be useful for further resolving the phylogenetic tree of placental mammals at different taxonomic levels and for better understanding the evolutionary dynamics of their genomes, i.e., the forces that shaped coding sequences in terms of selective constraints.

The paper describing the database is freely available from BMC Evolutionary Biology:

http://www.biomedcentral.com/1471-2148/7/241 OrthoMaM: A database of orthologous genomic markers for placental mammal phylogenetics Vincent Ranwez, Frederic Delsuc, Sylvie Ranwez, Khalid Belkhir, Marie-Ka Tilak and Emmanuel JP Douzery BMC Evolutionary Biology 2007, 7:241 (doi:10.1186/1471-2148-7-241)

We hope this will be of use to members of the community.

Frederic Delsuc and co-authors

–

Frédéric DELSUC (Chargé de Recherches CNRS) Laboratoire de Paléontologie, Phylogénie et Paléobiologie CC064 Institut des Sciences de l'Evolution UMR5554-CNRS Université Montpellier II Place Eugène Bataillon 34095 Montpellier Cedex 05 France Tel: (+33) 4 67 14 39 64 FAX: (+33) 4 67 14 36 10 Email: Frederic.Delsuc@univ-montp2.fr Webpage: http://frederic.delsuc.neuf.fr delsuc@isem.univ-montp2.fr delsuc@isem.univ-montp2.fr

Mus musculus samples

Dear Evoldir members,

I work on the colonization history of the house mouse (Mus musculus) in several Atlantic islands. I would be very interested to examine some samples from possible continental sources, especially from Africa (anywhere would be great, particularly North-East Africa) and South America. If anyone has access to specimens (tail tips, feet, toes, skin, etc) and would be willing to share them, I would be very grateful. Also, if you have a cat that is a good mouse hunter and sometimes leaves you some animals as presents on your door step that would be great as well! Please contact me (sofiagabriel@hotmail.com or sg542@york.ac.uk) for further info.

Thank you so much in advance,

Sofia

sg542@york.ac.uk sg542@york.ac.uk

Nb estimation using linkage

Dear EvolDir folks,

I have a sample from a single cohort of juvenile frogs and am wondering if I can apply the linkage disequilibrium method (as implemented in the NeEstimator program) to this sample to get an estimate of the effective number of the parents (*N*b) that produced the juvenile cohort. Can anyone verify or refute this? I have microsatellite genotype data for the juveniles as well as the adults, so I will have an *N*b estimate from the temporal method as well. I am hoping to use the LD method to get an additional estimate of *N*b.

Any of your comments on this issue will be greatly appreciated!

Thank you,

Ivan

Ivan C. Phillipsen Department of Zoology Oregon State University Corvallis, OR 97331-2914 philliiv@science.oregonstate.edu

phillipsen@gmail.com

New Evolution Education Journal

Dear EvolDir,

I am pleased to announce the official launch of the new journal Evolution: Education and Outreach, published by Springer and edited by Niles Eldredge and his son Greg. The journal is aimed at providing accessible and accurate discussions of evolutionary concepts, lesson plans, news, and other information to teachers at all levels as well as members of the public. The journal is available online without cost. The first issue can be found here:

http://www.springerlink.com/content/phj263762420/ If you have ideas for contributions, please see the webpage for author instructions:

http://www.springer.com/west/home/generic/search/results?SGWID=4-40109-70-17 3740503-0

Best wishes,

- Ryan Gregory

Dr. T. Ryan Gregory Assistant Professor Department of Integrative Biology University of Guelph 50 Stone Rd. E. Guelph, Ontario N1G 2W1 CANADA

http://www.genomesize.com/gregorylab/ rgregory@uoguelph.ca

Programs to detect selection

Dear Colleagues,

We have developed a easy to use program for selection detection based on the fdist Fst outlier method.

The software runs directly from the web, no installation required.

The major requirement is a recent version of Java installed (a link can be found on the application site)

If you are interested in selection detection using Fst-outlier methods, please check our application, LOSITAN. A preview release is available at: http://popgen.eu/soft/selwb/ Any issues, please don't hesitate to contact us, Tiago

tiagoantao@gmail.com

Requests for R

The National Evolutionary Synthesis Center (NESCent) is sponsoring a hackathon to improve the utility of R for comparative methods. What do you want to see done? We have an online single-question poll at http://snipurl.com/rhack , and/or you can write a response to hackathon2@nescent.org . The methods added will be a function of both user interest and developer interest and skill. More information about the hackathon is available at http://hackathon.nescent.org/ R_Hackathon .

Thank you,

The Organizing Committee From NESCent: Hilmar Lapp, Brian O'Meara, Samantha Price, Todd Vision, Amy Zanne From UC Berkeley: Steven Kembel

bcomeara@nescent.org

Sam Karlin

I just heard that Sam Karlin, who had a large impact on theoretical population genetics and on computational biology (as well as having many other achievments in mathematics) passed away on December 18. Here is an announcement: http://news-service.stanford.edu/news/2008/january9/karlin-010908.html —- Joe Felsenstein joe@gs.washington.edu Department of Genome Sciences and Department of Biology, University of Washington, Box 355065, Seattle, WA 98195-5065 USA

joe@gs.washington.edu

SelfishDNA Diseases

Selfish DNA and the genetic control of vector-borne diseases Catalysis Meeting access to public Wiki

Selfish genetic elements spread and maintain themselves in populations even though they have negative impacts on the fitness of organisms. They are of interest from an applied and a basic evolutionary perspective, and they are being studied from molecular and population dynamics/genetics perspectives. Although there are exceptions, most individual researchers take a single perspective in studying selfish DNA, interact with others who have that perspective, and tend to have only a superficial understanding and appreciation for work on selfish DNA conducted at different levels or with different goals. There has been recent interest in using selfish genetic elements to drive anti-pathogen genes into disease-vectoring pest populations in order to suppress transmission of human diseases such as dengue and malaria. We feel that the progress of research toward this goal has been hampered by a lack of interdisciplinary interaction. To help remedy this situation we held a workshop at NESCent on December 5,6 and 7th 2007which brought together researchers working on selfish DNA whose work is centered at different points along the continuum from basic to applied and from the molecular to population level. This workshop would fostered discussion among these researchers and we hope that it leads to new approaches for using selfish genetic elements to control vector-borne diseases. To broaden the reach of this workshop we have established a publically available wiki that can be reached at https://www.nescent.org/wg_selfishdna This wiki contains information on the workshop including pdfs of some of the presentations, pdfs of pertainent articles and preprints, as well as a link to user friendly computer simulation programs that track the spread of natural and synthetic selfish gene drive mechanisms and antipathogen genes. Some novel gene drive strategies are presented. If you have any comments on the content of the wiki or would like to add something to the wiki, please contact Fred_Gould@ncsu.edu

fred_gould@ncsu.edu fred_gould@ncsu.edu

Sequence assembly software

Hey all!!!

I am a graduate student in Molecular Phylogenetics Lab at Indian Institute of Science.

To assemble and crosscheck the sequence files, we need to buy a Sequence Assembly Software.

Please suggest some softwares that you are using for sequence assembly.

I would be glad if you will rate the software on a scale of 1-10 in terms of user satisfaction and software performance.

– Regards

Er. Rohini Bansal Ph.D. student Dr. Praveen Karanth's Lab CES, IISc, Bangalore-560012 India

bansalrohini@gmail.com

Sequence assembly software answers

Hi All,

Here is the compiled list of all the responses that i have received. Hope it is useful to you. :o))

Programs for sequence assembly:

* *

Geneious 3.5 (www.geneious.com)

PHRED/PHRAP applications available by request from the Green lab http://www.phrap.org/phredphrapconsed.html VectorNTI from Invitrogen features http://www.invitrogen.com/content.cfm?pageid=10071 Sequencher http://www.genecodes.com/ macvector (http://www.macvector.com/Products/macvectorassembler.html).

Codon Code Aligner (www.codoncode.com)

Vector NTI. it is free to academics.

freeware BioEdit. http://www.mbio.ncsu.edu/BioEdit/bioedit.html SeqMan, EditSeq and SeqBuilder programs of the Lasergene/DNAStar software for assembly and translation and MacVector for alignments. (http://www.dnastar.com/products/lasergene.php)

Se-Al

http://tree.bio.ed.ac.uk/software/seal/ – Regards

Er. Rohini Bansal Ph.D. student Dr. Praveen Karanth's Lab CES, IISc, Bangalore-560012 India

bansalrohini@gmail.com

Software BAPS 5 1

Hello all,

the most recent upgrade of BAPS software for population genetic analyses is now available also for 64-bit Windows and Linux systems, which enables handling much larger data sets as these systems can allocate more than 3GB RAM to a single process. Also, shortly after the recent announcement, the installation & usage for Mac OS X computers was simplified considerably by providing a script file that sets the paths needed by BAPS automatically.

The software can be obtained from:

http://web.abo.fi/fak/mnf//mate/jc/software/baps.html Hope you find these additions helpful!

Cheers, Jukka

bayesian@luukku.com

Software DAMBE

Dear Colleagues,

I have just uploaded a new version of DAMBE (4.5.66) at

http://dambe.bio.uottawa.ca/dambe.asp The installation instructions (as well as the installation package) are at

http://dambe.bio.uottawa.ca/-dambe_installation_instructions.asp It fixed a number of bugs (including a bug in the neighbour-joining method introduced perhaps quite sometime ago).

In particular, the new version has a few new genetic distances for phylogenetic studies with simultaneous estimation methods (see below). The traditional genetic distances were computed separately for each pair of sequences independent of other pairs. For example, the traditional K80 distance is derived from maximing the likelihood:

L_ij = Prob(sequences| d_ij, k_ij) where k_ij is the transition/transversion ratio. Such a distance is called an IE (independently estimated) distance and has been criticized for having three problems. First, they sometimes cannot be computed, i.e., inapplicable cases, especially for highly diverged sequences. Second, it is inconsistent because k_ij values are often different (i.e., k_12 <> k_13 <> k_23, etc.). These problems are exacerbated by limited sequence length. The third is insufficient use of information because the computation of pairwise distances ignores information in other sequences that should also contain information about the divergence between the two compared sequences. The DNADIST program in the PHYLIP package finds dij that maximizes Lij with a fixed transition/transversion ratio for all sequence pairs, but then one has to guess what transition/transversion ratio to use.

A simultaneous estimation method was presented by Tamura et al. (2004, PNAS) and implemented in MEGA4 for the TN93 model. In short, one find all distances as well as k1 and k2 that maximize

SL = Sum(lnL_ij).

The computation is through an iterative process. One first finds an approximate estimate of k1 and k2, keeps them fixed and find b_ij values that maximizes L_ij. Then one fixes then b_ij values and find k1 and k2 that maximizes SL, and so on. Finally one scales b_ij to d_ij.

The distance seems to perform outstandingly well and overcomes all three shortcomings we mentioned above associated with IE distances. This distance is terms “maximum composite likelihood” distance by Tamura et al. In DAMBE, it appears as “ML-CompositeTN93” and “ML-CompositeF84” in the menu for distance-based method with nucleotide sequences (Click ’Phylogenetics|Distance method|Nucleotide sequence’, with ML-compositeTN93 being the default). I will refer to them as ML-composite distance for short.

An alternative SE method is to use the least-square method. Take the TN93 model for example. For each pair of sequences, we have

SS_ij = (OP1_ij - EP1_ij)^2 + (OP2_ij - EP2_ij)^2 + (OQ_ij - EQ_ij)^2, where letters “O” and E stand for “observed” and “expected”, respectively.

We now find all d_ij and k1 and k2 that minimize

SS = Sum(SS_ij)

I have implemented this distance for both the F84 and TN93 models and they appear as “LS-compositeF84” and “LS-compositeTN93” in DAMBE’s menu for distance-based method (Click ’Phylogenetics|Distance method|Nucleotide sequence’). The distance seems to perform at least as good as ML-composite distances, and takes only about half as many cycles to converge.

I should appreciate your feedback.

For those who have not heard of DAMBE, it is a free integrated software package on the Windows platform for molecular sequence analysis. It recognize many different sequence formats, performs a variety of sequence alignment and phylogenetic analysis and is also a bioinformatics workbench (with position weight matrix and Gibbs sampler to identify function motifs, perceptron for identifying the differences between two group of sequences, dynamic programming algorithms for predicting RNA secondary structure and tRNA anticodon, HMM for protein secondary structure prediction, etc.). It takes only a few mouse clicks to install. To get started, just click ’File|Open standard sequence files’ and read in some sample files that come with DAMBE (in the C:\program files\DAMBE directory).

Best Xuhua

Dr. Xuhua Xia CAREG and Biology Department University of Ottawa 30 Marie Curie, P.O. Box 450, Station A Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 Fax: (613) 562-5486 URL: http://dambe.bio.uottawa.ca Xuhua.Xia@uottawa.ca Xuhua.Xia@uottawa.ca

Software TNT

One of the major programs for phylogenetic analysis, TNT (of Goloboff, Farris, and Nixon, 2003), formerly available for a license fee, has just been released as a free program, subsidized by the Willi Hennig Society. The program is available for download from its web site, http://www.zmuc.dk/public/phylogeny/tnt . Overview:

a.. Windows versions with GUI; all versions can be interactively driven with commands b.. a simple but powerful scripting language allows customization and "programming" of complex routines or simulations c.. Linux/Mac versions can run in parallel d.. Reads Nona/Hennig86 input data, as well as basic Nexus files. e.. Can export data and results easily to Nexus format f.. can overimpose legends on tree-branches (e.g. different support measures). Optimality criteria:

a.. analyses under pre-defined weights b.. analyses under implied-weights, either with standard or user-defined weighting functions (the latter including definition of clique-like weighting) c.. analyses under self-weighted optimization (i.e. dynamic weighting of character-state transformations) d.. standard (Fitch, Farris) characters, easily definable branched characters (=character-state trees), Sankoff (=step-matrix characters), continuous characters (from 0 to 65, with up to three decimals) e.. searches optionally collapse zero-length branches under different criteria (including SPR-TBR collapsing), or retain all distinct dichotmous trees Search options:

a.. exact ("branch-and-bound") searches applicable to relatively small data sets b.. random addition sequences plus TBR, applicable to medium sized data sets. c.. the fastest SPR-TBR swapping algorithms of any program d.. variety of search methods for large/complex data sets (sectorial searches, ratcheting and tree-drifting, tree-fusing and tree-hybridization) e.. recursive sectorial searches, using user-defined commands to analyze sectors f.. searches highly customizable via simple scripts g.. positive and negative constraints, flexibly defined h.. time-bound searches i.. can search for suboptimal trees (based on either fit difference and/or relative fit difference). Tree diagnosis:

a.. parsimonious mapping of character states b.. lists of synapomorphies c.. can summarize mappings or lists of synapomorphies based on sets of trees rather than one tree at a time d.. can display all most parsimonious reconstructions e.. counts of specific types of transformations f.. through the scripting language, it allows finding best state assignments with a fixed state at one or more nodes (for a given tree) Tree comparisons:

a.. strict, combinable components, majority, and frequency difference consensus trees b.. Semi-strict consensus supertrees, easy creation of MRP matrices (for subsequent supertree analysis under either parsimony or cliques) c.. finds taxa to prune to improve strict and combinable consensus trees d.. tree-distances: distortion coefficient, SPR-distances, agreement subtrees. Others can be easily calculated in conjunction with scripting language (e.g. number of "flippings", distance under MRP, triplets). e.. algorithms that help find taxa to prune to improve majority rule or frequency difference consensus trees, and group supports f.. easy comparisons of most similar groups between trees g.. comparisons of groups present in one tree but absent in another Group supports, randomization:

a.. generation of random trees (for testing in combination with scripts) b.. data permutation (alla PTP) c.. generation of random or simulated (jukes-cantor only) data sets d.. highly customizable jacknifing, bootstrapping, or symmetric resampling (searches can use any command defined by the user, or access scripts for analyzing resampled data sets in a special way) e.. Absolute and relative Bremer supports implemented natively (or easily with scripts) Scripting

a.. decision-making and control of loops b.. definition of variables (arrays with up to 5 dimensions) c.. easy access to internal variables to be used in decision making (number of taxa, trees, tree-scores, degree of resolution, branch lengths, tree-distances, etc.) d.. In Windows version, customizable dialogs e.. formatted output f.. easy access to taxon names, character names, branch-legends, etc., for use in formatted output g.. controls runs in parallel (Linux/Mac only), launching, monitoring, and controlling slave tasks. h.. tree-manipulations (including easy definition of branch-swapping routines) i.. allows manipulation of character-state reconstructions

Pablo A. Goloboff INSUE, CONICET, Instituto Miguel Lillo, Miguel Lillo 205 - 4000 S.M.Tucuman - Argentina Phone/FAX (+54381)-4232965

pablogolo@csnat.unt.edu.ar

UK systematists funding

The BBSRC Collaborative Scheme for Systematics Research (Co-Syst) is designed to provide short-term funding for new collaborative research in systematics and to support preliminary collaborative research that will form the basis of novel responsive mode proposals to either BBSRC or NERC. Applicants should be eligible to hold a UK Research Council grant. Further details from http://www.systass.org/awards/cosyst.shtml < http://www.systass.org/awards/cosyst.shtml >

"Julie A. Hawkins" <j.a.hawkins@reading.ac.uk>

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AdelaideU AncientDNA

Senior Research Associate (The Molecular Biology of Archaeology and Forensics) A 3-year Australian Research Council (ARC)-funded postdoc position is available at the Australian Centre for Ancient DNA in Adelaide from early 2008, to research and develop revolutionary new methods to extract and characterise DNA from a range of unusual ancient samples including sunken ship timbers, stone tools, hominid bones and teeth, and sediments. The project is an ARC LINKAGE collaboration with the National Geographic Society, Australian Federal Police, and Forensics South Australia. The main aim of the project is to re-design current ancient/damaged DNA approaches from the ground up, and to develop and extend recent new approaches to PCR such as SPEX (Brotherton et al. NAR 2007), and genomic library construction.

The candidate will need first-rate molecular biology knowledge and experience with an ability to work from a first principles basis, with minimal reliance on kits and pre-designed systems. The work will be experimentally challenging due to the difficult nature of the genetic templates, but this is a rewarding opportunity to undertake a complete re-design of current ancient DNA and molecular archaeological practice. An interest in ancient DNA, archaeology or natural history would be very useful, but the key requirement is expertise at the fundamental level in molecular biology and to a lesser extent, biochemistry.

The position will be supported by a 0.5 FTE technician, and will make use of the international quality ACAD facilities (<file://www.adelaide.edu.au/-ACAD>www.adelaide.edu.au/ACAD), and an extensive collection of >4,000 ancient samples from locations around the world covering the past 200,000 years.

ACAD is housed within the Department of Earth and Environmental Sciences, in the centrally located University of Adelaide (currently ranked 62nd in the world by the THES-QS). Research activities concentrate on molecular evolution, natural history, ancient DNA methods and practice, human evolution and forensics. ACAD is the ancient DNA node for the National Geographic Society's Genographic Project, using multiplexed SBE typing to analyse ancient human samples collected from around the world. Adelaide itself offers a very high standard of living (top 6 in the world, The Economist), with attractive weather, food, wine and beach environments, in an inexpensive setting with strong investment in Green Environments and Alternative Energy policies.

Further information about the position can be obtained from Prof. Alan Cooper, Dr Wolfgang Haak, Dr Kefei Chen or Dr Jeremy Austin and contact details are available at <file://www.adelaide.edu.au/-acad>www.adelaide.edu.au/acad Salary: (Level B) $66,700 - $79,207 per annum. Plus an employer superannuation contribution of 9-17% applies. Deadline: 31 January 2008. Please note the selection process is expected to take several months due to the timing of ARC funding and we expect to announce by late February/mid March. We anticipate a start date around April 2008.

You should have: * PhD or equivalent in Molecular Biology, with an interest/experience in biochemistry, archaeology/evolution, or forensics. * a strong commitment to excellence in research * a strong publication record commensurate with career stage Your application must: * include your rï¿½sumï¿½/Curriculum Vitae * address the selection criteria * include residency status * include the names, addresses and/or email details of three referees Email applications to maria.lekis@adelaide.edu.au or forward in duplicate to: Director, Australian Centre for Ancient DNA School of Earth & Environmental Sciences The University of Adelaide Darling Building South Australia 5005 Australia –

Prof. Alan Cooper ARC Federation Fellow Director, Australian Centre for Ancient DNA

Email: alan.cooper@adelaide.edu.au Ph: 61-8 -8303-5950/3952 Fax: 61-8-8303 4364

http://www.adelaide.edu.au/acad/ Mailing Address: Darling Building University of Adelaide North Terrace Campus South Australia 5005 Australia

alan.cooper@adelaide.edu.au

Barcelona DrosophilaChromosomeEvolution

Postdoctoral contract in Barcelona

We seek an enthusiastic and highly motivated person interested in carrying out research with the Group of Genomics, Bioinformatics and Evolution of the Universidad Autónoma de Barcelona on a project about the causes and consequences of chromosomal inversions in Drosophila (grant BFU2005-02237 funded by the Ministerio de Educación y Ciencia, Spain).

The postdoc will work on the distribution and evolution of the transposable element Galileo in the genus Drosophila. We have previously shown that this transposon is responsible for the generation of three polymorphic inversions in D. buzzatii. We also have bioinformatic evidence of a wide distribution of Galileo in the genus. We seek to determine the extent of the contribution of Galileo to chromosomal evolution

Recent publications of our group on this subject: Marzo et al. 2007. PNAS in press; Casals et al. 2005. Genetics 169:2047-2059; Casals et al. 2003. MBE 20: 674-685; Cáceres et al. 2001; Genome Res. 11:1353-64. Cáceres et al. 1999. Science 285: 415-418.

We will consider the candidate CV and will value previous experience with studies on transposable elements and experimental and bioinformatic techniques (cloning, Southern, PCR and RT-PCR, real time PCR, etc).

Period of the contract: February 2008-December 2009.

Total annual salary: ~30.000 euros

Application deadline: December 30, 2007

Applications. Candidates should send their application with CV and two names of researchers who know the candidate and can provide references (please include their e-mail address for contact) to

Dr. Alfredo Ruiz Gropo de Genómica, Bioinformática y Evolución Departamento de Genética y Microbiologia Facultad de Biociencias Universidad Autónoma de Barcelona 08193 Bellaterra (Barcelona)

Tel. 93-581-2729 Fax. 93-581-2387 E-mail: Alfredo.Ruiz@uab.es

Alfredo Ruíz Panadero <Alfredo.Ruiz@uab.cat>

CDC Atlanta InfluenzaEvolution

MODELING U.S. INFLUENZA DATA WITH CDC AND IMPERIAL COLLEGE

One postdoctoral position in biostatistics and mathematical modeling is currently available at the U.S. Centers for Diseases Control and Prevention, Atlanta, in close collaboration with MRC Centre for Outbreak

Analysis and Modeling, Imperial College London, UK

Open: present until March 2008

Length: anticipated for 2 years

Contacts:

- David Shay, CDC, USA dks4@cdc.gov

- Neil Ferguson, Imperial College, UK neil.ferguson@imperial.ac.uk

Salary: approximately $68,000 to $74,000 per annum, commensurate with training and experience

Location: U.S. Centers for Disease Control and Prevention, Atlanta, Georgia, USA

Project: understanding the spatiotemporal dynamics of seasonal influenza

A few studies have explored the inter-pandemic patterns of spatial spread of influenza, or the dynamics of genetic and antigenic evolution of influenza A viruses. This collaborative project between the Influenza Division, U.S. Centers for Disease Control and Prevention (CDC) and The MRC Centre for Outbreak Analysis and Modeling, Imperial College London, proposes to integrate these two aspects of influenza ecology and analyze influenza illness, excess mortality, and viral surveillance data collected by the Influenza Division, CDC. Influenza activity across the United States is monitored by several systems that operate on differing time and spatial scales. The influenza surveillance system includes influenza viral data, influenza-like-illness (ILI) data, excess mortality data, and data on the antigenic characterization of circulating viruses.

This collaborative project has several initial planned activities. First, datasets will be collated, cleaned, and normalized. At this stage, other datasets which could be relevant for this project will also be identified. Second, after examination of the consistency between the different data sources, epidemic patterns will be identified by using relevant methods for visualizing the data (e.g., time series, mapping, and movies) and a range of descriptive analysis. Spatial aspects of epidemics dynamics will be studied, including when and where epidemics start and how they spread across the United States and its territories. Influenza type and sub-type interactions will be investigated by examining the co-circulation and predominance of viruses during epidemics. Descriptive analysis methods which might be used include time series, wavelet and spatial correlation analysis. This work will allow the development of readily understandable and interactive representations of influenza activity for public health professionals and non-specialists, including policy makers.

The third component of the project will examine a variety of methods to use existing ILI and virus isolation data in further developing modeling of excess influenza-related mortality. Specifically, approaches to including simple mechanistic models of influenza-related mortality will be examined. A particular focus will be on regional or more finely geographically disaggregated models.

The fourth component of this project, which will be developed in parallel with the second and third, will explore hypotheses for the ecological drivers of the spatial dynamics of influenza transmission, influenza evolution, and the development of population immunity. By fitting space-time multi-strain models to surveillance and antigenic data, we will estimate immunity profiles of the population at the start and the end of each annual epidemic. The aim will be to highlight interactions between types and sub-types and to attempt to predict population immunity profiles from one season to subsequent seasons. An important part of this mechanistic modeling will be estimation of the effect of climate and other factors on the seasonality of influenza transmission in different U.S. regions. Analyses of this type are difficult to do with existing regression models, as the dynamical coupling between different regions (mediated by population movements) may induce strong correlations in disease incidence between locations.

Job description

The post holder will be involved in all aspects of the project, in collaboration with epidemiologists, statisticians, and virologists from CDC and mathematical modelers from Imperial College. He/she will be in charge of the collection and management of data, the development of innovative visualization methods and parts of the statistical analysis. He/she will also be involved in the development of mathematical models. The post holder will be expected to prepare and publish research papers in the peer-reviewed literature. The person appointed will be based at CDC in Atlanta, but will spend several weeks each year working with the Imperial College group in London; a postdoc from the Imperial College will also travel to Atlanta. It is expected that this post-doctorial

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

CornellU 2 QuantGenetics

USDA-ARS at Cornell University TWO Postdoctoral Positions in Quantitative/Population/Computational Genetics for Evolution by Artificial Selection

The Barley Coordinated Agricultural Project is a ground-breaking effort to apply association genetics to crop improvement in US elite barley germplasm. The data being created by this project is characterized by deep pedigrees, extensive marker data, population structure, inbreeding, and unbalanced design. To evaluate this data, we are assembling and adapting methods from plant, human and livestock genetics. These methods include imputation-based association mapping, genomic selection, and GxE analysis. The environment at Cornell includes nationally recognized research programs in population genetics, genomics and plant breeding, which will provide additional resources and stimulation.

Incumbents will work in the labs of Jean-Luc Jannink and Peter Bradbury on efforts to * Identify and make use of haplotypes in SNP data from barley inbreds, representative of North American elite and breeding pools. * Determine optimal QTL detection methods involving single-locus or haplotype methods * Scale-up genomic selection methods to datasets involving thousands of lines and markers * Apply data to the elucidation of the demographic and evolutionary history of elite barley

Preferred applicants should have a Ph.D. in quantitative, population, or computational genetics; knowledge of plant breeding; proven written and spoken communication skills and ability to work collaboratively. US citizens or Green Card holders are also preferred (others may apply but initial employment will be delayed). An excellent postdoctoral salary will be offered. Positions are for two years, extendible up to four. Earliest start date is 25 November 2007. The positions will remain open until good candidates are identified. A letter of interest in the position, C.V., and contact information for three references should be emailed to Jean-Luc Jannink and Peter Bradbury at: JeanLuc.Jannink@ars.usda.gov Peter.Bradbury@ars.usda.gov

– Jean-Luc Jannink, Small Grains Quantitative Geneticist USDA-ARS, Robert W. Holley Center for Agriculture and Health Phone +1 607 255 5266 Fax +1 607 255 6683 Email jeanluc.jannink@ars.usda.gov

Mailing Address: Cornell University Dept. of Plant Breeding and Genetics 407 Bradfield Hall Ithaca, NY 14853 USA

JeanLuc.Jannink@ARS.USDA.GOV

NatlUIreland Prokaryotic LateralGeneTransfer

Hi folks,I have a post-doc position available in my lab to work on the evolution of prokaryotic genomes and in particular the effect of LGT on metabolism.The position is available for 18 months and the total remuneration package equates to US$73,863/Euro 50,373/ STG 36,279 per annum, pro rata. This includes pension contribution and social insurance and the rate rises by 3.125% after one year.The work is entirely computational and will be carried out at the National University of Ireland Maynooth, which is located 15 miles/ 25 Km west of Dublin city.More details are available on request. The position is to start immediately.Kindest regards,James McInerney.Website: http://bioinf.nuim.ie/ james.o.mcinerney@nuim.ie james.o.mcinerney@nuim.ie

TulaneU FishMolecularEvol

A postdoctoral position is available in the Blum Lab < https://ent.tulane.edu/exchweb/bin/redir.asp?URL=http:/-/www.tulane.edu/ ˜ mjblum > in the Department of Ecology & Evolutionary Biology at Tulane University. The incumbent will engage in collaborative research exploring aspects of molecular ecology, landscape genetics, macroecology and/or biogeography of freshwater fishes using theoretical and empirical approaches. Topics of interest in the lab include: the use of genetic tools for assessing aquatic environmental condition; environmental determinants of hybridization among freshwater fishes; metapopulation dynamics of fishes in urban streams; the evolutionary origins of freshwater fish diversity across eastern North America; and island biogeography of amphidromous and secondary freshwater fishes. There is considerable flexibility in the focus of the research the incumbent will conduct, and the incumbent will be encouraged to develop new areas of expertise. However, it is imperative that any research that is undertaken facilitates interactions between the incumbent and members of the lab.

Preference will be given to candidates possessing in-depth knowledge of modern molecular techniques and quantitative skills. However, candidates who are carrying out innovative research and who have the desire to develop laboratory skills are encouraged to apply. An initial appointment will be for one year, with continuation for up to two additional years dependent upon performance. A starting date of January 2008 or a mutually agreeable date early in 2008 is strongly preferred. Salary will be commensurate with experience and qualifications. REQUIREMENTS: Ph.D. in ecology, genetics, or closely related field. Send via email attachment a letter of application, curriculum vitae, statement of research interests, and names and addresses of three references to Michael Blum at mjblum@tulane.edu. Tulane University is an Affirmative Action/Equal Employment Opportunity Employer. Women and minorities are encouraged to apply.

“Blum, Michael J ” <mjblum@tulane.edu>

UAarhus PlantInvasives

Two Postdoc positions are available in the beginning of next year (application deadlines the 31st of January and the 1st of February, respectively) at the section of Plant Biology, Department of Biological Sciences, Plant Biology, University of Aarhus Denmark.

The postdocs will work with the the physiological ecology and genetics of aquatic plants with emphasis on invasive and non-invasive species.

The call for applications can also be found at the department homepage:

http://www.biology.au.dk/biologi.stillinger < http://www.biology.au.dk/biologi.stillinger > (...choose English in the left corner..)

Tenna Riis, Assoc. Prof. PhD Dept. of Biological Sciences University of Aarhus Ole Worms Alle, Build. 1135 8000 ??rhus C Denmark Phone: +45 8942 4725 Cellphone: +45 6020 2641 Fax: +45 8942 4747

Tenna Riis <tenna.riis@biology.au.dk>

UArizona MulticellularityEvol

A POSTDOCTORAL POSITION is available in the laboratory of Dr. Richard E. Michod (http://www.eebweb.arizona.edu/Michod/) in the Department of Ecology and Evolutionary Biology at the University of Arizona (Tucson, AZ; http://eebweb.arizona.edu/). We are looking for a motivated, enthusiastic and independent individual with a strong background in evolutionary biology and/or genomics and molecular biology to address questions concerned with the evolution of multicellularity, using the green algal group, Volvocales, as a model-system. Experience working with green algae is not critical. Current projects in the lab include studying the genetic basis for the evolution of germ-soma differentiation, measuring life history trade-offs as colony size increases, and artificial selection experiments on body size in volvocalean green algae.

To apply, please e-mail (shanley@email.arizona.edu) with the following information: a statement detailing your research interests and qualifications, a CV, and the names and contact information of three references.

The initial appointment is for one year, with an additional two years' funding available conditional on satisfactory performance. The position is funded by an NSF grant, at 35K per year (plus benefits). The start date is flexible (as early as Feb. 1, 2008).

The University of Arizona is an EO/AA Employer.

nedelcua@email.arizona.edu nedelcua@email.arizona.edu

UBritishColumbia EvolMorph MarineProtist

Postdoctoral Research Position: Evolutionary Morphology, Marine Protistology Departments of Zoology & Botany University of British Columbia

Postdoctoral Research Position: Evolutionary Morphology, Marine Protistology Departments of Zoology and Botany University of British Columbia

The Laboratory of Protozoan Diversity and Evolution (http:// www3.botany.ubc.ca/bleander/index.html) is looking for a broadly trained, self-motivated and enthusiastic individual interested in exploring the evolutionary morphology and molecular phylogeny of marine predatory flagellates.

The lab is focused almost exclusively on characterizing uncultured (or difficult to culture) marine microeukaryotes using state-of-the- art approaches that incorporate fieldwork, light microscopy, scanning electron microscopy, transmission electron microscopy and molecular phylogenetics. Although the successful applicant will play a major role in developing specific projects, research centered on the discovery, biodiversity and character evolution of marine dinoflagellates, euglenids and meiofauna will be encouraged.

The applicant must have a Ph.D., excellent written and oral communication skills, and demonstrated interest and expertise in comparative organismal biology, macroevolution and systematics. Additional experience with any or all of the following is highly desirable: marine biology; endosymbiosis; light microscopy; FISH; transmission and scanning electron microscopy; image processing (e.g. Abobe Photoshop and Illustrator); standard molecular techniques associated with PCR, cloning and sequencing; molecular phylogenetic analysis; and the interpretation of ultrastructural data from eukaryotes. The research will involve routine field collections in nearby habitats, including the Bamfield Marine Sciences Centre (www.bms.bc.ca) located on the west side of Vancouver Island. The successful applicant will be reappointed each year for 3 years, contingent on satisfactory progress, and be expected to participate in the UBC Centre for Microbial Diversity and Evolution (http:// www.cmde.science.ubc.ca/). The postdoctoral research position is available in June of 2008, but the actual start date is negotiable.

If interested, please email a short cover letter outlining your research experience and interests, a curriculum vitae and contact information for 3 referees to:

Brian Leander Email: bleander@interchange.ubc.ca, Departments of Zoology and Botany, University of British Columbia, #3259-6270 University Boulevard, Vancouver, B. C. V6T 1Z4, Canada, Tel: (604) 822-2474, Fax (604) 822-6089

The closing date for applications is January 18, 2008, but the position will remain open until filled.

UBC hires on the basis of merit and is committed to employment equity. We encourage all qualified persons to apply. However, Canadians and permanent residents of Canada will be given priority.

bleander@interchange.ubc.ca bleander@interchange.ubc.ca

UCaliforniaRiverside EvolutionaryBiology

The UC Riverside Chancellor's Postdoctoral Fellowship for Cultivating Diversity in Science, Engineering and Mathematics solicits applications from individuals with a demonstrated commitment to increasing the number of underrepresented ethnic minority faculty members in research institutions. The program is open to individuals with doctoral degrees in Science, Engineering and Math who are committed to careers in academia, and whose teaching, research or service will help UCR address the barriers that prevent full participation of underrepresented minority groups in academic careers in the STEM fields. The program provides postdoctoral fellowships, research opportunities, mentoring and guidance in preparation for academic career advancement.

Deadline for applications is January 15, 2008

For full instructions and more information about the program, please see the following website (you may have to cut and paste the link into your browser):

http://academicpersonnel.ucr.edu/awards/-chancellorPostDocFell owship.php

Marlene Zuk Professor of Biology and Associate Vice Provost, Faculty Equity and Diversity University of California Riverside, CA 92521 USA

Phone: 951-827-3541 email: VPequity@ucr.edu

UCaliforniaRiverside FungalPopGenet

Postdoctoral position in fungal population genetics, University of California, Riverside

This position is being re-advertised due to the last candidate obtaining a permanent position prior to starting. We need someone ASAP so please only apply if qualified and ready to start work very soon.

A full-time postdoctoral position is available in the laboratories of Greg W. Douhan and Frank P. Wong in the Department of Plant Pathology and Microbiology at the University of California, Riverside. The focus of the research is to investigate the population biology of Pyricularia grisea, causal agent of gray leaf spot of turf and rice blast. This work is currently in progress, therefore, a qualified candidate would have the opportunity to immediately begin collecting genotypic data using AFLP and/or microsatellite markers from sampled populations. DNA has been extracted from a large collection of isolates and mating type data has already been collected. This could prove to be a fruitful position for an ambitious candidate since there could be many additional research opportunities to work on other projects within the two labs. Candidates should have a Ph.D. degree in plant pathology, genetics/genomics, bioinformatics/computational biology, or related disciplines. Proven ability to publish is highly desirable. Good analytical skills within population genetics and/or systematics are expected. Interest and/or experience working with fungi is not essential but is desirable. The position has guaranteed funding for one year with a high likelihood of multi-year extension of funding. Salary is commensurate with experience and qualifications, with a minimum of $32,000/year. Postdoctoral researchers receive full University of California benefits. Interested individuals should send a curriculum vitae, contact information for three references, electronic copies of at least two publications or manuscripts in progress that demonstrate the candidate^{1}s skills, and a cover letter describing their interest in the position to gdouhan@ucr.edu. Please put: "post doc" in the subject line of the email.

Greg W. Douhan,

Department of Plant Pathology and Microbiology, University of California Riverside, Ca 92521 Office: (951)-827-4130

Greg Douhan <gdouhan@ucr.edu>

UGeorgia PlantEvolutionaryGenet

UNIVERSITY OF GEORGIA DEPARTMENT OF GENETICS

POSTDOCTORAL POSITION IN PLANT ECOLOGICAL GENETICS

A postdoctoral position is available in my lab to examine the genetic basis of complex traits in plants. I am particularly interested in an individual with skills in QTL mapping, specifically genetic marker development in non-model species. The project is part of a larger project on the ecological genetics of adaptation in plants.

I am interested in hiring someone with some background in evolutionary or ecological genetics and with excellent bench skills. The ideal candidate will be organized, pay close attention to detail, and be able to work both independently and in collaboration with others. Independent side projects on the part of the postdoc are encouraged and will be supported intellectually and financially if feasible. A Ph.D. is required

There is also an opportunity for this postdoc to gain independent teaching experience (for extra pay) by teaching a small, 1-credit, discussion section for our undergraduate evolutionary biology course each semester.

The start date is flexible. The initial appointment is for one year, with an additional two years' funding available conditional on satisfactory performance. The annual salary for this position will be commensurate with experience, and includes benefits. The University of Georgia is an Equal Opportunity Employer and I encourage applications from candidates from groups underrepresented in the life sciences.

Please send me an e-mail (mauricio@uga.edu) with the following information: a statement detailing your interest and qualifications for the position, a CV, a statement of your research interests, and the names and contact information for 3 people who could write on your behalf. The position is available immediately and applications will be reviewed until the position is filled.

The Mauricio lab is a part of the diverse and interactive UGA Department of Genetics, for which more information can be found at http://www.genetics.uga.edu/ . Rodney Mauricio Department of Genetics Davison Life Sciences Building University of Georgia Athens, GA 30602-7223 mauricio@uga.edu http://www.genetics.uga.edu/mauriciolab –

Rodney Mauricio, Ph.D. Department of Genetics Phone: (706) 542-1417 University of Georgia FAX: (706) 542-3910 Athens, GA 30602-7223 e-mail: mauricio@uga.edu

Lab Web Page: http://www.genetics.uga.edu/mauriciolab PIRE Grant Web Page: http://www.genetics.uga.edu/pire Evolution at UGA: http://www.genetics.uga.edu/evolution mauricio@uga.edu mauricio@uga.edu

UIllinois HymenopteraSystematics

Postdoctoral Research Associate, University of Illinois (Parasitoid Wasp Systematics and Bioinformatics)

A 2-year postdoctoral research associate position is available in the Department of Entomology (http://www.life.uiuc.edu/entomology/index.html at the University of Illinois, Urbana-Champaign. The position is associated with NSF-funded research on braconid parasitoid wasps in the laboratory of Dr. James Whitfield (http://www.life.uiuc.edu/whitfield). The Department of Entomology has recently been ranked #1 nationally among Entomology graduate programs, and the postdoc will join a leading laboratory in insect molecular systematics with close ties to other top insect systematics labs both on campus and at the Illinois Natural History Survey.

Molecular systematics of the hyperdiverse genus /Heterospilus/

Funded by NSF RevSys 0717365, this project combines monographic taxonomic work on the speciose braconid wasp genus /Heterospilus/ in Costa Rica with a multigene phylogenetic exploration of the genus on a broader (world) geographic scale. The postdoctoral associate will assist Dr. Paul Marsh (http://www.life.uiuc.edu/whitfield/Paul_Marsh.html) with the taxonomic part of the study, databasing the taxonomic data and illustrations, designing online interactive identification keys, and helping author a Tree of Life webpage for the group. Parallel to this work, under the direction of Dr. Whitfield, a graduate student (position being advertised separately) will extract, amplify and sequence each of 3 genes from roughly 200 species of wasp, and conduct molecular phylogenetic analyses to test monophyly of the genus worldwide, and to explore relationships within the genus, especially for the neotropical fauna. For the postdoctoral position, some research experience in insect systematics is required, and experience with biodiversity informatics packages such as mx, Delta or LucID is highly desirable. The position is available as soon as Summer 2008.

Interested candidates should submit the following (preferably by email) to Dr. James Whitfield (jwhitfie@life.uiuc.edu):

1) A letter stating why you want to apply for the position, and why you think you would be the best person for this research. Please also include a broader perspective on your career and graduate school objectives. 2) A current curriculum vitae, including any previous research projects you have been involved with, honors, awards, publications and presentations. 3) A list of relevant field, laboratory and analytical techniques with which you have experience. 4) Names and contact information (email, phone, address) for at least 3 people who can supply reference letters.

We will begin assessing applications during late December. On order to receive full consideration for this position, please submit application materials by January 10 2007.

jwhitfie@life.uiuc.edu

UKansas PhylogeneticTheory

A POSTDOCTORAL POSITION is available in the laboratory of Dr. Mark Holder in the Department of Ecology and Evolutionary Biology at the University of Kansas (Lawrence, KS). The research will focus on theoretical and computational issues in systematics (particularly phylogenetics). The position is available for two years. At least one year will be devoted to developing software for inferring phylogenetic trees from unaligned sequences (simultaneous alignment and tree inference). Research topics for the other year of work could include topics initiated by the candidate, or current research projects in the Holder lab – these include the improvement of context-dependent model of protein- coding sequence evolution, and the development of robust methods of Bayesian phylogenetic analyses. Candidates will be expected to have completed a PhD in Biology, Statistics, Computer Science or a related field. Preferably the candidate will exhibit competence in at least one programming language (C, C++, python, Java, or Perl are preferred). The ideal candidate will be enthusiastic, motivated, have a strong background in phylogenetics, and have experience implementing statistical inference techniques in software.

Responsibilities and percent of time: 80% Experimental research 20% Publication of results

Required Qualifications: 1. Biology, Statistics, Computer Science or a related field 2. A strong background in bioinformatics as demonstrated by materials submitted through the application process, work experience, and letters of references, and/or previous publications.

Preferred qualifications: 1. Strong background in phylogenetics 2. Creative, enthusiastic and highly motivated 3. Programming skills 4. Strong background in computer science, math, and/or statistics. 5. Excellent oral and written communication skills

Salary: Based on experience of the candidate, but not less than $40,000 per year.

Fringe Benefits: Unclassified staff benefits as determined by the State of Kansas

The University of Kansas is an EO/AA Employer.

Target date of employment: May 01, 2008

Application details:

To apply, go to https://jobs.ku.edu and search for position #00206565.

You will be asked to provide: * current CV * statement of research interests, and * the names (and email contact information) for three references.

Amendments and news for this position will be posted at: http://people.ku.edu/ ˜ mtholder/postdoc Mark Holder

mtholder@ku.edu http://www.people.ku.edu/-˜mtholder/ Department of Ecology and Evolutionary Biology University of Kansas 6031 Haworth Hall 1200 Sunnyside Avenue Lawrence, Kansas 66045

lab phone: 785.864.5789 alt. phone: 785.371.4666

fax (shared): 785.864.5860

mtholder@ku.edu mtholder@ku.edu

ULiverpool Bioinformatics

Dear All,

A post-doctoral bioinformatics position is available in the School of Biological Sciences, Liverpool to work with Steve Paterson and Andy Cossins (Liverpool) and Charles Tyler (Exeter). This work is funded by the NERC PGP programme. Closing date is 1st Feb 2008.

You will join a research team investigating global gene expression responses of a number of environmentally important organisms. The project will involve the detailed bioinformatic interpretation of gene lists derived from microarray studies and includes the development of data pipeline tools and analytical methods. You should have a PhD with a background in computing or biological sciences and have experience of bioinformatics with the ability to work as part of a team. A track record of publication is desirable. The post is available for 2 years initially.

Ref: R-567079

Further details from the UoLiverpool HR website:

http://www.liv.ac.uk/working/job_vacancies/-research/R-567079.htm Informal enquiries to Steve Paterson

Dr. Steve Paterson Lecturer in host-parasite biology School of Biological Sciences University of Liverpool LIVERPOOL, UK L69 7ZB

Tel. 0151 795 4521 Mob. 0151 794 7668 Fax. 0151 795 4408 email s.paterson@liv.ac.uk Rm. 202 Biosciences Building http://pcwww.liv.ac.uk/-˜stevep11/PatHome.html Steve Paterson <s.paterson@liverpool.ac.uk>

UMassAmherst DarwinFellow

DARWIN FELLOW

The Graduate Program in Organismic and Evolutionary Biology at University of Massachusetts Amherst announces a two-year POSTDOCTORAL FELLOWSHIP/LECTURESHIP. OEB draws together more than 80 faculty from the Five Colleges (University of Massachusetts Amherst and Smith, Hampshire, Mount Holyoke and Amherst Colleges), offering unique training and research opportunities in the fields of ecology, organismic and evolutionary biology. Our research/lecture position provides recent PhD's with an opportunity for independent research with an OEB faculty sponsor as well as experience developing and teaching a one-semester undergraduate biology course. Position subject to availability of funds. 1st year salary: $30,000. 2nd year salary: $32,000. To apply, send curriculum vitae, three letters of reference, statements of research and teaching interests, and letter of support from your proposed OEB faculty sponsor. A list of faculty and additional information is available at www.bio.umass.edu/oeb .OEB Darwin Fellowship 319 Morrill Science Center 611 N. Pleasant Street University of Massachusetts Amherst Amherst, MA 01003 413-545-0928 darwin@bio.umass.edu Application review begins: 1/11/08 Start date: 8/17/08

The University of Massachusetts Amherst is an Affirmative Action/ Equal Opportunity Employer. Women and members of minority groups are encouraged to apply.

adam porter <aporter@ent.umass.edu>

UMichigan YeastEvolutionaryGenet

A POSTDOCTORAL POSITION is available in the laboratory of Dr. Jianzhi (George) Zhang (http://www.umich.edu/˜zhanglab/) in the Department of Ecology and Evolutionary Biology at the University of Michigan, Ann Arbor, Michigan. We are looking for a motivated and independent individual with a strong background in yeast molecular genetics or yeast functional genomics to address questions concerning the evolution of duplicate genes, evolution of reproductive isolation, and/or gene expression evolution. Experience in experimental yeast genetics is required and a strong interest in evolutionary genetics/genomics is a plus.

To apply, please e-mail jianzhi@umich.edu with the following information: a brief statement about your research interests and qualifications, a CV, and the names and contact information of 2-3 references.

The initial appointment is for one year, with the possibility of renewal conditional on satisfactory performance. The start date is flexible (as early as Feb. 1, 2008).

jianzhi@umich.edu jianzhi@umich.edu

UniCollegeCork BioinformaticsEpigenetics

UniCollegeCork.BioinformaticsEpigenetics

Our lab is seeking applications from highly motivated postdocs interested in applying bioinformatic and molecular evolutionary approaches to the identification and characterisation of genes under epigenetic regulation in eukaryotic genomes. We seek enthusiastic and highly motivated candidates with excellent and proven skills in bioinformatics and genetics (as demonstrated by their publication record). We particularly seek candidates who have proven proficiency in the following platforms and languages; Unix, Perl/Python, R, BioPerl/BioPython, Bioconductor, postgresql/mysql. Programming experience in C/C++/Java would also be advantageous. Prospective applicants should send an e-mail outlining your research interest and motivations, including; (a) your C.V. (please list publications and experimental skills) & (b) contact details and e-mail addresses for 3 referees to:

Dr. Charles Spillane, Genetics & Biotechnology Lab, Biochemistry Dept & Biosciences Institute, University College Cork, Cork, Ireland. E-mail: c.spillane@ucc.ie

Lab website: www.ucc.ie/spillane Deadline: 12th January 2008 UCC is an equal opportunities employer

Dr. Charlie SPILLANE, SFI Investigator & Senior Lecturer, Genetics & Biotechnology Lab, Dept of Biochemistry & Biosciences Institute, University College Cork (UCC), 2.10, Lee Maltings, Cork, IRELAND

[T] 00-353-21-4904124 (office) [E] c.spillane@ucc.ie [W] www.ucc.ie/spillane "Spillane, Charles" <C.Spillane@ucc.ie>

UOslo EvolutionaryTheory

Post-doctoral position in theoretical evolutionary biology

Available at the Center for Ecological and Evolutionary Synthesis (CEES), Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo

A postdoctoral research position is available to work with Prof. Thomas F. Hansen on topics in theoretical biology. The appointment is for two years and is funded through the University. Preferred starting date is as soon as possible. The general topic of the lab concerns the evolution of evolvability and the interplay between adaptation and constraints. These questions are approached through mathematical and computational modeling, through data analysis, and through development of new methods of statistical analysis. Several of the ongoing projects in the lab are focused on understanding how the structure of the genotype-phenotype map, including epistasis and pleiotropy, affects the variability and evolvability of phenotypic traits. We are studying genetic architecture both through dynamical modeling and through the development and application of statistical methodology. One possible project involves modeling of gene-regulatory networks with the aim of understanding the effects of network structure on evolvability. Other projects are focused on developing and applying methods for assessing evolvability, selection, and rates of evolution in time series or comparative data.

The position is flexible in regard to the exact topic of research, and the successful applicant can be involved in any one of several ongoing projects.

The position offers ample opportunity to work at the interface between theory and data analysis within a broader group of researchers and students with strong expertise in theoretical and statistical modeling. The successful candidate will be encouraged to pursue his/her own ideas as long as these fall within the broad topic of the lab.

We are seeking a candidate with interest in theoretical and conceptual issues of evolutionary biology and evolutionary genetics including the relationship between genotype and phenotype and the role of constraints in evolution. Expertise in one or more of the following areas is particularly relevant: Mathematical or computer modeling, statistics, developmental genetics, and population/evolutionary genetics. Applicants must hold a degree equivalent to a Norwegian doctoral degree. Please contact Thomas Hansen at the below address for more detail.

The CEES is a semi-autonomous interdisciplinary research group within the Department of Biology that combines the skills of population ecologists, evolutionary biologists, geneticists, and statisticians. It has a strong international flavor, and currently employs 13 faculty, 33 postdocs/researchers, 49 graduate students, and 16 associate scientists. The CEES has been awarded status as centre of excellence by the Norwegian Research Council, and is well funded.

The University of Oslo is an equal opportunity employer and seeks in particular to increase its number of female scientists. Women are therefore particularly encouraged to apply. The University of Oslo also wants more people with an immigrant background in permanent academic posts. Such people are encouraged to apply.

Contact Person: Professor Thomas F. Hansen tlf. +47 22854521, e-mail: thomas.hansen@bio.uio.no. Information about the centre can be found at: http://www.bio.uio.no/cees Pay Grade: 54-60 (NOK394700,- NOK439300, 50000 - 55000, $71000-$79000 depending on qualifications and seniority)

Application Deadline: January 22., 2008

Ref. No.: 07/14591

Application, CV (marked Ref. No.), confirmed certificates etc., up to 5 scientific papers (4 copies) as well as suggested research plan including a statement about the relevance of qualifications should be sent to: Faculty of Mathematics and Natural Sciences, attn. Senior Executive Officer Bente Schjoldager, P. O. Box 1032 Blindern, N-0315 Oslo, Norway.

Thomas Hansen <t.f.hansen@bio.uio.no>

UppsalaU AvianEvolutionaryGenomics

Post-doc in evolutionary genomics

at the Evolutionary Biology Centre, Uppsala University, Sweden Centre of Excellence in Evolutionary Genomics

Genome sequencing (6x coverage) of the second bird species to have its genome characterised - the zebra finch - has just been completed. A post-doc position focusing on evolutionary genomic and molecular evolutionary analysis of the zebra finch genome sequence is now available in Hans Ellegren's laboratory

The zebra finch is an important model species for neurobiology. and has led to several important discoveries. The production of new neurons in adult brain was first reported in zebra finch, which challenged the universally held dogma that neurogenesis does not occur in adults. Research in this species also demonstrated that active synthesis of estrogen in the zebra finch brain, causing masculine patterns of neural development and challenging the view of estrogen being a strictly gonadal steroid. Songbirds are unique among non-humans in their combination of vocal sophistication and experimental accessibility. Like humans, songbird vocalizations are learned and this learning process has close similarities to human speech. For example, FOXP2, the first gene linked to speech disorder in humans is also expressed in the neural song circuit of zebra finch, especially at times of vocal learning.

The project involves whole-genome analysis of molecular evolutionary processes in avian genomes. This will include analyses of, among other things, adaptively evolving genes, conserved non-coding DNAs, evolution of novel genes and expansion of gene families. The main source of data comes from the comparison of the chicken and zebra finch genomes, as part of the zebra finch genome sequencing project, however, there is also sequence data from additional bird species obtained through 454 sequencing. In addition, evolution of gene expression will be studied based on transcriptome profiling and population genomic analyses will be done based on large-scale SNP data.

The successful applicant must hold a PhD and should have experience from large-scale molecular evolutionary analyses using bioinformatic approaches. Programming skills are desirable. The position is for two years, with possibilities for extension, and is within a lab group of about 10 people including PhD students and international post-docs.

The position is immediately available and the search will remain open until the position is filled.

To apply, please send a CV, a description of research interest and the name and contact details of two references to Prof Hans Ellegren at Hans.Ellegren@ebc.uu.se (Dept of Evolutionary Biology, Norbyvägen 18D, SE-752 36 Uppsala, Sweden).

Further information about the laboratory can be found at http://www.egs.uu.se/evbiol/Persons/Hans.html – Prof Hans Ellegren Dept of Evolutionary Biology Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala

Phone: +46-18-4716460 Fax: +46-18-4716310 Email: Hans.Ellegren@ebc.uu.se

Lab home page: http://www.egs.uu.se/evbiol/index.html Personal home page: http://www.egs.uu.se/evbiol/Persons/Hans.html Hans.Ellegren@ebc.uu.se Hans.Ellegren@ebc.uu.se

UppsalaU CanieEvolution

Postdoctoral position in conservation genetics and/ or late Pleistocene population genetics of Canis species.

Fellow would be a member of the Quaternary Genetics group in the Department of Evolutionary Biology at the Evolutionary Biology Centre at Uppsala University, in Uppsala, Sweden. http://www.egs.uu.se/evbiol/Research/quaternarygenetics.html The Evolutionary Biology Centre provides a highly stimulating research environment and has one of the largest concentrations of evolutionary biologists in Europe. http://www.ebc.uu.se/index_eng.php Project involves population level genetic analyses of coyotes, wolves or jackals and modern, historic and/ or late Pleistocene populations.

The candidate must have a PhD in relevant field and should work well both as a member of the group and independently. To apply, please send letter of application including research interests, a c.v., and contact details for two or three references by e-mail (Jennifer.Leonard@ebc.uu.se). I can also be contacted for further information regarding group and/ or project. Position open until filled, but for full consideration, apply by January 10, 2008. Final applicant's c.v. must be approved by the funding foundation. Position is for one year and would be paid 18,000 SEK per month (approximately US$ 2,800/ month).

Preferred start date: early 2008.

– Jennifer Leonard Department of Evolutionary Biology Uppsala University Norbyvägen 18D SE-752 36 Uppsala (Sweden) Tel. +46-18-471 6466 Fax. +46-18-471 6310 Jennifer.Leonard@ebc.uu.se http://www.egs.uu.se/evbiol/Persons/Jennifer.html jennifer.leonard@ebc.uu.se jennifer.leonard@ebc.uu.se

UTuebingen Robot sex

I have funding for a 5-year, EU-funded postdoc position to work on virtual genetic recombination in robots ("robot sex") at the University of Tuebingen. This position is part of the large interdisciplinary network SYMBRION in which swarm robots are developed and used to study emergent properties (details on www.symbrion.org).

The position is available from 1st February 2008.

Work description 1. Development of a virtual genome for robots with all options to recombine and improve through selection and evolution. Testing this genome on a simulation platform for initial optimization and debugging before transplantation to real robots. 2. "Ecological experiments" in which the evolution of sexuality and gender is investigated using robots as an omnipotent model system (many options, in part depending on own interests and creativity, conflict and cooperation within and between the sexes, within and between "species"). 3. Attending SYMBRION meetings, reporting on progress to the other members of the framework. 4. Although the project itself has guaranteed core funding (salary and basic expenses), the successful candidate is expected to apply for additional external funding to generate a small research group with undergraduate and postgraduate students.

Required qualifications The preferred candidate has recently finished her/his Ph.D. degree in Theoretical Biology, with a subject in the broad field of the Evolution of Sex or Sexual Selection. Good programming and computer skills are essential in order to be able to share in the development of simulation tools within the network. Excellent communicative abilities (particularly in English), a natural tendency to work in teams, and to travel regularly to other partners are equally essential. The robot platform (electronics, hardware control) will be developed by other groups. Nevertheless, some experience in robotics or electronics may be useful in order to optimize communication with the other partners.

Working environment My group is particularly interested in the evolution of reproductive modes and antagonistic coevolution, e.g. between the sexes or between parasites and hosts. We work on a wide variety of organisms in the field as well as in the lab. The group consists of a core of 10 university-appointed staff (4 scientists) plus 15 students, 9 of which are Ph.D. students. See www.uni-tuebingen.de/evoeco for information.

We are a member of “EvE”, the Evolution and Ecology Forum Tuebingen, which is an association of 15 Professors from the Faculties of Biology, Geosciences, Informatics and from the Max-Planck-Planck Institute of Developmental Biology. EvE is currently developing into an interfacultary network studying the short-term and long-term consequences of organismal interactions.

Tuebingen is a small, historical, university town in a beautiful part of Europe, between the Black Forest and the Swabian Alb. The climate is continental, with cold winters and hot summers. Of particular importance for this project is the close vicinity to the University of Stuttgart (approx. 35 km), where the initiators of SYMBRION are located and where the robot platform is being developed. Tuebingen is quite cosmopolitan, with a strong foreign community. It is easy to get around with English, but learning a bit of German helps.

Application Please send pdfs of your application documents (cv, application letter, 3 names of possible referees) to nico.michiels@uni-tuebingen.de. Selection will start from 15 January 2008 and continue until the ultimate candidate has been identified. I am also happy to answer any questions you may have.

Nico K. Michiels (Prof.) Animal Evolutionary Ecology Zoological Institute, Faculty of Biology University Tuebingen Auf der Morgenstelle 28 E 72076 Tuebingen Germany

Tel. +49 7071 29 74649 Mobile +49 170 4758003 Fax +49 7071 29 5634

nico.michiels@uni-tuebingen.de http://www.uni-tuebingen.de/evoeco http://www.eve.uni-tuebingen.de

Nico Michiels <nico.michiels@uni-tuebingen.de>

UWashington EvolutionPlantDev

Postdoctoral Position in Evolution of Plant Development

Position available to study the genetic and developmental basis of flower diversity in the laboratory of Dr. Verï¿½nica Di Stilio at the University of Washington in Seattle, WA, USA. Research is on the basal Eudicot genus Thalictrum (Ranunculaceae), using an evolution of development approach towards understanding morphological diversification of flowers. Current focus is on transcription factors as key regulators of development, in particular belonging to the MYB and MADS box families, that regulate organ identity and tissue differentiation in the flower. Requirements: PhD in Plant Biology, Molecular, cellular, developmental, evolutionary biology or related field. Basic molecular biology and microscopy skills required. Ability to perform in situ hybridizations, transgenic techniques, molecular evolution and phylogenetic analyses desired. Funding is available for 2 years beginning as early as January of 2008. Review of applications will begin immediately and continue until the position has been filled. Please send CV, research statement and 3 reference contacts to: Verï¿½nica Di Stilio, Department of Biology, University of Washington, Hitchcock Hall 506, Box 351800, Seattle WA 98195-1800. E-mail: distilio@u.washington.edu

Verï¿½nica S. Di Stilio, PhD Assistant Professor Department of Biology University of Washington Hitchcock Hall 506 Box 351800 Seattle WA 98195-1800 (206) 616-5567 off (206) 685-4755 lab FAX (206) 616-2011

distilio@u.washington.edu

YaleU EvolutionaryMedicine

Postdoctoral Associate-To work on a project that utilizes the data of the Framingham Heart Study to investigate the genetic variance-covariance structure either of (1) age at menarche, age at menopause, age at death, biomarkers of inflammation, and associated SNPs to test hypotheses on the role of inflammation in aging or of (2) traits in the first two cohorts in the study and their relationship to phenotypic selection gradients to estimate the rate of evolution in a contemporary human population. Salary $40,000; position for one year with a second year possible given satisfactory performance. Starting date negotiable. Yale University is an Affirmative Action/Equal Opportunity Employer. Applications from women and minority are encouraged. Send applications by email to Stephen Stearns (stephen.stearns@yale.edu); include a statement of interest, a CV with publication list, and the coordinates of two referees. Application deadline is January 15, 2008. Position will remain open until filled.

stephen.stearns@yale.edu

YaleU GalapagosConsGenet

Post-doctoral position to work on Galapagos Giant tortoises or marine iguanas

We are looking for a person interested in joining our research group to work on the evolutionary genetics and conservation of two charismatic Galapagos reptiles: Giant Tortoises and marine iguanas. Our lab has been involved in studying these organisms for the past 15 years. The perfect candidate should have a demonstrated track record showing competence in any the general fields of evolutionary genetics, molecular systematics, phylogeography and conservation genetics. Knowledge of Spanish and capacity to work well in a large international group of scientist is important, as well as very good analytical and laboratory skills. Since funds for the salary are predicated on winning an internal fellowship sponsored by the Yale Institute for Biospheric Studies (Donnelly fellowship), and letters for candidate nomination by the sponsoring faculty need to be presented by December 7th 2007, I need to make a decision in the coming days. If interested ,please send a CV asap and go to the Caccone lab web page (http://130.132.86.97/labwebsite/gisella.html) for information on the projects and to the YIBS sites for specifics on the fellowship (http://www.yale.edu/yibs/-donnfellows.html). Competitive candidates for these fellowships are individuals with multiple scientific publications, which have recently completed or are about to complete their PhD. For further inquire contact Dr Caccone at Adalgisa.caccone@yale.edu by December 5, 2007 at the latest.

– Gisella Caccone YIBS-Molecular Systematics and Conservation Genetics Lab. ESC 140 Yale University 21 Sachem St., New Haven, CT, 06520-8106 USA Tel 203-432-5259 Fax 203-432-7394

adalgisa.caccone@yale.edu adalgisa.caccone@yale.edu

WorkshopsCourses

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BodegaBay California Phylogenetics Mar8-15

UC Davis WORKSHOP IN APPLIED PHYLOGENETICS at Bodega Marine Laboratory, Bodega Bay, California

March 8-15, 2008

sponsored by the

University of California, Davis and Bodega Marine Laboratory (additional financial support provided by the University of Rochester, Yale University, and NESCent)

Introduction. Phylogenetic methods have revolutionized modern systematics and become indispensable tools in evolution, ecology and comparative biology, playing an increasingly important role in analyses of biological data at levels of organization ranging from molecules to ecological communities. The construction of phylogenetic trees is becoming a methodology that is well-defined, with broad agreement on the central issues and questions. A nearly standard set of topics is now taught as part of the curriculum at many colleges and universities. On the other hand, application of phylogenetic methods to interesting problems outside of systematics is an area of special excitement, innovation, and controversy, and perspectives vary widely.

In March, 2008, for the ninth year, we will teach a workshop for graduate students interested in applying phylogenetic methods to diverse topics in biology. The one-week course will be an intensive exploration of problems to which modern phylogenetic tools are being applied. We cover a range of topics in biogeography, ecology, conservation biology, phylogenomics, functional morphology, macroevolution, speciation, and character evolution. The course starts with recent advances in phylogenetic methodology, and then focuses on methods and tools that can be brought to bear on these "applied" issues in the context of a given phylogeny.

The course will be held entirely at the Bodega Marine Lab on the Northern California coast, which has extensive computing resources and on-site housing. The course format will involve equal parts of lecture, discussion, and training in software and internet tools. One afternoon during the week will be left free for field trips to local natural areas.

Specific Topics to be Covered

* Finding, evaluating and interpreting phylogenetic trees; phylogenetic databases * Recent advances in tree reconstruction: Bayesian inference; stochastic optimization strategies; divide-and-conquer methods; Garli & other approaches * Analysis of character evolution–theory: parsimony, likelihood and Bayesian approaches; null models and statistical testing * Analysis of character evolution–form and function of complex character systems * Phylogeography; coalescent methods for inferring migration rates and patterns * Phylogenetic comparative methods * Phylogenetic perspectives on biodiversity and conservation biology * Data mining of sequence databases for phylogenetic analysis * Estimation of divergence times from sequence data * Species delimitation and phylogenetic taxonomy

Instructors for the main workshop.

* H. Bradley Shaffer * Peter Wainwright * Tom Near * Rich Glor * Phil Spinks * Justen Whittall * Brian O'Meara * Alan Lemmon * Emily Moriarty Lemmon * Robert Thomson * Bruce Rannala

plus guest lecturers!!

Prerequisites. Students should have some familiarity with phylogenetic methods through previous coursework. Some experience with PAUP, PHYLIP, or other programs for phylogeny reconstruction will be assumed.

Admission and Fees. Students will be admitted based on academic qualifications and appropriateness of research interests. The course fee is $450. This includes room and board at BML for duration of the course (arriving March 8, leaving March 15) and transportation from Davis to BML.

Application Deadline. Applications are due by January 15, 2008. Please send a completed application form (available at http://www.eve.ucdavis.edu/bodega/bodega08app.doc) and one letter of recommendation from your major advisor. Applications should be sent via email as PDFs to pqspinks@ucdavis.edu. Sorry, but due to the limited size of the class, postdocs and faculty are discouraged from applying. Students will be notified via e-mail by 20 January of acceptance.

Send all application materials to

Dr. Phillip Q. Spinks Section of Evolution and Ecology 2320 Storer Hall University of California Davis Davis, CA 95616 email:pqspinks@ucdavis.edu

pqspinks@ucdavis.edu pqspinks@ucdavis.edu

ImperialCollegeLondon MathModels Sep1-12

Of interest to some; reply to Ulrika (u.wernmark@imperial.ac.uk) cheers MAJ (sig at bottom)

Introduction to Mathematical Models of the EPIDEMIOLOGY & CONTROL OF INFECTIOUS DISEASES:

Short Course for Public Health Professionals, since 1990 1-12 September 2008 at Imperial College London

Our understanding of infectious-disease epidemiology and control has been greatly increased in recent years through mathematical modelling. Insights from this increasingly-important and exciting field are now in-forming policymaking at the highest levels, for pandemic influenza, SARS, HIV/AIDS, TB, malaria, foot-and-mouth disease and other infections.

Since 1990, this short course has 'demystified' mathematical modelling, and kept public-health professionals, policy makers, and medical and veterinary researchers, up-to-date with what they need to know about this fast-moving field. It is taught by active researchers in the world-leading Department of Infectious Disease Epidemiology (www.imperial.ac.uk/medicine/-research/researchthemes/publicandint/ide), which advises public health agencies, governments, international organisations, and pharmaceutical companies, and hosts the MRC Centre for Outbreak Analysis & Modelling, UNAIDS Epidemiology Reference Group secretariat, Partnership for Child Development, and the Gates Foundation-funded Schistosomiasis Control Initiative that has treated over 12 million children to date in six countries in Africa.

Participants need only a very basic mathematical ability (high school level is more than sufficient): most course participants do not use maths regularly, and calculation is done using Excel and the user-friendly modelling package, Berkeley Madonna; hence manipulation of equations is not required. We offer an optional 'maths refresher' day on Sunday 31 August, free of charge.

This programme will be of interest worldwide to public health professionals, policy makers, health economists, commissioning agencies, immunologists, medical, veterinary, biological and pharmaceutical scientists.

For further details visit the course website www.imperial.ac.uk/cpd/epidemiology/ which includes full information on how to apply for the course.

Please download a PDF of the course brochure here: http://www3.imperial.ac.uk/pls/portallive/docs/1/-31511700.PDF Should you have any queries please don't hesitate to contact me.

Best wishes Ulrika

Ulrika Wernmark

Programme Manager

Centre for Professional Development

Imperial College London

South Kensington Campus

58 Prince's Gate

London SW7 2AZ

Tel: +44 (0) 207 594 6886

Fax: +44 (0) 207 594 6883

Please visit our website at www.imperial.ac.uk/cpd Mark A. Jensen, Ph.D. Asst. Professor Dept. of Epidemiology & Biostatistics College of Public Health, and Dept. of Genetics Franklin College of Arts & Sciences University of Georgia N132 Coverdell Center Athens, GA 30602 maj@uga.edu

maj@uga.edu maj@uga.edu

RiodeJaneiro Phylogenetics Mar3-9

2008 EMBO World Practical Course: “Advanced Methods in Reconstructing Molecular Phylogenetic Relationships” March 3 to 9, 2008, Botanical Garden, Rio de Janeiro

The use of phylogenetic methods to reconstruct the evolutionary history of molecular sequences is a vital part of biological research. Such methods underpin studies on the evolution and epidemiology of plant and animal parasites and disease-causing organisms, they are needed to understand the contrasting roles of vertical and horizontal inheritance in genome evolution, and more generally they allow an objective analysis of the patterns and processes generating biological diversity. To carry out phylogenetic analysis properly, it is necessary to have a good understanding of the strengths and weaknesses, principles and applications of the key methods and approaches. The past few years have seen have an explosion in new methods of analysis including the application of Bayesian analysis methods in phylogeny reconstruction, the development of improved non-homogeneous models that much better represent the dynamics of sequence evolution, and the development of methods for high-throughput genome-wide analyses. This course has been designed to cater for these newest of methods and for understanding how they relate to the more traditional methods. We also address the strengths and weaknesses of all kinds of approach. Our goal is to teach technical sophistication without losing sight of the need for a critical attitude to data and analyses.

The web page for the 2006 course (http://-bioinf.ncl.ac.uk/molsys/) provides more information on content, but please be aware that both course and webpage are likely to be updated for the 2008 course.

Applying to come on the course >From past experience we expect that demand will outstrip the availability of places which we limit to around 25 students. EMBO also require that we have a gender and nationality balance on the course. We also try to ensure a mix of experience and biological backgrounds from the students who attend.

EMBO covers the costs of student accommodation and communal meals for the duration of the course only. It does not cover the cost of your travel to Rio. There may be some monies to help to cover the travel costs to Brazil of up to three students from outside of Western Europe and North America.

To apply please send a one page cover letter detailing why you wish to attend the course and what you hope to get out of it. Also send a two page CV giving details of your experience and any presentations or publications. Send your application by email to Martin.Embley@ncl.ac.uk to arrive by the closing date of January 1st 2008.

Martin.Embley@newcastle.ac.uk Martin.Embley@newcastle.ac.uk

UGroningen AvianEvolution

L.S.,

Could you please add this TopMaster Course announcement (as outlined below) to the EvolDir website?

Sincerely, yours

Prof. dr. ir. Jan Komdeur (Avian Evolutionary Ecology)

Animal Ecology Group Centre for Ecological and Evolutionary Studies University Groningen Biological Centre PO Box 14 9750 AA Haren The Netherlands Phone: + 31 50 363 2056 Phone secretary (Mrs. Joyce Rietveld): + 31 50 363 2040 Fax: + 31 50 363 5205 E-mail: j.komdeur@biol.rug.nl

TopMaster Program in Ecology and Evolution The University of Groningen is among the world leaders in biological research with centres of excellence and strong research groups in widely differing fields as evolutionary ecology and genetics, conservation biology, community, microbial ecology, theoretical biology, marine and ecology, and ecophysiology of plants. The Faculty of Mathematics and Natural Sciences of the University of Groningen aims for a leading position in education and research by offering a select number of TopMaster Programs. These international programs are designed to provide an optimal preparation for a subsequent PhD program and eventually for a scientific career. The TopMaster Program in Ecology and Evolution, organized by the Centre for Ecological and Evolutionary Studies (CEES), is linked to top-research groups in the Faculty. The teachers are all active researchers at different research departments within CEES, and as a student here you will come into close contact with researchers at the frontline of international science. Through intensive student-teacher interactions during courses, seminars and research projects, students get an intense training in modern research paradigms and techniques. The programme is highly selective and aimed at the brightest and most ambitious students from all over the world. All admitted students can apply for a scholarship. The two-year program starts each year in September. The deadline for application is 1 February 2008.

For more information on the TopMaster program and the admission procedure, check our website 'www.rug.nl/biologie/onderzoek/onderzoekinstituten/cees/topmaster/index', or contact Prof. Jan Komdeur (j.komdeur@rug.nl) or Ms. Trudeke Sanders (admissions@rug.nl).

J.Komdeur@rug.nl J.Komdeur@rug.nl

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.

Afterward

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.