
E v o l D i r

April 1, 2009

M o n t h i n R e v i e w

Foreword

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

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

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



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BrownU Genomics of Change Jun8-11

The American Genetic Association 2009 Symposium on:

The Genetics and Genomics of Environmental Change will be held at Brown University 8-11 June 2009

Registration Is now live at:

<http://www.brown.edu/Departments/EEB/aga/> Register by March 15 and save on Registration fees.

Hope to see you in Providence in June

Cheers

David Rand

David M. Rand Professor of Biology Department of Ecology and Evolutionary Biology Box G-W, 80 Waterman Street Brown University Providence, RI 02912 Voice: (401) 863-2890 (Office - Walter Hall 202) (401) 863-1063 (Lab - BioMed Center 516-518) Fax: (401) 863-2166 email: David_Rand@brown.edu web pages: <http://www.brown.edu/Departments/-EEB/rand/index.htm> <http://research.brown.edu/-research/profile.php?id=1100924991&r=1> David Rand <David_Rand@brown.edu>

**CapeTown Biodiversity Oct13-16
AbstractCall**

Dear Colleague,

The Call for Abstract (oral contributed papers or posters) of the Second DIVERSITAS Open Science Conference (OSC2) "Biodiversity and Society: Understanding connections, adapting to change" (13-16 October 2009, Cape Town, S-Africa) is open on the OSC2 website (<http://www.diversitas-osc.org/> < http://www.diversitas-osc.org/index.php?page=oral_papers >). To access abstract submission form and guidelines *(only on-line submission is accepted)*, please visit the conference website : http://www.diversitas-osc.org/index.php?page=oral_papers Note that the deadline to submit your abstract is *Tuesday 31 March 2009*.

*Could you please **advertise the Conference and the Call for Abstract in your newsletter, website and **network ? *

Thank you very much,

Yours sincerely,

Prof Hal Mooney, Chair SC-DIVERSITAS and Anne Larigauderie, ED DIVERSITAS

Person to contact : Manuelle Roville, DIVERSITAS OSC2 Coordinator : info-OSC2@diversitas-international.org

-

Ms. Manuelle Roville DIVERSITAS OSC2 Coordinator

DIVERSITAS Muséum national d'Histoire naturelle (MNHN) 57 rue Cuvier - CP 41 75231 Paris Cedex 05 France

Tel: + 33 1 40 79 80 44 Fax: + 33 1 40 79 80 45 Email: info-OSC2@diversitas-international.org Website: <http://www.diversitas-international.org> DIVERSITAS Open Science Conference 2 "Biodiversity and Society: Understanding connections, adapting to change" 13-16 October 2009, Cape Town, S-Africa www.diversitas-osc.org Diversitas OSC2 <info-OSC2@diversitas-international.org>

**Darwin Australia Darwin2009
Sep22-24**

We would like to invite you to the Charles Darwin Symposium 2009: Charles Darwin's contribution to science and society, to be held in tropical paradise in the city of Darwin, Australia.

Official symposium website: <http://www.cdu.edu.au/cdss2009/index.html> Program: <http://www.cdu.edu.au/cdss2009/program.html> Speakers: <http://www.cdu.edu.au/cdss2009/speakers.html>

Sponsors: <http://www.cdu.edu.au/cdss2009/sponsorship.html> Further links: <http://www.cdu.edu.au/cdss2009/links.html> About the September 2009 Charles Darwin Symposium:

The year 2009 marks the 200th anniversary of the birth of Charles Darwin and the 150th anniversary of his work *The Origin of Species*. Lesser known is the fact the 2009 also marks the 170th Anniversary of the naming of "Port Darwin" by Darwin's former shipmates on the 3rd voyage of the *Beagle*.

Through a combination of meticulous observation and innovative thinking, Darwin developed an explanation for the incredible variety of living things: that evolution is driven by natural selection.

This Symposium will provide an opportunity to appreciate, debate, and even challenge Darwin's findings, and will bring together an exciting range of speakers from around the globe.

Charles Darwin's scientific knowledge and rigour, acquired through human curiosity and ingenuity, have contributed significantly to the advancement of humanity.

About the Charles Darwin Symposium:

Charles Darwin Symposia are an initiative of the Charles Darwin University/Northern Territory Government Partnership Agreement and are supported by the NT Government.

The symposia are designed to encourage lively and informed debate on issues of importance to all Territorians. Through the symposia, the University seeks to engage with the wider community, inviting members of the public to participate in the debates, airing diverse points of view, and seeking to reach understandings on the issues under scrutiny.

The organisers of the symposia invite community leaders, academics and other experts from across the nation and internationally, to address the topics that are the focus of each symposia.

Opportunities are provided for the public to comment, question and critique the experts, as well as present their own perspectives on the matters at hand.

Register:

The symposium is free to attend, however we request that you register for catering purposes.

Register online <http://www.surveymethods.com/EndUser.aspx?A480ECF5ACE4F1FE> When & Where:

22-24 September,

Darwin Convention Centre, <http://www.darwinconvention.com.au/> Darwin, Australia
<http://en.travelnt.com/explore/darwin.aspx?cid=3Dwot08-darwin> Contact: email: cdss@cdu.edu.au
 Telephone, Darwin city, Australia: +61(0)8 8946 6202

Partner Events:

Darwin 200: Evolution & Biodiversity <http://www.evolutionbiodiversity2009.org/>
<http://www.cdu.edu.au/cdss2009/images/darwin200-logo.gif>
 Gold sponsor: <http://www.cdu.edu.au/cdss2009/images/smallercity.jpg> Mark.Schultz@cdu.edu.au

Germany SocialInsectEvolution Oct9-12 Registration

Registration for the 1st Meeting of the Central European Section of the IUSSI now open! For information and registration look at the following webpage! <http://ecology.bio.lmu.de/iussi/> – Prof. Dr. Susanne Foitzik Department Biologie II Verhaltensökologie Ludwig-Maximilians-Universität München Großhaderner Str. 2 D - 82152 Planegg / Martinsried Germany

Phone: + 49 89 / 2180 74 209 Fax: + 49 89 / 2180 74 221 e-mail: foitzik@zi.biologie.uni-muenchen.de

Susanne Foitzik <foitzik@zi.biologie.uni-muenchen.de>

Hinxton UK BrainEvolution Sep9-12

Evolution of Brain, Behaviour & Intelligence 9th - 12th September 2009 Venue: Wellcome Trust Conference Centre, Hinxton, Cambridge, UK Registration: https://registration.hinxton.wellcome.ac.uk/-display_info.asp?id=130 With kind regards Lucy

* Office Days: Monday, Tuesday, Wednesday & Thursday

Mrs Lucy Criddle Conference Organiser, Event Management Wellcome Trust Scientific Conference Programme Wellcome Trust Conference Centre Wellcome Trust Genome Campus Hinxton Cambridge CB10 1RQ UK

Tel: +44 (0)1223 495004 Fax: +44 (0)1223 495023 Email: l.criddle@wtconference.org.uk
www.wtconference.org.uk www.wellcome.ac.uk/-conference Lucy Criddle
 <l.criddle@wtconference.org.uk>

IowaCity SMBE 2009 Jun3-7 NextGenerationSeqSymposium

Dear all,

Submissions of abstracts for oral and poster presentations are now open for the symposium on

“Impact of Next Generation Sequencing on the Study of Evolution”

which is part of the upcoming Conference of the Society for Molecular Biology and Evolution in Iowa city, USA (3-7 June 2009).

DESCRIPTION OF THE SYMPOSIUM: Over the past years DNA sequencing technology has undergone massive improvements. The introduction of the so-called next- and next-next generation sequencing technologies has finally allowed to process millions of DNA sequences in a massive, parallel and miniaturized fashion (for reviews see Shendure J et Ji H, Nat Biotechnol, 26(10):1135-45, 2008 and Mardis ER, Annu Rev Ge-

nomics Hum Genet, 9:387-402, 2008). Not only these methods represent technological innovations in terms of increased throughput and reduced costs, but, more importantly, they are dramatically changing the way of planning experiments, opening new areas of investigation. The resulting impact on evolutionary genomics is enormous: applications range from sequencing of ancient genomes to intra-population variability, from ecological diversity to mutational dynamics of cancer cells. For the innovation, the number and the variety of involved areas, we propose a symposium dedicated to unravel the impact of next-generation sequencing on evolutionary biology. The aim of the symposium will be twofold: from one side it will disclose the new perspectives offered by these approaches, while from the other it will face the experimental and computational challenges of correctly treating the data (including potential error sources, data handling and validation methods). Such a symposium will be intersecting and complementary to other already accepted symposia (e.g. Mutation accumulation in eukaryotic genomes and Population genomics, to name two), helping to expand the technological and applicative aspects.

DEADLINE FOR ABSTRACT SUBMISSION: April 1st

CONFIRMED SPEAKERS:

- Mike Snyder, Yale University - Florian Kuchenbauer, Terry Fox Laboratory Canada

MEETING WEBSITE: <http://smbe2009.org> CONTACTS: - Francesca D. Ciccarelli, European Institute of Oncology Milan, Italy francesca.ciccarelli@ifom-ieo-campus.it - Anna De Grassi, European Institute of Oncology Milan, Italy anna.degrassi@ifom-ieo-campus.it

Hope to see you in Iowa City!

-

Francesca D. Ciccarelli, PhD Biocomputing IFOM-IEO-Campus Via Adamello, 16 20139 Milan, Italy tel +39-02574303053 fax +39-0294375990 web: <http://ciccarelli.group.ifom-ieo-campus.it/> francesca.ciccarelli@ifom-ieo-campus.it

IowaU SMBE2009
EpigeneticsEnvironmentEvolution
Jun3-7

Hello all,

This is a renewed invitation for submission of abstracts for oral and poster presentations for the symposium on “Epigenetics, Environment, and Evolution (EEE)”

during the annual meeting of the Society for Molecular Biology and Evolution at Iowa City, IA, USA (June 3-7, 2009).

6 15-minute slots will be available for contributed talks. Empirical studies on any system pertaining to the theme of the symposium are particularly encouraged for submission, so are some reviews with more theoretical components.

The deadline for abstract submission for consideration as a contributed talk has been changed to April 5th (all abstracts received after April 5th will be posters), but the deadline for early registration is still April 1st. For more general information about the meeting please go to <http://ccg.biology.uiowa.edu/smbe/>. Again, I would also like to invite all the other evolutionary biologists to come to this symposium during the SMBE2009 meeting, particularly if you have had enough fun in the innumerable parties for Darwin this year and just want some fresh air.

Looking forward to seeing you at Iowa City!

“Epigenetics, Environment, and Evolution (EEE)” Symposium Description:

Traditionally, the molecular study of evolution has been focused on DNA sequence variation. This is convenient, and it is also based on the dogmatic belief that has developed since the discovery of the double-helix structure of DNA, which is, any evolutionary change must be based on mutation at DNA sequence level. This is a grossly simplified understanding of biology and a rather outdated view about life. In the last decade, increasingly more evidences have revealed that epigenetic changes, i.e., modifications of nucleotides (e.g., methylation of cytosine) and/or histones (acetylation, methylation, etc.) without any change at DNA sequence level, particularly under the influence of the environment, could dramatically alter important life traits and such alteration is heritable at least to some degree. Increasingly more evidences suggest epigenetic regulation may have played fundamental, rather than just supplemental, roles in development (e.g., cell differentiation), adaptation to environment, and diseases (like the occurrence of cancer). All these suggest possibly important roles played by epigenetics and the environment in biological evolution. A symposium about the relationship between epigenetics, environment, and evolution is due, particularly in this year of Darwin. In this symposium, the roles played by the environment and epigenetics in evolution will be addressed with respect

to both molecular mechanisms and theoretical implications. Specific topics would include: (1) Can epigenetic changes alter important phenotypic traits? (2) How can the environment affect a genome's epigenetic state? (3) Are epigenetic alterations by the environment and subsequent phenotypic changes inheritable? (4) What does this mean for evolutionary theory?

Organizer:

Xianfa Xie Department of Biology, Brooklyn College, The City University of New York, Brooklyn, NY, USA
xianfaxie@brooklyn.cuny.edu

p.s. Please kindly forward this email to those who you know might be interested in this symposium but not on the evoldir email list (like some molecular biologists who have interests in mechanisms of evolution). Thanks!

Xianfa Xie <xixianfa@gmail.com>

KansasCity Genomics Jun11-14 EarlyRegDeadline

Frontiers in Arthropod Genomics

3rd ANNUAL ARTHROPOD GENOMICS SYMPOSIUM

June 11 - 14, 2009, in Kansas City, USA

www.k-state.edu/agc/symp2009

Deadline to Register at Early-Bird Rates: Friday, March 20, 2009

Other important deadlines:

*Poster Abstract Submissions: Friday, May 15

*Hotel Reservations: Thursday, May 21, or until room block is filled

KEYNOTE SPEAKERS:

*Fotis C. Kafatos, Imperial College London, "Evolutionary, functional and population genomics of mosquitoes: The perspective of a malariologist."

*William M. Gelbart, Harvard University, "Opportunities & Challenges for Arthropod Genomics and Informatics in the NextGen World."

FEATURED SPEAKERS:

* Volker Brendel, Iowa State University, "Opportunities and challenges for automated genome annotation

and modeling in a time of unlimited access to sequence data"

* Susan J. Brown, Kansas State University, "Profiling genome transcription during *Tribolium* development: From egg to eternity"

* Jay D. Evans, USDA-ARS Bee Research Lab, Maryland, "Chasing your honey: Genomic studies of honey bees and their pathogens"

* Marian R. Goldsmith, University of Rhode Island, "The new silk road: From *Bombyx* to butterflies"

* David G. Heckel, Max Planck-Institute for Chemical Ecology, Jena, Germany, "Insect defenses in chemical co-evolution: Transcriptional responses of the generalist herbivore *Helicoverpa armigera* to plant defense compounds, phytohormones, and insecticides"

* Kristin Michel, Kansas State University, "Mosquito salivary gland interactions with malaria parasites"

* Terence Murphy, National Center for Biotechnology Information/NIH, "Arthropod genome support at NCBI and the challenges of annotating genomes in the 21st century"

* Marcelo Ramalho-Ortigao, Kansas State University, "Sand fly functional genomics and beyond"

* Yoonseong Park, Kansas State University, "Evolutionary processes of the partnership between neuropeptides and their receptors"

* José Ribeiro, Laboratory of Malaria and Vector Research, NIH/NIAID, "An insight into the spitome of the blood sucking *Nematocera*"

* Denis Tagu, French Nat'l Inst. for Agricultural Research, Rennes, France, "Using the pea aphid genome to study phenotypic plasticity"

* Doreen Ware, Cold Spring Harbor Laboratory, "Annotation and comparative analysis of plant genomes"

* Stephen K. Wikel, University of Texas Medical Branch, Galveston, "Tick-host-pathogen research in the post-genomic era"

POSTER SESSIONS: There will be two poster sessions. A few platform presentations will be chosen from submitted poster abstracts. Abstract Submission Deadline: May 15, 2009.

SYMPOSIUM PROGRAM: The symposium sessions will begin Thursday evening, June 11, and continue on Friday and Saturday, with additional events on Saturday evening and Sunday morning. Speakers will present new insights from genomic approaches in arthropods and describe the development of tools for genomic analysis. Workshops will be held Thursday prior to the

Symposium and Friday evening. Activities will conclude by noon on Sunday, June 14.

ROUNDTABLE DISCUSSION: Sunday morning will highlight a roundtable discussion led by members of the ArthropodBase Consortium regarding the generation of integrated arthropod genome databases and tools for genome projects. Symposium attendees are invited to join the fun as we share our progress by providing feedback on these projects and proposing new possibilities.

REGISTRATION: The early registration fee is \$295 (\$150 for graduate and undergraduate students) on or before March 20, and will include a welcome reception Thursday evening, breakfast and lunch on Friday and Saturday, and breakfast on Sunday. After March 20, the registration fee is \$395 (\$225 for students).

VENUE: The symposium will take place at the historic Marriott Hotel in downtown Kansas City. Participants are invited to stay Saturday night for an optional evening of jazz and KC barbeque.

INFORMATION: Visit our website, www.k-state.edu/agc/symp2009, for complete details and brochure. Add your name to the Symposium mailing list, by sending your contact information to dmerrill@k-state.edu.

QUESTIONS: Contact us at (785) 532-3482 or dmerrill@ksu.edu.

Please share this announcement with colleagues and students!

SPONSOR: Center for Genomic Studies on Arthropods Affecting Human, Animal and Plant Health, Kansas State University

SYMPOSIUM ORGANIZING COMMITTEE

Robin E. Denell, Committee Chair

Susan J. Brown

Kristin Michel

Subbaratnam Muthukrishnan

Yoonseong Park

John Reese

Doris Merrill, Program Coordinator

K-State Arthropod Genomics Center

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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>

Leibniz ConservationBiology Sep21-24

Dear Colleagues,

On behalf of the Leibniz Institute for Zoo and Wildlife Research (IZW) and the European Association of Zoos and Aquaria (EAZA) we wish to extend a cordial invitation to participate in the "7th International Conference on Behaviour, Physiology and Genetics of Wildlife" between 21st and 24th September 2009 in Berlin, Germany.

Our webpage is now open for registration:

<http://www.izw-berlin.de/de/flink/7thIZW-Conference.html> < <http://www.izw-berlin.de/de/flink/7thIZW-Conference.html> >

Aim

To foster an exchange of ideas among international specialists from many disciplines working with free-ranging and captive animals. To achieve this aim we have secured an impressive list of plenary speakers and workshop organisers.

Main topics

* Behavioural Ecology * Stress & Disturbance * Reproduction Biology * Conservation Genetics * Conservation Biology

Plenary Talks

* Life History & Maternal Effects (Pat Monaghan, University of Glasgow, UK) * Stress & Disturbance (Marco Apollonio, Universita Sassari, Sardinia, Italy) * Reproduction Biology (David Wildt, Smithsonian National Zoological Park, USA) * Evolutionary Genomics in Conservation (Pierre Taberlet, Université Joseph Fourier, Grenoble, France) * Conservation Biology (Eric Dinerstein, Director of Science WWF USA, Washington, USA)

Workshops

* Evolutionary Genomics (Pierre Taberlet, Université Joseph Fourier, Grenoble, France & Simone Sommer, IZW)

* Communication in Mammals and Birds (Francesco

Bonnadonna, Centre d'Écologie Fonctionnelle et Évolutive, Montpellier, France & Martin Dehnhard, IZW)

* Welfare and Conservation (Eric Dinerstein, WWF-USA, Washington, USA & Marion L. East, IZW)

* Stable Isotopes, Nutrition and Energetics (Carlos Martinez del Rio, University of Wyoming, USA & Sylvia Ortmann, IZW; Christian Voigt, IZW)

* Behavioural Rhythms (Serge Daan, University of Groningen, The Netherlands & Anne Berger, IZW)

* Research by, in, with and for zoos, aquaria and other ex situ- institutions (Kirstin Leus, EAZA & IUCN/SSC: CBSG Europe, Antwerp, Belgium)

The workshop "Non-Invasive Monitoring of Hormones" will take place in the week preceding the Conference

(14th - 18th September 2009, Berlin). The workshop will be run by Martin Dehnhard, IZW; Rupert Palme, University of Vienna; and Michael Heistermann DPZ, Göttingen.

We are looking forward to welcome you, Kind regards,
Simone Sommer

Prof Dr Simone Sommer Evolutionary Genetics, Leibniz-Institute for Zoo- and Wildlife Research & Evolutionary Ecology, University of Potsdam Leibniz-Institute for Zoo- and Wildlife Research (IZW) Alfred-Kowalke Str. 17 D-10315 Berlin Tel. +49 30 5168 315 Fax +49 30 5126 104

"Sommer, Simone" <SOMMER@izw-berlin.de>

that support their growth. Since its recent resurgence, this topic became hotly debated, with evidence apparently supporting and denying the hypothesis.

Until very recently the EisE hypothesis was effectively untestable because of the constraints in analyzing microbial communities, especially for those organisms that are unculturable and/or difficult to identify by conventional (e.g. morphological) methods. Plus, of course, there is an acute shortage of taxonomic expertise for many groups. Modern molecular-based techniques may circumvent many of these problems and allow significantly a higher throughput of samples thereby increasing the quality and quantity of data. Such techniques are now being used to inform the debate around microbial biodiversity and biogeography. The symposium will provide an opportunity to review how far we have come and in which direction efforts might best be directed in the future.

Preliminary list of speakers Diego Fontaneto: body size and biogeography David Bass: Spatial patterns in protist distribution. David Williams: are there endemic species in small organisms? Mark Blaxter: spatial patterns in small animals, a morphological and phylogenetic approach. Wilhelm Foissner: possible reasons for protist endemism, with examples from bromeliads and floodplains. David Jenkins: underlying biological mechanisms. Luc De Meester: spatial scales, dispersal, and metacommunity dynamics. Joaquin Hortal: species concepts, theoretical and experimental biogeography and ecology.

For more information: diego.fontaneto@nrm.se
diego.fontaneto@unimi.it

Leiden Biogeography Aug13

Symposium: The importance of being small: does size matter in biogeography? Conveners: Diego Fontaneto, David Roberts, Juliet Brodie Location: Leiden, The Netherlands, August 13th 2009 Submission of abstract for talks or posters is now open: www.biosyst.eu (go to ->scientific program ->Symposia)

This symposium is based around the hypothesis of everything-is-everywhere (EisE) amongst small organisms. This hypothesis was proposed at the beginning of the 20th century for microbial diversity and, about ten years ago, extended to describe spatial patterns of diversity for any organism smaller than 2 mm, under the simple observation that microscopic organisms such as protists seem to be cosmopolitan, at least in habitats

LowellMA ENEBC EvolutionaryBiol Apr25

Sat. Apr. 25th 2009, Lowell, MA: A great opportunity for graduate and undergraduate students to present their research in a diverse, low-key environment! Students may register for either oral or poster presentations; sessions will be organized according to submission content, but past years' ENEBCs have featured projects ranging from molecule to ecosystem, with a heavy dose of evolutionary biology. Conference information and registration page available at

<http://www.uml.edu/enebc/> This year's ENEBC is hosted by the University of Massachusetts Lowell.

For further information, contact Brian Bettencourt at
Brian_Bettencourt@umt.edu or 978 934 2899.

bbettenc69@gmail.com

McMasterU DarwinsLegacy May25-29

The Origins Institute (OI) at McMaster University is planning to celebrate the sesquicentennial for Darwin's masterpiece, by staging a major international conference, May 25-29.

As the Associate Director for the OI and chair for the conference Scientific Organizing Committee, I am honoured and pleased to invite you to this event.

I copied below information about the planned conference. Additional information can be accessed at

<http://origins.mcmaster.ca/conferences.php> The OI was founded in 2004 as a transdisciplinary academy to explore fundamental questions in science through 6 origins themes (space-time, elements, structure in the cosmos - stars, planets, galaxies, life, species & biodiversity, humanity).

Additional information about the OI may be accessed at

<http://origins.mcmaster.ca> The OI emphasises transdisciplinary research and all talks will be delivered in a manner that will accommodate the broad scientific audience and topics that will be featured at the conference.

TITLE Darwinian's Legacy: Natural Selection as an Organising Principle in Science

DATE 2009 May 25-29

SCHEDULE The conference will comprise 9 half-day sessions and social activities. Each session will include one keynote addresses (approximately 50 minutes, plus 10 minutes for discussion), one invited speech (approximately 25 minutes, plus 5 minutes for discussion), and shorter contributed talks. Two poster sessions also will be held.

May 25, morning - Darwinian Science

May 25, afternoon - Selection (Natural, Sexual, and Kin) Mark Rausher

Social Reception (May 25, evening)

May 26, morning - Paleontology James Valentine

May 25, afternoon - Evolution & Development Brian Hall

May 26, evening - Public Lecture Steve Benner

May 27 morning - Cognition, Language, & Culture Christof Koch

May 27, afternoon - Social Outing (Niagara Falls)

May 27, evening - Winery Dinner

May 28 - Speciation & Adaptation Hopi Hoekstra

May 28, afternoon - Molecular Evolution Steven Benner

May 28, Conference Banquet (Royal Botanical Gardens)

May 29, morning - Emergent Complexity

May 29, afternoon - Origin of Life & Astrobiology David Deamer

May 29, evening - BBQ

On behalf of the Scientific Organising Committee, I hope that you will be able to accept this invitation.

Jon Stone (Associate Director) & Ralph Pudritz (Director)

Scientific Organising Committee: Walter Craig, Mathematics Daniel Goldreich, Psychology Ralph Pudritz, Astrophysics Ulrich Riller, Geology Rama Singh, Biology Jon Stone, Computational Biology

Jon Stone SHARCNET Chair in Computational Biology Associate Director, Origins Institute McMaster University Department of Biology Life Sciences Building (Office, Room 327; Laboratory, Room 325) 1280 Main Street West Hamilton ON L8S 4K1 CANADA Telephone number: CA +1 9055259140 Call (Office, +26136; Laboratory, +27676) Facsimile number: 905-522-6066 email address: jstoner@mcmaster.ca

"J. R. Stone" <jstoner@mcmaster.ca>

Moscow ComputationalMolecularBiol Jul20-23

Hello all,

the biennial Moscow Conference on Computational Molecular Biology (MCCMB'09) will take place in

Moscow, Russia on July 20-23, 2009. Despite its “local” title, MCCMB provides a forum for international and Russian scientists working in various areas of bioinformatics and computational genomics.

The working language of the conference is English.

Note that the deadline for abstract submission for talks is April 1st.

For more information, see: <http://mccmb.belozersky.msu.ru/2009/> Topics of interest

The topics of interest include, but are not limited to:

* Sequence analysis o statistics of DNA and protein sequences o functional annotation of DNA sequences and proteins * Structure of biopolymers o prediction of protein structure o interaction of proteins with ligands o classification of folds and structural motifs o prediction of RNA structure * Molecular evolution o phylogeny analysis; o evolution of genomes, regulatory systems and metabolic pathways o genome rearrangements * Genomics and proteomics o large scale genome analysis o metabolic and signal pathways o expression arrays o SNPs in medicine and population genetics o large-scale analysis of proteomes and protein-protein interactions o automated annotation of genomes and ontologies * Systems biology (models and networks). * Bioalgorithms. * Education in bioinformatics.

Calendar

Conference: July 20V23, 2009 Deadline for online registration: residents June 5, non-residents May 1 Deadline for submission of abstracts for oral presentations: April 1 Notification to authors: April 25 Deadline for submission of poster abstracts: June 5 Deadline for revised abstracts: June 5

yegor_bazykin@mail.ru

Portland SSE 2010 CallForSymposia Jun25-29

The 2010 annual meeting of the Society for the Study of Evolution will be held from June 25-29, 2010 in Portland, Oregon and hosted by Portland State University. The Council of the Society invites proposals for the two Society-sponsored symposia to be held in conjunction with the meeting. Symposium proposals should include: (1) a synopsis of the symposium theme (about one page); (2) a tentative list of speakers, including institutional affiliations, and topics; (3) a rationale for

the symposium explaining why this topic and this group of speakers are particularly appropriate for a Society-sponsored symposium; and (4) a statement that all potential speakers have been contacted and agree to participate in the symposium.

In evaluating symposium proposals, the Council will favor those proposals whose topics concern newly emerging fields, fields ripe for syntheses, and fields different from those that have been included in recent Society symposia. The Council particularly encourages proposals that include women, younger investigators and others traditionally underrepresented in Society symposia.

The Council will select two proposals for half-day symposia at its meeting in June 2009. All applicants will be notified of the Council’s decision in July. The Society provides partial travel support for organizers and participants in sponsored symposia. Details are available on request. To be assured of full consideration, proposals must be received at the following address by midnight Eastern Standard Time on May 18, 2009:

Dr. Charles B. Fenster, Executive Vice President The Society for the Study of Evolution Department of Biology University of Maryland College Park, Maryland, 20742 USA e-mail: CFenster@umd.edu Proposals can be sent as paper copies by mail or preferably as e-mail attachments in Word or RTF format (under subject heading: SSE Symposia Proposal). Please expect and request confirmation of receipt of the proposal.

Judy Stone <jstone@colby.edu>

Richmond Virginia SystemsBiol Jun16-19

*/The Third /**/Summit/**/ on Systems Biology - Microbial World and Beyond/*

*/June 16-19, 2009/**/, /**/Richmond/**/, /**/Virginia/**/, /**/USA/**/*

<http://www.vcu.edu/csbc/systemsbiologysummit/>
* *

Call for Abstracts/Papers

The Third Annual Summit on Systems Biology will be held on June 16-19, 2009, in historic Richmond, Virginia located two hours south of Washington, DC. The Summit is comprised of five scientific sessions and two workshops to bring together computational and experimental scientists in the area of microbial systems. The

third summit will discuss research directions and latest findings in the “omics” domain, as well as promote collaborations in microbial systems biology and related disciplines. Dr. Leroy Hood, Director of the Institute for Systems Biology, and Dr. Stuart Kauffman, of the University of Calgary and a past MacArthur Foundation Fellow, both pioneers in Systems Biology, are on the Summit Steering Committee. Keynote speakers include Dr. Stuart Kauffman and Dr. Jeremy Nicholson of Imperial College London. We invite active researchers in these and related fields to submit abstracts for review in response to this call /to participate with a *podium presentation or a poster at the conference.*

The five scientific sessions are:

* Microbial Engineering * Microbial Diversity and Ecology * Host-Pathogen Interactions * Human Microbiome * Evolution of Microbial Systems

The two workshops are:

* Tree of Life and Microbial Systems Biology * Gene Networks and Diseases

You are invited to submit a 1-page abstract by *April 9, 2009*.

Abstracts must be submitted as electronic files (preferred in Word or PDF format). Please use the format outlined in the template (download from the website, <http://www.vcu.edu/csbc/-systemsbiologysummit/abstracts.html>) to prepare the abstract and email it directly to both/ /zzhao@vcu.edu <mailto:zzhao@vcu.edu> and sysbiosummit@vcu.edu <mailto:sysbiosummit@vcu.edu>. Please use “Summit on Systems Biology: Abstract Submission” as the email subject line.

Authors of accepted abstracts will also be invited to submit a paper for potential publication in a special issue in Chemistry and Biodiversity < <http://www3.interscience.wiley.com/journal/106056929/home?CRETRY=3D1&SRETRY=0> >. Decisions on abstract acceptance for the conference will be announced on May 15, 2009. Contact: Dr. Zhongming Zhao (zzhao@vcu.edu <mailto:zzhao@vcu.edu>) and sysbiosummit@vcu.edu <mailto:sysbiosummit@vcu.edu>.

*Key Dates: *

Abstract submission deadline: *April 9, 2009** *

Abstract acceptance and paper/poster invitation notification: May 15, 2009

Early registration deadline: May 15, 2009

Manuscript (for special issue) submission deadline: August 1, 2009

– Zhongming Zhao, Ph.D. Asst. Professor of Bioinformatics Depts. Psychiatry and Human Genetics and Center for the Study of Biological Complexity Virginia Commonwealth University PO Box 980126, Richmond VA 23298-0126 Phone: (804) 828-8129 Fax: (804) 828-1471 <http://bioinfo.vipbg.vcu.edu/> zzhao@vcu.edu zzhao@vcu.edu

Rochester Nasonia2009 Aug7-9

Subject: Conference - Nasonia 2009 Nasonia is a genus of haplodiploid wasps that is emerging as a new genetic model. The genomes of three related inter-fertile species have been sequenced, and there is a growing set of genetic and genomic tools for studies of developmental, population, behavioral, and evolutionary genetics, included for QTL cloning. The 2009 Nasonia meeting will be held at Rochester New York, 7-9 August. If you are interested in learning more and possibly attending, please visit

<http://www.rochester.edu/College/BIO/nasonia/> . One topic of this meeting will be advances emerging from the Nasonia genomes.

Jack Werren <werr@mail.rochester.edu>

Sheffield Evolution of insect immunity Jul15-17 2

Royal Entomological Society International Symposium Insect Infection and Immunity: Evolution, Ecology and Mechanisms

In Sheffield, UK, July 15-17 2009

Deadline for abstracts: March 31 (Please submit abstracts for posters and talks to: ento2009@sheffield.ac.uk.)

Deadline for registration: May 1 (<http://www.royensoc.co.uk/register/index.php>)

The symposium on insect immunity, organized by Stuart Reynolds (Bath, UK) and Jens Rolff (Sheffield, UK) will consist of three plenary sessions running in the morning of each day. Speakers include:

George Dimopoulos (John Hopkins Malaria Research

Institute, USA)

Fotis Kafatos (Imperial College, UK)

Greg Hurst (University of Liverpool, UK)

Jean Luc Imler (Institut de Biologie Moléculaire et Cellulaire, Strasbourg, France)

Jacob Koella (Imperial College, UK)

Shelley Adamo (Dalhousie, Canada)

Brian Lazzaro (Cornell University, USA)

Paul Schmid-Hempel (ETH Zurich, CH)

Mike Siva-Jothy (University of Sheffield, UK)

The afternoon, organized by Klaus Reinhardt, Roger Butlin and Mike Siva-Jothy (all Sheffield, UK), includes the following thematic sessions with contributed talks and posters on:

Comparative Genomics (chair Casey Bergman, Manchester) Invited Speaker: Jack Werren, Rochester, USA

General Entomology (chair Mike Siva-Jothy, Sheffield) Stanislav Gorb, Kiel, Germany Paul Buckland, Sheffield, UK

Predation (chair Dirk Mikolajewski, Sheffield) Johanna Mappes (Jyväskylä, Finland) Robby Stoks (Leuven, Belgium)

Insect Immunity (chair Petros Ligoxygakis, Oxford)

Range Expansion (chair Janis Antonovics, Virginia/Sheffield) Jane Hill, York, UK Rosa Menendes, Lancaster, UK

Evening Plenary by Naomi Pierce, Harvard, USA:

“Nabokov meets Darwin: origin and evolution of blue butterflies”

The Society offers excellent support for students: students can apply for support of up to 50% of all costs (travel, accommodation, registration). Also, as conference dinners are very good networking opportunities, the dinner is only £15 for students. Early application is strongly recommended. Applications must be made by letter or email (bill@royensoc.co.uk) to the Registrar at the RES office and the deadline for receipt is 1st May 2009.

Daytime childcare is available on request (child-care.ento2009@sheffield.ac.uk).

Registration (<http://www.royensoc.co.uk/register/-index.php>) and program <http://www.royensoc.co.uk> Deadline: 1st of May

Please submit abstracts for posters and talks to: ento2009@sheffield.ac.uk. Deadline for talks: March 31

Jens Rolff <JOR@sheffield.ac.uk>

Sheffield InsectEvolution Jul15-17

Royal Entomological Society International Symposium

DEADLINE for Abstracts: April 1

In Sheffield, UK, July 15-17 2009

Deadline for abstracts: APRIL 1 (Please submit abstracts for posters and talks to: ento2009@sheffield.ac.uk.)

Deadline for registration: May 1 (<http://www.royensoc.co.uk/register/index.php>)

Plenary by Naomi Pierce, Harvard, USA: “Nabokov meets Darwin: origin and evolution of blue butterflies”

Scientific sessions:

Comparative Genomics (chair Casey Bergman, Manchester) Invited Speaker: Jack Werren, Rochester, USA

Evolutionary Ecology of Predation (chair Dirk Mikolajewski, Sheffield) Invited speakers: Johanna Mappes (Jyväskylä, Finland) Robby Stoks (Leuven, Belgium)

Insect Immunity (chair Petros Ligoxygakis, Oxford)

Range Expansion (chair Janis Antonovics, Virginia/Sheffield) Invited speakers: Jane Hill, York, UK Rosa Menendes, Lancaster, UK

General Entomology (chair Mike Siva-Jothy, Sheffield) Invited Speakers: Stanislav Gorb, Kiel, Germany Paul Buckland, Sheffield, UK

Student Travel Support:

The Society offers excellent support for students: students can apply for support of up to 50% of all costs (travel, accommodation, registration). Also, as conference dinners are very good networking opportunities, the dinner is only £15 for students. Early application is strongly recommended. Applications must be made by letter or email (bill@royensoc.co.uk) to the Registrar at the RES office and the deadline for receipt is 1st May 2009.

Daytime childcare is available on request (child-care.ento2009@sheffield.ac.uk).

A special symposium on is running in the mornings:

Insect Infection and Immunity:

Evolution, Ecology and Mechanisms

The symposium on insect immunity, organized by Stuart Reynolds (Bath, UK) and Jens Rolff (Sheffield, UK) will consist of three plenary sessions running in the morning of each day. Speakers include:

George Dimopoulos (John Hopkins Malaria Research Institute, USA)

Fotis Kafatos (Imperial College, UK)

Greg Hurst (University of Liverpool, UK)

Jean Luc Imler (Institut de Biologie Moléculaire et Cellulaire, Strasbourg, France)

Jacob Koella (Imperial College, UK)

Shelley Adamo (Dalhousie, Canada)

Brian Lazzaro (Cornell University, USA)

Paul Schmid-Hempel (ETH Zurich, CH)

Mike Siva-Jothy (University of Sheffield, UK)

Jens Rolff <jor@sheffield.ac.uk>

17-20, 2009.

More information about the Conference is on the Web Page:

<http://balkangendiv-conference.com> Registration is prolonged by the end of March 31, 2009. In case of need, please, contact Dr. Petar Zhelev University of Forestry, 10 Kliment Ohridsky Blvd., 1756 Sofia Bulgaria Fax: ++359 2 862 28 30, e-mail: zhelev@ltu.bg; peter.zhelev@abv.bg

Ladislav Paule <paule@stonline.sk>

StMalo France Biodiversity May17-20 DeadlineExtended

Sofia Bulgaria GeneticDiversity Jun17-20

Conference

“Balkans - Hot Spots of Ancient and Present Genetic Diversity ”

The Balkan Peninsula is a region with a very rich diversity both of plant and animal species. The recent studies have shown that due to many circumstances, like geographic situation, evolutionary and climatic factors, the biological diversity on Balkans is higher than in almost any other comparable area in Europe. Therefore, it is of particular importance to study the diversity and to share information among the scientists from different countries.

The conference will be organized by the University of Forestry, Sofia, with Bulgarian Botanical Society and Institute of Zoology of Bulgarian Academy of Sciences co-organizers.

The Scientific Program is organized in Plenary Lectures, Oral Presentations and Poster Sessions. The main topic of the conference will cover: - Paleobotany and history - Diversity, differentiation and phylogeography - Endemism - Migration from Balkan refugia - Introgression

The Conference will be held in Sofia, Bulgaria, on June

Dear colleagues,

Abstract submission and registration deadlines are extended to 9 march and 17 march 2009 respectively, for the:

International Conference on Polyploidy, Hybridization and Biodiversity ICPHB2009 that will take place at the Palais du Grand Large, Saint-Malo (France) on 17-20 may 2009.

Updated information is available at <http://www.icphb2009.univ-rennes1.fr/> , oral and / or poster contributions are welcome.

Scientific Committee: Ainouche M. (France), Alix K. (France), Chalhoub B. (France), Chen J. (USA), Chèvre A-M. (France), Colot V. (France), Comai L. (USA), Doyle J. (USA), DHont A. (France), Grandbastien M-A. (France), Jahier J. (France), Jenzcewski E. (France), Kovarick A. (CZ), Leitch A. (UK), Mittelsten Scheid O. (Austria), Pires C. (USA), Quixin S. (China) Rieseberg L. (Canada), Soltis P. (USA), Thiellement H.(France), Van de Peer Y. (Belgium), Veitia R. (France) , Wendel J. (USA)

M. L. AINOUCHE Evolution des Genomes et Speciation, Equipe MOB (Mecanismes à l'Origine de la Biodiversite) UMR CNRS 6553 Ecobio, Universite de Rennes 1 - CAREN Campus Scientifique de Beaulieu, Bat. 14A 35 042 Rennes Cedex France Ph. 33 (0)2 23 23 51 11 Fax 33 (0)2 23 23 50 47

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

Switzerland
EvolutionOfSexDetermination
Jun17-20 2

Evolution of sex-determination mechanisms Conference /workshop

There are 6 places left for this 3-days meeting (June 17-20, 2009) addressing the evolution of sex-determination mechanisms and sex chromosomes.

We have invited leading scientists in this area (D.Charlesworth, B.Rice, F.Janzen, M.Kirkpatrick, M.Beye, L.Beukeboom, RH Devlin) who will present syntheses of recent research on sex determination in vertebrates, invertebrates and plants, delineating the roles of environmental effects, sex-antagonistic genes, causes and consequences of recombination loss, sex-ratio selection, molecular mechanisms of sex determination, plus many other relevant topics. Participants will have the opportunity to present and discuss their work in this area.

The meeting will take place in the Hotel de la Sage (<http://www.hoteldelasage.com/>), in a picturesque small village of the Val d'Herens, Swiss Alps.

Fees (300) include meeting registration and full accommodation for the 3 days.

More info and registration at <http://www.unil.ch/dee/-page62605.html> Nicolas.Perrin@unil.ch

Trondheim ConservPopGenetics
May23-26 3

Conservation Genetics: Integrating Population Genetics and Conservation Biology

The networking programme ConGen within the European Science Foundation (ESF) announces a conservation genetics conference to take place in Trondheim, Norway, 23-26 May 2009. The conference integrates theoretical, experimental and applied approaches to conservation genetics, and will present up-to-date knowledge in population genetics, conservation and

evolutionary biology, and genomics, by leading researchers in these fields.

Local organisers are the Norwegian Institute for Nature Research (NINA), Trondheim, Norway, and the Norwegian University of Science and Technology (NTNU), Trondheim, Norway. The conference's scientific committee is Kuke Bijlsma, University of Groningen, Volker Loeschke, University of Aarhus, Juha Merilä, University of Helsinki, Isabelle Olivieri, Université Montpellier II, and Ettore Randi, Istituto Nazionale per la Fauna Selvatica.

Key speakers include John Avise, University of California at Irvine, Fred Allendorf, University of Montana, and Richard Frankham, Macquarie University, Australia. We also invite contributions as short oral presentations or posters.

The conference will be held at Rica Nidelven Hotel, Trondheim (Norway).

Information about the conference, with online registration, is available at

<http://www.nina.no/?ch=1000057> <
<http://www.nina.no/?ch=1000057> >

Deadline for registration has been postponed to 15 March 2009.

Best wishes,

Kjetil Hindar, Øystein Flagstad and Laila Saksgård, NINA Hans Stenøien, Gunilla Rosenqvist and Henrik Jensen, NTNU

"Hindar, Kjetil" <Kjetil.Hindar@nina.no>

UBritishColumbia MathBiol
Jul27-30

The Society for Mathematical Biology annual meeting will be held July 27-30, 2009 on the campus of the University of British Columbia in Vancouver. Please see the meeting web site:

<http://www.math.ubc.ca/Research/MathBio/-SMB2009/> Upcoming deadlines: Contributed talk proposal, May 10; Poster proposal, June 27; Early registration deadline, June 27.

Enquiries to: SMB2009@pims.math.ca
coombs@math.ubc.ca coombs@math.ubc.ca

UGuelph Frontiers Evolution May 20-21

Dear Colleagues, You are cordially invited to the 2009 Peter Yodzis Colloquium (May 20-21) at the University of Guelph on: The Frontiers of Evolution

This year the Yodzis colloquium on fundamental ecology celebrates Darwin's ideas with two days of talks that showcase science at the frontiers of evolutionary biology. The development of these emerging fields demonstrate how the theory of evolution is conceptually alive but also still incomplete.

Come join us May 20-21 to listen and discuss the present and future of evolution with: David S. Wilson (levels of selection) Richard Lenski (experimental evolution) Hans Thewissen (paleontology and genetics) Belinda Chang (molecular evolution) Ryan Gregory (evolution of the genome) Craig Albertson (evolution and development)

Please see our website for more details and registration: www.uoguelph.ca/Ecologicalcolloquia/ Where: University of Guelph, Guelph, ON 1 hour by car west of Toronto, Ontario.

When: May 20 - 21, 2009

Registration gives you: Participation in all of the day's talks and discussions Coffee breaks Social and Poster session

Registration for faculty is 150\$ per individual (before April 16th) and 200\$ after April 15th. Registration for grad students and postdocs is 75\$ per individual (before April 16th) and 100\$ after April 15th.

Schedule May 20: 8:00 - 8:45 Registration 8:45 to 9:00 Welcome (all talks are 60 min plus 15 min discussion)

Morning session 9:00 to 10:15 David S. Wilson (Binghamton University) 10:15 to 10:45 Coffee break 10:45 to 12:00 Richard Lenski (University of Michigan) 12:00 to 1:00 Lunch break Afternoon session 1:00 to 2:15 Belinda Chang (University of Toronto) 2:15 to 2:45 Coffee break 2:45 to 4:00 Craig Albertson (Syracuse University) Evening Social 4:30 to 7:00 Poster session and social mixer (Science Atrium)

May 21: 9:00 to 10:15 Ryan Gregory (University of Guelph) 10:15 to 10:45 Coffee break 10:45 - 12:00 Hans Thewissen (Northeastern Ohio Universities College of

Medicine) 12:00 to 1:00 Lunch break 1:00 - ? Panel discussion: Whither Darwin's Evolution?

Poster session on frontiers of evolution (May 20 evening social): We invite you to prepare a poster about your work at the frontiers of evolution. We will host a social along with the poster session where we can all meet, network and informally discuss evolution. We especially encourage grads and postdocs to show their recent work!

Our sponsors: University of Guelph College of Biological Sciences Depts. Of: Integrative Biology, Environmental Biology Faculty of environmental Sciences Biodiversity Institute of Ontario Ontario Agricultural College

LOOKING FORWARD TO SEEING YOU THERE!

Beren W. Robinson Assoc. Prof. Dept. of Integrative Biology University of Guelph Guelph, Ontario N1G 2W1, Canada

email: berenrob@uoguelph.ca Phone: 519-824-4120 x58968 Fax: 519-767-1656 Office location: Scie 2455 Lab location: Scie 2403

"Beren W. Robinson" <berenrob@uoguelph.ca>

UIdaho SSB Awards Jun12-17

Society of Systematic Biology Awards Available

Awards for Graduate Student Research

The Society of Systematic Biologists (SSB) announces the 2009 annual Graduate Student Research Awards competition. The purpose of these awards is to assist students in the initiation (first two years) of their systematics projects and in the collection of preliminary data to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: <http://systbio.org/?q=node/6>). Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply. Awards will range between \$1,200 and \$2000 and approximately seven awards will be made.

All application materials must be in electronic format. Applicants and their recommenders are strongly en-

couraged to use pdf format, rather than Word or some other application, to minimize difficulties in file transfer. We strongly recommend that applicants send all materials (except letters of reference) in a single pdf file. Letters of recommendation should be sent separately by the referees in pdf format or in the text of an e-mail; please include the full name of applicant in letters of recommendation. Applicants must submit 1. curriculum vitae (one page) 2. brief research proposal including objectives, methods, significance, and schedule (max. three single-spaced pages including literature cited and any figures and tables) 3. budget and budget justification (1 page) 4. two letters of recommendation; one letter must be from the student's current graduate advisor.

The research proposal must clearly state the current stage of the proposed research and the current year and status of the student. Please include e-mail contacts for the applicant in the application itself. Both Masters and Ph.D. students are eligible. Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work. Please email all application materials and queries to SSB Award Committee ssb-apps@life.illinois.edu. In the subject line of the email, please indicate the SSB Student Research.

To be considered for this year's award, application materials, including letters of recommendation, must be received electronically no later than March 31, 2009.

– Sydney A. Cameron Assoc. Prof. Department of Entomology and Program in Ecology, Evolution and Conservation Biology University of Illinois 320 Morrill Hall 505 S. Goodwin Ave. Urbana, IL 61801

ofc ph. 217-333-2340 lab ph 217-333-2170 cell ph 217 766-5631 scameron@life.illinois.edu

www.life.illinois.edu/scameron Sydney Cameron
<scameron@life.illinois.edu>

UIIdaho SSB ErnstMayrAward Jun12-17

Society of Systematic Biology Awards Available
Ernst Mayr Award (Graduate Student Award)

The Ernst Mayr Award is given to the presenter of the outstanding student talk in the field of systematics at the annual meetings of the Society of Systematic Biologists. The award consists of \$1000 and a set of available back issues of Systematic Biology.

Who is Eligible. Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to be considered (to join go to: <http://systbio.org/?q=node/6>). Previous Mayr award winners are not eligible. Application Procedure. Applications should be sent to the current SSB Awards Committee Chair (Sydney Cameron), at ssb-apps@life.illinois.edu. E-mail submissions are required. In the subject line of the email, please indicate the SSB award category as "Mayr Award".

Applicants should:

Submit a 400-word abstract of their talk to the SSB Mayr Awards Committee (ssb-apps@life.illinois.edu) by March 15, 2009. All candidates will be notified of their status no later than March 30, 2009. If selected as a Mayr candidate, during the meeting registration process (<http://evolutionmeetings09.org>) enter a note about being a Mayr candidate in the field concerning participation in a specific session. The deadline for the meeting submission is the same as for all other talks, i.e., April 5.

Judging. Based on the submitted abstracts, the Mayr Awards Committee (appointed by the Awards Chair) will select a maximum of 15 applicants for inclusion in the Ernst Mayr session at the 2009 Moscow, Idaho meetings, which will be held at a single venue in a separate session. Talks will be judged on creativity, quality, excellence of research, and quality of presentation. Abstracts should clearly indicate methods used, conclusions, and the relevance to systematics. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible.

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

Notification of Winner. The winner of the award will be announced at the SSB business meeting in Moscow, again during the banquet or awards ceremony at the conclusion of the Evolution Meetings, and an announcement will be published in Systematic Biology.

– Sydney A. Cameron Assoc. Prof. Department of Entomology and Program in Ecology, Evolution and Conservation Biology University of Illinois 320 Morrill Hall 505 S. Goodwin Ave. Urbana, IL 61801

ofc ph. 217-333-2340 lab ph 217-333-2170 cell ph 217 766-5631 scameron@life.illinois.edu

www.life.illinois.edu/scameron Sydney Cameron
<scameron@life.illinois.edu>

UIdaho SSE 2009 Activities Jun12-17

Conference: Evolution 2009 in Moscow, Idaho, is some 90 days away. We know that many of you will bring families, and that some will take the opportunity to enjoy some of the glorious back country. Whether you're a rafter, a hiker, a fisher, or a biker, you can't go wrong.

To give you a taste of the options, a bunch of your colleagues here in Moscow have put together a list of outdoors things for kids and grownups to do each day during the meetings, and a rafting trip right after the meetings. These are events that were created by locals once they learned about Evolution 2009. You sign up directly with them, and - ping - you're done.

The information is posted at: <http://sites.google.com/site/ev2009trips/Home>

Legal stuff: Because some of us organize the Evolution meetings at the University of Idaho, I want to spell out that the activities posted at the attached link are completely separate from Evolution 2009, and the university has no involvement in it whatsoever.

Dr. Olle Pellmyr Dept of Biological Sciences University of Idaho P.O. Box 443051 Moscow, ID 83844-3051 USA

phone 208.885.6807 (off) 885.8860 (lab)

pellmyr@uidaho.edu pellmyr@uidaho.edu

UIdaho SSE UndergradDiversity 2

Undergraduate Diversity at SSE/SSB 2009

For the seventh consecutive year, the Undergraduate Diversity at SSE/SSB program, funded by the Under-

graduate Research and Mentoring in the Biological Sciences (URM) program at NSF, will take place at the 2009 meeting of the Society for the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB) in Moscow, ID. This year we have teamed up with staff at the National Evolutionary Synthesis Center (NES-Cent) to send up to 25 undergraduates to the meetings to present posters and receive mentoring from graduate students, postdocs and faculty in evolutionary biology. For full information and links to the application portal see

<http://www.oeb.harvard.edu/faculty/edwards/-community/application.html>

The deadline for applications this year is April 1, 2009. However, proposals will be reviewed and accepted on a rolling basis, SO IT IS ADVANTAGEOUS TO APPLY EARLY. Applications can be made online through a special portal at the National Evolutionary Synthesis Center (NESCent) http://www.nescent.org/eog/signup_evolution09diversity.php. Applications consist of a title, author line and abstract of the poster to be presented by the undergraduate; a one-page statement of academic interests and career goals; and a letter of recommendation. The personal statement should address how attending the Evolution meetings will help meet these goals, and should indicate whether or not the student plans to attend graduate school, if this is known. The letter of recommendation, ideally from the undergraduate's research advisor, should indicate how inclusion of the student will increase diversity of the group participants. All materials required for application can be found at the NESCent application portal. Details on selection criteria are available at the program headquarters at

<http://www.oeb.harvard.edu/faculty/edwards/-community/application.html>

We can only accept applications from students who are US citizens or permanent residents. Applications will be accepted only from students registered or very recently graduated from U.S. institutions, including Puerto Rico (i.e., no later than having finished classes during the winter or spring semesters before the meeting) and traveling to the meeting from within the US. Students demonstrating a need for funds to attend SSE/SSB will be given preference, and will be selected so that as a group, they will maximize cultural diversity among undergraduates at the meetings.

You can also contact one of the program organizers for more information:

Scott V. Edwards (sedwards@fas.harvard.edu) Richard Kliman (rmkliman@cedarcrest.edu)

at NESCent:

Jory Weintraub (jory@nescent.org)

Jory Weintraub <jory@unc.edu>

UIowa SexRecomb May31-Jun3

“EVOLUTION OF SEX & RECOMBINATION: IN THEORY & IN PRACTICE”

May 31 - June 3, 2009 at the University of Iowa, Iowa City, USA

<http://cgg.biology.uiowa.edu/sexrec> The Roy J. Carver Center for Comparative Genomics and the Department of Biology at the University of Iowa announce an international conference on the evolution of sex & recombination taking place May 31 - June 3, 2009. The meeting will start on the evening of Sunday, May 31st with a reception and keynote talk (Graham Bell) and will conclude at ~1:00 pm on Wednesday, June 3rd.

This conference will immediately precede the 2009 Society for Molecular Biology and Evolution annual meeting (SMBE 2009: <http://smbe2009.org>), also located in Iowa City, on June 3-7, 2009. In order to integrate both meetings, an “overlap day” (June 3rd) will feature topics of clear interest to both sets of attendees.

The Sex & Recombination meeting was previously scheduled and fully organized for June 16-19, 2008, but was suddenly cancelled due to severe flooding in Iowa City. The organizers are pleased to note that a vast majority of the previously-scheduled attendees have committed to attend this meeting on the rescheduled dates.

Talks will be given by invited speakers at both the junior and senior level. There will also be some opportunities for contributed talks and posters to be given by conference attendees at all levels of seniority. A number of travel awards will be provided to deserving students and postdocs.

The deadline for abstract consideration for contributed talks and for travel awards will be April 16th, with decisions announced the following week. All attendees not selected for a contributed talk will be automatically slated to present their work as a poster.

Topics will include: Advantages of sexual reproduction
Experimental evolution of sex
Estimating recombination rates
Mating types & sex determination
Linkage, selection & population size
Sex chromosomes
Sex & pathogenesis
Sexual selection
Sexual conflict

Sponsorship for this meeting includes generous support from the American Genetic Association, but we encourage additional sponsorship inquiries. A symposium issue to be published in Journal of Heredity is planned.

Check the website for up-to-date information on confirmed speakers, details regarding registration, accommodation, etc. We anticipate opening registration within the next week (by March 23rd). Registration will be \$200 for grad students and postdocs and \$300 for faculty. Registration includes the closing banquet (and keynote: Michael Lynch) to be held on the evening of June 2nd.

All enquiries are encouraged and should be directed to the organizers: sexrec@uiowa.edu.

Facebook users: Join our official meeting group.

On behalf of the organizing committee,

John Logsdon –

John M. Logsdon, Jr., Ph.D. Associate Professor Director, Roy J. Carver Center for Comparative Genomics University of Iowa Department of Biology 319 335 1082 office 310 Biology Building 319 335 1083 lab Iowa City, IA 52242-1324 319 335 1069 FAX

email <john-logsdon@uiowa.edu> web <<http://www.biology.uiowa.edu/cgg/>>
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<<http://euplotes.biology.uiowa.edu>>

UIowa SMBE 2009 AbstractDeadlineExtended

Another SMBE 2009 Deadline Extended!

We are extending the abstract submission deadline for contributed talks for four additional days (to April 5, 2009). All abstracts received by April 5th can be considered for contributed talks in both symposia-related and general-topic sessions. However, the April 1st deadline for early registration fees remains in place (see: http://cgg.biology.uiowa.edu/smbe/registration_fees.php).

The registration and abstract submission process for SMBE 2009 is a two-step procedure (see: <http://cgg.biology.uiowa.edu/smbe/subform.php>). Thus, you are welcome to register and pay for the meeting prior to submitting your abstract. All contributed abstracts

received after April 5th will be automatically assigned to posters.

A few notes:

1. When submitting an abstract, please select the most appropriate symposium or general session for your work, as well as a second choice. See <http://cgg.biology.uiowa.edu/smbe/symposia.php> for up-to-date summaries of the SMBE 2009 symposia, including confirmed speakers. 2. If your work does not fit neatly into one of the symposia or general sessions, please apply for a contributed talk anyway. Selected talks will represent a wide diversity of topics. 3. A least three general (non-symposium-associated) contributed sessions will be held. However, depending on demand and available space, a few additional general sessions may be added to the program. 4. Some symposium-associated contributed sessions, if under-subscribed, will include talks on general topics. 5. We will consider adding a few additional topical sessions, as needed (e.g., transposable element evolution).

The above information may not be immediately reflected on the website.

General information on the meeting follows:

****SMBE 2009, Iowa City**** “Darwin to the Next Generation”

The 17th annual meeting of the Society for Molecular Biology and Evolution-SMBE 2009-will be held in Iowa City June 3-7, 2009, on the campus of The University of Iowa.

Visit our meeting website (<http://smbe2009.org>) for the most current information.

The SMBE 2009 scientific program will include 4 plenary talks and 23 symposia. The program will feature ~215 talks; more than half will be contributed talks selected on a competitive basis from submitted abstracts. We anticipate that 300-400 poster contributions will be highlighted in two evening poster sessions.

SYMPOSIA (see website for detailed descriptions and confirmed speakers):

* Biological networks from genes to populations * Epigenetics, environment & evolution * Evolution of networks * Genome evolution after polyploidy * Genomics of speciation & recent divergences * Historical roots of molecular evolution * Impacts of next generation sequencing on evolution * Insect evolutionary genomics * Molecular arms races * Molecular basis of speciation * Molecular evolution of biological complexity * Molecular evolution of functional noncoding sequences * Molecular evolution of plant:biotic interactions * Mutation accumulation in eukaryotic genomes * Origin &

evolution of animal genomes * Population genomics: selection, demography & mutation * Population genomics: theory, computation & adaptation * Primate functional & comparative genomics * Reproductive protein function & evolution * Sex-specific demography using the X * Teaching molecular evolution * Types of molecular evolution * Vanishing genomes

On behalf of the organizers, we'll see you soon in Iowa City! John

–

John M. Logsdon, Jr., Ph.D. Associate Professor Director, Roy J. Carver Center for Comparative Genomics University of Iowa Department of Biology 319 335 1082 office 310 Biology Building 319 335 1083 lab Iowa City, IA 52242-1324 319 335 1069 FAX

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john-logsdon@uiowa.edu john-logsdon@uiowa.edu

UIowa SMBE2009 AnimalGenomes Jun3-7

Dear all,

You are cordially invited to participate in the symposium on the “Origin and Evolution of animal genomes” to be held at the upcoming meeting of the Society for Molecular Biology and Evolution at the University of Iowa in Iowa City (June 3-7, 2009).

SYMPOSIUM DESCRIPTION: Multicellular animals (Metazoa) are relatively late arrivers on the scene of eukaryotic evolution and differ from other eukaryotes in their morphological organization, cellular composition, life cycles, and life styles. These differences should ultimately reflect information encoded in animal genomes but should also influence the evolution of animal genome architecture. The advent of high-throughput sequencing technology made it possible to obtain genomic information for both model and non-model species of animals and their closest phylogenetic relatives. Several new animal genomes have been published in the last year alone. This symposium will attempt to provide a synthesis of our current understanding of animal genome evolution and its relevance to organismal evolution in the group. In particular we

will focus on genomes of non-bilaterian animals as they are essential for reconstructing early stages in animal genome evolution.

ABSTRACT SUBMISSION DEADLINE:

April 1st for contributed talks

CONFIRMED SPEAKERS: T. Ryan Gregory, University of Guelph Kevin J. Peterson, Dartmouth College

MEETING WEBSITE: <http://smbe2009.org> CONTACT: Dennis Lavrov, Department of Ecology, Evolution and Organismal Biology, Iowa State University dlavrov@iastate.edu; 515-294-9091

Dennis V. Lavrov, Assistant Professor Department of Ecology, Evolution, and Organismal Biology, Iowa State University, 343A Bessey Hall, Ames, IA 50011 phone: (515) 294-9091; fax: (515) 294-1337 <http://www.eeob.iastate.edu/faculty/LavrovD/> dennis.lavrov@gmail.com

UIowa SMBE 2009 AwardsDeadlineExt Jun3-7

Deadlines Extended!

Due to some confusion regarding details for the Walter Fitch student awards, we have decided to extend the deadline for ALL award applications for three additional days (to March 19, 2009). This deadline extension includes the Fitch, Postdoc Travel, Grad Travel, and Undergraduate Diversity Mentoring Program Awards. The April 1 abstract deadline for consideration of contributed talks remains in place. (see: <http://cgg.biology.uiowa.edu/smbe/awards.php>)

Please note that: 1. all eight participants selected for the Fitch Symposium will automatically receive a travel award (in the same amount as Postdoctoral or Grad Student travel awards), 2. all applicants for the Fitch prize who are not selected for the Fitch symposium will be automatically considered for the Postdoctoral or Grad Student travel award. 3. all travel awards will be provided as reimbursement after the meeting. 4. you must register for the meeting prior to submitting an abstract for award consideration. 5. to apply for the travel (& Fitch) awards, you should register as a SMBE member, as this is required for award consideration. If the SMBE membership site is down, you can still register as a SMBE member on our meeting site (if so, be sure to become a SMBE member prior to award

decisions)

The above information may not be immediately reflected on the website.

General information on the meeting follows:

****SMBE 2009, Iowa City**** “Darwin to the Next Generation ”

The 17th annual meeting of the Society for Molecular Biology and Evolution-SMBE 2009-will be held in Iowa City June 3-7, 2009, on the campus of The University of Iowa.

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SYMPOSIA (see website for detailed descriptions and confirmed speakers):

* Biological networks from genes to populations * Epigenetics, environment & evolution * Evolution of networks * Genome evolution after polyploidy * Genomics of speciation & recent divergences * Historical roots of molecular evolution * Impacts of next generation sequencing on evolution * Insect evolutionary genomics * Molecular arms races * Molecular basis of speciation * Molecular evolution of biological complexity * Molecular evolution of noncoding genes * Molecular evolution of plant:other interactions * Mutation accumulation in eukaryotic genomes * Origin & evolution of animal genomes * Population genomics: selection, demography & mutation * Population genomics: theory, computation & adaptation * Primate functional & comparative genomics * Reproductive protein function & evolution * Sex-specific demography using the X * Teaching molecular evolution * Types of molecular evolution * Vanishing genomes

On behalf of the organizers, we'll see you soon in Iowa City! John

–

John M. Logsdon, Jr., Ph.D. Associate Professor Director, Roy J. Carver Center for Comparative Genomics University of Iowa Department of Biology 319 335 1082 office 310 Biology Building 319 335 1083 lab Iowa City, IA 52242-1324 319 335 1069 FAX

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euplotes.biology.uiowa.edu >
 john-logsdon@uiowa.edu john-logsdon@uiowa.edu

**UIowa SMBE2009
 Biological Networks Jun3-7**

Hello all,

Submission of abstracts for oral and poster presentations is open for the symposium on

“Biological networks from genes to populations: Applications & analytical approaches”

which will be held at the Society for Molecular Biology and Evolution Meetings in Iowa City, IA, USA (June 3-7, 2009). Please see the symposium description below. Empirical studies using network approaches are complementary to the theme of the symposium and are particularly encouraged for submission.

The deadline for abstract submission for consideration as a contributed talk is April 1st (all abstracts received after April 1st will be posters). If you would like to give an oral presentation of your work at this symposium, but have not registered and submitted an abstract yet, please so within the next week.

For more general information about the meeting, including registration and abstract submission, please see <http://cgg.biology.uiowa.edu/smbe/> Looking forward to seeing you at Iowa City!

“Biological networks from genes to populations: Applications & analytical approaches” symposium description:

Complex, multi-dimensional processes are characteristic of all levels of biological organization, from the diversification of gene families to the co-regulation of gene expression to the flow of genes among natural populations. A powerful tool for investigating these complex systems is to represent them in the form of networks (or graphs) describing both direct (pair-wise) and indirect (higher-order) interactions among variables. This symposium will cover active areas of evolutionary research focusing on the development of new methods to estimate realistically complex networks, the formal description of these networks, and models of network formation and function. The symposium will accommodate talks ranging from the theoretical to the empirical on any organism. Participants will be prompted to discuss and exchange ideas about “network thinking” its

importance as an organizing principle in evolutionary biology. Network thinking is both an analysis tool and way to visualize complex biological data empirically. Networks can be broadly applied to nearly all levels of evolutionary biology from gene regulation networks to population and community structure. This symposium will complement another symposium “The evolution of networks” as it will demonstrate the breadth of network application across multiple biological levels and discuss analytical approaches.

Organizers:

John Nason, Department of Ecology, Evolution and Organismal Biology; Iowa State University, Ames, USA
 Jeanne Serb, Department of Ecology, Evolution and Organismal Biology; Iowa State University, Ames, USA

Confirmed Speakers:

Rodney Dyer, Department of Biology, Virginia Commonwealth University, Richmond, USA (Invited)

Luay Nakhleh, Department of Computer Science, Rice University, Houston, Texas, USA (Invited)

Isabelle Peter, Division of Biology, California Institute of Technology, Pasadena, USA (Invited)

–
 Jeanne M. Serb Assistant Professor

Department of Ecology, Evolution, and Organismal Biology 245 Bessey Iowa State University Ames, IA 50011 USA

tel: 515-294-7479; FAX: 515-294-1337 serb@iastate.edu
<http://www.eeob.iastate.edu/faculty/profiles/SerbJ/-SerbJ.html> Jeanne Serb <serb@iastate.edu>

**UIowa SMBE2009
 Comparative Genomics Jun3-7**

Hello all,

Submission for abstracts for oral and poster presentations are open for the symposium on

“Primate Functional & Comparative Genomics”

To be held at the Society for Molecular Biology and Evolution Meetings in Iowa City, IA USA (June 3rd - 7th, 2009). We encourage submission of research that investigates primate genomic diversity, gene expression/regulation, selection, and genome organization in order to test hypotheses regarding human and nonhu-

man primate evolution, uniqueness, development, and disease. The deadline for abstract submission for consideration as a contributed talk is April 1st.

For more general information about abstract deadlines and the meeting please see <http://ccg.biology.uiowa.edu/smbe/> . Looking forward to seeing you in Iowa!

Primate Functional & Comparative Genomics Symposium Description: The amount of primate sequence data being produced each year has grown exponentially since the publication of the human genome. Are we any closer to pinpointing the genetic basis for uniquely human traits? This symposium will present current research that uses comparative and functional genomics to explore the genetic differences between humans and nonhuman primates (as well as between primates and other mammals) that underlie species-specific phenotypes. Talks included will use a combination of computational and experimental approaches to examine the origin and functional impact of species-specific changes in the genome and transcriptome. Development and use of innovative statistical methods and appropriate models for the analyses of high throughput genetic data are also welcome.

Confirmed Speakers: Philipp Khaitovich Comparative Biology Group, CAS-MPG Partner Institute for Computational Biology, Shanghai, P.R.China (Invited)

Katie Pollard Gladstone Institutes, University of California, San Francisco, USA (Invited)

Shyam Prabhakar Genome Institute of Singapore, SINGAPORE (Invited)

Organizers: Kirstin Sterner Department of Anthropology and Molecular Primatology Lab, New York University, New York City USA

Nelson Ting Department of Anthropology and Roy J. Carver Center for Comparative Genomics, University of Iowa, Iowa City USA

Yi Xing Department of Internal Medicine and Department of Biomedical Engineering, University of Iowa, Iowa City USA

nelson ting <nelson-ting@uiowa.edu>

UIowa SMBE 2009
EukaryoticMutAccumulation Jun3-7

Dear all,

Submissions of abstracts for oral and poster presentations are now open for the symposium on

“Mutation accumulation in eukaryotic genomes”

to be held at the upcoming meeting of the Society for Molecular Biology and Evolution at the University of Iowa in Iowa City (June 3-7, 2009).

SYMPOSIUM DESCRIPTION: The accumulation of harmful mutations is central to many biological questions of broad interest, from the inheritance and severity of disease to the importance of preserving genetic diversity. Answering these questions require that we acquire a comprehensive understanding of why, how, and whether harmful mutations accumulate at different rates and in different lineages. Recent applications of high throughput sequencing and gene expression technologies to the studies of mutation accumulation have greatly enhanced our understanding of this fundamental process. This symposium will bring together the most recent advances from across the spectrum of topics where mutation accumulation matters, from mitochondrial disease to the maintenance of sex.

ABSTRACT SUBMISSION DEADLINE: April 1st for contributed talks

CONFIRMED SPEAKERS: Joanna Elson, University of Newcastle upon Tyne David Rand, Brown University

MEETING WEBSITE: <http://smbe2009.org> CONTACT: Maurine Neiman, Department of Biology, University of Iowa, Iowa City, IA. maurine-neiman@uiowa.edu; 319-384-1814

Maurine Neiman Department of Biology University of Iowa maurine-neiman@uiowa.edu 319-384-1814 http://www.biology.uiowa.edu/faculty_info.php?ID=1409 “Neiman, Maurine” <maurine-neiman@uiowa.edu>

UIowa SMBE2009
InsectEvolGenomics Jun3-7

Dear Colleagues,

We invite you to attend the upcoming conference of the Society for Molecular Biology and Evolution and submit abstracts for the symposium on

INSECT EVOLUTIONARY GENOMICS: THE EVOLUTION OF DIVERSITY

Symposium Description: By many measures, insects

are the most successful of animal taxa. Insects make up more than half of all named species and inhabit virtually every terrestrial environment. In addition, they display tremendous morphological, behavioral, and developmental diversity. Insects have also played a key role in furthering our understanding of genetics and evolution. In fact, key insights into the importance of epigenetic mechanisms, gene shuffling, rates of protein evolution, and variation in gene expression have all been derived from analyses of insect taxa. This symposium will focus on emerging topics in insect evolutionary genomics. Our goal is to provide a forum in which investigators share information and discuss applications, directions, and ideas to ultimately further our understanding of evolutionary mechanisms underlying phenotypic diversity.

Confirmed Speakers: Dr. Jack H. Werren; University of Rochester Dr. Christina M. Grozinger; The Pennsylvania State University Dr. Hugh M. Robertson; University of Illinois

Deadline for abstract submission: DEADLINE APPROACHING!!!: April 1ST

Websites: http://cgg.biology.uiowa.edu/smbe/symposia.php?action=view&sym_ID=8 <http://cgg.biology.uiowa.edu/smbe/index.php> Contacts: Soojin V. Yi soojin.yi@biology.gatech.edu <http://www.yilab.gatech.edu/> and Michael A. D. Goodisman michael.goodisman@biology.gatech.edu <http://www.goodismanlab.biology.gatech.edu/> Michael A D Goodisman

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michael.goodisman@biology.gatech.edu
michael.goodisman@biology.gatech.edu

UIowa SMBE2009
SpeciationGenomics Jun3-7

Hi everybody,

This is an renewed invitation to participate in a symposium on the origin of species at SMBE 2009 (Iowa City June 3-7):

“Genomics of Speciation & Recent Divergences”

SYMPOSIUM DESCRIPTION: With the recent availability of full genome sequences in several pairs of closely related species, we are now at a stage where a genome-wide picture of species divergence is within reach. These new data are complemented by theory on the role of recombination in the divergence process and by statistical methods assessing gene flow during divergence. Recent studies have clearly shown that speciation history may be complex and that the genomes of incipient species diverge at strikingly heterogeneous rates. Although much of this heterogeneity may be accounted for by stochasticity of the genetic drift process, the role of natural selection in promoting or preventing genomic divergence between nascent species remains highly debated. For example, can genomic regions experiencing reduced introgression act as ³genomic islands of speciation², impeding gene flow of linked regions and thereby increase intergenomic divergence and drive reproductive isolation? In particular, while genomic co-adaptations developing independently in each species are believed to select against the transfer of genetic material from one species into the genomic background of the other, other forces such as balancing selection may actually favor introgression. This symposium will present the depth of scholarship and the variety of evolutionary processes involved in genomic divergence by conveying top researchers actively involved in studies on a wide range of organisms. We anticipate that it will be a nice opportunity to bring together genomicists for a fine-scale description of the heterogeneity of divergence across the genome with population geneticists for more precise, hypothesis-driven studies on candidate genes.

INVITED SPEAKERS: Michael Nachman, Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, USA

Sam Sheppard, Department of Zoology, University of Oxford, Oxford, UK

Sara Via, Department of Biology and Department of Entomology, Cornell University, Ithaca, USA

Andrew Whiteley, Department of Biology, Université Laval, Québec, Canada

Symposium website include links to speakers' websites: (http://cgg.biology.uiowa.edu/smbe/symposia.php?action=3Dview&sym_ID=3D5)

There will be six 15 min slots available for contributed

talks. The deadline for abstract submission for contributed talks is April 1st. Poster presentations are also welcome! (All abstracts received after April 1st will be posters.)

Visit the meeting website (<http://smbe2009.org>) for further information about the conference.

Looking forward to seeing you in Iowa!

/Johan Lindell, Niclas Backström, Vincent Castric, and Jody Hey

Contact info: Johan Lindell <johan.lindell@ebc.uu.se>
Department of Evolutionary Biology, Uppsala University, Sweden

Niclas Backström <niclas.backstrom@ebc.uu.se> Department of Evolutionary Biology, Uppsala University, Sweden

Vincent Castric <Vincent.Castric@univ-lille1.fr> CNRS, Université de Lille, France

Jody Hey <Hey@Biology.Rutgers.Edu> Department of Genetics, Rutgers University, United States

– Johan Lindell, Ph.D. FORMAS Postdoctoral Fellow

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UIowa SMBE2009 Symposium Epigenetics Jun3-7

Hello all,

Submission for abstracts for oral and poster presentations is open for the symposium on

“Epigenetics, Environment, and Evolution (EEE)”

To be held at the Society for Molecular Biology and Evolution Meetings in Iowa City, IA, USA (June 3-7, 2009). Please see the symposium description below. Empirical studies on any system pertaining to the theme of the symposium are particularly encouraged for submission.

The deadline for abstract submission for consideration

as a contributed talk is April 1st (all abstracts received after April 1st will be posters), which hopefully you have noticed from an early email sent out by the SMBE2009 organizers. If you would like to give an oral presentation of your work at this symposium but have not registered and submitted an abstract yet, hope you can do so within the next week.

For more general information about the meeting please see <http://ccg.biology.uiowa.edu/smbe/>. I would also like to invite all the other evolutionary biologists to come to this symposium during the SMBE2009 meeting, particularly if you have had enough fun in the innumerable parties for Darwin this year and are wondering if there are other mechanisms for evolution other than natural selection.

Looking forward to seeing you at Iowa City!

“Epigenetics, Environment, and Evolution (EEE)”
Symposium Description:

Traditionally, the molecular study of evolution has been focused on DNA sequence variation. This is convenient, and it is also based on the dogmatic belief that has developed since the discovery of the double-helix structure of DNA, which is, any evolutionary change must be based on mutation at DNA sequence level. This is a grossly simplified understanding of biology and a rather outdated view about life. In the last decade, increasingly more evidences have revealed that epigenetic changes, i.e., modifications of nucleotides (e.g., methylation of cytosine) and/or histones (acetylation, methylation, etc.) without any change at DNA sequence level, particularly under the influence of the environment, could dramatically alter important life traits and such alteration is heritable at least to some degree. Increasingly more evidences suggest epigenetic regulation may have played fundamental, rather than just supplemental, roles in development (e.g., cell differentiation), adaptation to environment, and diseases (like the occurrence of cancer). All these suggest possibly important roles played by epigenetics and the environment in biological evolution. A symposium about the relationship between epigenetics, environment, and evolution is due, particularly in this year of Darwin. In this symposium, the roles played by the environment and epigenetics in evolution will be addressed with respect to both molecular mechanisms and theoretical implications. Specific topics would include: (1) Can epigenetic changes alter important phenotypic traits? (2) How can the environment affect a genomes epigenetic state? (3) Are epigenetic alterations by the environment and subsequent phenotypic changes inheritable? (4) What does this mean for evolutionary theory?

Organizer:

Xianfa Xie Department of Biology, Brooklyn College,
The City University of New York, Brooklyn, NY, USA
xianfaxie@brooklyn.cuny.edu

p.s. Please kindly forward this email to those who you know might be interested in this symposium but not on the evoldir email list (like some molecular biologists who have interests in mechanisms of evolution). Thanks!

Xianfa Xie <xiexianfa@gmail.com>

UIowa SMBE2009
Symposium Evolution Networks
Jun3-7

Hi folks,

The call for oral and poster submissions to the symposium on:

“Evolution of Networks”

is now open.

The description of the symposium is below. We would encourage you to submit an oral presentation, however, the deadline is April 1st and all submissions after this deadline will automatically only be considered for poster presentation.

You can submit your abstracts here:

<http://cgg.biology.uiowa.edu/smbe/subform.php> The home page for the conference is here:

<http://cgg.biology.uiowa.edu/smbe/> Please pass this email on to others that you think might be interested.

http://cgg.biology.uiowa.edu/smbe/-symposia.php?action=3Dview&sym_ID=3D3 All

of biology consists of networks ' interactions and connections between agents. A network can be visualised as a graph, which consists of nodes (or vertices) linked together by edges (otherwise known as links, connections or arrows). The nodes represent the agents, the edges represent their interactions. Two nodes are joined by an edge if, and only if they interact or have some kind of relationship. Edges may be bidirectional (interactions go both ways) or unidirectional (A influences B but not the other way round). Networks and nodes within networks have properties such as connectivity, transitivity and whether or not they are scale-free. In a biological context, the likelihood that

an enzyme will be useful in an organism is measured in terms of what other enzymes, proteins and metabolites are present in that organism. A bacterial species can be described in terms of the network of gene sharing to which it belongs and in relation to other organisms that share homologous genes. The expression pattern of a gene in a genome is dependent on the expression pattern and functions of other genes and indeed the environment in which the genome is to be found. Crucially and perhaps of most interest to SMBE, these networks evolve over time. Organisms can both lose and duplicate genes, the external and internal environment changes, gene expression levels change and indeed new genes can be formed. New organelles are invented or acquired and old organelles are lost. In this symposium, we shall address the evolution of biological networks ' from metabolic networks to gene expression networks to gene-sharing networks, to the interaction between intracellular networks and the environment. The timing of this symposium is quite good. The nuts and bolts methods for understanding evolution at the sequence level are well worked out, the data from next-generation sequencing is revealing new metabolic modules that we never knew existed and network mathematics is being exported to molecular biology. Many students would benefit from a symposium where the evolutionary context of many network-based studies is presented.

– Dr. James O. McInerney, Bioinformatics Laboratory, Department of Biology, National University of Ireland, Maynooth, Co. Kildare, Ireland. P: +353 1 708 3860 F: +353 1 708 3845 E: james.o.mcinerney@nuim.ie – Work — <http://bioinf.nuim.ie/>

james.o.mcinerney@nuim.ie

UIowa SMBE Teaching MolEvol
Jun3-7

UIowa SMBE Jun 3-7

Teaching Molecular Evolution: Effectively Incorporating the into Education

Hi everyone,

This is an invitation to participate in a symposium on Teaching Molecular Evolution at SMBE 2009 (Iowa City June 3-7):

Moore, manager of the Science & Society Program at the European Molecular Biology Organization

(EMBO), last May called for a stronger infusion of the molecular aspects of evolution into secondary school curricula in Europe (Moore 2008). Moore argued that, of the most fascinating and definitive examples supporting evolution X those made in the past four decades using gene-sequencing technology and bioinformatics X are largely absent from European secondary school curricula. The same certainly can be said for the US, and the problem is not restricted to secondary education, but spills into the university curriculum as well.

The stuff is indeed important. If we really want our students to understand evolution, it is critical that they understand fundamental ideas about biochemical evolution, molecular clocks, phylogenetics (tree-thinking), and development (evo-devo). However, an overemphasis on analysis of DNA sequences holds the potential to push organisms themselves into the background (Gee 2008), preventing students from understanding evolution via insights best gained from studies of comparative morphology or the analysis of fossils in a cladistic framework.

So, what's the best way to incorporate Molecular Evolution into our students' overall evolutionary biology education? This SMBE symposium will explore this question by bringing together speakers who teach molecular evolutionary principles in courses ranging from Introductory Biology to specialized courses in Molecular Evolution. In addition, we will include speakers who represent molecular evolution education outreach, authors of textbooks used in Evolution and Molecular Evolution courses, and evolution education researchers.

Our primary goals will be to identify and explore problems our students have understanding evolutionary concepts, and how we can best use molecular evolutionary principles to help them overcome these difficulties.

References Gee H (2008) The March of the Mighty Molecule. <http://network.nature.com/people/henrygee/blog/2008/05/01/march-of-the-mighty-molecule>. Accessed Dec. 29, 2008.

Moore A (2008) Science teaching must evolve. *Nature*, 453: 31-32. doi: 10.1038/453031a.

Invited speakers include Andrew Moore, Editor-in-Chief, *BioEssays* (tentative), David Baum, Univ. of Wisconsin, and Hopi Hoekstra, Harvard University.

We are looking for six speakers (15 minutes each), who will be selected for contributed talks via submitted abstracts. We are looking for people who will tell us about the cool things they are doing in evolution education. We are hoping to find people who are taking a truly integrative (and pedagogically sound) approach to evolution education.

lution education.

The deadline for abstract submission for contributed talks is April 1st. Poster presentations are also welcome!

Visit the meeting website (<http://smbe2009.org>) for further information about the conference.

See you in Iowa!

UPDATE: Abstract deadline for award consideration: March 16th Early registration closes: April 1st Abstract deadline for consideration as contributed talk: April 1st (all abstracts received after April 1st will be posters) Abstract deadline for inclusion in the program book: May 15th

Jim Smith <jimsmith@msu.edu>

UMichigan UsingPhylogenies Mar14

Registration is still available for the 5th Annual Early Career Scientists Symposium to be held at the University of Michigan on March 14.

The Symposium examines how phylogenies have been integrated into the field of ecology, thus providing an evolutionary perspective on the origin and maintenance of ecological communities. The symposium participants will address a range of questions from across the Tree of Life. How does the evolutionary history of a species influence its interaction with other species? What are the mechanisms of such influences and how does ecological context influence further evolution? What are the consequences of the feedback between ecology and evolution for community structure and dynamics? The symposium will also include an open mike discussion, poster presentations by graduate students, complimentary lunch and a dinner reception.

Eight outstanding scientists have been selected to present their work. The speakers include:

Jeannine Cavender-Bares, University of Minnesota (keynote speaker). Rose L. Carlson, Harvard University Liliana M. Dávalos-Alvarez, SUNY Stony Brook Erika Edwards, Brown University Matthew Helmus, Xishuangbanna Tropical Botanical Garden, Kunming, China Steven W. Kembel, University of Oregon John Paul, Colorado State University Enrico Rezende, Universitat Autònoma de Barcelona Nathan G. Swenson, Harvard University Herbaria

Further information about the symposium, and registration is available at the following web site:

<http://sitemaker.umich.edu/ecss2009/home> Christopher Dick <cwDick@umich.edu>

UNebraska Evolution Sep2-4

We are holding a major symposium on evolution here at the University of Nebraska at Kearney, September 2-4, 2009. Would you please place an advertisement for this event on your web site. Our conference's web page is located at www.evolution2009.org. We are very excited about the lineup of speakers that we have for the symposium, including Jack Horner, Randy Moore, and a representative of the J. Craig Venter Institute. Thank you for your assistance.

Best,

Brad Ericson, Professor of Biology Biology Department, BHS 301C University of Nebraska at Kearney Kearney, NE 68847 (308)865-8912 ericsonb@unk.edu

Brad L Ericson <ericsonb@unk.edu>

UWisconsinMadison StatGenetics May4-6

Symposium: Statistical Genetics of Livestock in the Post-Genomics Era May 4-6, 2009 University of Wisconsin - Madison

The web site of the symposium "Statistical Genetics of Livestock in the Post-Genomic Era" is finally up and running. Please check out the following link:

<http://www.wisc.edu/dysci/sglpge/> We have a great list of invited speakers, plus there will be a poster session for contributed papers, so please join us if you're available in early May.

Sincerely,

Dr. Kent Weigel and Dr. Guilherme Rosa Symposium co-chairs

The Symposium organization acknowledges funding support from the USDA-NRI 43.0 Animal Genome Program.

–

Guilherme J. M. Rosa Assistant Professor Department of Dairy Science University of Wisconsin - Madison

444 Animal Science Building 1675 Observatory Dr. Madison, WI 53706 USA

Phone: + 1 (608) 265-8617 Fax: + 1 (608) 263-9412 E-mail: grosa@wisc.edu <https://mywebspaces.wisc.edu/~grosa/web/>

"Guilherme J. M. Rosa" <grosa@wisc.edu>

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*** Please disseminate widely to students at your institution ***

The Centre for Research and Conservation (CRC) of the Royal Zoological Society of Antwerp (RZSA) is offering a PhD Scholarship in the project:

Mate Choice & patterns of adaptive variation in the European Black Vulture (*Aegypius monachus*)

The Black Vulture has an extensive but discontinuous Palearctic distribution extending from the Iberian Peninsula across southern Europe through the central Asian Plateau to Mongolia and China. Since the early 1950's, in response to anthropogenic effects, the wild European distribution has shown a dramatic decrease with extirpations from the majority of its European range. In 1987, in an effort to help conserve and re-establish populations within Europe, the Black Vulture Conservation Foundation (BVCF) and the European Association of Zoos and Aquaria (EAZA) established a European Endangered species Programme (EEP), coordinated by Animal Park Planckendael in Mechelen, Belgium. Despite successful reintroductions (in Spain and France), the breeding success of this EEP is relatively low mainly because of lack of hatching success. It was hypothesised that the low percentage of fertilized/viable eggs may be due to genetic incompatibility between paired birds, either in terms of genome wide heterozygosity or specifically at the Major Histocompatibility Complex (MHC) and closely linked Olfactory Receptor & Vomeronasal Genes (OR & VR genes), together called the 'immuno-olfactory super-

complex' (IOS). Although birds have been used extensively for studies of sexual selection and mate choice, relatively little work has focused on the role of the IOS. Those studies that have taken place have usually been on passerine or fowl species. As such, data from this study will form a unique contribution to IOS research in raptor populations. Furthermore, we will integrate the analysis of semiochemicals with the genetic analysis as the odourant profiles might represent condition-dependent signals that reflect not only variation at the IOS genes but an individual's overall genetic variation. To test/strengthen the hypothesis that these signals are condition-dependent, we will compare the data against traditional parameters including: body measurements and parasite loads (ectoparasites and blood parasites) to estimate condition. Hence the project will encompass multidisciplinary aspects involved in breeding success including the genetic basis (MHC), the molecules involved (semiochemicals), their receptor genes (OR & VR), to the effect on the condition of the organism involved (parasitic load, hatching/breeding success and survival) and the effect on conspecifics (mate choice and pair bonding).

If IOS profile is an important component of mate choice in this species, then IOS screening will be excellent tool for informing the movement of individuals among institutions and the assignment of pairs within the captive breeding program, and as such is in keeping with the aims and objectives of the European Action Plan for this species. Investigation of IOS variation in the fragmented wild populations will also be used to inform the setting of conservation management units in the field. The structure observed at the genes under selection will influence decisions on translocations (e.g. the avoidance of breaking up co-adapted gene complexes).

The broad aims of the project are to a) evaluate the pedigree and breeding success using studbook data as well as molecular (microsatellite DNA) data, b) use

captive individuals from among the European Zoo EEP collection, as well as samples from wild/released populations within Europe, to assess the role of IOS genotype in female mate choice, c) to compare genetic data with existing observational data from behavioural studies, and d) to contrast IOS variation against existing (and new) mtDNA and microsatellite data to detect signatures of adaptive variation.

Promotor: Prof Dr Erik Matthysen - Group of Evolutionary Ecology - University of Antwerp

Copromotors: Dr Jill Shephard & Dr Peter Galbusera - Royal Zoological Society of Antwerp, CRC ; Dr David Richardson - School of Biological Sciences, University of East Anglia

There is also the opportunity for the successful candidate to be involved in applied zoo-research and related activities of the Centre for Research and Conservation (CRC). The CRC is a government-funded research division of the Royal Zoological Society of Antwerp (RZSA) and is active both within the society's grounds (Antwerp Zoo, Wild Animal Park Planckendael and the local nature reserve "De Zegge"), in its own field-based conservation projects in Cameroon and Brazil, and as a research partner in various other projects with an in-situ component. Performing scientific research helps the Royal Zoological Society of Antwerp accomplish its mission to contribute to worldwide nature conservation and education.

The successful candidate should have:

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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>

BathU EvolutionaryGenetics Shorebirds

NERC-funded PhD studentship at University of Bath: Evolutionary genetics of breeding systems in shorebird populations

Supervisors: Prof Tamás Székely (Bath), Dr Patricia Lee (Swansea), Dr Steve Dorus (Bath) & Prof Terry Burke (Sheffield)

Mating systems, pair bonds and parental care are highly variable traits within and between shorebird

populations. The Biodiversity lab at the University of Bath is carrying out a series of studies to reveal the selective processes that has shaped breeding system variation. Two fundamental issues, however, have remained elusive: (i) what is the role of local adaptation driving breeding system variation? (ii) are these adaptations related to genes and genomes?

The objective of the NERC-funded studentship is to develop, test and use molecular markers (SNPs and microsatellites) to measure population differentiation. The project has a field component given that the Biodiversity Lab works with a range of species in exotic locations. However, the emphasis of the project is on evolutionary and molecular approaches. We anticipate that the markers will be useful for establishing population-level differentiation between breeding populations, and estimating migratory routes. This will provide the link between migratory strategies and breeding system variation for genetically differentiated populations. Establishing the connection between breeding and migrating shorebirds may also impact upon conservation strategies for managing shorebird populations.

This project will suit a student with strong interest in molecular ecology, conservation genetics and behavioural ecology. The ideal candidate should have good general laboratory skills with understanding of DNA sequencing, and statistical analyses of mitochondrial and/or nuclear sequence data.

There is a significant field component in the project, and we expect the student will spend substantial time sampling shorebird populations in Europe, Asia and Africa, often working in hostile environments (Arctic, tropics). The student will be trained in field biology, molecular ecology, behavioural ecology and statistical analyses.

Application deadline: 30 April 2009.

For further details on how to apply, please visit this website: <http://www.bath.ac.uk/bio-sci/postgrad/-phd/opportunities.html> All enquiries concerning this studentship should be directed to Dr Emma Lawrence e.l.lawrence@bath.ac.uk

Funding Notes: This is a fully NERC-funded studentship 3.5 years, and are available for UK/EU students who have been resident in the UK for at least the 3 years prior to the start of the research programme.

Dr. PLM Lee Senior Lecturer Department of Environmental and Molecular Biosciences Wallace Building Swansea University Singleton Park SWANSEA SA2 8PP United Kingdom p.l.m.lee@swansea.ac.uk

"Lee P.L.M." <P.L.M.Lee@swansea.ac.uk>

BathU Shorebird Evolutionary Genetics

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Dr. PLM Lee Senior Lecturer Department of Environmental and Molecular Biosciences Wallace Building Swansea University Singleton Park SWANSEA SA2 8PP United Kingdom p.l.m.lee@swansea.ac.uk

P.L.M.Lee@swansea.ac.uk P.L.M.Lee@swansea.ac.uk

Canberra Orchid Population Genetics

Australian Postgraduate Award Industry (APAI) PhD Scholarship * * * * *The Australian National University, Canberra, Australia* Applications are now open for a 3 year APAI PhD scholarship. The position is funded by a multidisciplinary Australian Research Council Linkage grant. Applicants wishing to pursue a PhD as part of this multidisciplinary project are sought in one of the following three areas: (1) Chemical Ecology, (2) Population Genetics, (3) Climate Change modelling or a combination of these fields. Applicants must hold either a First Class Honours Science Degree, a Master Degree in Science or equivalent qualification. A sound scientific background in one of the above three fields or a combination of these fields is essential. Evidence of research excellence as demonstrated by publications is highly desirable. Ref No: LP0989338 APAI Closing date: April 20, 2009. For details: <http://cos.anu.edu.au/HDR/Scholarships.php> For further information: rod.peakall@anu.edu.au <<mailto:rod.peakall@anu.edu.au>>

– Michael Whitehead PhD candidate Botany and Zoology School of Biology ANU College of Medicine, Biology and Environment. Australian National University Canberra ACT 0200 Telephone: +61 (0)2 6125 4172 Facsimile: +61 (0)2 6125 5573 Email: michael.whitehead@anu.edu.au

michael.whitehead@anu.edu.au
michael.whitehead@anu.edu.au

CarletonU Evolution of Sex

Graduate Position: Evolution of Sex ' Carleton University ' Root Gorelick

I am looking for new graduate students (MSc or PhD) to develop evolutionary theory of origin and maintenance of sex. Our research includes epigenetic origin of meiosis; heterochrony in syngamy; evolutionary history and implications of gynogenesis/hybridogenesis; shortening of sex chromosomes; heritable effects of maternal thermoregulation of parthenogenetic and outcrossing reptiles; and thermoregulation of sex in plants. While most of our work is theoretical, we have several empirical collaborations. Additional information can be found at <http://www.carleton.ca/~rgorelic>. If interested, please send your cv, summary of research experience and interests, and contact details of at least two referees to Root_Gorelick@carleton.ca <mailto:Root_Gorelick@carleton.ca>.

Root Gorelick, Ph.D. Department of Biology and School of Mathematics & Statistics Carleton University 1125 Colonel By Drive Ottawa, Ontario K1S 5B6 Canada

Voice 613-520-2600 ext. 1586 URL www.carleton.ca/~rgorelic E-mail Root_Gorelick@carleton.ca

Root_Gorelick@carleton.ca

DalhousieU Conservation

Support for a PhD position is expected to become available at Dalhousie University (Halifax, Nova Scotia, Canada) for research in conservation genetics and/or comparative phylogeography of fish in temperate regions. The student will develop a research project that uses molecular genetic and phenotypic approaches to examine issues in adaptive radiation and conservation genetics and/or phylogeography of fish in Patagonia or in Labrador. The successful candidate should have experience with molecular techniques and should have a strong interest in population genetics and statistics. The position is expected to start in the 2009/2010 academic year, pending funding approval and is contingent

upon acceptance to the Department of Biology graduate program. Potential applicants may consult the following: Ruzzante et al 2006 *Mol Ecol* 15:2949-2968, and 2008 *Mol Ecol* 17: 2234-2244, Zemplak et al 2008, *Mol Ecol* 17: 5049-5061, as well as Palstra et al 2007 *ME* 16:4504-4522 and Palstra and Ruzzante 2008 *Mol Ecol* 17: 3428-3447.

If interested please send an e-mail application including CV, names and addresses of two to three referees and a statement describing the reason(s) for your interest in this research to: Daniel E Ruzzante, Associate Professor and Canada Research Chair in Marine Conservation Genetics, Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4J1.(email: daniel.ruzzante@dal.ca, <http://myweb.dal.ca/~ruzzante>)

Daniel Ruzzante, Associate Professor Canada Research Chair in Marine Conservation Genetics Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4J1 phone: (902) 494-1688 fax: (902) 494-3736 e-mail: daniel.ruzzante@dal.ca

<http://myweb.dal.ca/ruzzante> <http://-patagonia.byu.edu> Canada Research Chairs <http://-www.chairs.gc.ca> Daniel.Ruzzante@DAL.CA

ImperialCollegeLondon BacteriaPhageCoevolution

Applications are invited for a NERC PhD studentship to start October 2009 under the supervision of Dr Ivana Gudelj in the Department of Mathematics, Imperial College London.

Title: Mathematical modeling of bacteria-phage co-evolution

Project outline: In the year that sees the bicentenary of Darwins birth and 150th anniversary of the publication of his seminal work *The origin of species*, a successful candidate will have an exciting opportunity to join a team of mathematicians and experimental biologists working on fundamental question in evolutionary ecology. For example, how can we account for both within and between species diversity? Why do ecosystems differ in the number of species they contain? The project will approach these problems by using mathematics and laboratory mini-ecosystems containing *E.coli* bacteria and their viral parasites phages.

It is widely acknowledged that much of the genetic and

phenotypic polymorphism in nature is generated and maintained by co-evolutionary interactions. Bacteria and phages have not only proven to be an extremely useful model system for studying co-evolutionary diversification but also understanding the impact viruses have on bacterial evolution is an important problem in its own right. The student will work on the development and analysis of mathematical models of bacteria-phage co-evolution that combine systems biology with population biology. The models will be parameterized, tested and revised in collaboration with the experimental lab of Dr Samantha Forde, Ecology and Evolutionary Biology Department, University of California at Santa Cruz.

The studentship will be full-time for three years at the standard NERC rate. Candidates should have a first or a good upper second class honours degree in mathematics or a related theoretical discipline. Applicants with a relevant MSc such as applied mathematics, mathematical biology or theoretical biology would be welcome. The position is open to UK citizens and EU citizens with an appropriate qualification who have been resident or studied in the UK for three years. For an informal discussion of the project please contact: Dr Ivana Gudelj, i.gudelj@imperial.ac.uk.

Applicants should send a CV, including a brief personal statement as well as contact details of two academic referees, either electronically to r.svanidze@imperial.ac.uk or by post to Rusudan Svanidze, Department of Mathematics, Imperial College London, 180 Queens Gate, London, SW7 2AZ.

The studentship may be offered to a suitable candidate at any time and so early application is encouraged.

Ivana Gudelj <i.gudelj@imperial.ac.uk>

Imperial Community Evolution

PhD Studentship

The Grantham Institute for Climate Change

Supervision: Dr Tim Barraclough.

Project Title: The evolutionary responses of complex ecosystems: simulated responses of ecosystems to environmental perturbation (3 years)

Project Summary: Predicting the outcome of current environmental change scenarios is hampered by the lack of theoretical understanding of how ecological

and evolutionary dynamics interact in complex ecosystems. Previous models have explored such questions, but these have suffered from simplistic or biologically unrealistic assumptions about the underlying ecological and evolutionary mechanisms. To overcome these limitations, this project will use meta-analyses of a) lab and field evolution experiments, b) ecophysiological data and c) food web data on the trophic interactions among component species within ecosystems to develop simulation models of ecosystems that fall within biologically realistic ranges of key parameters (such as evolvability, connectivity, species abundances etc). Simulations will then be run on high performance computer facilities to explore the interaction between ecological dynamics (changes in species abundances and distribution) and evolutionary dynamics (genetic adaptation to changes) under different scenarios of environmental change. The key aim will be to estimate the likely contribution of evolutionary and ecological change to the responses of ecosystems to different aspects of environmental change. How resilient are systems in terms of their ability to adapt to new environmental conditions?

Training and expertise: the student will receive training in evolutionary and ecological theory, computer modelling, database assembly, statistical analysis, and the mathematical biology of complex systems. You will join a lively group at Silwood Park campus working at the interface between evolutionary biology and ecology, and on the application of these topics to climate change research.

Applications must be completed online at: <http://www3.imperial.ac.uk/pgprospectus/howtoapply/-applicationforms> . Once you have submitted your application, please e-mail the Grantham Institute on granthamphd@imperial.ac.uk to inform us which project you have applied for. If you have already applied but wish to be considered for a Grantham studentship please e-mail us at the same address (granthamphd@imperial.ac.uk)

Closing date 31 March 2009

Dr Timothy G. Barraclough, Reader in Evolutionary Biology

Division of Biology, Imperial College London, Silwood Park Campus, Ascot, Berkshire, SL5 7PY, UK E-mail: t.barraclough@imperial.ac.uk Telephone: +44 (0)207 594 2247 Fax: +44 (0)207 594 2339 Web-page: www.imperial.ac.uk/people/t.barraclough ** MSc course in Ecology, Evolution and Conservation ** www3.imperial.ac.uk/naturalsciences/courses/pg/ls/ecology

Timothy Barraclough <t.barraclough@imperial.ac.uk>

ImperialC UK
DiseaseEvolutionGenomics

Subject:

MOLECULAR EPIDEMIOLOGY, GENOMICS AND EVOLUTION OF THE FROG-KILLING FUNGUS *BATRACHOCHYTRIUM DENDROBATIDIS*

The chytrid fungus, *Batrachochytrium dendrobatidis* (Bd), is causing global declines in amphibian biodiversity. The PhD project will explore the emergence of this pathogen across Europe by developing new molecular epidemiological techniques to genotype lineages of the pathogen for the following tasks:

1. Collecting and identifying Bd isolates from across Europe with increased / attenuated virulence
2. Using high-throughput genome sequencing to identify SNPs, and characterising these in European isolates of the pathogen
3. Using phylogenetics to identify the number of times that Bd has been introduced into Europe and identifying the principle vectors

This studentship is tied to the new European project 'RACE: Risk Assessment of Chytridiomycosis to European amphibian biodiversity' and will involve substantial amounts of work in the field, as well as the laboratory, and with other member research groups. Fieldwork involves travel to islands (Sardinia/Mallorca) and mountainous regions (Pyrennees/Alps) so the candidate needs to be physically fit.

The successful candidate will be strongly motivated and capable of independent work, and will have an excellent degree in Life Sciences, preferably with a Masters degree in Genetics/Bioinformatics. If you wish to discuss the studentship, please contact Dr Matthew Fisher (matthew.fisher@imperial.ac.uk; <http://www1.imperial.ac.uk/medicine/people/matthew.fisher/>)

All students will belong to the Graduate School of Life Sciences and Medicine which provides a full programme of training in research and transferable skills. Further details of the Division can be found at <http://www1.imperial.ac.uk/medicine/about/divisions/ephpc/ide/> You should send one hard copy, and an electronic version, of a full CV, including two original references, and a letter stating why you are

interested in studying for this PhD to Matthew Fisher, DIDE, Imperial College London, Norfolk Place, London, W2 1PG.

Please note that candidates must fulfil College admissions criteria. Closing Date: 15th April

It is anticipated that interviews will be held during the week commencing 20th April

“Fisher, Matthew” <matthew.fisher@imperial.ac.uk>

KentStateU 2 PlantEvolEcol

Two Graduate Student Positions in Plant Evolutionary Ecology

Funding is available for two graduate students to work with Andrea Case (Kent State University, Ohio, USA) and Christina Caruso (University of Guelph, Ontario, Canada) on an NSF-funded research project. We are investigating the causes of population sex ratio variation in a gynodioecious plant (*Lobelia siphilitica*) across eastern North America. This project combines field experiments, controlled crosses in the greenhouse, and genotyping using microsatellite markers to determine how different mechanisms of evolution, as well as any differences in population history, contribute to variation in population sex ratio across *L. siphilitica*'s range. There is ample opportunity for students to develop independent research associated with the project.

One Ph.D position is available in the Department of Biological Sciences at Kent State University. The student would participate in lab work as well as fieldwork in Ohio and Indiana. Familiarity with basic molecular techniques (DNA extraction, PCR, sequencing) and using genetic markers will be helpful. Stipends cover 12-mo salary, tuition and fees. Students have the option, but are not required, to teach. Details of how to apply to the program are available at http://bioweb.biology.kent.edu/GraduateProgram/How_to_apply.html Prior to submitting a formal application for the Kent State position, candidates should send a brief statement of interest and CV to acase@kent.edu.

One Ph.D or M.Sc. position is available in the Department of Integrative Biology at the University of Guelph. The student will be responsible for overseeing controlled crosses in the greenhouse and conducting fieldwork in Ontario and Iowa. Applicants should have academic background and research experience in ecol-

ogy and/or evolutionary biology. Experience working with plants in the greenhouse and field would be helpful. Information on the graduate program in Integrative Biology is available at <http://www.uoguelph.ca/ib/grad/graduate.shtml> Prior to submitting a formal application for the Guelph position, interested candidates should send an unofficial transcript, CV (including references), and a brief statement of interest to carusoc@uoguelph.ca.

We strongly encourage applicants from underrepresented groups.

– Dr. Andrea Case Asst. Professor of Biological Sciences Kent State University Box 5190 Kent OH 44242-0001 USA Office: 245 Cunningham Hall Phone: 330-672-3699 acase@kent.edu <http://bioweb.biology.kent.edu/FacultyPages/Case/>
 – Christina M. (Chris) Caruso Assistant Professor Department of Integrative Biology University of Guelph Guelph, Ontario N1G 2W1 Canada 519-824-4120 x52030 carusoc@uoguelph.ca <http://www.uoguelph.ca/ib/people/faculty/caruso.shtml>
 “CASE, ANDREA” <acase@kent.edu>

LundU PlantSystematics

Lund University announces the following vacancy:

PhD studentship in Evolution within the discipline of Plant Evolution and Systematics

With placement at the Department of Ecology, Section for Plant Ecology and Systematics, Faculty of Science, Lund University.

Reference Number: N 2009/119 Starting Date: As soon as possible Information: Prof. Honor C. Prentice +46 46 2228971 (+46 73 5968334) Honor.C.Prentice@ekol.lu.se Prof. Anders Tunlid +46 46 2223757 (+46 70 3140067) Anders.Tunlid@mbioekol.lu.se Worker's unions at Lund University: OFR, SACO och SEKO

Project title: Allelic variation and protein function in a plant community context

Project description: This interdisciplinary project represents a collaboration between the Section of Plant Ecology and Systematics, and the Section of Microbial Ecology within the Department of Ecology, Lund University.

The project will focus on genomic ecology and commu-

nity genomics and will develop a novel system for the study of gene variation and function in the context of natural plant communities. Molecular differentiation will be investigated at a pair of loci coding for a key metabolic enzyme, phosphoglucose isomerase (PGI), in the wild plant *Festuca ovina*, and the distribution and function of individual PGI alleles will be explored in natural populations within grassland plant communities on the Baltic island of Uland. The project will involve characterization of sequence differentiation between the multiple alleles at the two loci and the development of allele-specific primers. Relationships between individual alleles and fine-scale niche-variation within natural grassland communities will be investigated and the functional consequences of the allelic variation will be inferred through analyses of predicted protein structures.

The PhD project will be linked to the Research School in Genomic Ecology within the Centre for Genomic Ecology (CGE). Genomic ecology represents a new interdisciplinary field on the interface between ecology, evolutionary and molecular biology, and genomics. The long-term goal of CGE is to achieve an integrated understanding of the molecular, evolutionary and ecological mechanisms and processes that are involved in the generation of the immense diversity of form and function that characterizes living organisms. The Research School in Genomic Ecology will provide the PhD student with access to advanced courses and opportunities for placements in other laboratories as well as a stimulating social network. Further information about CGE and the research school can be found at <http://www.ekol.lu.se/research/genomic-ecology>. Qualifications: Applicants should have a Master's degree (or equivalent) in biology, with specialization in botany, plant ecology, plant genetics, molecular ecology, molecular genetics, or a similar subject area. Experience with molecular techniques is a central requirement for the position. Competence with univariate and multivariate statistics, bioinformatics and plant cultivation is also a desirable merit. A very good knowledge of written and spoken English is required. A valid driving licence is also a desirable merit.

Additional information: A Swedish PhD represents four years of full-time study. Of these four years, three years are devoted to research activities and one year is devoted to advanced course work, in which course points are obtained via attendance at research-level courses given in Lund or elsewhere in Europe.

Regulations concerning appointment as a full PhD student can be found in HF 5 Chap 1-7 and SFS 1998:80. Also consult the admission regulations found at: <http://www.science.lu.se/o.o.i.s/4964> An educational stipend

is awarded for the first 18 months of full-time study, following which time the student is appointed as a full doctoral student. Regulations concerning educational stipends for doctoral students can be found in SFS 1995:938 and 1998:81. Regulations concerning appointment as a full PhD student can be found in HF 5 Chap 1-7 and SFS 1998:80. Those who hold an educational stipend or a doctoral student appointment must first be accepted for postgraduate study. To be accepted, a student must be judged to have the competence necessary to complete a course of postgraduate study. In addition to pursuing postgraduate studies, the doctoral student may also perform other duties - including teaching and administration - according to the specific regulations. The university strives for a more even gender representation within postgraduate education.

Applications are made on a specific application form found on the web site: <http://www.science.lu.se/o.o.i.s/13456> The application must reach the Registrar, Kansli N, Lund University, Box 118, SE-221 00 Lund, Sweden, not later than Wednesday 8 April 2009. All

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MaxPlanck Ploen HostParasiteCoevolution

PhD position at Max-Planck Institute for Evolutionary Biology, Department of Evolutionary Ecology, Ploen (Germany) : Molecular basis of host-parasite co-evolution

We invite highly motivated students with background in Evolutionary Biology to apply for a PhD position in the MPI-Evolutionary Biology. The applicant should have a Diplom/Master in Molecular Biology (or its equivalent). The candidate will collaborate with the team working on immunogenetics, immunology, population genetics, parasitology, and behavioural ecology both in the lab and in the field. More information about the department's research interests can be found under: <http://www.evolbio.mpg.de/english/abteilungen/evolutionsoekologie/> . The successful candidate will work on the molecular aspect of host-parasite co-evolution. Research goals will include identifying genes that may shed light on the evolutionary

mechanisms acting on both the host and its parasite thereby leading to their co-evolution. Research will be conducted on our established model organism stickleback (*Gasterosteus aculeatus*) and its parasites. English is the working language in the lab so we encourage Germans, as well as foreign students, to apply. Moreover, the Max Planck Society is an equal opportunity employer and encourages female scientists and scientists with disabilities to apply.

The institute is located in Plön, Northern Germany. It offers a stimulating research environment focusing on evolutionary biology with links to the Christian Albrechts University Kiel, and the Leibniz Institute for Marine Sciences (IFM-Geomar) in Kiel. The Institute provides state-of-the-art laboratories and equipment, including facilities for genome analysis. To apply, please send your CV containing a short research statement and list of publications (if available), and address of three references by email to milinski@evolbio.mpg.de or samonte@evolbio.mpg.de. The position will remain available until filled.

Prof. Dr. Manfred Milinski Executive Director Max-Planck-Institute for Evolutionary Biology (former Max-Planck-Institute of Limnology) Department of Evolutionary Ecology August-Thienemann-Strasse 2D-24306 Ploen, Germany direct: +49-(0)4522763254 Sec: +49-(0)4522763253 Fax: +49-(0)4522 763 310 email: milinski@evolbio.mpg.de website: <http://www.evobiol.mpg.de/> irene samonte <irenesamonte@yahoo.com>

McGillU PollenMovement

McGill University. Plant Reproductive Biology

As part of a NSERC Strategic Network Grant to the Canadian Pollination Initiative, we are seeking to recruit a Masters or Ph.D. degree student to work on the reproductive biology and genetics of native and cultivated blueberries (*Vaccinium* spp.) in Canada. The work will entail the development and application of molecular genetic tools to study the movement of pollen in natural and cultivated stands, with an emphasis on studying the impact of pollinators, plant population structure, and inbreeding depression on patterns of fruit set. The project has both field and lab components, and involves collaboration with a team of researchers across the Canada.

Please e-mail you Curriculum Vitae and cover let-

ter describing your career goals to: Prof. Daniel Schoen, Biology Department, McGill University (daniel.schoen@mcgill.ca)

Daniel Schoen <daniel.schoen@mcgill.ca>

New Zealand Stick Insect Genomics

Genomics of cold tolerance adaptations in New Zealand alpine stick insects

The Allan Wilson Centre for Molecular Ecology and Evolution and Landcare Research has funding for a Ph.D. position in genome evolution of stick insects. The Ph.D. student will be supervised by Thomas Buckley at Landcare Research, Auckland and will be enrolled at the University of Auckland. They will receive training in genomics, entomology, bioinformatics, population genetics and phylogenetics. The student will be co-supervised by Richard Newcomb (University of Auckland) and Allen Rodrigo (Bioinformatics Institute, University of Auckland). The successful candidate will receive a scholarship of \$25,000 per year for three years and \$5,000 per year for fees.

The New Zealand stick insect genus *Micrarchus* contains several species of which one is restricted to the high alpine zone of the South Island. Other species are restricted to the lowlands of the North and South Islands. This project will involve gathering transcriptome data from alpine and lowland *Micrarchus* species via pyrosequencing to identify candidate loci involved in cold tolerance. The function of these loci will then be assessed using quantitative PCR. Genetic variation at loci showing a clear association with cold tolerance will be measured within and between species. The historical phylogenetic pattern will be reconstructed using markers isolated from the transcriptome data. Patterns of gene flow between the alpine and lowland species at cold tolerance loci and background loci will be compared.

For enquiries please contact Thomas Buckley at the email address below. Applications close by April 10th 2009. Potential candidates should submit a CV, grades, and two references:

Thomas Buckley Landcare Research buckleyt@landcareresearch.co.nz +64-9-574-4116

<http://www.landcareresearch.co.nz/research/-biosystematics/invertebrates/phasmatodea/> <http://www.landcareresearch.co.nz/research/biocons/>

genetics/staff_page.asp?staff_num=1110 <http://www.allanwilsoncentre.ac.nz/> Richard Newcomb: <http://www.hortresearch.co.nz/index/page/578> Allen Rodrigo: <http://www.cebl.auckland.ac.nz/people.php> Thomas Buckley Landcare Research Private Bag 92170 Auckland New Zealand

buckleyt@landcareresearch.co.nz Phone +64-9-5744116 Fax +64-9-5744101

BuckleyT@landcareresearch.co.nz

Nice France EvoDevo

PhD Position: Gene-environment interactions in development and evolution (Institute of Developmental Biology and Cancer, Nice, France)

A PhD fellowship is available to study how developmental processes respond to environmental variation and how such responses evolve. We use *Caenorhabditis* nematodes as study organisms and our approaches encompass developmental genetics, intra- and interspecific comparative analyses, experimental evolution and ecology.

The successful candidate will be highly motivated and participate in the planning of the project. This 3-year position is funded by the French National Center for Scientific Research (CNRS) and open to all nationalities.

Starting date: Fall 2009

Our research team has recently been created at the Institute of Developmental Biology and Cancer (IBDC) in Nice. The focus of our group is to apply integrative approaches to the study of developmental systems and their evolution. The IBDC is an international research institute hosting a large number of teams working on diverse topics in development, cell biology and cancer. The institute, located in the city centre, has excellent research facilities and provides an interactive scientific environment.

To apply, send a summary of your research interests and future plans, CV, names and contact information for three references to Christian Braendle (braendle@unice.fr), BEFORE April 15, 2009. Informal inquiries welcome. For more information, please visit: <http://www.unice.fr/isdbc/> Christian Braendle Institute of Developmental Biology and Cancer CNRS UMR 6543 University of Nice Sophia-Antipolis, Parc Valrose

Batiment des Sciences Naturelles, etage 7 06108 NICE cedex 2 FRANCE Tel +33 (0) 4 92 07 68 97 Fax +33 (0) 4 92 07 68 56 braendle@unice.fr <http://www.unice.fr/-isdbc> Christian.BRAENDLE@unice.fr

Norwich UK PlantGeneticDiversity

Ph.D. studentship at the John Innes Centre and the University of East Anglia, Norwich, UK

The role of genetic diversity in securing food production <http://www.jic.ac.uk/STUDENTS/search/details.asp?id=3D769> The research concerns the possibility of exploiting genetic diversity to secure long-term food supplies. In field trials, crops with high levels of genetic diversity have similar mean yields to those of pure varieties but their yields are more stable across different environments. Genetically diverse crops could therefore have a crucial role in maintaining a stable food supply in future despite unpredictable variation in the climate and reduced ability to rely on chemical inputs derived ultimately from fossil fuel.

The aim of the studentship is to test if, in a genetically diverse population, competition between plants within local patches in a field maintains the average yield (seed production) despite the environment being variable or even unpredictable. The experiments will use Arabidopsis as a model organism because it allows experiments to be done with greater replication and more precise control of the environment than is possible with any arable crop plant.

The student will be supervised by James Brown at the John Innes Centre and Tove Jørgensen at the University of East Anglia. See <http://www.jic.ac.uk/staff/-james-brown/> and http://biobis.bio.uea.ac.uk/biosql/-fac_show.aspx?ID=3D362 for more information about their research.

For further details and information about how to apply, see <http://www.jic.ac.uk/STUDENTS/search/details.asp?id=3D769> James Brown and Tove Jørgensen

james.brown@bbsrc.ac.uk james.brown@bbsrc.ac.uk

Paddington UK DiseaseEvolution

The Department of Infectious Disease Epidemiology (DIDE) has one 3-year studentship funded by NERC. The student will be based at the St Marys Campus, Paddington and will commence in October 2009.

The studentship will pay UK/EU tuition fees and a stipend of £16,500 The studentship is available to UK nationals or EU nationals, who have lived in the UK for at least three years immediately preceding the date of an award. For full eligibility details please see the following NERC requirements <http://www.nerc.ac.uk/-funding/available/postgrad/eligibility.asp> Owing to funding restrictions applications from overseas candidates cannot be considered.

Title of Project

Molecular Epidemiology and Evolution of the Frog-Killing Fungus *Batrachochytrium dendrobatidis*

The chytrid fungus, *Batrachochytrium dendrobatidis* (Bd), is causing global declines in amphibian biodiversity. The project will explore the emergence of this pathogen across Europe by developing new molecular epidemiological techniques to genotype lineages of the pathogen for the following tasks:

1. Collecting and identifying Bd isolates from across Europe with increased / attenuated virulence
2. Developing an informatics-system to integrate EU genotypes into the global Bd genotyping scheme and exploring evolutionary relationships
3. Using phylogenetics to identify the number of times that Bd has been introduced into Europe and identifying the principle vectors

This studentship is tied to the new EU project 'RACE: Risk Assessment of Chytridiomycosis to European amphibian biodiversity' and will involve substantial amounts of work in the field, as well as the laboratory, and with other member research groups.

The successful candidate will be strongly motivated and capable of independent work, and will have a excellent degree in Life Sciences, preferably with a Masters degree. If you wish to discuss the studentship informally, please contact Dr Matthew Fisher (matthew.fisher@imperial.ac.uk; <http://www1.imperial.ac.uk/medicine/people/-matthew.fisher/>)

All students will belong to the Graduate School of Life Sciences and Medicine which provides a full programme of training in research and transferable skills. Further details of the Division can be found at <http://www1.imperial.ac.uk/medicine/-about/divisions/ephpc/ide/> You should send one hard copy, and an electronic version, of a full CV, including two original references, and a letter stating why you are

interested in studying for this PhD to Matthew Fisher, DIDE, Imperial College London, Norfolk Place, London, W2 1PG.

Please note that candidates must fulfil College admissions criteria. For an informal discussion please contact Matthew Fisher, 020 7594 3787 matthew.fisher@imperial.ac.uk

Closing Date: 15th April

It is anticipated that interviews will be held during the week commencing 20th April

d.henk@imperial.ac.uk d.henk@imperial.ac.uk

TrentU PopulationGenetics

Population genetics/Conservation genetics

I am looking for a highly motivated and productive graduate student to work on one of several research projects (depending on personal interest) that include the conservation genetics of endemic plants in Ontario (Hills thistle), the population genetics of pitcher plants, or the evolutionary genetics of the common reed (*P. australis*). All projects would involve a field component for sampling purposes and ecological study, plus laboratory genetics work which would be conducted at Trent University. Applicants should have research experience in lab work, as well as a broad interest in microevolutionary processes.

Applicants should send a letter with a statement of research interests and relevant experience, curriculum vitae with a list of publications (if any), copies of academic qualifications, and the names and e-mail addresses of three referees as a single pdf file to Joanna Freeland (joannafreeland@trentu.ca; <http://people.trentu.ca/joannafreeland>) by March 15.

joannafreeland@trentu.ca

UEdinburgh PlantTaxonomy

MSc Degree/Postgraduate Diploma in the Biodiversity and Taxonomy of Plants

Royal Botanic Gardens Edinburgh/ University of Ed-

inburgh

Programme Philosophy The MSc in Biodiversity and Taxonomy of Plants was established by the University of Edinburgh and the Royal Botanic Garden Edinburgh (RBGE) to address the growing worldwide demand for trained plant taxonomists and whole-plant scientists. A detailed knowledge of plants and habitats is fundamental to their effective conservation. To communicate such knowledge accurately and effectively, training is required in plant taxonomy ' the discipline devoted to plant diversity and evolution, relationships, and nomenclature. The MSc is perfect for those wishing to develop a career in many areas of plant science: n Survey and conservation work in threatened ecosystems n Assessment of plant resources and genetic diversity n Taxonomic research n Management of institutes and curation of collections n A stepping stone to PhD research and academic careers

Edinburgh is a unique place to study plant taxonomy and diversity. The programme and students benefit widely from a close partnership between RBGE and the University of Edinburgh (UoE). RBGE has one of the world's best living collections (15,000 species across our four specialist gardens ' 5% of world species), an herbarium of three million specimens and one of the UK's most comprehensive botanical libraries. The School of Biological Sciences at UoE is a centre of excellence for research in Plant Sciences and Evolutionary Biology. Recognised experts from RBGE, UoE, and from different institutions in the UK deliver lectures across the whole spectrum of plant diversity. Most course work is based at RBGE, close to major collections of plants, but students have full access to the extensive learning facilities of the university.

Aims and Scope The MSc provides biologists, conservationists, horticulturists and ecologists with a wide knowledge of plant biodiversity, as well as a thorough understanding of traditional and modern approaches to pure and applied taxonomy. Apart from learning about the latest research techniques for classification, students should acquire a broad knowledge of plant structure, ecology, and identification.

Programme Structure This is an intensive twelve-month programme and involves lectures, practicals, workshops and essay writing, with examinations at the end of the first and second semesters. Topics covered include: n Functions and philosophy of taxonomy n Evolution and biodiversity of the major plant groups, fungi and lichens n Plant geography n Ecology of plants and ecosystems n Conservation and sustainability n Production and use of floras and monographs n Biodiversity databases n Phylogenetic analysis n Population and conservation

genetics n Tropical field course, plant collecting and ecology n Curation of living collections, herbaria and libraries n Plant morphology, anatomy and development n Molecular systematics

Fieldwork and visits to other institutes are an integral part of the course. There is a two-week field course to Belize in which students are taught field collection and identification of tropical plants ecological survey techniques. The summer is devoted to four months of a major scientific research project of the student's choice or a topic proposed by a supervisor. These research projects link in directly with active research programmes at RBGE.

Entry Requirements Applicants should ideally hold a university degree, or its equivalent, in a biological, horticultural, or environmental science, and above all have a genuine interest in plants. Relevant work experience is desirable but not required. Evidence of proficiency in English must be provided if this is not an applicant's first language.

Funding The course is currently supported by eight Natural Environment Research Council studentships that are open to EU students only (see <http://www.nerc.ac.uk/funding/>). Other international funding bodies have supported overseas students in the past. Further information can be found on our website.

Further Information For further details on the programme, including a course handbook please visit the RBGE website: <http://www.rbge.org.uk/education/-professional-courses> You can also contact the Course director or Education Department at RBGE, or the Postgraduate Secretary of the University of Edinburgh:

MSc course Director, Dr Louis Ronse De Craene Royal Botanic Garden Edinburgh Tel +44 (0)131 248 2804 Email: l.ronsedecraene@rbge.ac.uk Postgraduate Secretary, The University of Edinburgh School of Biological Sciences, Darwin Building The King's Buildings, Edinburgh EH9 3JR, UK

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UExeter MaternalEffectsEvolution

Three PhD opportunities available at the Centre for

Ecology & Conservation, University of Exeter Cornwall Campus Open to EU students

Geographic variation and the evolution of maternal effects

Primary supervisor: Professor Allen J. Moore

Deadline for applications: 27 March 2009

This project is part-financed by the European Union, European Social Fund

Maternal effects, where mothers influence offspring traits via maternally-influenced environments, are a common source of variation in life history traits. Maternal effects are expected to have evolved as adaptations however little work has examined how maternal effects evolve. In this study you will compare maternal effects in tropical and temperate populations of the large milkweed bug, *Oncopeltus fasciatus*, to determine the scope for maternal effects to evolve in response to environmental stress or change. Although maternal effects provide a source of environmental variation for offspring, differences among mothers in their effects can be genetic and therefore evolve. In addition to examining differences in the extent, timing and importance of maternal effects among populations, genetic variation underlying maternal effects in different populations will be compared. [<http://biosciences.exeter.ac.uk/postgraduate/newposts.php#maternal>]

For informal enquiries contact Professor Allen Moore at A.J.Moore@exeter.ac.uk

Geographic variation and evolved responses to food stress

Primary supervisor: Dr Patricia J. Moore

Deadline for applications: 27 March 2009

This project is part-financed by the European Union, European Social Fund

One way in which insects respond to food stress is to resorb oocytes and re-invest that energy into somatic maintenance. Oosorption can occur through apoptosis, programmed cell death of the oocytes. The large milkweed bug, *Oncopeltus fasciatus*, has a broad geographic distribution, from Costa Rica to southern Canada. Previous research has suggested that tropical populations are more adapted to food stress than temperate populations. In this project you will examine how ovarian apoptosis varies between tropical and temperate populations, and the ecological and genetic influences on this variation. The central questions are "Does food availability lead to population differentiation? Is there sufficient variation in the expression of a conserved mechanism to permit geographic vari-

ation in apoptosis?" [<http://biosciences.exeter.ac.uk/postgraduate/newposts.php#foodstress>]

For informal enquiries contact Dr Patricia Moore at P.J.Moore@exeter.ac.uk

Sett Menus: The ecological & evolutionary origins & consequences of individual foraging behaviour in group-living badgers

Primary supervisor: Dr Stuart Bearhop

Deadline for applications: 27 March 2009

This project is part-financed by the European Union, European Social Fund

The extent to which individuals of a species vary in their exploitation of different food resources is an important feature of foraging ecology and is likely to be an key component of the ecological and evolutionary dynamics of populations, although these ideas have rarely been tested. Variation in diet occurs at many levels: within individuals (over seasons, with age and social rank) and among individuals (between sexes, over different spatial and social scales). Diet at the species level is therefore a composite of multiple sources of variation in individual foraging choices. In group-living animals, social structure constrains dietary variation by imposing territorial limits on foraging and, potentially, by inducing either socially or genetically heritable foraging traits. Disentangling the influence of heritable and environmental components of dietary specialisations therefore requires knowledge of both genetic and environmental components. As a consequence the processes driving foraging specialisations and their evolutionary consequences remain poorly understood.

This PhD will use combination of stable isotope analysis, radio-tracking, long term pedigree data and theoretical modelling to address a series of questions relating to the development and persistence of individual and group level foraging specialisations in badgers. The study will evaluate the fitness consequences of different foraging preferences and will be among the first to attempt to unravel the roles of the natal environment versus heritability in establishing such specialisations, investigating the ontogeny of specialisation and modelling factors that may act as constraints. As the likelihood of TB transmission has been shown to be related to badger foraging behaviour, a better understanding of the factors driving foraging specialisations could be important in the

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UFribourg Evolutionary Genetics

PhD position in evolutionary genetics

Project: The genetics of reproductive isolation and ecological trait differences in European Populus

Supervision: Christian Lexer, University of Fribourg, Switzerland

A PhD position is available in the newly established lab of Christian Lexer. I am looking for a highly motivated candidate with interests in the fields of evolutionary biology and population genetics. The PhD fellowship is university-funded, and the project will be tightly linked with a British NERC-funded research project on the ecological & evolutionary genomics of species isolation in European Populus, which involves a postdoc, two other PhD students, and several collaborating labs in the EU and USA.

The PhD project will address the genetics of reproductive isolation and ecological trait differences in natural hybrid zones of *Populus alba* and *P. tremula*. It is based on molecular genetic data which my group has gathered over the last several years, and on recent advances in the use of admixed populations and hybrid zones for addressing key questions in ecology & evolution. Key aspects of the PhD project will be (1) to study the molecular population genetics of genetic loci involved in barriers to introgression, (2) to study the genetic basis of ecological trait differences in natural populations. This involves both, experimental lab work (sequencing, microsatellites, SNPs, interactions with related transcriptomics project) and ecological field work (assessing the effects of traits on tree biotic interactions). Depending on the interests of the student, there can be a stronger focus either on the lab or on the field component. In any case, an interest in the use of new tool s in computational biology is essential.

The starting date is negotiable (any time from July 2009 onwards). Funding from the university is for three years (annual salary is ca. CHF 40'000). Knowledge of French or German is helpful in every day life, but the working language in the group is English. A Diploma or Masters degree (or equivalent) in biology or related subject is necessary for admission. Fribourg is a lively town with over a quarter of the population being students. It is located ca. 30 minutes from the Alps, close to other cities such as Berne and Lausanne and just a

little over an hour from Geneva.

To apply, please send an e-mail with the application materials in a single pdf file to Christian Lexer (christian.lexer@unifr.ch). Application materials should include a CV, a list of publications, and a short (less than one page) statement of research interests. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 30 March will be given full consideration. Interviews will take place end of April or early May.

Further information and address for application: Dr. Christian Lexer, Associate Professor of Evolutionary Biology E-mail: christian.lexer@unifr.ch, Tel: +41 26 300 88 68 Web: <http://www.unifr.ch/biol/ecology/lexer/index.html> For more information about Ecology & Evolution in Fribourg see <http://www.unifr.ch/biol/ecology/> christian.lexer@unifr.ch christian.lexer@unifr.ch

UFribourg EvolutionPlantInvasions

1 PhD & 1 Post-Doc Position in Evolutionary Ecology of Plant Invasions, University of Fribourg, Switzerland

Rationale

The proposed project will be the first one that considers the importance of polyploidy and herbivores for invasions simultaneously. Our leading hypothesis is that herbivore pressure and assemblage will, at least partially, explain the predominance of specific cytotypes both in the native and introduced range. The *Centaurea stoebe* L. (syn. *C. maculosa* Lam.) (Asteraceae) system provides an excellent model system to study these interactions, and we take advantage of the large knowledge already available on this plant and its herbivores. Native to Europe where it occurs as a diploid (2x) and a tetraploid (4x) cytotype, the species is highly invasive in North America, where nearly exclusively only 4x plants have been found. Several specialist insect herbivores have been introduced to North America for its biological control, with only partial success so far.

We seek two highly motivated researchers to help clarifying underlying mechanisms of this most successful plant invasion as a complement to various presently ongoing studies that we carry out in collaboration with both national (through NCCR Plant Survival) and in-

ternational partners. We plan to (i) explore the relationship between type and amount of herbivory and the occurrence of the two cytotypes of *C. stoebe* in its native range by a European-wide survey combined with a replant/transplant experiment, (ii) carry out a series of experiments to analyze interactions between two selected specialist herbivores and the *C. stoebe* cytotypes, and (iii) investigate more generally into the role of generalist herbivores for plant invasions (in collaboration with Urs Schaffner, CABI Europe-Switzerland and our US counterparts).

Requirements

- PhD position: Master Thesis in Biology, preferentially in ecology and evolution

- Post-Doc position: doctoral degree in plant ecology and evolution

For both positions, knowledge of, and experience in one or several of the following areas of research is desirable: experimental (field) ecology and evolutionary biology, invasion biology, plant-herbivore interactions, experimental design and statistical analysis; furthermore, fluency in English and driver's license will be required.

Salary and conditions

The positions are funded by the Swiss National Science Foundation, and start April 1, 2009. Salaries: PhD c. 43'000 SFr/year for 3 years; Post-Doc dependent on age and status, gross salary in the first year about CHF 70'000, for 2-3 years.

Applications

Applicants should e-mail their CV and publication list, together with a short motivation letter and a summary of research experience and interests, and the names of two professional referees to Heinz.mueller@unifr.ch. Please indicate your earliest possible, and your ideal start.

For further information, please contact:

Prof. Dr. Heinz Müller-Schärer, D  partement de Biologie, Unit   Ecologie & Evolution, Universit   de Fribourg, Chemin du Mus  e 10; CH-1700 Fribourg, SWITZERLAND; tel: + (41) (0) 26-300 88 35/50 cf. my research website at <http://www.unifr.ch/biol/ecology/muellerschaerer/group/mueller/> for further information and recent publications on this subject.

Heinz M  ller-Sch  rer <heinz.mueller@unifr.ch>

UFribourg PlantInvasions

There is a strong evolutionary component in the study because we will test the hypothesis that old, coevolved communities respond fundamentally differently to plant invasions than new communities with which the invasive plant has not evolutionary history.

Advert:

PhD position on plant invasions at CABI Europe-Switzerland & University of Fribourg

Rationale The plant species *Centaurea stoebe* (spotted knapweed), introduced from Central Europe into North America during the late 19th century, has become a model for research on the ecological and evolutionary causes and consequences of invasions. We presently explore the role of rapid evolutionary processes in the invasion success of *C. stoebe*, and try to elucidate the complex interactions between *C. stoebe* and natural enemies both in the native and the introduced range.

We are now seeking a PhD student highly motivated to work on the environmental impact of *C. stoebe* and of other invasive plant species. The field experiments aim to assess the effects of invasive plants on above-ground and below-ground ecosystem properties, and on studying the recovery of ecosystems after successful control of the invasive plant. These studies will be conducted at various sites in Europe and in North America to assess the response of communities that share (native range) or not share (introduced range) a coevolutionary past with *C. stoebe*. New ideas and complementary studies are of course highly invited.

The position will be with Dr. Urs Schaffner, CABI Europe-Switzerland, Delémont, Switzerland and Prof. Dr. Heinz Müller-Schärer, Dep. of Biology/Ecology & Evolution, University of Fribourg, Switzerland, and is embedded in the National Centre of Competence in Research (NCCR) 'Plant Survival' (<http://www2.unine.ch/nccr>), funded by the Swiss National Science Foundation. The work place will be at the CABI Europe-Switzerland Centre in Delémont, and the student will be affiliated to the University of Fribourg. We offer a stimulating research environment in an international context. The CABI Centre in Delémont has more than 50 years of expertise in classical biological control and invasion ecology and has a worldwide network of collaborators (<http://www.cabi.org/>-

[datapage.asp?iDocID=373](http://www.cabi.org/datapage.asp?iDocID=373)).

Requirements - Master Thesis in Biology, preferentially in Ecology & Evolution - Knowledge of, and/or experience in one or several of the following areas of research is desirable: experimental field ecology, community ecology, soil ecology. - Fluency in English and driver's license

Salary and conditions The position is planned to be filled by 1 May 2009 and is available for 3 years. Salaries are according to the guidelines of the Swiss National Science Foundation (gross salary is roughly CHF 42'000). The successful candidate will be enrolled in the NCCR doctoral school with a large offer of specific lectures and practicals.

Applications Applicants should send their complete CV and the names of two professional referees by e-mail to Urs Schaffner (see address below). We start evaluating the applications by 27 March 2009.

For further information, please contact: Dr. Urs Schaffner, +41 32 421 48 77, e-mail: u.schaffner@cabi.org. <http://www.cabi.org/peopleDetail.asp?StaffNo=S0001> Prof. Dr. Heinz Müller-Schärer, 41 26-300 88 35/50, e-mail: heinz.mueller@UNIFR.CH. <http://www.unifr.ch/biol/ecology/muellerschaerer/group/mueller/>

Urs Schaffner <u.schaffner@cabi.org>

UHawaiiHilo ConservationBiol

Graduate Scholarship in the Tropical Conservation Biology and Environmental Science (TCBES)

M.S. Program at the University of Hawaii at Hilo

<http://www2.hawaii.edu/~tcbes/>

Application deadline for graduate scholarship is 1 April 2009. A Bachelor's degree in biology is preferred with courses or experience in ecology, evolutionary biology, or genetics.

Join a team that examines the mechanisms of speciation using multiple varieties of *M. polymorpha*, a common, endemic Hawaiian tree species that appears to be in the process of diversification. This project includes molecular, field, and greenhouse methods to contrast patterns of neutral and expressed genetic variation among habitat-associated varieties and to quantify the fitness of intra-specific hybrids. These studies will allow estimation of the strength of isolation of the gene pools

of varieties on the same and different islands, insight into the molecular genetic changes that accompany divergence into multiple varieties, and determination of the stage and strength of reproductive barriers between varieties. The graduate scholar will receive training in field and molecular methods and will contribute to the overall project, while also conducting thesis research.

The successful applicant will receive \$22,000 annual salary, will enroll in the TCBES Program in August 2009, and will join a vibrant research community in evolutionary genetics at UH Hilo, comprising faculty, postdocs, and graduate and undergraduate students.

Students of Native Hawaiian, Pacific Islander, or other under-represented ancestries are especially encouraged to apply. For information on the TCBES Program and application procedures, visit: <http://www2.hawaii.edu/~tcbes/>. Please direct questions to Dr. Elizabeth Stacy (estacy@hawaii.edu www2.hawaii.edu/~estacy/).

Elizabeth Stacy Assistant Professor Department of Biology TCBES Graduate Program University of Hawai'i at Hilo 200 West Kawili Street Hilo, HI 96720 Phone: 808-933-3153 Fax: 808-974-7693

estacy@hawaii.edu estacy@hawaii.edu

UHelsinki 2 EvolutionaryGenetics

Department of Biological and Environmental Sciences, University of Helsinki, invites applications for

2 Doctoral Student Positions in Evolutionary Genetics

The Doctoral Students will be a part of the Ecological Genetics Research Unit (EGRU). The assignments will begin during spring 2009 (start date is flexible) and continue through 2011, possibly longer. EGRU is part of the Finnish Centre of Excellence in Evolutionary Genetics and Physiology (<http://www.coe.fi>). Supervisor of the project will be Prof. Juha Merilä. The research work is done in collaboration with other members of EGRU.

Both of the PhD-projects aim to investigate genetics of local adaptation in sticklebacks using various genetic (population genetic, genomic and quantitative genetic) approaches. One of the projects is focused on nine-spined sticklebacks (*Pungitius pungitius*), and in particular, genetic basis of body size differentiation among Fennoscandian populations. The other project focuses

on three-spined stickleback (*Gasterosteus aculeatus*) differentiation in scale of the Baltic Sea, with strong emphasis on comparative study of neutral and adaptive differentiation. Apart of fundamental evolutionary dimensions, both projects involve possibilities for more applied work in the context of conservation genetics and adaptation to changing environmental conditions.

A successful candidates for these positions are interested on evolutionary genetics, conservation genetics and population genomics problems, and/or problems in ecological and evolutionary biology in general. A background in population genetics/genomics is desirable.

We are looking for individuals with a Masters or equivalent degree in Biology or Genetics, who are highly self-motivated and can work both independently and in a team. Capacity to face intellectual challenges, willingness to learn new skills and explore new intellectual territories are qualities expected from the candidates. The working language will be English. Proven skills in English are required for admission to post graduate study program (minimum 550 points from TOEFL PBT, or grade A, B or C from CAE/CPE).

An overview of our past and current research can be found at <http://www.helsinki.fi/biosci/egru> and <http://www.coe.fi>.

The salary will be based on level 2 of the demands level chart for teaching and research personnel in the salary system of Finnish Universities. In addition, the appointee will be paid a salary component based on personal work performance (the total salary will vary between 1785 - 2201 EUR per month).

The application should include a complete - CV - Publication list (if available) - A scanned academic transcript (list of grades in university courses) - A statement of research interests and motivation for applying this position not exceeding two pages - Two reference letter to send directly to

Applications should be addressed to the Faculty of Biosciences and sent to Department of Biological and Environmental Sciences, Johanna Paananen, P. O. Box 65 (Viikinkaari 1), FIN-00014 University of Helsinki, to arrive no later than 4st April 2009. More information on positions is available from Prof. Juha Merilä (email. juha.merila@helsinki.fi).

More information about Finland, University of Helsinki, and Department of Biological and Environmental Sciences can be found from the following links: <http://www.helsinki.fi/en/index.html> (city) <http://www.helsinki.fi/university/> (university) <http://www.helsinki.fi/bio/english/> (department) Further information about University of Helsinki Interna-

tional Staff Services <http://www.helsinki.fi/intstaff/>
Helsinki, March 16, 2009 Administration Office

Johanna Paananen <johanna.paananen@helsinki.fi>

ULiverpool SeaBirdPhysiologyEvolution

UNIVERSITY OF LIVERPOOL School of Biological Sciences

NERC funded Studentship Eligibility: UK citizens and UK-resident (3 years+) EU citizens ONLY

Exploring the links between metabolism and fitness using seabirds as models Dr. J.A. Green jonathan.green@liverpool.ac.uk <<mailto:jonathan.green@liverpool.ac.uk>> and Dr. M. Berenbrink michaelb@liverpool.ac.uk <<mailto:michaelb@liverpool.ac.uk>>

Energy is the currency of life and understanding how animals gain, use and store energy is essential in helping us to understand how they function in their environment. Quantification of energetics enables us to understand the shape of the functional response curve between resource availability and reproductive success. This is particularly important as animals face changing environments and competition for their food resources.

Models predict that animals which maximise their energy gain while minimising their energy intake are likely to have greater fitness. The proposed project will investigate the links between rates of energy expenditure and performance in natural populations of seabirds. This should allow repeatability and heritability of these traits to be investigated and the relative importance of genotypic and phenotypic effects assessed. Seabirds are an ideal model for studies of this type as they are long-lived, philopatric, and show considerable reproductive skew. As a result, multiple generations of successful individuals can be found breeding alongside less successful individuals. The student will measure basal metabolic rate (BMR) and possibly field metabolic rate and determine how these traits are related to breeding success at different scales, while accounting for confounding effects such as age and seasonality. Measuring these variables will allow a number of conflicting hypotheses to be tested. Do successful animals have a low BMR which allows them to consume less food and pass more to their chick? Will successful animals have a high BMR, indicative of a high capacity to work and

gain resources from their environment?

Opportunities exist for study in a number of different populations of seabirds, both at home and abroad, and the student will be expected to undertake fieldwork on isolated islands. Within the broad framework of the proposed project, there may be chances to develop experimental/manipulative approaches to answer these key questions.

Training :

Skills which will be learned during this project will include: Planning and executing expeditions and fieldwork. Ornithological/fieldwork techniques such as animal handling, biometric measurements and monitoring of breeding. Ecophysiological techniques including respirometry, the heart rate method and overall dynamic body acceleration (ODBA). Complex data handling in a variety of disciplines. Parametric statistics. Calculation of repeatability and heritability. Energy budget modelling. Writing and submission of data for publication. The student will need to train and apply for a Home Office Licence and will become familiar with the issues surrounding the ethics of experimentation on wild animals. The project will involve liaison with the governing and licensing authorities of the field sites.

References: Blackmer, A.L., Mauck, R.A., Ackerman, J.T., Huntington, C.E., Nevitt, G.A. & Williams, J.B. (2005) Exploring individual quality: basal metabolic rate and reproductive performance in storm-petrels. *Behavioral Ecology* 16, 906-913.

Nespolo, R.F. & Franco, M. (2007) Whole-animal metabolic rate is a repeatable trait: a meta-analysis. *Journal of Experimental Biology* 210, 2000-2005.

Wendeln, H. & Becker, P.H. (1999) Effects of parental quality and effort on the reproduction of common terns. *Journal of Animal Ecology* 68, 205-214.

Applications are invited from students who either hold or expect to obtain, a First or Upper Second class Honours degree in a relevant subject. Application by email, indicating the project(s) of interest (and supervisors) in priority order, giving the reasons for this, together with a c.v. including the names and contact details of two academic referees, should be sent as soon as possible to: Mrs. Linda J. Marsh, Research Support Office, School of Biological Sciences, The Life Sciences Building, Crown Street, Liverpool L69 7ZB (email: biolres@liverpool.ac.uk <<mailto:biolres@liverpool.ac.uk>>, Fax: 0151 795 5122). Please indicate where you first saw the project(s) advertised.

Dr Jonathan A Green Lecturer in Marine Biology

School of Biological Sciences University of Liverpool

Crown Street Liverpool L69 7ZB UK

Tel: +44 (0) 151 795 4385 Fax: +44 (0) 151 795 4400

www.liv.ac.uk/marinebiology

Jonathan.Green@liverpool.ac.uk

Jonathan.Green@liverpool.ac.uk

by Dr Mark Brown (<http://www.rhul.ac.uk/Biological-Sciences/AcademicStaff/Brown/index.html>).

For further details and application procedures, please go to: <http://www.rhul.ac.uk/Biological-Sciences/-Vacancies/index.html#PhD> For specific information about the project, please email mark.brown@rhul.ac.uk

MARK.BROWN@RHUL.AC.UK

ULondon EvolutionaryBiol

A PhD position in evolutionary ecology is available in the School of Biological Sciences, Royal Holloway, University of London, UK

Title: Local adaptation in a generalist multi-host parasite of bumble bee queens

Research outline: All animals have parasites, and parasites are one of the most important selective pressures on the ecology and evolution of their hosts. While we know a lot about parasites that utilize only one host species, most parasites can use multiple host species. The ecological and evolutionary implications of multiple-host use for both the parasite and the hosts are unclear. The nematode parasite *Sphaerularia bombi* is a parasite of the queens of numerous bumble bee species. Parasitised queens are castrated and behaviourally manipulated by the nematode to maximize its own reproduction. Understanding how this parasite impacts bumble bees is important for two reasons. First, it will provide novel insights into the ecology and evolution of multiple-host parasites. Second, bumble bees are essential pollinators of both wild and agricultural flowering plants, but they are currently in significant decline throughout Europe and North America. *Sphaerularia bombi* may both control bumble bee populations and arbitrate competition among bumble bee species. Consequently, understanding the dynamics of this complex host-parasite system has clear implications for the maintenance of biodiversity. We have developed novel experimental protocols to enable controlled infections and experiments in the lab. Our recent work has suggested that this highly virulent parasite exhibits local adaptation to its suite of host species. This project will combine field-work with controlled laboratory infections and multi-generational selection experiments to examine the dynamics of local adaptation in this system. Results from this work will increase our understanding of multi-host parasites in general, as well as illuminating the dynamics of an important parasite of declining pollinators. The project will be supervised

Umea EvolutionInForestHabitats

PhD position in Molecular Ecology

A Ph. D. position in the field of Molecular Ecology (4 years full time) is available at the Department of Wildlife, Fish and Environmental Studies, at SLU, Umeå, Sweden. The position is funded by the Swedish research council, FORMAS. We are looking for a doctoral student who is broadly interested in applying genetic methods to quantify evolutionary and ecological processes in wild populations. The particular Ph. D. project aims to improve our understanding of browsing dynamics in forest habitats, particularly factors affecting individual foraging patterns and cost-benefit trade-offs.

Qualifications: The successful candidate will be a highly motivated person with a firm theoretical understanding of behavioral and evolutionary ecology, and a strong commitment to basic science. Applicants must have completed a Master degree (or equivalent) in Animal Ecology within the last 3 years. Experience of field and laboratory work, proficiency in writing, data base management and statistics will be valued highly. The position is open to anyone meeting these qualifications.

Closing date: Please send your application, marked with reference number 848/09, to "the Registrar, SLU, P.O. Box 7070, S- 750 07 Uppsala, Sweden" or electronically to "registrator@slu.se" no later than April 29th, 2009. Candidates using the electronic submission route should be prepared to complement the electronic application with hard copies on short notice. A complete application should include: 1) short cover letter indicating the reasons for applying and long-term career goals, 2) copy of the Master thesis (or equivalent work), 3) copy of University grades, 4) CV (maximum 2 pages), 5) summary of research experience, and 6) copies of any published or in-press papers (if applicable), and 7) the names of two references (who may be asked to provide a written reference). Shortlisted can-

didates can expect to be called for interview.

For further inquires please contact Göran Spong at goran.spong@vfm.slu.se. END of add.

Göran Spong Department of Wildlife, Fish and Environmental studies SLU (Swedish Agricultural University) SE-90187 Umeå, Sweden +46 730350641

Göran Spong <Goran.Spong@vfm.slu.se>

UMissouriColumbia CompGenomics

Graduate research assistantship in computational comparative genomics.

The University of Missouri-Columbia's Informatics Institute (MUII) is accepting a limited number of late applications to the Doctoral Program in Informatics. As part of this program, one research assistantship is available in my laboratory. Potential thesis topics include a) developing evolutionary models of the processes of sequence evolution, gene duplication and gene loss in eukaryotes b) assembly and annotation of large scale sequence data (from 454/Solexa instruments) from vertebrates and their microbial associates c) inference and analysis of metabolic networks from mammalian species using comparative genomics.

More information on my research interests can be found at <http://web.missouri.edu/~conantg> . Informal enquiries can be made to Gavin Conant, conantg@missouri.edu.

Applications should be submitted as soon as possible: detailed instructions are available at: <http://muii.missouri.edu/index.php?pid=3D14> Gavin Conant

F21C Animal Reproductive Biology Group 163B Animal Science Research Center 920 East Campus Drive University of Missouri Columbia, MO 65211 Phone: 573-882-2931 Email: conantg@missouri.edu Web: <http://web.missouri.edu/~conantg> conantg@missouri.edu

UppsalaU SexDetermination

Graduate student position available at the Department of Evolutionary biology, Uppsala University

A graduate student position in Evolutionary Genetics/genomics is available at the Department of Evolutionary Biology at Uppsala University. This position offers an opportunity to explore a wide range of evolutionary paradigms, from the genomic consequences of selfing vs outcrossing, to the early steps in the evolution of sex chromosomes.

Our research group uses the filamentous ascomycete genus *Neurospora* as a model system. *Neurospora* is well suited for studies on reproductive systems since its closely related species exhibit a wide spectrum of reproductive behavior. Furthermore, we use the mating-type chromosome of *Neurospora tetrasperma* as a simple, general, model for studies of the early evolution of sex chromosomes from autosomes. It shares features with the complex sex chromosomes found in the animal and plant kingdom, but is not affected by complex sex-biased evolutionary forces such as sexual selection and male biased mutation rate.

The PhD-project can be developed after the interest of the applicant, but should preferably involve large scale SNP-typing and/or high throughput sequencing of natural populations of *Neurospora*.

The Program in Evolutionary Biology (<http://www.egs.uu.se/evbiol/index.html>) is situated in the Evolutionary Biology Centre in central Uppsala. The working atmosphere is international with English as working language. The Evolutionary Biology Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, with research programs including ecology, systematics, genetics, genomics, and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 40 minutes with train from Stockholm.

Required qualifications for applicants are 1) a MSc in Biology, Genetics, Evolutionary Biology, Microbiology or related field, 2) experience in one or several of the following areas: bioinformatics, population genetics, evolutionary biology, genetics, microbiology, mycology, and 3) demonstrated communication skills in English.

The position is for four years. Start date fall 2009. Review of applications will begin immediately and continue until the position is filled.

To apply, send NO LATER THAN APRIL 15: your CV, including contact information for two references, and a cover letter stating your research interest to: Dr Hanna Johannesson, hanna.johannesson@ebc.uu.se.

hanna.johannesson@ebc.uu.se
hanna.johannesson@ebc.uu.se

UppsalaU SpeciationGenomics

A 4-year PhD position is available at the Department of Evolutionary Biology at the Evolutionary Biology Centre in Uppsala, Sweden to study Speciation Genomics.

Background

The study of speciation mechanisms remains one of the major challenges in fundamental biological research. With the advent of the genomic era it has become possible to study the genetic underpinnings of reproductive isolation (RI). Hybrid zones, often referred to as natural laboratories of evolution, are ideal systems to unveil the barriers that keep gene pools from merging. The European crow hybrid zone where Carrion Crows (*Corvus [corone] corone*) and Hooded Crows (*Corvus [corone] cornix*) meet is an often cited textbook example of hybridization. In a narrow zone that stretches across Europe, they produce viable hybrids that backcross into the parental populations. Morphological, ecological and behavioural evidence suggest almost complete RI. This is traditionally interpreted in terms of allopatric speciation leading to genome wide incompatibilities upon secondary contact. Contrary to the pronounced RI, genetic evidence reveals unexpectedly low levels of differentiation between the two taxa. Behavioural and theoretical work suggests that divergence may be rooted in sexual imprinting solely based on differing plumage characteristics.

The project

We use several approaches to understand the genetic architecture of this hybrid zone including candidate genes and uninformed genome scans making use of next-generation sequencing approaches. Recent evidence suggests that differences in expression profiles may play an important role in the initial steps of species differentiation. In the crow system there is a clear hypothesis that genes involved in plumage coloration may be invoked in the divergence process. The applicant will study expression patterns in the different crow taxa quantifying expression divergence and identifying the genes that may contribute to phenotypic differences. The work will be done in close cooperation with the Max Planck Institute of Ornithology in Radolfzell, Germany, where birds are raised. Methodologically, the project will include laboratory work as well as bioinformatic downstream analyses. The successful applicant should show a combination of molecular, evolutionary

and population genetic experience. She/he should not be afraid of handling large data sets and is ideally familiar with programming (e.g. Unix Shell, Perl). The student will be jointly supervised by Dr Jochen Wolf and Prof Hans Ellegren. Starting date is open to discussion.

Infrastructure

The Evolutionary Biology Centre is one of world's leading research institutions in evolutionary biology that successfully bridges a broad variety of disciplines in the biological sciences. It is situated in the beautiful small town of Uppsala in Sweden, that offers rich opportunities in cultural and outdoor activities and is strongly influenced by the 40 000 students living here. The Department of Evolutionary Biology excels in many aspects of genetics and evolution and offers an inspiring atmosphere in an international group. Our interests include molecular evolution and evolutionary genomics with a primary focus on birds. We form part of a recently launched Centre of Excellence, the Uppsala Centre for Evolution and Genomics (<http://www.uceg.uu.se>).

For further information visit our website: <http://www.egs.uu.se/evbiol/Persons/Hans.html>

Send your application including a letter describing research interests, CV and two letters of recommendation to Dr. Jochen Brock Wacain Wolf at wolf@evolbio.mpg.de. Applications should be submitted before April 20th.

Dr. Jochen Brock Wacain Wolf

Department of Evolutionary Biology Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

phone: ++46 18 471 6468

fax: ++46 18 471 6310

< <http://www.egs.uu.se/evbiol/Persons/Jochen.html>
> <http://www.egs.uu.se/evbiol/Persons/Jochen.html>

Jochen Wolf <wolf@evolbio.mpg.de>

UReading modelling selection ancient DNA

UNIVERSITY OF READING School of Biological Sciences

NERC CASE funded Studentship Eligibility: UK cit-

izens and UK-resident (3 years+) EU citizens ONLY
CASE partner: Natural History Museum

Project title. The application of computational statistics and population genetics to ancient DNA data from historical collections. Supervisors

Dr Mark Beaumont (m.a.beaumont@reading.ac.uk), Dr Robert Prys-Jones (Natural History Museum; CASE partner; r.prys-jones@nhm.ac.uk), Dr Jim Groombridge (Durrell Institute of Conservation and Ecology, University of Kent; J.Groombridge@kent.ac.uk)

Project description. This project is a collaboration between theoretical and empirical biologists with the aim of using data from historical collections to infer the demographic and evolutionary history of populations. Such data may come from historical records or may be obtained from ancient DNA genotyping of museum specimens (Groombridge et al, 2000). In the last 10 years computer-intensive statistical methods have been developed (Wang and Whitlock, 2003; Beaumont, 2003; O'Hara, 2005; Bollback et al., 2008). It is potentially possible to measure selection coefficients, population sizes, recombination rates, and migration rates using historical data. A method is available, based on Markov chain Monte Carlo (MCMC), that can infer population sizes and selection coefficients for a 3-locus model, including linkage, dominance and epistasis. This has been applied to model temporal changes in morph frequency in the land snail *Cepaea nemoralis*.

The aim of this CASE studentship will be to extend and test the framework that has already been developed. Large data sets on *Cepaea nemoralis* populations sampled over the last century are available to test hypotheses concerning the mode of selection operating in *Cepaea*. Ancient DNA data are also available to test the hypotheses that all gene frequency changes are neutral (e.g. Shepherd et al, 2005). Data from Dr Robert Prys-Jones and Dr Jim Groombridge, Durrell Institute, Kent, will be used to model changes in gene frequencies over time using ancient DNA from endangered bird species. The student will be based at the University of Reading, but will be expected to spend some time with the CASE partner, Dr Prys-Jones, at the Natural History Museum.

The successful candidate will be expected to have an aptitude for mathematical modelling and programming. Ideally, it is hoped that this project will attract a student with a degree in mathematics, statistics, or computer science, interested in moving into computational biology. The candidate will also have the opportunity to generate their own data by genotyping samples, and thereby obtain training in practical molecular genetics.

References Beaumont, M.A. (2003) Estimation of population growth or decline in genetically monitored populations. *Genetics* 164: 1139-1160.

Bollback JP, York TL, Nielsen R (2008) Estimation of 2N(e)s from temporal allele frequency data. *Genetics* 179, 497-502.

Groombridge, J. J., C. G. Jones, M. W. Bruford and R. A. Nichols (2000) Ghost' alleles of the Mauritius kestrel. *Nature* 403: 616.

O'Hara RB (2005) Comparing the effects of genetic drift and fluctuating selection on genotype frequency changes in the scarlet tiger moth. *Proceedings of the Royal Society B-Biological Sciences* 272, 211-217.

Shepherd LD, Millar CD, Ballard G, et al. (2005) Microevolution and mega-icebergs in the Antarctic. *Proceedings of the National Academy of Sciences of the United States of America* 102, 16717-16722.

Wang JL, Whitlock MC (2003) Estimating effective population size and migration rates from genetic samples over space and time. *Genetics* 163, 429-446.

HOW TO APPLY Please send your application to Sarah Swan [s.m.swan@reading.ac.uk] in the admissions office. Your initial application should comprise the following: 1) a copy of your curriculum vitae, 2) names, addresses and e-mail addresses of at least two academic referees, 3) a covering letter stating why you want to do this project and why you are a good candidate. The closing date for applications is Friday April 3rd and we intend to hold interviews on Monday April 20th. If you have any queries about the project itself, please contact the supervisor directly by e-mail.

Mark A. Beaumont, School of Biological Sciences Philip Lyle Research Building PO Box 68 University of Reading Whiteknights Reading RG6 6BX U.K.

Tel 0118 378 7707 Fax 0118 931 0180 Email: m.a.beaumont@reading.ac.uk WWW: <http://www.rubic.rdg.ac.uk/~mab/>

USheffield DiseaseEvolution

PhD Studentship Available at University of Sheffield

Project: "Understanding the indirect effects of vaccination programmes: a community ecology approach"

Supervisors: Owen Petchey, Amy Pedersen & Andy Fenton

We invite highly motivated students to apply for a PhD studentship (NERC directly funded, UK citizens only) to develop theoretical models of host-parasite community ecology. The studentship will be part of a larger NERC funded project studying co-infection dynamics in a wild mouse population in the UK. A background in mathematical biology and/or quantitative ecology is recommended, but not essential.

Research outline: In natural systems, individual host organisms are often co-infected by a number of different parasite species. These parasites exploit a range of host tissues and resources, making resource competition between parasites likely. The host's immune system attacks parasites, which can cause indirect interactions, such as apparent competition, between parasites. Viewing the parasites, resources, and immune system as a community of interacting players is an emerging area in the field of parasitology. However, many uncertainties exist about within-host parasite communities. How much resource competition occurs between parasite species? What is the functional form of the response of the immune system to parasite intensity? How strong are tradeoffs between different components of the immune system? What are the strengths of direct and indirect interactions between parasites? The aims of this research will be to develop within-host parasite models based on a community ecological approach to address these questions. In addition, an applied consequence of the interactions between parasites, resources, and immune responses is their effects on treatment and vaccination strategies. Since successful vaccination can be viewed as the extinction of a species from a community, a significant aim of the project is to use methods from community ecology to explore the potential indirect consequences of vaccination programmes.

Applications will be accepted until March 27th.

The position will start in September 2009 and be based in the Department of Animal and Plant Sciences, University of Sheffield. Under special circumstances the studentship could be taken up in the Institute of Evolutionary Biology at the University of Edinburgh.

Please see this web page (<http://tinyurl.com/dx7fpx>) and email Amy Pedersen (a.pedersen@sheffield.ac.uk), Owen Petchey (o.petchey@sheffield.ac.uk) or Andy Fenton (a.fenton@liverpool.ac.uk) for more information.

To submit an application, go to: <http://www.shef.ac.uk/aps/prospectivepg/applications.html>

— Amy B. Pedersen Royal Society Incoming Research Fellow Department of Animal and Plant Sciences University of Sheffield Alfred Denny Building Western

Bank Sheffield S10 2TN UK

Email: a.pedersen@sheffield.ac.uk Office: +44(0) 114 222 4692 Lab: +44(0) 114 222 0060 Web:<http://www.shef.ac.uk/aps/staff/acadstaff/pedersen.html>
a.pedersen@sheffield.ac.uk a.pedersen@sheffield.ac.uk

UStirling SeedDispersal

Following the withdrawal of a candidate, a three year full-time PhD studentship has become available in the School of Biological and Environmental Sciences at the University of Stirling, United Kingdom.

Application closing date: Wednesday 25th March 2009 for an expected start date in October 2009.

Project description

Waterborne Seed Dispersal of *Alnus glutinosa* Gaertn in a River Catchment and Landscape Connectivity of Riparian Woodlands

Black alder, *Alnus glutinosa* Gaertn, is the most abundant native tree in Scottish riparian woodlands where it plays a key ecological role. Despite its importance in riparian ecosystem function, the population genetics *A. glutinosa* has been little studied. Long-distance water dispersal of seeds believed to be driven by flowing water, temporary flooding or wind drift at the water surface while wind dispersal should contribute to short distance dispersal. This project proposes to investigate the relationship between river flow dynamics and spatial patterns of alder seedling recruitment and river margin colonisation via waterborne seed dispersal in a river catchment using a landscape genetics approach. Field activities will be based in Scotland; in the river Tay catchment which contains large areas of undisturbed alder dominated floodplain habitat of high nature conservation value. Laboratory activities will involve the development of genetic markers and high throughput genotyping to detect the parentage of recruited seedlings by parentage analysis. The possibility of integrating ecological and genetics data in a geographically-explicit model may be considered to predict how river management disturbance affects tree population dynamics.

The project will require a combination of field work, molecular biology, data analysis and modelling. If you wish to discuss the project informally please contact Dr Cecile Bacles (c.f.bacles@stir.ac.uk <<mailto:c.f.bacles@stir.ac.uk>>).

The entry qualification for postgraduate studentships is a first class or upper second class honours degree in a relevant biological sciences subject, or an appropriate M.Sc. degree. More information about our graduate school programme may be found on our website (<http://www.sbes.stir.ac.uk/information/postgrad/index.html>).

The studentship covers stipend and will pay UK/EU tuition fees. The studentship is available to UK or EU nationals. Owing to funding restrictions applications from overseas candidates cannot be considered.

Individuals with a background in population genetics and a keen interest in restoration ecology are encouraged to apply. Please send a CV with contact details of two referees and a letter describing your research interests and your motivation to work on the project to Dr Cecile Bacles, preferably by email to c.f.bacles@stir.ac.uk <<mailto:c.f.bacles@stir.ac.uk>>, at the School of Biological and Environmental Sciences, University of Stirling, Stirling FK9 4LA UK before Wednesday 25th March, with invitations for interview expected to follow shortly after the application deadline.

– Academic Excellence at the Heart of Scotland. The University of Stirling is a charity registered in Scotland, number SC 011159.

c.f.bacles@stir.ac.uk c.f.bacles@stir.ac.uk

UZurich ComputationalEvolutionaryBiol

WAGNER Andreas, Prof. aw@bioc.uzh.ch six digit code:010000

PhD thesis in computational evolutionary biology

A three-year Ph.D. studentship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to study robustness and evolvability in large metabolic networks, using computational approaches. The successful candidate will have a strong background in bioinformatics and computational biology. Fluency in a major scripting language such as perl, and experience in software development is a must. Also necessary is a strong background in biology. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further. We are looking for an individual with a Masters Degree or

equivalent, who is highly self-motivated and can work independently. The working language in the laboratory is English. German skills are not essential.

The Wagner lab at the University of Zurich studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Ongoing projects range from laboratory evolution experiments in yeast to human population genomics. A sample of our research can be found at <http://www.bioc.uzh.ch/wagner/>. *Lab members are a group with very diverse backgrounds, research projects, and nationalities. They are unified by their interests in evolution and /or fundamental organizational principles of life. **

Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch: CV including publication list (if available), a scanned academic transcript (list of grades in university courses), a statement of research interests not exceeding two pages, and three references. Please include the word COMP09 in the subject line. The application deadline is March 30, 2009. The earliest starting date is August 1, 2009.

–

Christiane Gujan Administrative Assistant of Prof. A. Cafilisch and Prof. A. Wagner Zurich University Institute of Biochemistry Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Tel. 0041 (0)44 635 55 49 Fax 0041 (0)44 635 68 62

Christiane Gujan <gujan@bioc.uzh.ch>

UZurich EvolutionaryTheory

PhD position in Evolution and Ecology

We are looking for a highly motivated PhD student to work on evolutionary theory. Specifically, the student will develop models of bacterial and plasmid evolution. Plasmids can transfer horizontally, from bacterium to bacterium, and they seem to carry a biased set of genes, such as those involved in antibiotic resistance or virulence, or genes that promote cooperation with other bacteria. We wish to ask why, and when, such genes should transfer horizontally, rather than in-

tegrating themselves into the host chromosome.

The focus of the project is very broad, and will touch on cooperation and conflict, virulence evolution, eco-evolutionary feedbacks and also address the levels-of-selection problem. The project will mostly involve evolutionary modeling, but will also involve close collaboration with empiricists. Students who wish to address the problem using bioinformatics or microbial experiments will be encouraged to do so.

Zurich is located less than one hour from the Alps, and is a small but vibrant city that is regarded to have one of the best standards of living in the world. There is a large international community and it is well connected to all major European cities.

The successful applicant will be supervised by Dr Daniel Rankin (<http://www.rankin.sk/>), a theoretical evolutionary biologist interested in a wide range of topics, from social evolution to the link between evolution and ecology. The position will be based in the Computational Biology and Bioinformatics Group, led by Professor Andreas Wagner (<http://www.bioc.uzh.ch/~wagner/>). The group is very international and consists of a very diverse range of individuals who work on a wide range of interesting evolutionary topics.

The candidate should have a diploma/MSc degree and have studied in one of the following fields: evolutionary biology/ecology, mathematics, microbiology or economics. Experience with modeling will be an advantage, but is not necessary. The working language of the group is English, and knowledge German is very helpful but not necessary.

To apply, please send an E-mail with the applicants cover letter, CV and short (<1 page) statement of research interests and experience in a single pdf file to d.rankin@access.uzh.ch. Please mention "PhD position" in the subject of e-mail. Please additionally give the names and contact details of two or three people willing to write letters of recommendation. Deadline for applications is Friday 24th April 2009. The position, funded by the Swiss NSF, is available to start immediately and will be for three years. The student will receive

Further information: Dr Daniel Rankin (<http://www.rankin.sk/>)

E-mail: d.rankin@bioc.uzh.ch, Tel: +41 44 63 56143 or +41 78 648 9905

For more information about the group in Zurich see: <http://www.bioc.uzh.ch/wagner/> — Dr Daniel J. Rankin Department of Biochemistry University of Zurich Building Y27, Winterthurstrasse 190 CH-8057

Zurich, Switzerland

<http://www.rankin.sk/> e-mail: d.rankin@bioc.uzh.ch

Office: +41 (0)44 63 56143 Fax: +41 (0)44 63 56862

d.rankin@bioc.uzh.ch d.rankin@bioc.uzh.ch

UZurich ForestDiversity

2 PhD Positions, Institute of Environmental Sciences, University of Zurich: Structure and Functioning of Forest Ecosystems

We are looking for well-motivated candidates for PhD projects on the diversity, stability and functioning of forest ecosystems. The projects will extend work on the relationship between diversity and functioning of ecosystem in grasslands (<http://www.uzh.ch/uwinst/>) to forest ecosystems. One project will be associated with the Sabah Biodiversity Experiment in Malaysian Borneo (experience of tropical would be advantageous) and the other project will work with data from temperate forests.

Applicants need to hold a relevant Honours or (preferably) Masters degree. You should have a good background in ecology and experience of the relevant forest ecosystems would be advantageous. The project will require knowledge of statistics and programming (particularly using R and C). The projects are collaborations between the groups of Andy Hector, Lindsay Turnbull at the University of Zurich (<http://www.uzh.ch/uwinst/>) and external groups, particularly Drew Purves at Microsoft Research, Cambridge, U.K.

Start date: From April 2009.

Working language: English

Salary: 40 - 45,000 CHF.

Please send a short relevant electronic CV and application letter to weilen@uwinst.uzh.ch entitled: Your-NameCV.ext.

PhD Position, Institute of Environmental Sciences, University of Zurich:

Data-Constrained Plant Growth Modelling

How do plants grow? How do they allocate photosynthate to different structures such as leaves, roots and flowers in different environments, and how do they make such decisions? This project seeks to understand plant growth with the simplest possible assumptions

and will use extensive data sets and modelling to approach this problem from an entirely new angle. The project will involve extensive computer modelling including both simulations and fitting models directly to data. The project may also include new data collection depending on the interests and aptitudes of the successful candidate.

We are looking for a well-motivated person to conduct this research, culminating in a PhD from the University of Zurich, Switzerland. Applicants need to hold a good, relevant first degree and have some experience with computer modelling. They must also be able to work in a team with other students and post-docs. A background in statistics and some knowledge of plant ecology is also desirable. The project is funded by Microsoft Research, UK and the successful candidate will receive extensive help and technical support from this source. The project will be based in Zurich, where the successful candidate will be expected to live. The

project is co-supervised by Dr. Lindsay Turnbull (University of Zurich) and Dr. Drew Purves (Microsoft Research, UK) and requires an immediate start.

Key reference: Turnbull, L. A., Paul-Victor, C., Schmid, B. & Purves, D. W. (2008) *Ecology*, 89, 1352.

Working language: English

Salary: 40 - 45,000 CHF.

Please send your CV and application to: lindsayt@uwinst.uzh.ch. Please label your attached CV file: "CV.applicant.name.doc"

Maja Weilenmann Verwaltungsassistentin Institut für Umweltwissenschaften Universität Zürich Winterthurerstrasse 190 8057 Zürich Tel. ++41 (0)44 635 61 24 Fax ++41 (0)44 635 57 11 weilen@uwinst.uzh.ch < <http://www.uzh.ch/uwinst/> > <http://www.uzh.ch/uwinst/>

Maja Weilenmann <weilen@uwinst.uzh.ch>

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**BarnardC NewYork Temporary
EvolTeaching**

Adjunct Assistant Professor Ecology & Evolution*

The Department of Biological Sciences at Barnard College, Columbia University, seeks an Adjunct Assistant Professor to teach three courses in 2009-10: an upper-level lecture covering the ecology and/or evolution of a group of organisms chosen by the candidate and an upper-level lab on the same topic in the Fall 2009 semester, as well as an upper-level lecture course in Ecology in the Spring 2010 semester. Applications for individual courses will be considered.

Applicants should send a cv and a list of three potential contacts for letters of recommendation to: Ecology and Evolution Search Committee, Dept. of Biological Sciences, Barnard College, 3009 Broadway, New York, NY 10027 (e-mail:biologyjob@barnard.edu).

Barnard College is an Equal Opportunity Employer. Women and members of under-represented minorities are encouraged to apply.

“Hilary S. Callahan” <hcallahan@barnard.edu>

BowdoinCollege LabInstr MarineBiolEvolution

Position Announcement Laboratory Instructor in Evolution and Marine Biology at Bowdoin College <https://careers.bowdoin.edu/> Posting Number: 0600351

Bowdoin College invites applications for a full-time academic year, benefits-eligible Laboratory Instructor position beginning in August of 2009. The Biology Department is looking for an enthusiastic, self-motivated individual to work with faculty to help teach laboratory sections in Biology of Marine Organisms (Fall semester) and Evolution (Spring semester).

Responsibilities include: Coordinate laboratory setup and implementation; help teach weekly laboratory sections and field trips; provide technical assistance to students; contribute to writing lab protocols; grade lab reports; and supervise student assistants.

Education/Skills Requirements: Applicants must possess a BS in biology with an emphasis in ecology or evolution (MS is strongly preferred); excellent oral and written communications skills; strong organizational skills and problem-solving abilities; and an ability to provide individual and group instruction with sensitivity to different learning styles. Candidates should ideally be familiar with marine intertidal ecosystems; ma-

rine invertebrate form and function; molecular, genetic and systematic techniques in evolution; experimental design, data/statistical analysis; and the use of computers in data acquisition and analysis.

Experience Requirements and/or Equivalents: Experience teaching labs using laboratory equipment and techniques, including cellular and molecular technologies where appropriate, or field-related techniques. Demonstrated supervisory and project coordination experience required. Experience in teaching both field-based and lab-based laboratories is preferred.

lgordon@bowdoin.edu lgordon@bowdoin.edu

Fisheries Louisiana ConservationGenetics

Position Title: Laboratory Technician Where: National Marine Fisheries Service, Marine Mammal Genetics Lab Classification: Full-time Contract position. Must be US citizen Location: Lafayette, LA Starting Salary: Commensurate with qualifications and experience Start Date: Position is open immediately. I would prefer to have the position filled no later than May 1st, 2009 Application Deadline: March 16, 2009 (applications will be considered until position is filled)

Job Summary: The Marine Mammal Molecular Genetics Laboratory of the NMFS Southeast Fisheries Science Center is seeking a highly motivated laboratory technician to join an active lab investigating population genetics and evolutionary histories of a variety of marine mammal species.

Responsibilities include: Assisting in the daily operation of the lab including ordering supplies, preparation of reagents.

Performing standard molecular biology laboratory procedures: DNA extractions, PCR, DNA sequencing, microsatellite genotyping.

Database entry.

Qualifications: A Masters degree in appropriate field of technology or science such as Biological Sciences, Molecular Biology, or Genetics.

Demonstrated research experience with DNA extractions and PCR, DNA sequencing and microsatellite data collection.

Familiarity with genetic analyses of sequence and/or microsatellite data and facility with standard computer

software programs.

A strong work ethic, the ability to work independently and enthusiasm for research in molecular and evolutionary genetics.

Strong organizational skills and attention to detail.

Experience running an ABI capillary sequencer is preferred

Send a letter of application and description of experience, CV/resume, and names of three professional references to Patricia Rosel, NOAA Fisheries, 646 Cajundome Blvd., Suite 234, Lafayette, LA 70506 or email to patricia.rosel@noaa.gov.

Patricia.Rosel@noaa.gov

France Field Assist Turtle Evolution

Field assistant in evolutionary ecology of European swamp turtles

We are looking for a field assistant to participate in a project on European swamp turtles (*Emys orbicularis*) from May to July 2009 at the Research Station Petite Camargue Alsacienne in France (www.camargue.unibas.ch).

The work will include caring for the about 80 swamp turtles living in the station's outdoor enclosures, capturing the turtles, observing breeding behaviour, locating nests and collecting eggs for artificial incubation in the lab. The applicant is expected to stay for the entire field season from the beginning of May to the end of July. Applicants should preferably have some knowledge of French or German.

The field site is situated in the nature reserve Petite Camargue Alsacienne in France, about 10 km north of Basel (Switzerland). We cannot cover travel expenses, but we offer free accommodation and use of the infrastructure at the research station. The assistant will receive 400 Euros to cover living expenses.

The position will be filled as soon as possible. Applications should be in English, French or German, and should include, in one single pdf or word file, a curriculum vitae and a letter of motivation. Please provide names and email addresses of two persons who are willing to write a letter of recommendation, and send applications by email to both of the following addresses:

Dr. Valentin Amrhein pca.recherche@orange.fr

Christian Rust christian_rust@hotmail.com

valentin amrhein [<pca.recherche@orange.fr>](mailto:pca.recherche@orange.fr)

Groningen Research Technician MolEvolGenetics

Research Technician A A research technician position is available at the Centre for Ecological and Evolutionary Studies (CEES) at the University of Groningen. The candidate will join a recently started research group that studies parasitoid-host interactions to unravel the evolutionary genomics of adaptations. The overall aim of the research group is to identify what genomic features (e.g., SNPs, transposons, epigenetic regulation) enable a rapid evolutionary response to adverse environmental conditions. The research technician will participate in various projects within the research group.

Requirements and duties The candidate will have a degree (BSc/HBO or equivalent) in a relevant subject (such as molecular biology or genetics), affinity with evolutionary biology, extended experience with molecular biology techniques and ideally will have worked with *Drosophila* previously. You will have excellent organisational and research skills, and a positive attitude to learn and troubleshoot new methods. The main duties include experimentation in molecular biology, genetics and insect biology, as well as meticulously carrying out routine fly work.

Additional conditions of employment Applications are invited for an experienced research technician, who will carry out research work and maintain fly and parasitoid stocks for Evolutionary Genomics research. The University of Groningen can offer you a salary dependent on qualifications and work experience from 1902,- (scale 7, number 0) up to a maximum of 2324,- (scale 7, number 4) gross per month for a full-time position. The position will be available for a period of 3 years, starting as soon as possible.

Additional information For more information you may contact Dr. Bregje Wertheim, e-mail address: b.wertheim@rug.nl. Or additional information can be obtained through one of the following links. About the organization: <http://www.rug.nl> About the Evolutionary Genetics group: <http://www.rug.nl/biologie/-onderzoek/onderzoekGroepen/evolutionaryGenetics/-index> Application Cover letters in English language, including a personal motivation (important!), a curriculum vitae, and the names and addresses of

three referees (including telephone number and E-mail address), to be sent before 23 March 2009 to: vmp@rug.nl. Also send an electronic copy of your application to b.wertheim@rug.nl. When applying for this job always mentions the vacancy number 209077.

Bregje Wertheim Rosalind Franklin Research Fellow
Evolutionary Genetics Biological Centre University of Groningen Postbus 14 9750 AA Haren The Netherlands
tel: +31 50 3639039 e-mail: b.wertheim@rug.nl

IBIS Chief Editor

CHIEF EDITOR WANTED FOR IBIS

The British Ornithologists' Union is one of the world's oldest and most respected ornithological organisations with an international membership stretching across all continents. In 2008, the BOU celebrated 150 years supporting ornithology.

The BOU publishes Ibis, the international journal of avian science, four times per year and is seeking a Chief Editor to lead the editorial team.

IBIS - THE INTERNATIONAL JOURNAL OF AVIAN SCIENCE Ibis is an international journal with a reputation for publishing high quality papers in avian science, covering a range of topics, including ecology, conservation, behaviour, palaeontology, taxonomy and new species. The current editorial team is made up of a Chief Editor and five Editors, and is supported by a Journal Manager (responsible for coordinating the journal's peer review process) and an international Associate Editorial Board. Further details about the journal can be found at <http://www.ibis.ac.uk>. Ibis has been published continuously since 1859.

CHIEF EDITOR We are seeking a Chief Editor who will oversee the handling and publishing of papers in Ibis. The Chief Editor must be a highly motivated, decisive, outstanding communicator, and must act with the highest probity. They must have an excellent understanding of their own field of avian science, as well as of the wider discipline, and have experience of refereeing and the editing process, including dealing with electronic manuscript processing.

This is a part-time freelance position with a current annual remuneration of £4,740 inclusive of travel and other expenses. An appointment will be made with an agreed start date before July 2009.

KEY RESPONSIBILITIES - Work with the editorial team and Journal Manager to oversee manuscript processing from submission to publication - Pre-screen submitted manuscripts for suitability for the journal, make decisions based on editors' recommendations, and overseeing manuscript revision and editing with the editors - Identify key established or emerging subject areas for the journal to focus on - Solicit the submission of high quality manuscripts in all areas relevant to the journal - Use opinion from fellow scientists/practitioners to drive changes in procedure, to develop initiatives and/or to feed into general discussions on journal strategy - Promote Ibis and the British Ornithologists' Union when attending conferences - Work with senior BOU staff, appointed Council members and the publisher's representative in the management of the journal - Work closely with the journal publisher's staff to ensure the journal keeps to its publication schedule - Contribute to the journal's strategic development plan and its annual appraisal - Attend annual meetings in the UK with the publishers (Wiley-Blackwell), the editorial team and BOU Council - Help to identify new associate editors

SELECTION CRITERIA - Strong, current publication record - Knowledge and understanding of the subject area, complementary to that of the editorial team, - Experience of refereeing (essential) and of editorial work (highly desirable) - A good understanding of electronic manuscript handling systems (Ibis uses Manuscript Central) - Ability to work independently and also as an editorial team member - Ability to manage the editorial team and Associate Editor Board - Ability to deal with authors efficiently, professionally and respectfully - Ability to think strategically and act decisively - Commitment to the post and to the goals of the BOU

TO APPLY Applications and informal enquiries: Applicants should send a CV, plus a letter stating what you have to offer Ibis and how you would develop the journal over the next five years to Steve Dudley, BOU Senior Administrator, steve.dudley@bou.org.uk. Informal enquiries should also be directed to Steve.

CLOSING DATE 27 March 2009. Interviews will be held on 17 April.

The BOU is a Registered Charity in the UK no. 249877
Steve Dudley <steve.dudley@bou.org.uk>
stevedudley@btconnect.com

Program Manager Kansas State University, Manhattan, Kansas

Program Manager sought for a newly funded, five-year program designed to integrate graduate students in the biological sciences, physics and geosciences into science courses at Junction City High School, Junction City, Kansas. The program theme emphasizes the nature of scientific inferences about objects or events that we cannot directly experience or manipulate. The successful candidate will take a leadership role in developing and implementing this new graduate training program. Specific responsibilities include leading a one-credit course for the graduate student fellows during the academic year and providing ongoing feedback to the students, facilitating graduate student involvement with teachers and administrators in the Junction City school district, overseeing research experiences for teachers, assisting with development of a summer training institute and a spring capstone meeting, designing several additional training activities during the academic year, and participating in program assessment activities. Opportunities for scholarly research in science education are possible.

Required Masters or Ph.D. in one of the science content areas or in education or bachelors degree plus five years of experience in scientific research and/or science education. Desirable experience in any of the following areas: scientific research, teaching at the high school level, involvement with K-12 school districts, web development. We seek an individual who is highly motivated, ambitious, possessing excellent communication and organizational skills, and who is able to work in a collegial manner with a diverse group of colleagues as well as independently within the project parameters established by the principal investigators and project collaborators. Salary will be nationally competitive, commensurate with qualifications. Desired start date: May 2009.

Kansas State University is located in Manhattan, Kansas (www.ci.manhattan.ks.us), a pleasant community of ca. 50,000 located in the Flint Hills of northeastern Kansas, about two hours from Kansas City. Local recreational opportunities include a large lake/park system, diverse outdoor activities, athletic events, and a rich program in the performing arts. Manhattan also serves as the regional center for education, health care, commerce, entertainment and communications.

Candidates should submit a letter of interest, curriculum vitae and representative reprints, and arrange to have letters of recommendation sent by three academic and/or professional references. It is preferred that the application be submitted electronically to: [\[ogy@ksu.edu\]\(mailto:ogy@ksu.edu\). If electronic submission is not feasible, materials may be mailed to: Dr. Carolyn J. Ferguson, Division of Biology, 104 Ackert Hall, Kansas State University, Manhattan, KS 66506-4901 \(phone: 785-532-3166\). Review of applications will begin 23 March 2009, and continue until the position is filled.](mailto:biol-</p>
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Kansas State University is an Equal Opportunity/Affirmative Action Employer and actively seeks diversity among its employees. Background check required.

Carolyn J. Ferguson Assoc. Professor and Curator of the Herbarium (KSC) Division of Biology, Ackert Hall 313 Kansas State University Manhattan, KS 66506-4901

Office ph: 785-532-3166 Herbarium ph: 785-532-6619
Fax: 785-532-6653

www.ksu.edu/biology/faculty_pages/ferguson.html

www.ksu.edu/herbarium www.biodis.ksu.edu

ferg@ksu.edu ferg@ksu.edu

LaTrobeU EvoDevo

Three continuing (tenured) positions are available in the Genetics Department, School of Molecular Sciences, La Trobe University, Melbourne.

The positions specify a background in evolutionary genetics, especially EvoDevo using model organisms, genomics/bioinformatics, and/or evolutionary biology and population genetics.

Position information and application procedures are available at

<http://www.latrobe.edu.au/pc/jobs.htm> Please post on EvolDir

Regards

Warwick Grant

Associate Professor Warwick Grant Reader Genetics Department La Trobe University Bundoora, Vic., 3086 AUSTRALIA

+61 3 9479 5067 office +61 3 9479 2480 fax

Warwick Grant <W.Grant@latrobe.edu.au>

MaxPlanckInst EVA Leipzig EvolutionaryGenomics

Junior Group Leader in Evolutionary Genomics

The Department of Evolutionary Genetics at the Max Planck Institute for Evolutionary Anthropology (MPI-EVA) invites applications for a junior research group leader focused on population and comparative evolutionary genomics of humans and the great apes. The position is intended to complement the Department's existing strengths in genomics and bioinformatics to address fundamental questions on the evolution of humans and the great apes. We are particularly interested in candidates who use rigorous comparative evolutionary and population genetic approaches to analyze large-scale genomic data. The successful candidate will have access to state-of-the-art computational and molecular biology laboratory resources, including extensive next-generation sequencing capacity, and the opportunity to be involved with several ongoing research projects in the Department, including next-generation sequencing of the Neandertal (for more information see <http://www.eva.mpg.de/neandertal/index.html>) and bonobo genomes, population genetic analyses in the great apes, and evolutionary transcriptomics. Funding for the position is guaranteed for five years and includes support for post-doctoral fellows, Ph.D. students, and research/laboratory costs.

The institute is English-speaking and provides a dynamic and highly collaborative research environment, uniting international scientists from genetics, primatology, anthropology, linguistics, and psychology. The MPI-EVA is in Leipzig, Germany, a pleasant city of 500,000 inhabitants situated two hours from Berlin and three hours from Prague. To apply, send a cover letter, curriculum vitae, statement of research experience and interests, and contact information for at least three references to: Svante Pääbo, Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, D-04103 Leipzig, Germany or as a single electronic document (pdf) to mittag@eva.mpg.de (preferred). Review of applications will begin on April 10th and continue until the position is filled. Please send inquiries regarding the position to Svante Pääbo (paabo@eva.mpg.de). Further information on the MPI-EVA is available at <http://www.eva.mpg.de/english/index.htm>. For equal qualifications, preference will be given to the underrep-

resented sex in the relevant type of position, to minorities, and to persons with disabilities.

jeffrey.m.good@gmail.com

MaxPlanckInst EVA Leipzig EvolutionaryGenomics 2

This is a REVISED announcement:

Group Leader in Evolutionary Genomics

The Department of Evolutionary Genetics at the Max Planck Institute for Evolutionary Anthropology (MPI-EVA) invites applications for a research group leader focused on population and comparative evolutionary genomics of humans and the great apes. A group leader is similar in rank to an assistant professor (non-tenure track) and does not involve any teaching obligations. Funding for the position is guaranteed for five years and includes support for post-doctoral fellows, Ph.D. students, and research/laboratory costs.

The position is intended to complement the Department's existing strengths in genomics and bioinformatics to address fundamental questions on the evolution of humans and the great apes. We are particularly interested in candidates who use comparative evolutionary and population genetic approaches to analyze large-scale genomic data. The successful candidate will have access to state-of-the-art computational and molecular biology laboratory resources, including extensive next-generation sequencing capacity, and the opportunity to be involved with several ongoing research projects in the Department, including next-generation sequencing of the Neandertal (for more information see <http://www.eva.mpg.de/neandertal/index.html>) and bonobo genomes, population genetic analysis in the great apes, and evolutionary transcriptomics.

The institute is English-speaking and provides a dynamic and highly collaborative research environment, uniting international scientists from genetics, primatology, anthropology, linguistics, and psychology. The MPI-EVA is in Leipzig, Germany, a pleasant city of 500,000 inhabitants situated two hours from Berlin and three hours from Prague.

To apply, send a cover letter, curriculum vitae, statement of research experience and interests, and contact information for at least three references to: Svante Pääbo, Max Planck Institute for Evolutionary Anthropology, Deutscher Platz 6, D-04103 Leipzig, Ger-

many or as a single electronic document (pdf) to mit-tag@eva.mpg.de (preferred). Review of applications will begin on April 10th and continue until the position is filled. Please send inquiries regarding the position to Svante Pääbo (paabo@eva.mpg.de). Further information on the MPI-EVA is available at <http://www.eva.mpg.de/english/index.htm>. For equal qualifications, preference will be given to the underrepresented sex in the relevant type of position, to minorities, and to persons with disabilities.

jeffrey.m.good@gmail.com

MntLakeBioStation SummerAssist

Needed: Assistant to the Station Manager

The Mountain Lake Biological Station (University of Virginia) is located in Pembroke, Virginia, just a half hour drive from Blacksburg. Applications are currently being accepted for a full-time seasonal Assistant to the Station Manager, to work April - August 2009. This position provides administrative, financial, and general operational support. Duties include providing clerical support, answering telephones, greeting visitors, copying, faxing, sorting mail, station deliveries, and assisting the Station Manager with billing, purchasing of supplies, and receiving. This position also assists with maintaining the shop and stockroom, ensuring shop safety issues are reviewed and communicated. Ensure records on equipment use are maintained and accurate. Will assist researchers and students with building experimental apparatuses, providing repair, coordination, and movement of station equipment and furnishings. Waste removal, recycling duties, cleaning duties, and trail maintenance are also needed. A high school diploma is required. Knowledge of office reception, office procedures, accounting, and bookkeeping is preferred. Experience with Microsoft Word, Excel, and Access is helpful. Please apply on-line at: <https://jobs.virginia.edu>; Posting Number 0603212.

The University of Virginia is an Equal Opportunity/Affirmative Action Employer.

“De Marco Rehm, Anne (amd8c)”
<amd8c@virginia.edu>

Paddington UK ResAssist DiseaseEvolution

Research Assistant In Molecular Mycology

Division of Epidemiology, Public Health & Primary Care, Department of Infectious Disease Epidemiology

Salary Range £26,580 - £29,550 per annum

An exciting opportunity has arisen for a Research Assistant within the Department of Infectious Disease Epidemiology in the Division of Epidemiology, Public Health and Primary Care based at the St Mary's campus, Paddington.

You will join a successful team which has a strong interest in the biology, ecology, genetics and genomics of fungal pathogens of humans and wildlife and a chance to be involved with three projects: The functional genomics of the SE Asian pathogenic fungus *Penicillium marneffei*, the genetics of *Penicillium chrysogenum* and the biology of the amphibian chytrid fungus *Batrachochytrium dendrobatidis*. Work will involve molecular genetics, bioinformatics, model work and there will be opportunities for fieldwork.

You will be a graduate with a degree in Biology or associated Life Science and have experience in Molecular techniques such as PCR/Sequencing as well as be able to both work effectively within a team environment and independently.

This is a full time post for a fixed period of two years in the first instance.

For informal enquiries please contact Dr Matthew Fisher (Telephone 020 759 43787 or email matthew.fisher@imperial.ac.uk).

Our preferred method of application is online via our website <http://www3.imperial.ac.uk/employment>. Please complete and upload an application form as directed.

Alternatively, if you are unable to apply online, please contact Kasia Parfieniuk on 020 7594 3627 or email sm-recr@imperial.ac.uk to request an application form.

Reference number: SM036/09.

Closing date: 16 March 2009

d.henk@imperial.ac.uk d.henk@imperial.ac.uk

PennStateU BioinformaticsProgrammer

Bioinformatics Programmer available in the lab of Dr. Claude dePamphilis at Penn State University (< <http://cwd.huck.psu.edu/> ><http://cwd.huck.psu.edu/>). With funding from NSF's Plant Genome and Tree of Life programs, we are studying the evolution of flowers and early angiosperms (< <http://www.floralgenome.org/> ><http://www.floralgenome.org/>), parasitic plants (< <http://ppgp.huck.psu.edu/> ><http://ppgp.huck.psu.edu/>), and monocots (< <http://www.aspb.org/publicaffairs/news/monocot.pdf> ><http://www.aspb.org/publicaffairs/news/monocot.pdf>) through detailed analysis of transcriptome and genome sequences. We are looking for an experienced Programmer to maintain and develop new databases [e.g., < <http://fgp.bio.psu.edu/tribedb/index.pl> ><http://fgp.bio.psu.edu/tribedb/index.pl>], analysis pipelines, and original analysis methods to gain novel insights into the evolutionary history of genomes, gene families, and the Tree of Life. The successful candidate will be fluent in bioinformatics programming, including scripting languages and web development (Perl, and ideally R, MySQL, and php). This job will be filled as a level 3 or level 4, depending upon the successful candidate's education and experience. Minimum educational and work-related experience requirements are: Bachelor's degree in Bioinformatics (Master's degree preferred) plus four years of related experience or an equivalent combination of education and experience. This is a fixed-term appointment funded for one year from date of hire with excellent possibility of re-funding. Electronically apply on Job #F-29776 at < <http://www.psu.jobs> >www.psu.jobs. A complete application will include a Penn State employment application, a cover letter referencing this job number and describing experience and professional goals, and a curriculum vitae with contact information for three referees. Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

– Claude dePamphilis email: cwd3@psu.edu Professor of Biology Department of Biology and phone: 814-863-6412 (office) Huck Institutes of Life Sciences 814-863-6413 (lab) 405B Life Sciences Building fax: (814) 863-1357 Penn State University website: <http://www.fgp.huck.psu.edu/cwd/> University Park,

PA 16802 website2: <http://www.floralgenome.org/> website3: <http://chloroplast.cbio.psu.edu/> Claude dePamphilis <cwd3@psu.edu>

PuertoRico FieldResAssist

Field assistant for rhesus monkey research on Cayo Santiago, Puerto Rico.

We are looking for a volunteer to assist on a project examining kin recognition on a semi free-ranging rhesus macaque population on Cayo Santiago, Puerto Rico (see <http://ucm.rcm.upr.edu/cayosan.html>). The project is being undertaken in the Lab of Dr Anja Widig, Max Planck Institute for Evolutionary Anthropology, Leipzig (Germany) (see <http://www.eva.mpg.de/-pks/index.html>). The volunteer will work alongside Dr Dana Pfefferle (<http://www.dana-pfefferle.de>).

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

Carrying out playback experiments is a protracted and patience challenging task, including many hours of waiting for the correct situation. Thus you must be able to maintain a positive attitude. You also must be willing to work in a small team setting and have demonstrated a willingness to follow instructions. The ability to work in tropical conditions and the willingness to adapt to a foreign culture is needed. You also have to feel comfortable being far away from family and friends. Although the work can be demanding, being close to habituated primates is very rewarding and a great experience.

The language in our team is English. The successful candidate must have medical insurance, a valid IACUC certificate (www.citiprogram.org) and a TB-test from within the last six months.

There is NO financial support available for airfare, health insurance, housing and food.

Shared accommodation can often be found very cheaply

in Punta Santiago (e.g. \$200 per month).

To apply, candidates should email a brief cover letter outlining their interests, experience, and why they wish to undertake work on the project. They should attach a CV which includes at least contact details of one academic reference. Please only send email applications.

Term of Appointment: From 1st October till 20th December.

Application Deadline: Open till position is filled.

Contact Information: Dana Pfefferle danapfefferle@googlemail.com

danapfefferle@googlemail.com

StonyBrookU LabTech YeastRegulatoryEvolution

A Research Support Specialist position is available in the laboratory of Dr. Joshua Rest in the Department of Ecology and Evolution at Stony Brook University. We are an interdisciplinary team that combines experimental and computational approaches to study fundamental questions about the evolution of gene and protein regulatory systems.

Brief Description of Duties: Perform large-scale serial growth competitions in yeast.

* Perform large scale serial growth competitions, including regular serial dilutions, relative fluorescence measurements, and associated data collection. * Construct and validate yeast strains; design primers; transform strains. * Perform ancillary competition validation: flow cytometry; large-scale RNA and DNA isolation; pyrosequencing. * Data analysis and integration. * General lab maintenance.

Salary: \$34,975 - \$45,200 Required Qualifications: Bachelor's degree. Ability to demonstrate professional competence in research activities. Course work and laboratory experience with molecular biology protocols and equipment. Preferred Qualifications: Two years of laboratory experience either in yeast genetics or in high throughput biological analysis, such as cell culture or expression microarrays. For additional information on the Department or its activities, please visit <http://life.bio.sunysb.edu/ee/restlab/index.htm>. For more information about this position, or to apply online, please go to: <http://tinyurl.com/labtech> or <http://naples.cc.sunysb.edu/Admin/>

CampusJob.nsf/ebb5a78b9e8848868525659c0072eafe/-1b090b4ec1c469f1852575710062a1f4?OpenDocument
joshrest@gmail.com

Taipei MicrobialDiversity

Positions: Ecology, Microbial Diversity and Computational Genomics

The Biodiversity Research Center of the Academia Sinica (BRCAS, see homepage at <http://-biodiv.sinica.edu.tw/>), Taipei, Taiwan, invites applications for tenure track positions in terrestrial ecology, marine ecology, microbial diversity and computational biology. The rank is open, though junior scientists are preferred. Candidates with a research interest in ecology, microbial diversity, microbial genomics, or bioinformatics are encouraged to apply. Candidates with good postdoctoral research experience are preferred.

BRCAS is in an expansion mode, with many tenure-track openings. The center is strong in marine biodiversity and molecular and genomic evolution and has recently set up a sequencing core with one 454 and one Solexa machine. The center wishes to strengthen research in ecology (especially terrestrial ecology), microbial diversity and computational genomics. The positions will be open until filled; however, the first review will be conducted in the second week of June 1. An applicant should submit the names and e-mail addresses of three references along with CV (including a list of publications), 3-5 representative papers (pdf files), and a statement of past achievements and future research interests to Ms. Miao-Suey Lin (zomslin@gate.sinica.edu.tw).

wli@uchicago.edu

TexasAM CC LabCoordinator

Are you just finishing your Master's degree in Biology (or a related field) and looking for a job or know someone who is? We are looking for a broadly trained individual to serve as Laboratory Coordinator mainly for our intro bio labs who is interested in teaching

and willing to try new teaching methods, especially at a Hispanic-Serving Institution that is becoming a research intensive university.

Details can be found at: <http://www.sci.tamucc.edu/openpositions/biolab.html> .

Deb Overath

R. Deborah Overath, Ph.D. Assistant Professor of Biology Local Program Director Hispanic Leaders in Agriculture and the Environment Department of Life Sciences (ST 312) 6300 Ocean Drive, Unit 5800 Texas A&M - Corpus Christi Corpus Christi, TX 78412

Phone: (361) 825-2467 Fax: (361) 825-2742

“Overath, Deborah” <Deborah.Overath@tamucc.edu>

Texas Christian U Evolutionary Microbiology

We are initiating a job search for a tenure-track position in microbiology. The research area is open and we would hope the posting would appeal to many of the users of EvolDir.

Thanks for your time, Amanda

Microbiologist-Texas Christian University seeks a tenure-track Assistant Professor. The position is available Fall, 2009, but a Spring, 2010 start is also possible. Review of applicants will begin immediately and will continue until the position is filled. Responsibilities include participating in team-taught courses for Biology majors, teaching Microbiology, and conducting independent research. See www.bio.tcu.edu/microbiologist.htm for more information. Applicants should send a curriculum vita including a statement indicating teaching and research interests and experience, and should arrange to have three letters of recommendation sent to: Dr. Giri Akkaraju, Biology Department, Box 298930, Texas Christian University, Fort Worth, TX 76129. TCU is an EEO/AA employer.

Thanks,

Amanda

Amanda M. Hale Assistant Professor, Biology Dept. Texas Christian University 2800 S. University Dr. Room 432 Winton Scott Hall Fort Worth, TX 76129 office phone: 817-257-6182 fax: 817-257-6177 a.hale@tcu.edu <mailto:a.hale@tcu.edu>

<http://www.bio.tcu.edu/faculty/hale.htm> < <http://www.bio.tcu.edu/faculty/hale.htm> >

“Hale, Amanda” <a.hale@tcu.edu>

UAlaska Symbiosis

Position Title: Research Professional Plant-Microbe Interactions Institute of Arctic Biology, University of Alaska Fairbanks, AK USA

Move to the edge geographically and technologically! We are seeking a Research Professional to design, develop and optimize cutting-edge molecular methods in the last frontier - Alaska. This person will carry out independent efforts in support of the Plant-Microbe Interactions Research Focus Area of the EPSCoR Program at the University of Alaska (see <http://www.alaska.edu/epscor/>). The goal of the Plant-Microbe Interactions Research Focus Area is to better understand how mutualistic and pathogenic bacteria and fungi influence vegetation structure in Alaska under a changing climate. Emphases include ectomycorrhizal associations and biological nitrogen fixation. Participating faculty include Mary Beth Leigh, Christa Mulder, Sanjay Pyare, Roger Ruess, Lee Taylor and Jeffrey Welker. See <http://www.iab.uaf.edu/>, <http://www.uaa.alaska.edu/enri/> and <http://www.uas.alaska.edu/envs/index.html> . Qualifications include background in genetics, molecular biology and plant or microbial biology. Experience with DNA extraction, PCR, cloning, sequencing and sequence analysis are required, while familiarity with PLFA analyses or next-generation sequencing are desirable. The home location will be in the Institute of Arctic Biology at the University of Alaska, Fairbanks. Opportunities will be provided for participation in preparation of journal articles and grant proposals.

Requirements: A BS in Biology, Biochemistry, Microbiology or a related field is required. MS or PhD degrees are preferred.

Minimum salary: \$40,664 for 12 months Start Date: April-May-June 2009 Contact: fft@uaf.edu

To apply, go to www.uakjobs.com/applicants-Central?quickFind=66242 ltaylor@iab.alaska.edu ltaylor@iab.alaska.edu

UGroningen MarineEvolutionaryBiolChair

The Centre for Ecological and Evolutionary Studies (CEES) at the University of Groningen (The Netherlands) has a vacancy for a full professor in Marine Evolutionary Biology. The successful candidate is expected to build up a dynamic research programme that ideally combines observational and experimental approaches with a strong evolutionary perspective.

More detailed information can be obtained from: <http://www.rug.nl/> choose <job opportunities>

or directly:

<http://www.academictransfer.nl/vacaturebank/-zoeken/index.cfm?fuseaction=detail&vacature.id=-RFNZO6A6&startrow=1&welkesoort=-vacbank&orgid=00300&zijpad=0> suggested short title: Groningen.Marine Evolutionary Biology Chair

Regards. Leo

Prof. Dr. Leo W. Beukeboom Evolutionary Genetics Centre for Ecological and Evolutionary Studies University of Groningen Kerklaan 30 NL-9751 NN Haren P.O. Box 14 NL-9750 AA Haren The Netherlands Phone +31 50 363 8448 (direct) or 2092 (secr.) Fax +31 50 363 2348 Email l.w.beukeboom@rug.nl <http://www.rug.nl/biologie/evogen> Leo Beukeboom <l.w.Beukeboom@rug.nl>

ULiverpool 2ResTech ParasitePopulations

Two full-time research technician positions are available in the School of Biological Sciences, University of Liverpool, UK

Title: Assessing the stability of parasite communities through perturbation experiments

Two full-time research technician posts are available to join a project studying the parasite communities of small mammals (wood mice) in the wild. This is part of a NERC-funded grant led by Amy Pedersen,

Owen Petchey (University of Sheffield) and Andy Fenton (University of Liverpool), involving both fieldwork (small-mammal trapping) and laboratory assays.

Both posts are based within the Division of Population and Evolutionary Biology in the School of Biological Sciences, Liverpool, and will be responsible for conducting the small-mammal trapping at our field sites on the Wirral, Merseyside. We are looking for a Senior technician (Grade 6; £25,623 - £27,183) that has extensive experience with small-mammal trapping. The Graduate technician (Grade 5; £22,126 pa) will receive training in small-mammal trapping and techniques in parasitology. Opportunities will be available for both technicians to develop their research interests within this host- parasite system.

The Senior technician should have relevant experience and ideally hold a Home Office personal licence for handling small mammals. Both technicians will be required to undertake the majority of the intensive trapping on the project, and so should be familiar with organising and conducting fieldwork. Both technicians should hold valid UK driving licences. The posts are available for 3 years, starting in May 2009.

Closing date for receipt of applications is 20 March 2009.

For the Grade 6 Senior technician (Ref: S-569346/WWW) application and specific job description, please go to: http://www.liv.ac.uk/working/-job_vacancies/technical/S-569346.htm

For the Grade 5 Graduate technician (Ref: S-569345/WWW) application and specific job description, please go to: http://www.liv.ac.uk/working/job_vacancies/technical/S-569345.htm

For specific information about the project, please email Amy Pedersen (a.pedersen@sheffield.ac.uk) and/or Andy Fenton (a.fenton@liverpool.ac.uk).

— Amy B. Pedersen Royal Society Incoming Research Fellow Department of Animal and Plant Sciences University of Sheffield Alfred Denny Building Western Bank Sheffield S10 2TN UK

Email: a.pedersen@sheffield.ac.uk Office: +44(0) 114 222 4692 Lab: +44(0) 114 222 0060 Web:<http://www.shef.ac.uk/aps/staff/acadstaff/pedersen.html>
Amy Pedersen <a.pedersen@sheffield.ac.uk>

UOxford Tech Evolution

DEPARTMENT OF ZOOLOGY, UNIVERSITY OF OXFORD

Technician in Evolutionary Ecology & Entomology
Grade 3: starting salary £17,026

A Technician (Grade 3) is required for six months to cover maternity leave, to work on a BBSRC-funded project entitled 'Aphid secondary symbionts: from model system to crop pests'.

It has recently been shown that facultative bacterial (secondary) symbionts have a remarkably wide range of effects on the biology of their aphid hosts. These include increasing resistance to natural enemies, improved performance on certain host plants, and resistance to heat shock. We seek a technician to help explore this symbiosis. The project involves the experimental creation of novel aphid-symbiont combinations to investigate how host and bacterial genotypes interact to affect aphid fitness and how the symbiont may influence clonal competition and aphid population dynamics under different environmental conditions. This includes any possible effects of symbionts on indirect interactions between aphid species mediated by natural enemies.

You should have a strong interest in biology and enjoy working in a laboratory environment and as part of a team. You should have an aptitude for work where attention to detail and record keeping is critical. Ideally you should have experience working with insects in laboratories, and also with basic molecular genetic techniques.

This is a collaborative project involving the Universities of Oxford (Prof. Charles Godfray (charles.godfray@zoo.ox.ac.uk) and Dr. Margriet van Asch (Margriet.vanAsch@zoo.ox.ac.uk), University of York (Dr. Julia Ferrari) and Imperial College London (Dr. Frank van Veen). Informal enquiries about this post are welcome.

Further particulars and application forms can be downloaded from <http://www.zoo.ox.ac.uk/jobs/adverts/-at09012.pdf> or are available from the Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS, E-mail; recruit@zoo.ox.ac.uk The position is available in May 2009. Applications, enclosing a CV, covering letter and contact details of two referees, should be sent to the above address, quoting reference number AT09012. The closing date for applications is noon on 3 April 2009.

Margriet van Asch Dept. of Zoology University of Oxford Tinbergen Building South Parks Road OX1 3PS Oxford Phone: +44 1865 271253 Email: mar-

griet.vanasch@zoo.ox.ac.uk

UPuertoRico 2YearResTech InvertebrateCollection

Scientific Research Technician â UPRM Invertebrate Collection

A two-year full time position is available for a scientific research technician at the Department of Biology, University of Puerto Rico at Mayagüez (UPRM). The position plays a key role in a project aimed at reorganizing and digitizing the UPRM invertebrate collection. The chosen candidate will coordinate and perform curatorial activities such as specimen preservation and identification, specimen barcoding, georeferencing, databasing, and digital imaging. Prior experience with any of these tasks is advantageous, as is the ability to use biodiversity databases and web design applications. An undergraduate or advanced degree in invertebrate zoology is preferred; knowledge of English and Spanish or a willingness to learn is desirable.

The salary is adjusted to the UPRM pay scale and includes a full benefits package covering social security, health insurance, and a holiday bonus. The position is limited to U.S. citizens. To apply, please send a CV, names and contact information of two references, and letter of interest to Nico Franz, franz@uprm.edu. Applications will be reviewed immediately until the position is filled.

Nico M. Franz Department of Biology University of Puerto Rico PO Box 9012 Mayagüez, PR 00681

Phone: (787) 832-4040, ext. 3005 Fax: (787) 834-3673 E-mail: franz@uprm.edu Website: <http://academic.uprm.edu/~franz/> Nico Franz <franz@uprm.edu>

UppsalaU EvolutionaryGeneticsGenomics

Two faculty positions in EVOLUTIONARY GENETICS AND GENOMICS

at the Evolutionary Biology Centre, Uppsala Univer-

sity, Sweden

One as Assistant Professor in Evolutionary Genetics and Genomics http://www.personalavd.uu.se/-ledigaplatser/471foass_eng.html One as tenured Assistant Professor in Evolutionary Genomics http://www.personalavd.uu.se/ledigaplatser/-472bitrlekt_eng.html The positions are within the Department of Evolutionary Biology (<http://www.egs.uu.se/evbiol/index.html>), which is situated in the Evolutionary Biology Centre in central Uppsala. The Department includes the lab groups of Hans Ellegren, Anders Gotherstrom, Hanna Johannesson, Mattias Jakobsson and Jennifer Leonard. The working atmosphere is international with English as working language. The Evolutionary Biology Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, with research programs including ecology, systematics, genetics, genomics, and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 40 minutes with train from Stockholm.

See the links to the full advertisements given above for further information including how to apply. Deadline is April 20. Information inquires can be made to Professor Hans Ellegren (hans.ellegren@ebc.uu.se).

Hans Ellegren <hans.ellegren@ebc.uu.se>

UppsalaU EvolutionaryPlantEcol

Associate Professor/Senior Lecturer in Evolutionary Plant Ecology

(with the possibility of being employed as Professor)

Department of Ecology and Evolution, Evolutionary Biology Centre, Uppsala University

The position includes teaching at graduate and undergraduate level, research and some administration. The holder of the position is expected to contribute actively to applications for external research grants and to the development of the research and teaching of the department.

In ranking eligible candidates, equal importance will be given to scientific and teaching skills. When judging scientific proficiency special importance will be given to research qualifications within population ecology and

evolutionary plant ecology.

More detailed information about the position and information about how to apply can be found <http://www.personalavd.uu.se/ledigaplatser/engindex.html>

Closing date for application is May 6, 2009

For further information about the position, please contact Professor Jon Agren telephone +46-(0)18-471 2860 or email Jon.Agren@ebc.uu.se

The Evolutionary Biology Centre of Uppsala University offers a vibrant research environment and bridges a broad range of disciplines in the biological sciences. Information about the Evolutionary Biology Centre and the Department of Ecology and Evolution can be found at www.ebc.uu.se

Jon Ågren Plant Ecology/Dept of Ecology and Evolution Evolutionary Biology Centre Uppsala University Villavägen 14 SE-752 36 Uppsala Sweden

Phone: +46-18 471 2860 Telefon: 018-471 2860

Jon Ågren <jon.agren@ebc.uu.se>

UppsalaU StatisticalGenomics

Dear members of EvolDir,

Even though the following job announcement is for a post-doc position, it is actually considered as an open rank position and more experienced researchers are also invited to apply for it.

The research area is statistical genomics, dealing with the theoretical and practical issues related to the analysis of SNP genotypes (obtained for example from Illumina Bovine 50K Bead Chip) from several breeds of dairy cattle populations from all around the world.

Best regards,

Hossein Jorjani, PhD

POSITION ANNOUNCEMENT Across Country Genomic evaluation, Post-doc position at the Interbull Centre

JOB DESCRIPTION A growing number of Interbull member countries participating in international genetic evaluations are using genomic information in the national genetic evaluations of dairy cattle populations. Thus, Interbull Centre has started to address issues related to the 'integration of genomic evaluations into the international genetic evaluations'. A network of inter-

nationally renowned scientists is already supporting Interbull Centre on these issues. In order to intensify and speed up Interbull Centre's effort in this area a post-doc position is announced for a period of two years.

The area of research includes validation of national genomic evaluations and how the information on conventional and genomic predicted genetic merits should be combined with each other in an international evaluation.

QUALIFICATIONS Candidates should have a Ph.D. in animal breeding or related fields (e.g. quantitative genetics, statistical genetics). A background in genetic evaluation is essential. Candidates should have demonstrated evidence of good scientific capabilities, including strong analytical, biometrical and computational skills, and a willingness to work collaboratively. The working language at the Interbull Centre is English.

INTERBULL BACKGROUND Interbull, a permanent sub-committee of the International Committee for Animal Recording, is a professional organization offering international genetic evaluations and other services to its members in more than 40 countries worldwide. Interbull plans are realized at its operational unit, the Interbull Centre, based under contract at the Department of Animal Breeding and Genetics (DABG), Swedish University of Agricultural Sciences (SLU), Uppsala. At DABG, more than 60 researchers and PhD students are involved in quantitative and molecular genetics research, including genomic evaluation.

LOCATION Interbull Centre, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden. Uppsala is situated 30 minutes north of Arlanda international airport and 45 minutes north of Stockholm, the capital of Sweden. It is one of the major university cities in Sweden and offers an attractive mix of history, culture, modern hi-tech industry and a Nordic nature.

STARTING TIME We expect the holder of the position to start as soon as possible.

APPLICATION We welcome your application marked with ref no 559/09. Applicants should submit a complete curriculum vitae, and two names and contact information of personal references, to the Registrar of SLU, P.O. Box 7070, S-750 07 Uppsala, Sweden or registrar@slu.se no later than March 31, 2009.

For additional information about the position you can contact João Dürr or Dr. Hossein Jorjani (Hossein.jorjani@hgen.slu.se)

You can also see the job announcement in the following link:

<http://personal.slu.se//LEDANS/2009-559.pdf> Hossein Jorjani, Associate Professor

Interbull Centre Department of Animal Breeding & Genetics Swedish University of Agricultural Sciences

Box 7023 S - 75007 Uppsala Sweden

Phone : + 46 (0)18 671964 Fax : + 46 (0)18 672648

e-mail: hossein.jorjani@hgen.slu.se

URL : www.hgen.slu.se : www.interbull.org

UVirginia AssistantProfessor

We are initiating a job search, and although we've entitled the position "Ecologist," the definition of research areas are broad enough that we would hope to attract applications from many of the users of EvolDir.

David E. Carr Research Associate Professor, Environmental Sciences Director, Blandy Experimental Farm

Date: 27 February 2009

Institution: University of Virginia

Position: Research Assistant Professor in Ecology

The University of Virginia's Blandy Experimental Farm seeks to hire an Ecologist at the Research Assistant Professor level.

Academic appointment is within the University's Department of Environmental Sciences, and the position is based at Blandy, an environmental field station located in Virginia's Shenandoah Valley. The position's distribution is 50% research and 50% administration. The successful candidate is expected to establish an extramurally funded research program, attract and mentor successful graduate students, and mentor undergraduate researchers. Area of research is open but should complement existing strengths at Blandy and strengthen connections with the Departments of Environmental Sciences and Biology. Possibilities include (but are not limited to) invasive species ecology, restoration ecology, landscape ecology, and agroecology. Administrative responsibilities include oversight of Blandy's undergraduate and graduate research programs and working with other faculty to make Blandy a leader in environmental research and outreach.

Ph.D. in biology, environmental science, or a closely related discipline is required. Postdoctoral experience is preferred. Applicants must provide evidence

of high-quality research. For more detailed information about the position refer to www.virginia.edu/blandy-ecologist.htm. This is a non-tenure track position with an initial three year contract, renewable pending successful review.

To apply, please complete a Candidate Profile on-line through Jobs@UVA (<https://jobs.virginia.edu>) and attach a cover letter briefly highlighting your research experience and potential as a research administrator, curriculum vitae, and a statement of research interests. Search for Posting Number 0603195. Please arrange for three letters of recommendation to be sent to Dr. David Carr, Search Committee Chair (dec5z@virginia.edu). Review of applications will begin on March 31, 2009, however the position will remain open until filled.

Questions regarding the position can be sent to Dr. Carr, and questions regarding the candidate profile process or Jobs@UVA should be directed to Judy Masi (jmasi@virginia.edu).

The University of Virginia is an equal opportunity/affirmative action employer. Women and members of underrepresented groups are strongly encouraged to apply.

“David E. Carr” <dec5z@virginia.edu>

ZoolSoc London ResTech WaspGenomics

Job: Research technician on wasp behaviour and genomics project

Institute of Zoology Zoological Society of London

Research Technician Evolutionary Biology/Behavioural Ecology

15 months contract Salary £20,525 p.a. pro rata (including London weighting) Depending on relevant experience

The Institute of Zoology, based at Regents Park, London, is the research arm of the Zoological Society of London. The Institute is funded by HEFCE through the University of Cambridge and has excellent research facilities.

We would like to appoint a Research Technician for 15 months, starting 1st May 2009, to assist with research on social behaviour and evolution. The successful candidate will provide laboratory and field support for a NERC funded project on the evolution of social behaviour in primitively eusocial paper wasps. The position will involve use of a range of techniques in molecular biology, including RNA and DNA purification, microsatellite analyses and gene expression analyses (qPCR). The work will also involve 4 months field work at the Smithsonian Tropical Research Institute in Panama, using radio-tagging technology to study wasp behaviour.

Candidates should have a BSc or equivalent in biological sciences and excellent skills in molecular biology. Experience working with DNA, RNA and quantitative PCR is desired. Fieldwork experience involving insects and/or behavioural observations would be an advantage, but is not essential as full training will be provided.

For further information, please see <http://www.zoo.cam.ac.uk/ioz/> or contact HR Dept., ZSL, Regents Park, London NW1 4RY. Informal enquiries should be directed to Dr Seirian Sumner (Seirian.Sumner@ioz.ac.uk).

Interested candidates should email a cover letter and their CV, together with the names and addresses of two academic referees to Human Resources Department (HR@zsl.org) by 20th March 2009. Shortlisted applicants will be invited for interview in late March.

Seirian Sumner <seirian.sumner@gmail.com>

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AFLP bands extraction method choice

Dear all,

I am currently planning to do an AFLP genome scan with two closely related species, in order to detect regions of their genome that display a high level of divergence (see for ex. Wood et al. Mol Ecol 2008). The original AFLP genome scan will be performed on an ABI 3730 sequencer. However since we would like to further characterize the outlier loci, we will need to run again the selective amplification and to load it into a gel, then excise bands of interest, reamplify and clone them. This will probably be done with many primer pairs.

We never performed that in our lab, and I am wondering what is the most robust/efficient/precise/safe/quick way to do it. We cannot do radiolabelling in our lab. As far as I know, people most of the time use one of the followings:

- Silver stained acrylamide gel. Allows precise electrophoresis and to keep the gel for later use. Maybe quite labour intensive if many gels have to be run?
- Precast Spreadex (Elchrom) gels. Seems precise and safe, but one needs to cut the bands with a UV table within a few minutes. Also as far as I know the maximum length of a spreadex gel is 8 cm, and this seems small to me to precisely excise a band.
- Nusieve agarose. I am not sure this is realistic. Maybe two steps

electrophoresis: 1/ the whole amplification, cut around the band of interest, reamplify then 2/ load this second amplification with fewer bands into an adequately concentrated agarose gel.

Does someone have experience with that? Can anyone suggest other options?

Any help/advice greatly appreciated.

Matthieu

PS: We have currently no vertical acrylamide electrophoresis apparatus but this can be purchased.

Matthieu Boulesteix Postdoctoral Research Associate
Imperial College London Silwood Park Campus Buckhurst Road, Ascot, Berkshire, SL5 7PY, UK

Tel +44 (0)20 7594 2306 m.boulesteix AT imperial
DOT ac DOT uk

A Keast passing

Dr. Allen Keast passed away yesterday, 8 March, at about noon, in Kingston General Hospital where he was admitted about three weeks ago due to an infection in his heart. He was in his 87th year.

Allen was born November 15, 1922 in Sydney, New South Wales, Australia. He was an avid naturalist from his earliest boyhood, a passion that he pursued in university and throughout his career. Following high

school, Allen served in the Australian Army, being stationed for some 20 months in New Guinea. Upon completion of his military service, Allen attended the University of Sydney from 1946 to 1950 when he was awarded a B.Sc. with first class Honours. He continued his education at Sydney, while also holding a post as Assistant curator of Birds, Reptiles and Amphibians at the Australian Museum, and earned an M.Sc. degree in 1952. In 1953 Allen was awarded the Peter Brooks Saltonstall Scholarship at Harvard for his PhD studies. At Harvard, Allen was the first graduate student supervised by one of the leading evolutionary biologists of our time, Professor Ernst Mayr. He also worked with the renowned comparative anatomist, Alfred Sherwood Romer. After earning his PhD in 1955, Allen became Curator of Birds, Reptiles and Amphibians at the Australian Museum in Sydney, a position he held from 1955 to 1960. He then held a Visiting Researcher position at the Edward Grey Institute at Oxford University, as well as an appointment in 1962 as Visiting Biologist in South African National Parks, Pretoria, South Africa.

Allen joined the Biology Department at Queen's University in Kingston, Ontario, Canada in 1962, as Assistant Professor and quickly moved up through the ranks to Full Professor, a position that he held until his retirement in 1989.

Allen had a very strong interest in Australian natural history and he was also keenly interested in functional morphology and the role of evolution in shaping adaptations and hence community structure. He recognized that the fauna of the very isolated island-continent of Australia was very different from that of the southern continents of Africa and South America and this led Allen to produce major works on evolution in the Southern continents. Upon coming to Queen's, and finding himself in Canada, Allen was faced with a different biota in the cold-dominated, highly seasonal north temperate region, and he saw an opportunity to study biogeography and the forces molding community structure on a much smaller scale ' that of the fish fauna in the isolated lakes of southern Ontario. He established a field program at the Queen's University Biological Station (QUBS) at Lake Opinicon, and for more than 30 years examined comparative morphology and competition in those fish communities.

Through his career at Queen's, Allen trained many undergraduates and at least 27 graduate students. He published at least 50 primary research papers, 60 book and conference chapters and 7 books on biogeography. His work served to draw the attention of the world's ecologists and evolutionary biologists to the unique biogeography of Australia. In the Canadian lakes, his second field of research on the ecology of fish communi-

ties, he was a leader in demonstrating that the ecology of fishes changes dramatically as they grow. He recognized and took advantage of the unique opportunity that lakes provide ' that of a suite of organisms locked in isolation in a common environment, often competing for common resources. Over the 25 years he studied fish communities in Eastern Ontario's myriad lakes, especially at the Queen's University Biological Station, he produced another 30 scientific papers in this field.

One of Allen's great strengths was to synthesize. During his career, he edited or co-edited numerous volumes on evolution, biogeography and the relationships of biota. One of his more significant works was a 1980 volume on "Migrant Birds in the Neotropics" co-edited with Eugene Morton, that focused attention on issues of conservation for species that inhabit multiple regions throughout their life cycle.

As Professor Emeritus following his retirement, Allen maintained an active interest in field studies, and especially in writing. He maintained an active interest in the department, and especially in the Biology Station, right up until his death. He will be greatly missed by many friends and colleagues.

Allen was predeceased by a younger brother, John. He is survived by his sister, Janet Baker, who with her husband, Sid, lives near Seattle.

His funeral will be held this Friday March 13, 2009 in Kingston, Ontario, Canada.

For further information please contact Sandy Berg at sberg@kos.net

Sue Bertram <Sue_Bertram@carleton.ca>

Analyzing GO terms

Hello List,

I have a question concerning the evolutionary analysis of different gene sets from the same organism using GO terms.

Here is what I want to do: I have a tree over which I trace gene content, so a more basal node will have only a subset of the genes a terminal node (species A) has. The analysis I am looking for should compare the different nodes in respect to their genes and give information on how the genes differ in function/role (if at all). The expectation is that genes at a more basal node will overall fall into a different functional category

as those genes gained towards the tip (Species A).

GO terms are the most straight-forward data I can get my hands on, so I was hoping to find a way to use them as a basis for the analysis. However, given that GO terms are a bit of a mess (not strictly hierarchical, to begin with - and several GO terms / gene), I am looking for examples of how to do this. GO Slim was one thing I looked into, but I couldn't find really good tools for that.

To put it a little different - I need to bin genes into discrete categories based on GO terms in order to compare sets of genes so that I can check whether they differ in function. On top of that, the sets of genes are nested - but that's a minor detail and probably not entirely relevant to the original question.

Any advice (programs, publications, etc) would be greatly appreciated!

Cheers, Marc

-

Marc P. Hoepfner PhD student Department of Molecular Biology and Functional Genomics Stockholm University, 10691 Stockholm, Sweden

marc.hoepfner@molbio.su.se Tel: +46 (0)8 - 164195

Marc Höpfner <marc.hoepfner@molbio.su.se>

Barrier 2 2 software

Hi all, I am having difficulty downloading Franz Manni's free program Barrier 2.2 from the website (<http://www.ecoanthropologie.cnrs.fr/spip.php?article91>). When I click on the download link, I am redirected to another page that doesn't have anything to download. I really would like to use this software soon. Would anyone who already has the program and accompanying files be willing to email them to me? I would really appreciate it!

Thanks in advance,

Ivan

Ivan C. Phillipsen Department of Zoology Oregon State University 3029 Cordley Hall Corvallis, OR 97331-2914 philliiv@science.oregonstate.edu

phillipsen@gmail.com

Barrier 2 2 software answers

Hi all, Recently I asked if anyone could send me a copy of Franz Manni's Barrier 2.2 program. I had also emailed Franz himself. He responded and said that the website's (<http://www.ecoanthropologie.cnrs.fr/spip.php?article91>) < <http://www.ecoanthropologie.cnrs.fr/spip.php?article91> > download link would be up and running again soon. In the meantime, he said to email him directly: manni@mnhn.fr.

Thanks to those of you who responded.

Ivan

Ivan C. Phillipsen Department of Zoology Oregon State University 3029 Cordley Hall Corvallis, OR 97331-2914 philliiv@science.oregonstate.edu

phillipsen@gmail.com

BigDye dilutions for ABI310 answers

Dear Evoldir members,

Here are the replies I received to my original posting: "I'd be grateful to anyone who could tell me about their experiences of diluting BigDye for the ABI 310 capillary sequencer. I'd also be interested to hear from anyone who has tried the dLUTE SEQ DNA Sequencing BigDye Dilution Reagent on the ABI 3130."

For those who asked, information about the dLUTE SEQ DNA sequencing reagent can be found at http://www.nucleics.com/DNA_sequencing_tools/-DNA-sequencing-dlute-seq.html Thanks,

Paul

-

Dear Dr. Bloor, While I can't address diluting bigdye, I can say that I've used what we call 'quarter reactions.' This saves us considerable reagents. Taken from my institute's Nucleic Acid facility:

"1/4 Reaction: For each reaction add the following reagents to individual tubes:

Terminator Ready Reaction mix (Big Dye) 2 ul Big Dye Sequencing Buffer 5X 1 ul Primer 1ul (3.2 pmol) Template See table for Template guidelines Water To 11 ul

Total volume 11 ul”

http://mercury.bio.uaf.edu/core/protocols/_cyclesequencingrxn.html This has worked very well for us, and I reliably get clear sequences.

I hope this saves you as much time and money as it has saved us.

Best Wishes, Kevin Colson

—

Hi Paul,

You can dilute the big dye to 1/8 reactions routinely (compared to ABI protocols) and sometimes you can get away with 1/16, but it also depends on amount of template and length of your PCR product. We did this with a 310, then 3100, and now 3130. It is very routinely done.

I haven't tried the reagent that you mention below and I am interested to find out what you hear. Who makes that reagent?

thanks, Sarah

—

BigDye v3.1

my sequencing reactions are

1ul BigDye 1ul 3.33uM primer 1ul PCR product (EXO-SAP clean) 7ul 1x BigDye buffer

—

Hi Paul,

I have used up to 1/8 dilution of Big Dye terminators on various ABI platforms. Most commonly I use 0.5 ul in 10 ul reaction. Never had a problem with diluted Big Dye. ABI want us to use more because it's so damn expensive! Some people also use home-made buffer rather than shelling out for their original stock. Of course ABI claim the reactions don't work as well but big facilities make their own on a regular basis.

Good luck,

Birgit

—

Hi,

I use 1 to 0.3 uL big dye per sequencing reaction (10uL). Maybe one can go less.

I have tried the dLUTE kit with no success. I only

tried it twice but neither time did I get any results and I gave up. Because it that kit differs at every step (has its own precipitation, for example) troubleshooting will require commitment. Maybe it is worth it.

Good luck,

Kathryn

—

I always use a 1/8 dilution (0.5 ul Ready Reaction mix in a 10 ul reaction, run on a 3130xl sequencer if that makes a difference), with good results. I don't think going above 1/4 improves things much (though I admit I haven't done many controlled experiments). There are people who use 1/16 or less, but the few times I've tried it, I've had poor results. I think your PCR has to be extremely clean, and the amounts of primer and template DNA exactly right, for that to work.

The full recipe I use per reaction is 0.5 ul BigDye, 1.8 ul 5x buffer, 2.4 ul water, 0.3 ul primer (10 uM), 5 ul template+water (ratio depending on template concentration).

Karl

— Dear Paul,

In my previous lab, we successfully used 0.5 ul BD/10 ul reaction. I've attached my excel template that calculates the master mix with the appropriate amount of dilution buffer (2nd sheet also has the template amounts we used).

Given the ridiculously high price of the dilution buffer from ABI, I asked for recipes on evoldir a few years back and have attached the answers I got. We ended up purchasing the buffer from Teknova, as recommended by Rosanna Giordano (see product numbers in the .doc file) you get a huge amount for ~\$40 and it worked great.

Good luck! Leslie

—

I have no experience with the 310, but with the 37030xl. But i can say that 0.5 ul in a 10ul reactionm works just fine. Our reactions contain 5.9 ul ddH2O, 2 ul 2x seq buffer (we make our own), 0.6 ul primer (10 nmol), 0.5 ul BigDye, 1 ul PCR (SAP/EXO cleaned and undiluted). This works in 95% of situations. hope this helps –mark

—

I've gotten good results (just as good as at full strength) using 1/4X and 1/8X dilutions. I got the idea from Travis Glenn (who probably has recipes at his website). I use a 310.

—
 We did some tests and used to dilute ours to $\frac{1}{4}$ what is suggested by ABI, and that worked fine. I'd be curious to hear what other people have found. Camille
 —

Dear Paul,

>From my perspective, the 310 should not be very different from the other capillary sequencers. However, I used it very long time ago.

The BigDye dilution will depend mainly on the sequencing cleanup

— / —

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>

BlockingSolution DNAHybridization

Dear all,

we have a problem with hybridization of nucleic acids (or rather bacteria) on membranes using fluorescin-labelled probes.

We have formerly used a ready-made solution for hybridization and blocking called "Liquid block" produced by Amersham. Obviously the company does not produce this any longer and is not willing to tell what it contained (Tris, Casein and probably a few other things).

Could anyone who has also run out of their stocks of "Liquid block" are now using?

Thanks

Heike Feldhaar

Dr. Heike Feldhaar Behavioural Biology University of Osnabrück Barbarastr. 11 (Room 35/145b) D-49076 Osnabrück Germany

phone: +49 (0)541 969 3805 fax: +49 (0)541 969 2862

e-mail: feldhaar@biologie.uni-osnabrueck.de

"Feldhaar, Heike" <Heike.Feldhaar@Biologie.Uni-Osnabrueck.DE>

Bootstrapping PHIST

Dear Colleagues,

We would like to test whether 3 pairwise PHIST estimates, and 3 Pi estimates are significantly different from one another (single locus - mtDNA HVR). I understand one method of doing so is by bootstrapping. Is this the preferable method, and does anyone know of a program that would automate these calculations? (Arelquin and FSTAT would appear to require data from at least 4-6 loci). Alternatively, instructions for doing this 'by hand' would be greatly appreciated.

Thanks very much, Mark de Bruyn

Mark de Bruyn <markus.debruyn@gmail.com>

Collaborator needed

Insect neurobiologist needed for collaboration on a project involving sound production in cicadas. Must have familiarity with auchennorhynchan nervous systems. Project will involve making live preparations of cicada specimens such that they can be electrically stimulated to produce sound. Must be able to provide own equipment (electrodes, wave generator, etc.). Location of project to be determined (but must occur within U.S.), and may be conducted in collaborator's facilities, depending on the logistics involved. We will pay expenses and a stipend, and collaborator will be an author on any papers resulting from the research. Please send resume and a brief letter outlining your experience and qualifications for this work to the address below by 15 March 2009:

Dr. John Cooley Yale University Department of Ecology and Evolutionary Biology Osborn Memorial Laboratories 165 Prospect Street New Haven, CT 06520-8106

tel: (203) 432-7214 email: john.cooley@yale.edu home page: <http://magicicada.org/cooley/contact.html> cicada@magicicada.org

[http://biology.ucsd.edu/labs/markow/
/stockcenter.ucsd.edu](http://biology.ucsd.edu/labs/markow/stockcenter.ucsd.edu) <http://->
Therese Markow
<tmarkow@ucsd.edu>

Crayfish micros

Dear Evoldir readers,

I am looking for microsatellite markers that may amplify in white-clawed crayfish (*Austropotamobius palipes*) and would be very interested to hear from anyone who has been or is currently working on microsatellite studies in crayfish species, or who has done any cross-amplification of microsatellite markers amongst different crayfish species.

Jim Groombridge

Dr. Jim Groombridge Senior Lecturer in Biodiversity Conservation Durrell Institute of Conservation & Ecology University of Kent Canterbury Kent CT2 7NZ, UK Email: J.Groombridge@kent.ac.uk Website:<http://www.kent.ac.uk/anthropology/dice/-dicestaff/jimg.html> J.Groombridge@kent.ac.uk

Dmelanogaster Dsimulans strains

The San Diego Species Stock Center <https://stockcenter.ucsd.edu/> has obtained new isofemale strains of *D. melanogaster* and *D. simulans* from Africa and Mexico. These Isofemale lines are available until July 1st 2009:

Drosophila simulans: (36) 33-isofemale lines from Masiaca, Sonora (near the border with Sinaloa), Mexico (2009) 3-isofemale lines from Lujeri, Malawi (2009).

Drosophila melanogaster: (8) 7-isofemale lines from Masiaca, Sonora (near the border with Sinaloa), Mexico (2009) 1-isofemale line from Lujeri, Malawi (2009). Please the stock center directly if you are interested in purchasing any of these lines.

Therese Ann Markow, Professor Amylin Chair in Life Sciences Section of Ecology Behavior and Evolution Division of Biological Sciences Muir Biology Building 2215 9500 Gilman Drive University of California at San Diego La Jolla, CA 92093-0116

Email: tmarkow at ucsd.edu Phone: (858) 246 0095 Laboratory: (858) 246 0402 FAX:(858) 534-7108

Freezers Revco vs Sanyo

I am in need of a new -80. I have always used Revco, but that is because that's what I have experience with. Does anyone have any experience with Revco vs Sanyo -80 Freezers? Thanks Paul

Dr. Paul H. Barber Department of Ecology and Evolutionary Biology 621 Charles E. Young Dr. South University of California Los Angeles Los Angeles, CA 90095 Phone: 310-794-5349 Fax: 310-206-3987 <http://www.eeb.ucla.edu/Faculty/Barber> The Diversity Project: <http://www.eeb.ucla.edu/Faculty/-Barber/Intro.htm> Coral Triangle PIRE Project: <http://sci.edu.edu/impa/ctpire.html> Paul Barber <paulbarber@ucla.edu>

Lobelia samples

I am seeking samples of *Lobelia* species, especially *L. dortmanna* (North American or European) and *L. kalmii*, for a study of genetic variation within and among populations. Ideally, I would like samples from 5 - 10 individuals per population but I would gladly accept smaller samples, and I would be happy with either seed or leaf material. If you have access to materials that you would be willing to share, please contact me at benmontg@indiana.edu to arrange details. Any help would be appreciated! Regards, Ben Montgomery Indiana University

benmontg@indiana.edu benmontg@indiana.edu

Microsats amplification

Hi,

We've encountered a strange problem with fluorescently labeled microsat markers in a gastropod - all are amplifying well (and produce distinct bands on agarose gels) but when we genotype them on our sequencer, we get extremely weak (in most cases unscorable) peaks. This problem is taxon-specific: in a fish that we run along as a control, we get PCR products with approximately the same concentration, but the peaks are easily scorable, so there doesn't seem to be anything wrong with our reagents.

Changing the number of cycles (we've tried between 30 and 40) and/or salt concentration (2.5 - 6 mM) doesn't solve it.

Perhaps someone in this forum has come across the same problem?

Thanks for any suggestions, Peter

Peter.Teske@bio.mq.edu.au

Dr Peter R. Teske Postdoctoral Researcher Molecular Ecology Lab Dept. of Biological Sciences, E8C Macquarie University Sydney, NSW 2109 Australia Phone: +61 2 9850 8203 Fax: +61 2 9850 8245 E-mail: Peter.Teske@bio.mq.edu.au Website: <http://www.bio.mq.edu.au/molecularecology/people.htm> Publications: http://www.ru.ac.za/academic/departments/botany_research/peter/ Peter.Teske@bio.mq.edu.au Peter.Teske@bio.mq.edu.au

NESCent Biodiversity DataCenter

*** Please disseminate widely to students at your institution ***

CYBERINFRASTRUCTURE SUMMER TRAINEESHIPS 2009

VIRTUAL DATA CENTER FOR BIODIVERSITY, EARTH, ECOLOGICAL, AND EVOLUTIONARY SCIENCE DATA

http://hackathon.nescent.org/-Cyberinfrastructure_Summer_Traineeships_2009

Summer traineeships are available for up to four students and postdocs interested in informatics as applied to scientific data ranging from the fields of biodiversity, ecology, and evolutionary biology. The program provides a unique opportunity for undergraduate, masters, and PhD students as well as postdocs to obtain hands-on experience writing and

extending open-source software as part of a distributed collaborative software development team building a Virtual Data Center (VDC) that includes major data and metadata repositories in those fields.

Trainees accepted into the program will receive a stipend (\$4,500), and with the exception of attending one meeting near the beginning and one near the end of the 3-month program period may work from their home, or home institution. Travel costs incurred in connection with the meetings will be reimbursed. Each student will have at least one dedicated mentor to show them the ropes and help them complete their project.

Initial project ideas are listed on the website. These range from validation of metadata and identifier resolution, to supporting LSID and semantic-web compliant PURLs for digital data objects, to implementing modern web-service APIs, to cataloging the diversity of metadata schemas. The project ideas are flexible and can be adjusted in scope to match the skills of the student. We also welcome novel project ideas that dovetail with student interests.

The traineeships are supported by a National Science Foundation (NSF) grant to a consortium of major repositories for biodiversity, earth and environmental, ecological, and evolutionary science. The consortium includes the LTER Network Office, the U.S. Geological Survey, NASA and Oak Ridge National Laboratory, the Global Biodiversity Information Facility (GBIF), the National Evolutionary Synthesis Center (NESCent), and the National Center for Ecological Analysis and Synthesis (NCEAS). It aims to develop the cyberinfrastructure and technologies necessary to build a Virtual Data Center (VDC) based on a network of existing and new physical repositories ("nodes") that interoperate using open standards and protocols. The network will enable discovery of as well as open, stable, and secure access to data in any of its member nodes.

TO APPLY: Students apply online. Instructions for applying are at the website (see "When you apply"), along with program rules and eligibility requirements. The 15-day application period for students opens on Monday March 30th and runs through Monday, April 13th, 2009.

INQUIRIES: `vdc-twg {at} ecoinformatics {dot} org`. We strongly encourage all interested students to get in touch with us with their ideas as early as possible.

Cyberinfrastructure Traineeships Website: http://hackathon.nescent.org/-Cyberinfrastructure_Summer_Traineeships_2009

2009 NESCent Phyloinformatics Summer of Code (NESCent's participation in the Google

Summer of Code; managed separately; postdocs not eligible; ***student application period ends April 3rd***) http://hackathon.nescent.net/-Phyloinformatics_Summer_of_Code_2009 To sign up for quarterly NESCent newsletters: <http://www.nescent.org/about/contact.php> Todd Vision and Hilmar Lapp National Evolutionary Synthesis Center <http://nescent.org>

NESCent Coding

*** This is a reminder about the student application deadline. *** Please disseminate widely to students at your institution. ***

PHYLOINFORMATICS SUMMER OF CODE 2009 - STUDENT APPLICATION DEADLINE IS APRIL 3

http://hackathon.nescent.org/-Phyloinformatics_Summer_of_Code_2009 The Phyloinformatics Summer of Code program provides a unique opportunity for undergraduate, masters, and PhD students to obtain hands-on experience writing and extending open-source software for evolutionary informatics under the mentorship of experienced developers from around the world. The program is the participation of the US National Evolutionary Synthesis Center (NESCent) as a mentoring organization in the Google Summer of Code(tm) (<http://code.google.com/soc/>).

Students in the program will receive a stipend from Google (and a T- shirt solely available to successful participants), and may work from their home, or home institution, for the duration of the 3 month program. Each student will have at least one dedicated mentor to show them the ropes and help them complete their project.

NESCent is particularly targeting students interested in both evolutionary biology and software development. Project ideas are listed on the website and range from hardware acceleration for phylogenetic inference, to support for phyloinformatics standards within the BioPerl and BioRuby toolkits, to alignment of next-gen sequencing data, to ontology term markup for biocuration, to semantic interoperability of web-services, to 3D-printing of phylogenies. All project ideas are flexible and many can be adjusted in scope to match the skills of the student. We also welcome novel project ideas that dovetail with student interests.

TO APPLY: Instructions are at the website (see "When

you apply"). You can find GSoC program rules and eligibility requirements at <http://socghop.appspot.com>. ***The 12-day application period for students ends on Friday, April 3rd, 2009, at 19:00 UTC (3pm EDT, 12pm PDT).***

INQUIRIES: phylosoc@nescent.org. We strongly encourage all interested students to get in touch with us with their ideas as early as possible.

2009 NESCent Phyloinformatics Summer of Code: http://hackathon.nescent.net/-Phyloinformatics_Summer_of_Code_2009 Google Summer of Code FAQ: <http://socghop.appspot.com/document/show/program/google/gsoc2009/faqs> Cyberinfrastructure Traineeships (managed separately from GSoC; postdocs also eligible): http://hackathon.nescent.org/-Cyberinfrastructure_Summer_Traineeships_2009

To sign up for quarterly NESCent newsletters: <http://www.nescent.org/about/contact.php> Todd Vision and Hilmar Lapp National Evolutionary Synthesis Center <http://nescent.org> hlapp@nescent.org

Nst Gst phylogeographic signature

Hi all,

I'm trying to use the approach suggested in SPAGeDi 1.2 (O. Hardy and X. Vekemans 2007) to test for the existence of a significant phylogeographic signal, using mtDNA sequence data. However there is an issue that is not entirely clear to me: in cases when a $Nst > Gst > 0$ but the slope of pairwise Nst vs geographic distance is not significant, what could be plausible explanations? Can anyone give me any suggestions about this issue or can suggest some paper, book, that could be of help if further questions or doubts storm me?

many thanks

Marco Carriso

Univ. of Rome La Sapienza Italy Dep. Plant Biol. P.le Aldo Moro 5

marcocarriso@yahoo.it

Qiagen gel extractions kit

Dear Colleagues,

About a year ago I posted a message about problems with gel purifications (low yields and absorbance around 230 nm on Nanodrop). We never resolved the problem until a colleague has just been in touch with Qiagen again. Now they admit that they increased the salt concentration in the QG buffer and recommend to increase the incubation time with PE to aid with the salt removal. My colleague change to the Promega kit and gets good results! If you still have Qiagen kit sitting around and encounter the same problem my suggestion is to increase the incubation period with PE and maybe also do 2 washes.

I would be interested to hear you experience.

Good luck, Birgit

bhmm2@cam.ac.uk

Birgit Meldal <bhmm2@medschl.cam.ac.uk>

QuantGenetTextbook draft chapters

We are (slowly) finishing the companion volume to our 1997 “Genetics and Analysis of Quantitative Traits” textbook, namely volume 2, “Selection and Evolution of Quantitative Traits”.

Drafts of 24 out of the planned 47 chapters, and drafts of all five Appendices are now posted at: <http://nitro.biosci.arizona.edu/zbook/NewVolume.2/-newvol2.html> Given that roughly 900 (typeset) pages have been posted, it is recommended that the table of contents pdf be downloaded first to get an overview and see where material of interest to you might be posted.

New drafts will be posted as they come online, roughly one-two/month.

Please feel free to use this material in courses, etc. We only request feedback for errors, missing topics, etc.

cheers

bruce

Bruce Walsh University of Arizona

Bruce Walsh <jbwalsh@u.arizona.edu>

R code species extinction

Dear all,

Does anyone know of a software/R code available to implement the “field of bullets” model of species extinction?

best,

Marc Stephens stephensmarc29@yahoo.com.br

Relative branch length score

Hi all,

I would like to ask if what is the recommended software to use that will give a score to the branch length of a leaf node in a rooted tree relative to its topological position, i.e., the number of internal nodes in between such leaf and the root of the tree.

Thanks,

– Dr. Albert J. Vilella Ensembl Comparative Genomics <http://www.ebi.ac.uk/~avilella/> European Bioinformatics Institute - EMBL Wellcome Trust Genome Campus, Cambridge, UK

avilella@ebi.ac.uk

Resampling PhiST answers

Hi all, please see my original query to EvolDir below and (few) replies. If any further suggestions are forthcoming please e-mail me: markus.debruyne@gmail.com
Thanks, Mark

Dear Colleagues,

We would like to test whether 3 pairwise PhiST estimates, and 3 Pi estimates are significantly different from one another (single locus - mtDNA HVR). I understand one method of doing so is by bootstrapping.

Is this the preferable method, and does anyone know of a program that would automate these calculations? (Arelquin and FSTAT would appear to require data from at least 4-6 loci). Alternatively, instructions for doing this 'by hand' would be greatly appreciated.

Bootstrapping Fst and friends is done over loci, so it should be easy...

There are methods for bootstrapping over populations, but I'm not convinced by them in general (O'Hara, R.B. and Merilä, J., 2005. *Genetics* 171: 1331-1339), and for 2 populations, it'll obviously be difficult to bootstrap.

You should be able to construct a parametric bootstrap, by re-sampling the data from a multinomial distribution, with probabilities equal to the observed allele frequencies. This might be worth testing first, though - I'm not sure how much of a bias is induced if you have rare alleles that are not in the sample.

Bob O'Hara

Bob O'Hara Department of Mathematics and Statistics
P.O. Box 68 (Gustaf Hällströmin katu 2b) FIN-00014
University of Helsinki Finland

Hi Markus,

Regarding your query to evoldir. The reason Fstat etc require multiple loci to bootstrap confidence intervals is that the unit used for bootstrapping is the locus. Thus it is not possible to sample randomly from a distribution of loci unless you have more than one. Moreover, it has been shown that the bootstrap method can be very unreliable when performed across less than five loci. It is possible to bootstrap across other units (e.g. individuals) but you have to ask the question - where is my uncertainty? Is it that the individuals in your sample are a representative random sample from your population; or is it that your locus is a representative sample of the genome? In all likelihood your locus/loci are a very small sample of the entire genome, which is why you want to estimate the C_{is} . This is the case for most population genetics studies that use a relatively small number of loci to infer neutral genetic diversity (and the process acting upon it) as a sample from a potentially very large genome, hence the tendency to bootstrap across multiple loci. In your case bootstrapping is not an option I'm afraid - you have nothing to bootstrap! There may be some other tests that are more applicable and I hope you will get some answers from your query that will help. I would also say that p values are not the be all and end all. If your tests show large biological differences than you should focus on that.

All the best

Matt

Dr Matthew Oliver Research Fellow School of Biological Sciences University of Aberdeen Zoology building
Tillydrone Avenue Aberdeen AB24 2TZ UK

markus.debruyn@gmail.com

Scoring package AFLP analysis

Dear Evoldir members,

We have recently released an R CRAN library to automatize the scoring of AFLPs; RawGeno. The library includes: - An objective scoring solution for AFLPs - Visualization and Preliminary analyses (PCR plates checking, PCoA, heatmap) - Exporting functions to other programs (Paup, MrBayes, Structure and others)

Finally, RawGeno includes a Graphical User Interface to simplify its use; command line users can also program routines.

RawGeno can be downloaded from: <http://sourceforge.net/projects/rawgeno/> More details at: <http://www.biomedcentral.com/1471-2105/10/33>

Feel free to contact us if any further developing / debugging is needed.

Nils ARRIGO

ARRIGO Nils Ambroise <nils.arrigo@unine.ch>

Selfpublishing SpeciesDescriptions

Subject: ICZN and self-publishing of species names

Dear all,

Evoldir subscribers interested in taxonomy and nomenclature please read on.

A self-proclaimed taxonomist is erecting dozens of new species every month in a series of self-published papers, based on information the scientific community generally considers extremely dubious. Until recently, this has mainly concerned Australian snakes, but the latest papers totally revise the North American rattlesnakes and have caused uproar in North American herpetological circles.

PDFs of the papers, in a self-published journal called "The Australasian Journal of Herpetology", can be found here:

<http://www.smuggled.com/AJHFP1.htm> <http://www.reptileforums.net/forums/snakes/62848-rattlesnake-taxonomy-paper.html> Note the first website is blocked on some servers!

The papers are distributed in hard copy and so count as "published" and valid under ICZN rules (International Code of Zoological Nomenclature): as the journal states, "Print copies are distributed to major libraries and institutions that satisfy deposit requirements of the ICZN, ANL and similar bodies."

New species will continue to be described in self-published works for the foreseeable future unless the ICZN tightens rules on what counts as published (e.g. only journals indexed by Science Citation Index and books with an ISBN number and a recognised scientific publisher).

Do Evoldir members think taxonomy benefits - or is seriously hampered - by the ICZN formally recognising species, in self-published works?

I would encourage Evol Dir members to petition the ICZN if they have strong views on this matter: to date, they have strenuously resisted including peer review etc in the requirements for a species name to count as "published". The ICZN committee can be contacted here:

<http://www.iczn.org/Commissioners.htm> Regards,

Martin Brown

Email: mbrownaustralia@gmail.com

M Brown <mbrownaustralia@gmail.com>

Software NOBLAST JAMBLAST

Dear Evoldir members,

I am happy to announce the release of the: NOBLAST and JAMBLAST softwares freely available with source code, docs, packages and standalone executables available for a variety of systems (linux windows, sources..) from SourceForge: <http://sourceforge.net/projects/NOBLAST> <http://sourceforge.net/projects/JAMBLAST> General presentation:

NOBLAST(New Options for BLAST) provides:

1) a new extended user-friendly tabular output for-

mat that can be directly analysed with any spreadsheet (OpenOffice, Excel...) and/or any database engine (e.g. MySQL) without any use of a parser. This new option extends (-m parameter) the blastall, blastcl3 and blastpgp software and is available for various NCBI BLAST programs: Blastn, Blastp, Blastx, Tblastn, Tblastx, Mega BLAST and Psi BLAST.

2) distributed/parallel BLAST functionality with exact E-value adjustment when split database are used.

NOBLAST is an open source patch for blastall, blastcl3, blastpgp and formatdb from the NCBI toolkit.

JAMBLAST (Java Application Manager for BLAST results) is an additional Java cross-platform application which can be used optionally for the management of the BLAST outputs produced by NOBLAST, using MySQL. It also offers visualization, sorting, i, exporting... of the results according to user-deicriteria.

citation: Lagnel J, Tsigenopoulos CS, Iliopoulos I (2009) NOBLAST and JAMBLAST: New Options for BLAST and a Java Application Manager for BLAST results. *Bioinformatics* 25: 824-826.

<http://www.ncbi.nlm.nih.gov/pubmed/19181685>

Please, feel free to report any comments to me and enjoy...

Jacques Lagnel

Jacques Lagnel Hellenic Centre for Marine Research (HCMR) Institute of Marine Biology/Genetics Gournes Pedidos P.O.Box 2214 Heraklion 71003 Crete, Greece

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Tel. + 302810 337719 Fax: + 302810337820

- Hellenic Center For Marine Research, Crete Network Operation Center This message has been scanned for viruses and dangerous content by MailScanner, and is believed to be clean.

lagnel@her.hcmr.gr lagnel@her.hcmr.gr

Software RAxML 7 1 0

Dear Community,

RAxML has recently been updated and is now available for download as RAxML-7.1.0 at <http://www.kramer.in.tum.de/exelixis/software.html> I am still working on an updated Manual so please consult the on-line help via "raxmlHPC -h".

This is the alpha release, so please expect a lot of bugs, weird program outputs etc.

To report bugs send me an email and please send me all input files, the exact invocation, details of the HW and operating system, as well as all error messages printed to screen.

The MPI version does not work yet, only Pthreads and the sequential version work. A Windows version will be made available later-on once RAxML 7.1.0 is stable.

To compile:

sequential: "make -f Makefile.gcc" Pthreads: "make -f Makefile.PTHREADS"

New features:

* Improved parallel load balance for Pthreads version when conducting per-partition branch length estimate * Binary (Morphological) and Secondary Structure models implemented * Estimate of GTR model of amino acid substitution * Added LG model of protein substitution * Computation of RF and WRF tree distances * Implementation of significantly faster methods to operate on bipartitions of trees * Implementation of WC and FC Bootstrap convergence criteria, they can be executed on the fly or a posteriori * For details on the bootstrap method see N.D. Pattengale, M. Alipour, O.R.P. Bininda-Emonds, B.M.E. Moret, A. Stamatakis: "How Many Bootstrap Replicates are Necessary?". Proceedings of RECOMB 2009 preprint at <http://lcbp.epfl.ch/-bootstopping.pdf> * Rapid Bootstraps now feasible under CAT, GAMMA, as well as GAMMA+P-Invar * Parsimony ratchet implementation * 4 Algorithms to classify sequences from environmental samples into a given reference tree (to be described in more detail)

I have fixed various bugs and slightly changed the search algorithms and command line interface.

Comments and suggestions are always welcome.

Best regards,

Alexis

– Dr. Alexandros Stamatakis, Junior Research Group Leader

The Exelixis Lab Bioinformatics Unit (I12) Department of Computer Science Technische Universität München

Tel: +49 162 8541515 (Mobile) +49 89 28919434 (Office) Fax: +49 89 28919414 Skype: stamatak Email: stamatak@cs.tum.edu WWW: <http://www.kramer.in.tum.de/exelixis/> Room: 01.08.061

stamatak@in.tum.de stamatak@in.tum.de

SpiderSocialEvolution collaboration India

I am seeking arachnologists or ecologists in India that are interested in establishing collaboration on social evolution within the spider genus *Stegodyphus*, which contains one social and multiple subsocial species in India. The project will require sampling of spiders with the aim of conducting population genetic and phylogenetic analyses.

Please contact:

Dr. Trine Bilde Trine.bilde@biology.au.dk

Associate Professor in Evolutionary Ecology Department of Biological Sciences University of Aarhus Ny Munkegade 1540 8000 Aarhus C Denmark

<http://www.biology.au.dk/trine.bilde.htm> Trine Bilde <trine.bilde@biology.au.dk>

Stenamma ant samples

Dear Evolutionary Biologists,

I am a graduate student at the University of California, Davis and I work on the systematics of the ant genus *Stenamma*. One of my goals is to produce a broad-scale phylogeny of the genus. However, I have not been able to obtain fresh specimens from Europe or Asia. If you have any recently collected specimens preserved in 90-100% etoh I would be very grateful if you could send me a few. The genus is a cold hardy cryptic group, whose members are most often encountered in forest leaf litter samples (Winkler or Berlese). Please let me know if you can help in any way.

Best regards, Michael

– Michael G. Branstetter Department of Entomology University of California, Davis One Shields Ave Davis, CA 95616 lab ph. 530-752-9977

Michael Branstetter <mgbranstetter@ucdavis.edu>

Stress adapted flies

Desiccation Selected Flies Seek Home

Students of Howard Rundle and I are at the conclusion of a desiccation selection experiment with *D. melanogaster*, and neither of us plans to hold onto the populations. Here is a quick overview for anyone interested in adoption.

The lines were founded in 2005 from LHm stock (a California population collected in the late 80s and domesticated in Bill Rice's lab). The selected lines are unusual in having two different eye colours installed (3 desiccation wild-type populations and 2 desiccation brown-eyed populations, and matched controls that undergo starvation) in order to facilitate studies of mate choice and sperm competition. They are kept at census sizes of 1200-1300 adults and have been selected for 88 generations now. They resist stress over 4x longer than controls or ancestors (close to 2 days in zero humidity).

Anyone who has tried selection on this character will know that it is a serious chore, which is all the more reason we'd like to see these lines go to a good new home. For more information, we have a recent paper in *J. Genetics*' special issue on evolutionary genetics (<http://www.ias.ac.in/jgenet/Vol87No4/383.pdf>) or contact me for details.

Thanks, Adam Chippindale chippind@queensu.ca

Adam Chippindale <chippind@queensu.ca>

Sturgeon problems

Dear evoldir members

I am PhD student and I am going to study about *gdf9* in sturgeons (*Acipenser*), but I have difficulties to sampling (peeling the ovum and isolating the follicle layers). I would appreciate receiving advices in this regards.

Best regards Mahtab

mahtab yarmohammadi
<mahtab_yarmohammadi@yahoo.com>

Summer of code

*** Please disseminate widely to students at your institution ***

PHYLOINFORMATICS SUMMER OF CODE 2009

http://hackathon.nescent.org/-Phyloinformatics.Summer_of_Code.2009 The Phyloinformatics Summer of Code program provides a unique opportunity for undergraduate, masters, and PhD students to obtain hands-on experience writing and extending open-source software for evolutionary informatics under the mentorship of experienced developers from around the world. The program is the participation of the US National Evolutionary Synthesis Center (NESCent) as a mentoring organization in the Google Summer of Code(tm) (<http://code.google.com/soc/>).

Students in the program will receive a stipend from Google (and possibly more importantly, a T-shirt solely available to successful participants), and may work from their home, or home institution, for the duration of the 3 month program. Each student will have at least one dedicated mentor to show them the ropes and help them complete their project.

NESCent is particularly targeting students interested in both evolutionary biology and software development. Initial project ideas are listed on the website. These range from hardware acceleration for phylogenetic inference, to tree visualization within a wiki, to alignment of next-gen sequencing data, to development of a reusable ontology term markup module for biocuration. All project ideas are flexible and many can be adjusted in scope to match the skills of the student. We also welcome novel project ideas that dovetail with student interests.

TO APPLY: Apply online at the Google Summer of Code website (<http://socghop.appspot.com/>), where you will also find GSoC program rules and eligibility requirements. The 12-day application period for students opens on Monday March 23rd and runs through Friday, April 3rd, 2009.

INQUIRIES: phylosoc@nescent.org. We strongly encourage all interested students to get in touch with us with their ideas as early on as possible.

2009 NESCent Phyloinformatics Summer of Code: http://hackathon.nescent.net/-Phyloinformatics.Summer_of_Code.2009 Google

Summer of Code FAQ: <http://socghop.appspot.com/document/show/program/google/gsoc2009/faqs>

Cyberinfrastructure Traineeships (managed separately from GSoC; postdocs also eligible): <http://hackathon.nescent.org/> Cyberinfrastructure_Summer_Traineeships_2009

To sign up for quarterly NESCent newsletters: <http://www.nescent.org/about/contact.php>

Todd Vision and Hilmar Lapp National Evolutionary Synthesis Center <http://nescent.org> Hilmar Lapp <hlapp@nescent.org>

Texas creationism

Please forward the following appeal for help to Evoldir members. Thanks! -Dan Bolnick danbolnick@mail.utexas.edu

Begin forwarded message:

Click to view this email in a browser

Dear Colleagues,

The Texas State Board of Education is considering several changes to the state science curriculum that will undermine effective coverage of evolution in high-school biology classes. Proposed anti-evolution language will also put pressure on textbook publishers to incorporate creationist criticisms of evolution or else risk being excluded from the monolithic Texas textbook market.

The board members are receiving thousands of emails from creationists supporting the current curriculum draft. To keep scientifically unfounded arguments out of our schools' biology classes, we need help from each and every one of you. Please email the 15 members of the State Board and urge them to

- (1) adopt the scientifically sound curriculum standards drafted by a working group of teachers and scientists in December, and
- (2) reject amendments to these standards that have been proposed by anti-evolution members of the State Board of Education.

Below, we provide instructions on how to contact State Board of Education members. Although we include a form letter below, we encourage you to personalize the email. Below, we also provide a succinct explanation of the current status of curriculum revision in Texas.

Sincerely,

The 21st Century Science Coalition (www.texasscientists.org)

Dr. D.I. Bolnick University of Texas at Austin Dr. R.E. Duhrkopf Baylor University Dr. D. Hillis University of Texas at Austin Dr. B. Pierce Southwestern University Dr. S. Sarkar University of Texas at Austin

PS If you know of colleagues who have not yet signed the 21st Century Science Coalition statement, please forward them this e-mail or direct them to www.texasscientists.org. What you can do to help

Please email members of the State Board Of Education, encouraging them to adopt the original draft of the standards proposed by working groups in December.

You can email the entire SBOE directly at sboeteks@tea.state.tx.us.

Here is a template for an email to the SBOE (we encourage you to personalize this):

To the Texas State Board of Education,

As a scientist and active researcher and educator, I am writing to urge you to support sound science education in Texas. In particular, I request that you adopt the Biology and Earth Sciences TEKS draft as originally proposed by the Working Groups. These working groups are composed of educators and scientists with deep expertise in science, and their proposed TEKS drafts should be given unreserved support without amendment.

In particular, I object to the recent changes made to the highschool TEKS (subchapter C) section 112.34 (c) 7.B: "analyze and evaluate the sufficiency or insufficiency of common ancestry to explain the sudden appearance, stasis, and sequential nature of groups in the fossil record;" This language inaccurately insinuates that the fossil record supports long-standing creationist arguments that existing species were created as they exist today. The present wording is misleading. I also object to changes to section 112.36 (c) 8.A, which now read: "evaluate a variety of fossil types, proposed transitional fossils, fossil lineages, and significant fossil deposits and assess the arguments for and against universal common descent in light of this fossil evidence" ; Transitional fossils are not "proposed" - they are clearly documented based on detailed anatomical measurements. Also, the phrase "arguments for and against universal common descent" is a common creationist phrase that inaccurately suggests that there is credible scientific data arguing against common ancestry.

In conclusion, please revert to the original working

group version of the science TEKS, and resist additional changes that are not approved by the working groups of scientists and educators.

Sincerely,

YOUR NAME

YOUR QUALIFICATIONS

YOUR AFFILIATION/POSITION

Some suggestions for emailing the SBOE

1. You can specify in your email to sboeteks@tea.state.tx.us that you wish your message to reach particular SBOE members. It may help if you take advantage of this and vary your tone depending on which members you are writing to. For instance, the Science Supporters [Bob Craig; Mary Helen Berlanga; Pat Hardy; Rene Nunez; Mavis Knight] cast difficult votes to support evolution in the TEKS, and are being hammered by angry emails from creationists. When emailing these members, please be sure to thank these five for their consistent support of the science standards AS WRITTEN BY THE WORKING GROUPS, and urge them to continue to oppose amendments to the standards or efforts to revert to problematic language that

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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>

Tree of Life Poster

Dear Evolutionary Biologists

A friend of mine is a teacher at a Swiss high school and is looking for posters that depict the tree of life (not too heavy on the phylogenetic part, but accurate in the relationships, with nice colorful pictures of organisms, maybe even with more than just the animals). A quick search on the internet showed me that (at least in Switzerland) there are not many good posters available in online shops.

Do you know about any good resources (I am sure there are), where you can order such posters? Or other interesting items that are interesting and fun for kids to look at (and concern evolution)? It just occurred to me that I, as an evolutionary biologist, should be able to provide such information, especially in the Darwin year!

Cheers

Dominik

—

Dominik Refardt Theoretical Biology Institute of Integrative Biology, ETH Zürich ETH Zentrum CHN J14 Universitätsstrasse 16 CH-8092 Zürich Switzerland

Phone: +41 44 6327102 Fax: +41 44 6321271 Email: Dominik.Refardt@env.ethz.ch

dominik.refardt@gmail.com

Trichloris pluriflora mating system

Hello, EvolDir,

I was wondering if anyone has any information on the rate of self fertilization in *Trichloris pluriflora* (aka *Chloris pluriflora*, multiflower false Rhodes grass)?

Any insight would be much appreciated.

Many thanks, Jenn DeWoody jdewoody@yahoo.com

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Canberra CSIRO DemographicModeling

OCE Postdoctoral Fellowship 2008 - Genetic and demographic modelling

CSIRO Plant Industry, Canberra \$69K - \$76K plus Superannuation Ref No: 2009/231

Applications are invited for a three-year OCE Postdoctoral fellowship to develop mathematical simulation models of the genetic and demographic dynamics of self-incompatibility in invasive plant populations. The successful applicant will work with a small team of molecular population geneticists and plant ecologists examining how self-incompatibility affects the reproductive output of wild radish populations in Australia and the implications for the development of weed control strategies.

The successful applicant will be a mathematical population modeller or ecological geneticist with experience in developing simulation models that integrate both genetic and demographic processes. The main responsibility will be to work with a small team of molecular population geneticists and plant ecologists to develop population models to explore how self-incompatibility affects invasive plant population dynamics using wild radish as a primary model system.

As a member of the research team you will also undertake glasshouse experiments to determine the importance of dominance relationships in determining evolutionary dynamics of self-incompatibility and the long-term effects on reproductive performance.

You will have excellent written and oral communication skills and the ability to work as part of a team.

Candidates should have, or will shortly satisfy the requirements for a PhD in population genetics or ecological genetics with strong experience in mathematical simulation modelling and should have no more than three years of work experience since graduation.

For more information and to lodge your application please visit our website https://recruitment.csiro.au/-asp/Job_Details.asp?RefNo=2009%2F231 Applications close 20 April 2009

Katem.Smith@csiro.au

Columbia Bioinformatics

Postdoctoral Fellowship in Bioinformatics

The International Center For Tropical Agriculture (CIAT) is seeking applications for a Postdoctoral Research Fellowship in Bioinformatics. The position offers an outstanding career opportunity for a young re-

searcher interested in genomics in the context of international agriculture. The researcher will be part of a multidisciplinary team working on genetic improvement of beans, cassava, forage grasses species and rice.

Research areas: - Implement and organize data mining (sequences, gene annotation, QTL data, FSTs, etc.) for different crops (rice, bean, cassava). - Implement annotation pipelines to establish links between sequence annotation data and phenotypic characterization. - Develop bioinformatic tools to detect sequence-based genetic markers (SNPs, SSRs, SFPs)

Requirements: Applicants must have, or expect to hold by March 31, 2009, a Ph.D degree preferably in the field of bioinformatics/computational biology or genomics. Experience in computer programming such as: Perl, R, python, CSS, PHP and knowledge of statistics software are required.

Screening of CVs for this position will begin immediately and will continue until the position is filled.

Enquiries and applications, including an application letter, a curriculum vitae, and the names and contact details of three professional references (including telephone, fax numbers, and e-mail address), should be sent to Olga Lucia Cruz (o.l.cruz@cgiar.org)

Closing date for applications: March, 31, 2009

CIAT is one of 15 not-for-profit Centers funded mainly by various countries that make up the Consultative Group on International Agricultural Research (CGIAR), private foundations, international and regional organizations. CIAT conducts socially and environmentally progressive research aimed at reducing hunger and poverty, and preserving natural resources in developing countries. The Center offers internationally competitive salary packages, is an equal opportunity employer and believes that the diversity of its staff contributes to excellence. CIAT is interested in increasing this diversity of its staff and particularly encourages applications from both women and developing country professionals.

We invite you to learn more about CIAT by accessing our web site at www.ciat.cgiar.org Monica Cecilia Munoz-Torres <mcm262@georgetown.edu>

DalhousieU Apicomplexan Genomes

Junior Fellow Postdoctoral Research Position: Insights

into the origin of apicomplexan genomes.

Institutions: CIFAR Program in Integrated Microbial Biodiversity; Department of Biochemistry and Molecular Biology, Dalhousie University; Departments of Zoology & Botany, University of British Columbia.

Position details: The successful candidate will be a broadly trained, self-motivated and enthusiastic individual interested in exploring the early evolutionary history, genomics and molecular biology of apicomplexan parasites. The project represents a collaborative effort between the Slamovits Lab at Dalhousie University, Halifax, NS (www.biochem.dal.ca/faculty/facultypages/slamovits/) and the Leander Lab at the University of British Columbia, Vancouver, BC. (www.botany.ubc.ca/bleander/).

Required skills: The applicant must have a PhD in a relevant discipline, excellent written and oral communication skills, and demonstrated expertise in comparative biology, evolutionary biology, standard molecular biology techniques (DNA/RNA methods) and computational methods including phylogenetic analysis and sequence editing/management. Additional experience with any or all of the following is highly desirable: marine biology and fieldwork; invertebrate anatomy and dissection; light microscopy, eukaryotic cell culture. Locations: The main location is Halifax, Nova Scotia although the candidate is expected to spend time for field-oriented research and sample processing in the Leander Lab in Vancouver. This may involve a stay at the Bamfield Marine Sciences Centre (www.bms.bc.ca) located on the west side of Vancouver Island. Starting date and duration: The appointment may begin as early as September 1, 2009. The successful applicant will be appointed for 2 years, with the potential to extend to a third year contingent on satisfactory progress and funding availability.

Project description V Background: This project aims to shed light into the origin of the genomes of apicomplexan parasites. Apicomplexans are among the most harmful pathogens of humans and livestock, making these parasites economically important and focal organisms for medical research. In a continuous effort to understand better the biology of these parasites, several apicomplexan genomes have been completely sequenced and more are on the way. While multiple full genomes represent a great deal of data compared to many other eukaryotic groups, the extreme divergence in sequence and genome architecture among species and lineages precludes comprehensive comparative genomic analysis involving representatives of different apicomplexan lineages. This panorama is further obscured by the highly unusual genome composition in some groups

(e.g. 80%AT in Plasmodium genomes). In order to reconstruct an accurate picture of the origin and evolution of apicomplexan genomes, we need to acquire data from organisms representing lineages that appear to have retained a large number of ancestral characteristics. Current evidence suggests that gregarines and colpodellids form the stem group from which all other apicomplexans are derived and are expected to provide unparalleled insights into the basic genomic characteristics from which each lineage evolved their unique properties. In comparison to the wealth of genomic data from human or zoonotic apicomplexan parasites, genomic data from these basal apicomplexans is very scarce.

i Outline of the Proposed Research and Methods: The project involves the generation and analysis of EST and genomic surveys of gregarine species from coastal BC invertebrates and possibly other related protists. The initial stage of the project involves collection of invertebrate hosts from coastal BC and Vancouver Island locations and further processing in the lab to recover gregarine material and prepare high quality DNA/RNA for sequencing. At a second stage, genome and transcriptome sequence surveys will be carried out through genomic/cDNA library construction or second-generation sequencing in order to generate large amounts of sequence data. The candidate will curate and annotate the raw data using powerful computational resources available from the CGEB at Dalhousie University. In addition to sequence generation, curation and basic analysis, the candidate is expected to conduct

quality research on questions relevant to the interests of either or both groups. Such questions include, but are not limited to, exploring the relationships between genomic reduction, genome plasticity and gene expression, the study of the basic properties of apicomplexan gene regulation, gain insight into plastid evolution in alveolates, improve the phylogenetic backbone of apicomplexans and

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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>

Ecole Normale Supérieure de Lyon, University of Lyon, France

A postdoctoral position is available in the lab of Philippe Oger. The lab will combine computational and experimental approaches to studying the adaptation of prokaryotes to life under high hydrostatic pressure (termed piezophily). Three different scenarios supported by experimental evidence actually coexist to explain this adaptation, which involve either the occurrence of specific genes, the fine tuning of gene regulation or a more generalized adaptation of protein structures to high pressure conditions. Our long-term goals are to better understand at what level the adaptation to high pressure in prokaryotes occurs. The project details are flexible, but will focus on comparing the genomes of sequenced known piezophiles with closely related known piezosensitives to extract relevant genomic divergences linked to piezophily that can be tested experimentally using the tools developed in the lab for the in situ characterization of molecules and enzymatic activities.

Lyon is the second town of France, reputed for its gastronomy. It offers a very strong research environment. Ecole Normale is a small University-like structure located in the south of the town (www.ens-lyon.fr), with 13 labs engaged in research from Pure and Applied Mathematics to Earth Sciences. There is plenty of opportunity to interact with other labs, and especially the “Laboratoire de Biométrie et Biologie évolutive” of the University of Lyon (<http://lbbe.univ-lyon1.fr/>), with whom the program is developed.

To apply, please email a CV, brief description of research experience and interests, and contact information for at least two references to poger@ens-lyon.fr. The position can begin any time after April 1, 2009.

Phil Oger Earth Sciences Laboratory Ecole Normale Supérieure de Lyon Université de Lyon 46 Allée d'Italie 69364 Lyon cedex 07 poger@ens-lyon.fr

Phil Oger, PhD Laboratoire de Sciences de la Terre Ecole normale supérieure de Lyon University of Lyon 46, allée d'Italie 69364 Lyon cedex 7 (France)

phone: +33 (0) 472 728 792 fax: +33 (0) 472 728 677 email: Philippe.oger@ens-lyon.fr

philippe oger <philippe.oger@ens-lyon.fr>

Two Post-Doc Positions in Speciation Gene and Meiotic Drive in *Drosophila* in Emory University

Two post-doc positions funded by NIH are available starting on April 1, 2009 in the lab of Yun Tao at the Emory University Department of Biology on mapping, cloning and molecularly characterizing genes involved in meiotic drive and speciation in *Drosophila simulans*. The start date is flexible from April to middle summer, 2009. The initial appointment will be one year but extendable up to four years. Postdoc salary follows NIH standard.

The goals of the project are (1) to characterize two meiotic drive systems (Winters and Durham) in *D. simulans*; (2) to characterize the speciation genes between *D. simulans* and *D. mauritiana*; (3) to trace the molecular evolution of the genes involved in meiotic drive and speciation; and (4) finally to test the theory that meiotic drive is a major mechanism leading to speciation. Some background of the project can be found in the three publications (Tao et al. 2001 PNAS 98: 13183-8; Tao et al. 2007a PLoS Biology 5(11): e292; Tao et al. 2007b PLoS Biology 5(11); e293.)

Candidates for these two positions should have demonstrated expertise in one or more of the following areas: *Drosophila* genetics, standard molecular biology lab techniques, small RNA, bioinformatics, molecular evolution, evolutionary genetics (experimental or theory). Candidates are expected to be highly motivated, independent, eager to learn new skills and explore new intellectual territories. Successful applicants are encouraged to develop new and independent research projects in the broad field of evolutionary genetics, particularly in genetic conflicts and speciation.

Interested applicants should contact Yun Tao (y tao3@emory.edu; 404-727-0815) with a cover letter, CV, a one-page statement of career development and research interests, and the names of three or more references. The applications will be reviewed immediately until the positions are filled.

Yun Tao Assistant Professor Department of Biology
Emory University 1510 Clifton Rd. Atlanta, GA 30322
404-727-0815

y tao3@emory.edu

Yun Tao <y tao3@emory.edu>

Frankfurt Phylogenetic Diversification

The Biodiversity and Climate Research Centre (BiKF) has recently been founded by the Senckenberg Gesellschaft fuer Naturforschung, the Goethe@~PUniversity Frankfurt am Main, and additional partners. It is funded by the Federal State of Hesse through its Initiative for the Development of Scientific and Economic Excellence (LOEWE). The mission of the Centre is to carry out internationally outstanding research on the interactions of biodiversity and climate change at the organism level. The Project Area A (Evolution and Climate) invites applications for a

PostDoc Position: Phylogenetic Diversification and Climate Change in the Cenozoic PG A1 [Ref. #A03] BAT IIa

We are looking for a scientist with a strong research focus at the interface of biology, geography and informatics. The successful applicant will cooperate with various groups of biologists and palaeontologists working on the reconstruction of phylogenetic trees with traditional and molecular methods. She or he will be responsible for data standardisation and assessment, and accomplish modelling of current and past eco space and climate space of different plant and animal groups. The successful applicant will be in charge of organizing advanced training courses. Participation in university teaching and an active role in the acquisition of external funds is highly desired.

Applicants should hold a Ph.D. in biology, geography, bioinformatics, informatics or in another relevant subject and have a strong publication record. Expertise in the following areas is expected: modelling approaches (e.g. ecological niche modelling, reconstruction of habitat suitability, also in the past), geographic information systems (GIS), data management and statistics. Experience in programming is desired. Very good written and oral communication skills in English and the interest in joining a multidisciplinary team are required. Knowledge of German would be an advantage, and at least the willingness to learn basic German is required. Salary and benefits are according to a public service position in Germany (BAT IIa, approx. 58.800 Euros gross per annum). The Research Centre BiKF advocates gender equality. Women are therefore strongly

encouraged to apply. Equally qualified severely handicapped applicants will be given preference.

The contract shall start as soon as possible and will be restricted to 24 months. Review of the applications starts March 16th 2009 and will continue until the position is filled. The duty station will be Frankfurt am Main, Germany. Please send your application by e-mail, including 1) a cover letter outlining relevant background and work experience, 2) a full curriculum vitae, including a list of publications, 3) copies of educational certificates, 4) names and addresses of two referees, to Prof. Dr. h.c. V. Mosbrugger, Scientific Coordinator Biodiversity and Climate Research Centre, Senckenberganlage 25, D 60325 Frankfurt am Main, Germany. Email to Service and Finances: recruiting@senckenberg.de. For enquiries about the position and the contract conditions please write to Prof. Dr. B. Stribrny (Email: bernhard.stibrny@senckenberg.de) and for scientific enquiries to Prof. Dr. Annette Klussmann-Kolb (Email: [Klussmann\[minus\]Kolb@bio.uni\[minus\]frankfurt](mailto:Klussmann[minus]Kolb@bio.uni[minus]frankfurt) (mailto:Kolb@bio.uni[minus]frankfurt).de) or Dr. Alexandra Mueller (Email: alexandra.muellner@senckenberg.de).

Ursula.Maurer@senckenberg.de
sula.Maurer@senckenberg.de

GeorgiaTech QuantGenet

Quantitative Biology Postdoc @ Georgia Tech

A postdoctoral position in quantitative biology is available under the direction of Prof. Joshua Weitz (Biology, Georgia Tech). The postdoc will join an interdisciplinary research group of biologists, physicists, and computational scientists. The postdoc will collaborate on research focusing on viral dynamics and evolution, at the molecular and ecological scales, as well as have the opportunity to develop new projects at the interface of integrative biology, bioinformatics & dynamical systems.

The position, starting in August 2009, provides competitive salaries and benefits and will be based in the School of Biology. The initial appointment is for one year, with renewal up to three years subject to satisfactory progress and mutual agreement. The start date is flexible.

REQUIREMENTS: (1) PhD in computational biology,

physics, mathematics, microbiology, ecology or related area; (2) Demonstrated research excellence; (3) Strong quantitative skills; (4) Strong oral and written communication skills. Ideal candidates from the biological sciences should have experience with scientific programming. Ideal candidates from the physical/mathematical sciences should have prior exposure to research in the biological sciences. However, outstanding applicants looking to broaden their field of interest will also be considered.

TO APPLY: Applications should be emailed to [<jsweitz@gatech.edu>](mailto:jsweitz@gatech.edu) and consist of (1) a cover letter describing your interest in the position, (2) the names and contact information for three references, (3) a curriculum vita (including publications). Applications will be reviewed starting from March 15, 2009, and continue until the position is filled.

ABOUT THE GROUP: The Weitz group is supported by grants from the Burroughs Wellcome Fund, the James F. McDonnell Foundation, DARPA, and the National Science Foundation. For more information, consult the Weitz group website: <http://ecothery.biology.gatech.edu> or contact Joshua Weitz: [jsweitz \(at\) gatech.edu](mailto:jsweitz@gatech.edu).

Joshua S. Weitz Assistant Professor School of Biology & Physics Georgia Institute of Technology 310 Ferst Dr. Atlanta, GA 30332

email: jsweitz@gatech.edu phone: 404-385-6169
 office: Cherry Emerson 219 group: <http://ecothery.biology.gatech.edu/> web: <http://www.biology.gatech.edu/faculty/joshua-weitz/> Check out our recent articles:

Small-scale copy number variation and large-scale changes in gene expression <http://www.pnas.org/content/early/2008/10/21/0806239105.abstract>
 Collective decision making in bacterial viruses <http://www.biophysj.org/cgi/content/abstract/biophysj.108.133694v1> jsweitz@gatech.edu

Leibniz EpidemiologyModeler

The Leibniz Institute for Zoo and Wildlife Research (IZW)

in Berlin is Germany's premier wildlife research institute and funded by the federal government of Germany and the state government of Berlin (<http://www.izw-berlin.de> < <http://www.izw-berlin.de/> >). The IZW

focuses on the life histories and mechanisms of evolutionary adaptations of mammals and birds and their conservation in natural and anthropogenically influenced environments. The institute operates within the fields of evolutionary ecology and genetics, wildlife diseases and reproduction biology and management, has excellent facilities like a high-throughput genomic sequencing facility at the recently founded "Berlin Consortium for Genomics in Biodiversity Research" and is currently expanding its research programme. For this purpose the institute is seeking to appoint

for the Research Group Evolutionary Ecology:

1 spatial or epidemiological modeller - number 10/2009

responsible for the GIS-lab and software to develop own and expand our current research on modelling spatial processes in wildlife ecology and/or wildlife epidemiology. The successful candidate will have extensive experience in GIS and a track record in modelling of spatial processes in the ecological or epidemiological domain, be enthusiastic to interact with scientists from a wide variety of fields and a strong interest in wildlife, conservation and evolutionary issues. Experience with field research or interdisciplinary teams will be an advantage.

All positions are tenure-track positions and initially limited to three years. All are available immediately, with starting dates negotiable. The IZW is determined to increase the proportion of women in successful scientific careers and particularly encourages female scientists to apply. Applications will be considered until the positions are filled but preferably reach us by 30th April 2009. Please direct informal enquiries to Heribert Hofer (E-mail: direktor@izw-berlin.de, phone: ++(49)-30-5168101, fax ++(49)-30-5168110) and submit your CV, publication list, grants, a letter indicating your research interests and experience and the names and contact details of three referees to Gabriele Liebich, Leibniz Institute for Zoo and Wildlife Research, P.O. Box 601103, D-10252 Berlin, Germany, E-Mail: liebich@izw-berlin.de <<mailto:liebich@izw-berlin.de>> , fax: +49-30-5126104.

"Sommer, Simone" <SOMMER@izw-berlin.de>

Lyon SexChromosomeEvolution

Postdoctoral position on the origin and evolution of young plant sex chromosomes

An ANR-funded postdoc position (2 years) is avail-

able in Gabriel Marais' lab at the University of Lyon (France).

The project will focus on *Silene latifolia* a dioecious plant species with X and Y chromosomes. This species is emerging as a model species for the understanding of the evolution of sex chromosomes. The aim of the project will be to use the genomic resources that have recently become available in *S. latifolia* (BAC sequences, ESTs and microarrays) to investigate several points in relation to the origin and evolution of XY in this species: XY recombination suppression, Y degeneration, and sex determination. We collaborate on this project with Prof. Alex Widmer's lab (ETH Zurich).

We seek a highly motivated candidate with skills in data analysis and a strong interest in genome evolution and evolutionary biology in general. A PhD in one or several of the following fields is expected: bioinformatics, genomics, molecular evolution, population genetics, biostatistics. The applicant does not need to be a French speaker.

We are part of the Bioinformatics and Evolutionary Genomics group, which includes about 25 people (including Laurent Duret and Manolo Gouy). The BGE group has a long-standing experience in bioinformatics and offers a very stimulating scientific environment (highest rate by CNRS at last evaluation in 2006). We have a vast range of locally available bioinformatics tools and excellent computing facilities (UNIX servers, PC clusters). Our weekly lab meeting and journal club are held in English. Find more details at <http://lbbe.univ-lyon1.fr/> . Lyon is the 2nd largest French city. Its city center has been classified "world heritage" by UNESCO and Lyon is considered French capital of gastronomy. Excellent public transports exist within the city (metro, bus, tramway, public bikes), and to the nearby Alps, Paris (two hours by train) and the rest of Europe.

To apply, please send to Gabriel Marais (email: marais@biomserv.univ-lyon1.fr): a letter describing your research motivation and experience, a CV including publication list, full contact details of two scientific referees.

The position should start on fall 2009. Annual gross salary will be about 28,000 euros. Review of materials will begin late April and will continue until the position is filled. For further information, please contact:

Dr. Gabriel Marais Bioinformatics and Evolutionary Genomics group Institute for Biometrics and Evolutionary Biology University of Lyon Campus de la Doua, Villeurbanne Email: marais@biomserv.univ-lyon1.fr Website: <http://lbbe.univ-lyon1.fr/-Marais-Gabriel-.html?lang=en> Gabriel Marais

<marais@biomserv.univ-lyon1.fr>

MaxPlanckInst EvolutionaryBiol

Max Planck Institute for Evolutionary Biology - Post-doctoral research Position in evolutionary molecular biology/bioinformatics

The Max Planck Institute for Evolutionary Biology is seeking an evolutionary molecular biologist to join the department of evolutionary ecology. The position is for at least 2 years and would start as soon as possible. A further extension to maximally 5 years is possible.

***Project** *The successful applicant will participate in advancing a new supermodel of evolutionary genomics, the three-spined stickleback. Our primary goal is to conduct a large scale screening project for genome-wide adaptive genetic variation in different populations of the three-spined stickleback. The screen for polymorphic sites (e.g. SNPs) within and among populations/ecotypes involves massively parallel sequencing (454 technology) of both, expressed sequence tags, and enriched selected areas of the genome. The successful applicant will perform bioinformatic processing and analysis of the data, but he/she will also be strongly involved in the biological interpretation of data. The overall goal is to establish a new evolutionary tool for studying the genetics of adaptation in the model organism three-spined stickleback.

***Background** *The candidate should have a PhD in molecular biology, bioinformatics or any related field. Practical experience in either state of the art molecular techniques or computer-based large-scale sequence analysis, including bioinformatic programming/scripting and biostatistics are required. Expertise in next generation sequencing technologies and a good publication record would be advantageous.

***Working environment** *Details about the department's research activities can be found under: <http://www.evolbio.mpg.de/english/abteilungen/-evolutionsoekologie/index.html> As a Max Planck Institute we can offer labs and technical equipment at the highest standards, including facilities for genome analysis. The successful candidate will collaborate with the team including PhD students and postdocs as well as with Prof. Thorsten Reusch from the Leibniz Institute for Marine Sciences (IFM-Geomar), Prof. E Bornberg-Bauer (University of Münster) and Prof. Monika Stoll (Leibniz-Institute Münster) who

co-supervise the bioinformatic methods.

Our Institute is located in Plön, a small village in a beautiful landscape with many lakes and rivers around. It supports especially outdoor activities. In the vicinity are two major cities (Kiel and Lübeck) as well as the Baltic Sea. Additionally, Hamburg is reachable by train or car in 90 minutes. The institute maintains links to the Christian Albrechts University of Kiel, and the Leibniz Institute for Marine Sciences (IFM-Geomar). The MPI for Evolutionary Biology has three departments (evolutionary ecology, evolutionary genetics and evolutionary theory) and therefore offers a stimulating scientific environment dedicated to evolutionary biology. The working language at the institute is English.

The Max Planck Society is an equal opportunity employer and encourages female scientists and scientists with disabilities to apply.

Please send your application including a complete CV, a list of publications and the contact information of three references by e-mail (milinski@evolbio.mpg.de <mailto:milinski@mpil-ploen.mpg.de>). Review of applications begins 31.03.09 and will be continued until position is filled.

Prof. Manfred Milinski Director Max-Planck-Institute for Evolutionary Biology Department of Evolutionary Ecology August-Thienemann-Strasse 2 D-24306 Plön, Germany

Direct: +49-(0)4522 763 254 Fax: +49-(0)4522 763 310 Email: milinski@evolbio.mpg.de <http://www.evolbio.mpg.de/> eizaguirre@evolbio.mpg.de eizaguirre@evolbio.mpg.de

MichiganStateU EvolutionaryEcol

Post-doctoral Position in Evolutionary Ecology at Kellogg Biological Station, Michigan State University.

I am searching for a creative, motivated post-doc interested in evolutionary ecology. Applicants may propose their own research project or collaborate on one of the current lab projects investigating how rapid environmental changes impact the ecology and evolution of species interactions. Ongoing lab projects include studies on: 1) the demographic, community, and evolutionary consequences of global warming; 2) plant evolutionary responses to long-term nitrogen deposition; or 3) the impact of temporal variation on weed evolutionary responses in agro-ecosystems. For more de-

tails on research conducted in the Lau lab see <https://www.msu.edu/~jenlau/>. The primary responsibility of the post-doc will be to develop a new project or take the lead on one of the above-mentioned existing projects, including implementation of experiments, data analysis, and manuscript preparation. The post-doc will be housed at Michigan State University's Kellogg Biological Station ([http://www.kbs.msu.edu/\[1\]](http://www.kbs.msu.edu/[1])) in Hickory Corners, Michigan.

Applicants must have (or nearly so) a Ph.D. in Ecology, Evolution, Plant Biology or a related field, and should have experience performing large manipulative field and/or greenhouse experiments, analyzing data, and completing manuscripts. Two years of funding are available. The position is available immediately, although the start date is flexible. Interested parties should email a cover letter explaining why they are interested in the position, a CV, and a brief statement of research interests to jenlau@msu.edu. Evaluation of applications will begin 17 April 2009 and continue until the position has been filled.

Jennifer Lau Assistant Professor Kellogg Biological Station and Dept. of Plant Biology Michigan State University jenlau@msu.edu phone: 269-671-2107 fax: 269-671-2104

Links: — [1] <http://www.kbs.msu.edu/> jenlau@msu.edu

Montpellier Integrative Algorithms For Phylogenomics

A 24 months post-doctoral position is available to work on “integrative algorithms for phylogenomics” in the Science University of Montpellier, France (<http://www.univ-montp2.fr/>).

Keywords: Algorithms, phylogenetics, comparative genomics, tree reconciliation, divergence dates, combinatorics, statistics, parallel computing.

The work will be advised by Vincent Berry from the Methods and Algorithms for Bioinformatics team of the LIRMM lab (http://www.lirmm.fr/mab/-sommaire_english.php3) and Vincent Ranwez from the Molecular Phylogeny team of the ISEM lab (<http://www.isem.cnrs.fr/spip.php?rubrique380&lang=en> <<http://www.isem.cnrs.fr/spip.php?rubrique380&lang=en>>). The subject is in the scope of the two groups, combinatorial algorithms on one side and molecular

evolution on the other.

Applicants should have a strong background in Bioinformatics, Algorithms and/or Statistics, as well as good programming skills. A reasonable understanding of evolutionary biology is also required. The successful candidate will interact with both biologists and computer scientists in the context of a research project funded by the ANR (National Research Agency). The objective of this project is to design efficient methods and algorithms to infer species and genes trees, but also duplications and horizontal transfer events by modeling genome evolution mechanisms. This project is in collaboration with the LBBE lab in Lyon, France. Applicants are invited to refer to <http://www.lirmm.fr/-phylarlane> and to advisor's home pages for more details on the project and related papers.

The LIRMM and ISEM lab offer a highly stimulating scientific environment, being part of the largest european site in Agrosiences and part of a Biology & Health competitiveness pole. Montpellier is a university town, hosting one of the oldest universities in France. It benefits from excellent weather conditions and enjoys proximity with the Mediterranean sea, with Spain and Italy.

This job opportunity is available to start any month in 2009 and is addressed to students with a PhD degree or in the process of obtaining it (the thesis should be written by the start of the contract).

Please send a CV and motivation letter to both Vincent Berry (vberry@lirmm.fr <<mailto:vberry@lirmm.fr>>) phone: +33 467 41 85 48 and Vincent Ranwez (vincent.ranwez@univ-montp2.fr <<mailto:vincent.ranwez@univ-montp2.fr>>) phone: +33 467 14 36 97

Frederic.Delsuc@univ-montp2.fr
Frederic.Delsuc@univ-montp2.fr

RoslinInst Edinburgh StatisticalGenetics

Royal Dick Veterinary Studies: Research Fellow

The job holder will conduct research on developing and applying methods for QTL and association mapping, on methods for mapping loci controlling gene expression (eQTL) and on the implementation of these methods in user-friendly tools. The successful candidate will be actively involved in collaborations at local, national

and international level. The job requires a PhD in statistical, quantitative, or population genetics or a PhD in bioinformatics with proven numerical skills. Candidates with a PHD in statistics, physics or mathematics, wishing to embark on an exciting career in genetics are also invited to apply.

This post will be based at Roslin Institute. Please contact DJ de Koning (DJ.deKoning@roslin.ed.ac.uk) for further information.

The Roslin Institute is a BBSRC Institute associated with the Royal (Dick) School of Veterinary Studies, the number one-ranked Veterinary School in the UK in the 2008 Research Assessment Exercise. The Institute undertakes research within the framework of BBSRC Institute Strategic Programmes focussed on the health and welfare of animals, and applications of basic animal sciences in human and veterinary medicine, the livestock industry and food security. Roslin is a member of the Easter Bush Research Consortium (EBRC).

Application ONLY via www.jobs.ed.ac.uk reference 3010636

DJ de Koning

Genetics and Genomics The Roslin Institute and R(D)SVS, University of Edinburgh Roslin Bio-Centre, Midlothian EH25 9PS, Scotland UK phone +44(0)131 5274258 fax: +44 (0)131 4400434 DJ.deKoning@Roslin.ed.ac.uk exciting new project: www.genesys.ac.uk "dj dekonig (RI)" <dj.dekonig@roslin.ed.ac.uk>

Andalucia.

The post-doc will conduct research on variability and selection in the Major Histocompatibility Complex (MHC) comparing native, captive and invasive populations of the same bird species, and its interplay with a wide array of pathogens determined by PCR. A strong background in MHC studies or at least on other aspects of molecular ecology is required. Applicants should preferably have a Ph.D. in molecular ecology or related fields. The position is funded for two years. Gross salary is around 40.000 Euros/year.

Applications should be conducted BEFORE MARCH 31, 2009, electronically to the Consejería de Innovación, Ciencia y Empresa de la Junta de Andalucía with a complementary copy sent as soon as possible to Jose L. Tella (tella@ebd.csic.es). The electronic application to the Consejería de Innovación, Ciencia y Empresa de la Junta de Andalucía is compulsory to be eligible for the position.

Dr. Jose L. Tella Professor of Research Department of Conservation Biology Estacion Biologica de Doñana C.S.I.C. Avda. M. Luisa, s/n 41013 Sevilla Spain

E-mail: tella@ebd.csic.es Fax: (34) 95 4621125 <http://www.ebd.csic.es/carnivoros/personal/tella/>

See new web page under construction: <http://www.elaficano.com/pepe/index.html> Joaquin Munoz <quini@ebd.csic.es>

Sevilla MHC Biological Invasions

Postdoctoral Position in MHC and biological Invasions

A postdoctoral position is available at Estación Biológica de Doñana (EBD-CSIC, <http://www.ebd.csic.es>) in Sevilla to work on MHC variability in invasive populations of exotic birds within the Excellence Research Project 'Las aves exóticas invasoras como transmisoras de patógenos: enfermedades emergentes y procesos de selección en los hospedadores' - 'Exotic invasive bird species and pathogen transmissions: emergent diseases and selection processes in hosts' - led by Dr. Jose L. Tella (<http://www.ebd.csic.es/carnivoros/personal/tella/>). The Project is funded by the Secretaria General de Universidades, Investigación y Tecnología de la Consejería de Innovación, Ciencia y Empresa de la Junta de

StanfordU Evolutionary Genomics

Stanford University, Evolutionary genomics

A postdoctoral position is available in the lab of Hunter Fraser. The lab will combine experimental and computational approaches to studying the evolution of gene expression within and between species. Our long-term goals are to better understand 1) how new mutations affect gene expression; 2) what selective pressures act on these mutations; and 3) how changes in gene expression contribute to the evolution of other phenotypes. The project details are flexible, but ideally will focus on producing and/or analyzing genome-wide gene expression (RNA-seq) and transcription factor binding (ChIP-seq) data from multiple species. Preference will be given to candidates with both experimental and computational experience, and familiarity with high-throughput sequencing (Solexa/SOLiD), chromatin immunoprecipitation, or quantitative/statistical genetics is a plus.

Stanford is an extremely stimulating environment, with many labs engaged in research on evolution and genomics. There is plenty of opportunity to interact with other labs, for example in the monthly evolutionary genomics joint lab meeting that includes labs from several departments.

To apply, please email a CV, brief description of research experience and interests, and contact information for at least two references to hunter[at]alum.mit.edu. The position can begin any time after September 1, 2009. Salary and benefits are very competitive.

For further information please see the lab's website, <http://www.stanford.edu/~hbfraser/>. Hunter Fraser Assistant Professor Department of Biology Stanford University Stanford, CA hunter[at]alum.mit.edu

"Fraser, Hunter B." <hunter_fraser@merck.com>

The working language of the CMPG lab and of the Institute is English. More information on lab research activities can be found on <http://cmpg.unibe.ch> Interested individuals should email a motivation letter, a CV with a list of publications, and the names and emails of two references to laurent.excoffier@iee.unibe.ch

Application deadline is April 5th 2009

– Laurent Excoffier

Computational and Molecular Population Genetics (CMPG) Institute of Ecology and Evolution, University of Bern 6, Baltzerstrasse, CH-3012 Bern, Switzerland Tel: +41 31 631 30 31 Fax: +41 31 631 48 88 Email (NEW): laurent.excoffier@iee.unibe.ch <http://cmpg.unibe.ch/people/excoffier.htm> Computational Population Genetics Swiss Institute of Bioinformatics (SIB) <http://www.isb-sib.ch/groups/-Computational.Population.Genetics.htm> Laurent Excoffier <laurent.excoffier@iee.unibe.ch>

UBern PopulationGenetics

The CMPG lab is looking for a motivated population geneticist or evolutionary geneticist to fill a

2 1/2 years post doc position in population genetics

The successful candidate will work within the framework of a EU funded project addressing the question of the conservation of biodiversity in a changing and heterogeneous landscape.

He/she will more specifically study the effect of habitat fragmentation on the genetic diversity and the adaptability of populations at various geographical and temporal scales. Spatially explicit modeling and genetic simulation tools developed in our lab will be used for this purpose, and several extensions will need to be developed.

Advanced knowledge of population genetics (coalescent theory) and computational skills (Linux/Windows) are required. Since the research project will be done in collaboration with several other European labs, good organizational and communication abilities are essential. Additional knowledge in statistical genetics and computer programming (C/C++/Java/R) are a plus.

Starting date is Summer 2009, but negotiable. Salary follows the Swiss NSF scale, and is about 70,000 CHF per year. The successful candidate is also expected to be involved in light teaching and administrative duties.

UChicago Recombination

POSTDOC IN POPULATION GENETICS, UNIVERSITY OF CHICAGO

A postdoctoral position in population genetics is available in Molly Przeworski's group in the Human Genetics Dept. at the University of Chicago.

The research will focus on variation in recombination rates among humans and primates, but the specific project is flexible. In addition to recombination, work in the group currently focuses on a wide range of topics, from natural selection in humans and other primates to the evolution of regulatory regions.

Our group shares space and weekly lab meetings with those of Jonathan Pritchard and Matthew Stephens and enjoys close ties with other members of the Human Genetics and Ecology & Evolution departments, notably Anna Di Rienzo, Dick Hudson and Carole Ober. Moreover, it benefits from the large and outstanding community of researchers in population genetics, statistics and genomics at the University of Chicago.

Applicants for the position must have either a background in population genetics or come from a quantitative field (such as statistics or computer science) and have a strong interest in genetics. Programming and bioinformatics skills are essential. Informal inquiries as well as applications (including a CV,

copies of relevant publications and two letters of recommendation) should be emailed to Molly Przeworski at <mfp@uchicago.edu>.

Molly Przeworski Dept. of Human Genetics Dept. of Ecology and Evolution University of Chicago
<http://przeworski.uchicago.edu/> mfp@uchicago.edu
 mfp@uchicago.edu

UEastAnglia WarblerFitness

The following postdoc position has become available again due to the previously chosen candidate being unable to take up the position

Telomeres as biomarkers of costs and quality in the Seychelles warbler

UEA SCHOOL OF BIOLOGICAL SCIENCES

SENIOR RESEARCH ASSOCIATE Ref: RA519

29,704 to 35,469 per annum

This NERC funded postdoctoral position is available from June 2009 for a period of two years and nine months to undertake a comprehensive longitudinal study of telomere shortening in a wild avian population. The researcher will help to develop and then utilise molecular protocols to screen for telomere length in the Seychelles warbler. You must have, or shortly obtain, a PhD (or equivalent) in a relevant discipline, have a keen interest in understanding life history trade-offs and senescence and have practical experience in modern molecular techniques.

Closing date: 12 noon on Thursday 2 April 2009. This is a readvertisement but previous applicants are welcome to apply.

Further particulars and an application form are available on our website: www.uea.ac.uk/hr/jobs/ <file:///C:/Documents%20and%20Settings/k483/Local%20Settings/Temporary%20Internet%20Files/OLK1A\www.uea.ac.uk/hr/jobs/> or Tel. 01603 593493.

David S Richardson Centre for Ecology, Evolution and Conservation School of Biological Sciences University of East Anglia e-mail: david.richardson@uea.ac.uk Norwich NR4 7TJ ph: (44) 01603 591496 ENGLAND fax: (44) 01603 592250

http://biobis.bio.uea.ac.uk/biosql/fac_show.aspx?ID=325

“Richardson David Dr (BIO)”
 <David.Richardson@uea.ac.uk>

UEdinburgh DiseaseEvolution

A full-time Postdoctoral Research Associate position is available in the Institute of Evolutionary Biology, University of Edinburgh, UK

Title: Assessing the stability of parasite communities through perturbation experiments

A post-doc position is available starting on May 1, 2009 to work on co-infection dynamics in a wild mammal population in the UK. This will be part of a NERC funded grant led by Amy Pedersen (University of Edinburgh), Andy Fenton (University of Liverpool) and Owen Petchey (University of Sheffield) to quantify within-host parasite interactions and assess the stability of parasite communities. This work will involve a combination of fieldwork (small mammal trapping), laboratory assays, and theoretical modelling.

The postdoc will help manage the field trapping programme, conduct laboratory assays for parasite identification, carry out data analysis and help develop the parasite community models. Experience in small mammal trapping, disease ecology and mathematical modelling are recommended but not essential. The postdoc will have the unique opportunity to link experimental field based approaches with a community ecology theoretical framework to better understand the role of parasite interactions in shaping host-parasite communities.

The post will be for up to 36 months and will be based within the lab of Amy Pedersen at the Institute of Evolutionary Biology (<http://www.biology.ed.ac.uk/research/institutes/evolution/>) & Centre of Infection, Immunity and Evolution (CIIE; <http://ciie.bio.ed.ac.uk/>) at the University of Edinburgh.

The salary range is £28,200 - £33,780, dependent on experience.

Applications will be accepted until April 3, 2009.

For the Postdoctoral Research Associate (Ref. #: 3010681) application and specific job description, please go to:

http://www.jobs.ed.ac.uk/vacancies/index.cfm?fuseaction=vacancies.detail&vacancy_ref010681

For specific information about the project, please email Amy Pedersen (a.pedersen@sheffield.ac.uk) and/or Andy Fenton (a.fenton@liverpool.ac.uk).

— Amy B. Pedersen Royal Society Incoming Research Fellow Department of Animal and Plant Sciences University of Sheffield Alfred Denny Building Western Bank Sheffield S10 2TN UK

Email: a.pedersen@sheffield.ac.uk Office: +44(0) 114 222 4692 Lab: +44(0) 114 222 0060 Web:<http://www.shef.ac.uk/aps/staff/acadstaff/pedersen.html>
a.pedersen@sheffield.ac.uk a.pedersen@sheffield.ac.uk

UFlorida HumanGenetics

A NSF-funded postdoctoral position (1 year, renewable for 1-2 more years) is available in Connie Mulligan's lab at the University of Florida.

Two NSF-funded projects are currently ongoing and the successful candidate can work on one or both: 1) Investigation of human dispersals throughout the Horn of Africa and Arabia. We have an extensive collection of samples from this region and we are focused on finding new ways to analyze molecular genetic data in order to reconstruct human history. 2) Investigation of the genetic and cultural underpinnings of complex diseases that exhibit racial inequalities, using hypertension as a model phenotype. We are working with Lance Gravlee, a cultural anthropologist, to rigorously test heritable and environmental variables that contribute to the risk of hypertension in collaboration with the African-American community in Tallahassee, FL.

Qualifications: A strong background in genetic data collection (DNA sequencing, SNP detection, STR analysis etc.) and data analysis (simulation analysis, gene association analysis, computer programming, etc) is essential. The right candidate will help us achieve our research goals with their expertise and interest in one or more of: (1) synthesizing genetic, cultural, archaeological, and/or linguistic data, (2) theoretical population genetics, (3) statistical genetics, (4) bioinformatics, or (5) your specialty that doesn't quite fit into one of the prior categories. There are excellent opportunities for the successful candidate to develop new lines of research as well as productive collaborations outside the lab.

To apply: via email, send a CV, a statement of research interests, and the names and contact information (including email and phone) for three references. Applications and inquiries should be addressed to Connie Mulligan at cmulligan@ufl.edu.

Review of materials will begin May 1 and will continue

until the position is filled. Start date is flexible with an optimal start in Aug, 2009. Salary is commensurate with experience. Position may be extended for a total of three years. Informal inquiries prior to submitting a formal application are welcome. AA/EOE.

Connie J. Mulligan, PhD Associate Professor, Department of Anthropology Associate Director, UF Genetics Institute 1376 Mowry Rd, PO Box 103610 University of Florida Gainesville, FL 32610-3610 Telephone: 352-273-8092 Fax: 352-273-8284 Email: cmulligan@ufl.edu<<mailto:cmulligan@ufl.edu>> Website: <http://www.clas.ufl.edu/users/mulligan/-Webpage/index.html> cmulligan@UFL.EDU cmulligan@UFL.EDU

UFribourg EvolutionPlantInvasions

1 PhD & 1 Post-Doc Position in Evolutionary Ecology of Plant Invasions, University of Fribourg, Switzerland

Rationale

The proposed project will be the first one that considers the importance of polyploidy and herbivores for invasions simultaneously. Our leading hypothesis is that herbivore pressure and assemblage will, at least partially, explain the predominance of specific cytotypes both in the native and introduced range. The *Centaurea stoebe* L. (syn. *C. maculosa* Lam.) (Asteraceae) system provides an excellent model system to study these interactions, and we take advantage of the large knowledge already available on this plant and its herbivores. Native to Europe where it occurs as a diploid (2x) and a tetraploid (4x) cytotype, the species is highly invasive in North America, where nearly exclusively only 4x plants have been found. Several specialist insect herbivores have been introduced to North America for its biological control, with only partial success so far.

We seek two highly motivated researchers to help clarifying underlying mechanisms of this most successful plant invasion as a complement to various presently ongoing studies that we carry out in collaboration with both national (through NCCR Plant Survival) and international partners. We plan to (i) explore the relationship between type and amount of herbivory and the occurrence of the two cytotypes of *C. stoebe* in its native range by a European-wide survey combined with a replant/transplant experiment, (ii) carry out a series of experiments to analyze interactions between two se-

lected specialist herbivores and the *C. stoebe* cytotypes, and (iii) investigate more generally into the role of generalist herbivores for plant invasions (in collaboration with Urs Schaffner, CABI Europe-Switzerland and our US counterparts).

Requirements

- PhD position: Master Thesis in Biology, preferentially in ecology and evolution

- Post-Doc position: doctoral degree in plant ecology and evolution

For both positions, knowledge of, and experience in one or several of the following areas of research is desirable: experimental (field) ecology and evolutionary biology, invasion biology, plant-herbivore interactions, experimental design and statistical analysis; furthermore, fluency in English and driver's license will be required.

Salary and conditions

The positions are funded by the Swiss National Science Foundation, and start April 1, 2009. Salaries: PhD c. 43'000 SFr/year for 3 years; Post-Doc dependent on age and status, gross salary in the first year about CHF 70'000, for 2-3 years.

Applications

Applicants should e-mail their CV and publication list, together with a short motivation letter and a summary of research experience and interests, and the names of two professional referees to Heinz.mueller@unifr.ch. Please indicate your earliest possible, and your ideal start.

For further information, please contact:

Prof. Dr. Heinz Müller-Schärer, DA@partement.de Biologie, Unit@ Ecologie & Evolution, Universit@ de Fribourg, Chemin du Mus@e 10; CH-1700 Fribourg, SWITZERLAND; tel: + (41) (0) 26-300 88 35/50 cf. my research website at <http://www.unifr.ch/biol-ecology/muellerschaerer/group/mueller/> for further information and recent publications on this subject.

Heinz Müller-Schärer <heinz.mueller@unifr.ch>

UHouston EvolutionaryBioinformatics

An NIH-funded postdoctoral position (two years at least) is available in Dan Graur's lab at the University of Houston.

Applicants should have a broad appreciation of molecular evolutionary theory and bioinformatics and an aptitude for modeling and molecular data analysis. The specific research subject is flexible and negotiable. The overall goal of the funded project is to study multiple-sequence alignment and its effects on subsequent analyses. Independent research in any other branch of theoretical molecular evolution and bioinformatics is encouraged as well.

A PhD in Biology or a related field, experience in computer programming, familiarity with biological databases, bioinformatic packages, and statistical tools.

To apply: send, via email, a CV, a statement of research interests, some reprints or preprints, and the names and contact information for two references. Applications and inquiries should be addressed to Dan Graur at dgraur@uh.edu.

Dan Graur, Ph.D. John and Rebecca Moores Professor Department of Biology & Biochemistry University of Houston

369 Science & Research Building 2 4800 Calhoun Road Houston, TX 77204-5001

Voice: 713-743-7236 Fax: 713-743-2636 Homepage: <http://nsm.uh.edu/~dgraur/> Office: Room 352 Lab: Room 335

dgraur@gmail.com

ULondon EvolutionaryGenetics

Research Associate (3 year fixed contract) in the Laboratory for Molecular Palaeobiology

School of Biological Sciences, Royal Holloway University of London, UK.

The salary for this position is £31,838 per annum inclusive of London Allowance

We are seeking an enthusiastic, well-organized and experienced Postdoctoral Fellow for a three-year position in the School of Biological Sciences, Royal Holloway, University of London. This individual will work on the UK portion of the CLIMIGRATE project, a part of the FP7 ERA-NET program BiodivERsA.

The project will generate ancient DNA data from a suite of taxa to determine how species respond to climate change at the population level. We will use these data to evaluate, adjust and improve existing forecast-

ing models to more accurately predict future responses. This work forms part of an international collaboration between Dr Ian Barnes (RHUL, London), Professor Nigel Yoccoz (Tromsø, Norway) and Dr Love Dalen (Stockholm, Sweden) and will likely lead to high quality publications.

Our general research involves the use of DNA recovered from palaeontological and archaeological remains - ancient DNA. We have previously employed ancient DNA techniques to investigate mobility and population change in a range of taxa including brown bears (Valdiosera et al. 2007, *Molecular Ecology* 16, 5140; Barnes et al. 2002, *Science* 295, 2267) and woolly mammoth (Barnes et al. 2007, *Current Biology* 17 1072); our current research expands our taxonomic focus and methodological approach (see <http://www.rhul.ac.uk/-biological-sciences/AcademicStaff/Barnes/>).

Candidates must be highly motivated, capable of independent work, and have a relevant degree and experience. Proven ability in the application of molecular biology techniques to ecological and evolutionary questions is also essential. Knowledge of ancient DNA, phylogenetic and population genetic methods, and Late Pleistocene climate and environments are desirable.

The project is funded by the Natural Environment Research Council as part of the FP7 ERA-NET program BiodivERsA.

For informal enquiries please contact Dr Ian Barnes (ian.barnes@rhul.ac.uk).

Further Details please visit our website

<http://www.rhul.ac.uk/Personnel/JobVacancies/-AcademicResearch.html> or contact Human Resources on 01784 414241, email: recruitment@rhul.ac.uk

Please quote the reference number X0209/5255.

ian.barnes@rhul.ac.uk ian.barnes@rhul.ac.uk

ULouvain MosquitoEvolution

Postdoctoral Fellowships on invasive mosquitoes

Framework

The globalization of the exchanges and global warming create suitable conditions for the spread of invasive species and the (re)emergence of vector-borne diseases in the temperate-zone countries such as Belgium. The MODIRISK project, in place for 2 years, have pro-

vided data on the distribution of endemic and invasive mosquitoes in Belgium. In that context, an exotic species was identified in a single place, without immediate danger of diseases transmission. However, complementary analyses are planned.

The aim of this postdoc study is to determine the potential risks for human being. Trophic preferences will be evaluate by sequencing PCR products of the cytochrome b gene of mitochondrial DNA from blood fed mosquitoes. Detection of virus from field-collected mosquitoes, and avian samples will be done by a Reverse Transcriptase PCR (RT-PCR) assay.

Field population analyses will be also perform.

Missions -Demographic surveillance of the invasive species populations -Determination of the trophic preferences of three mosquitoes species (*Ochlerotatus japonicus*, *Anopheles plumbeus*, *Culex pipiens*) (PCR assay) -Determination of the infectious status of the three species (RT-PCR assay). -Study about larval competition of the invasive species

Skills and profile

- PhD in ecology, medical entomology, biology.
- Advanced experience in major molecular biology techniques.
- An experience in the domains of mosquitoes if possible
- Autonomy, motivation, initiative, analysis and synthesis ability.
- Good written and spoken communication skills in English and French.
- Driving licence needed

Duration : 12 months

Applicant should email to David.Damiens@uclouvain.be with a short statement of research interests, Curriculum Vitae, Publication list, contact information for three references. Position is available immediately

David Damiens Thierry Hance Université Catholique de Louvain, Ecology and Biogeography Unit Croix du Sud, 4-5 (Carnoy) B-1348 LOUVAIN-LA-NEUVE, Belgique Tel +32 10 47 3031 Fax : +32 10 47 3490 E-mail : David.Damiens@uclouvain.be

thierry.hance@uclouvain.be

thierry.hance@uclouvain.be

UmeaU macroevolution

A 2-year postdoc position: phylogenetic studies of the role of speciation in macroevolution

Umeå University, Sweden. Dept. Ecology & Environmental Sciences

A much debated issue in evolutionary biology is the relation between micro- and macroevolution, in particular the question whether or not differences between species are the cumulative effect of microevolutionary processes taking place in established species. The research group of Dr. Folmer Bokma investigates that question by using phylogenetic analyses of nucleotide sequences, gene (co-)expression, and morphological traits. Highly motivated candidates with relevant expertise in bioinformatics, molecular genetics, or mathematical statistics are encouraged to get in contact.

The position is available at the earliest possible time point. For further information, please contact Dr. Folmer Bokma, Department of Ecology and Environmental Sciences, (+46 90 786 7121) or folmer.bokma@emg.umu.se, or look at www.emg.umu.se/projects/macroevolution/. To qualify for the position you should have a PhD degree or equivalent, preferably not more than three years old. Your application, in English, must include a short summary (max 1 page) of your previous experience, a short description (max. 1 page) of how you could contribute to the research, a curriculum vitae with a list of publications, and names and contact details of three references.

Your complete application, marked with reference number 315-197-09, should be sent to jobb@umu.se (state the reference number as subject) or to the Registrar, Umeå University, SE-901 87 Umeå, Sweden to arrive March 31, 2009 at the latest. Documents sent electronically should be in MS Word or PDF format.

Folmer Bokma Dept. Ecology & Environmental Science Umeå University, Sweden folmer.bokma@emg.umu.se

ence on local adaptation. The successful applicant will genotype sticklebacks from natural populations, perform common garden breeding experiments, and analyse genetic and phenotypic data. As a joint project of the research groups of Professor Göran Englund (spatial fish ecology) Professor Frank Johansson (phenotypic plasticity) and Dr. Folmer Bokma (phylogenetics) this offers an interesting, cross-disciplinary scientific environment. Highly motivated candidates with relevant expertise in ecology and molecular genetics are encouraged to get in contact. Previous experience with stickleback research is considered an advantage.

The position is available at the earliest possible time point. For further information, please contact Dr. Folmer Bokma, (+46 90 786 7121) or folmer.bokma@emg.umu.se, or look at <http://www.emg.umu.se/projects/macroevolution/>. To qualify for the position you should have a PhD degree or equivalent, preferably not more than three years old. Your application, in English, must include a short summary (max 1 page) of your previous experience, curriculum vitae, list of publications, and names and contact details of three references. Union information is available from SACO, +46-(0)90-786 53 65, SEKO civil, +46-(0)90-786 52 96 and ST, +46-(0)90-786 54 31. Documents sent electronically should be in MS Word or PDF format. Your complete application, marked with reference number, should be sent to jobb@umu.se (state the reference number as subject) or to the Registrar, Umeå University, SE-901 87 Umeå, Sweden to arrive April 24, 2009 at the latest.

Folmer Bokma Dept. Ecology & Environmental Science Umeå University, Sweden folmer.bokma@emg.umu.se
folmer.bokma@emg.umu.se
folmer.bokma@emg.umu.se

UmeaU SticklebackGenetics

2-year postdoc position: stickleback ecological genetics Umeå University, Sweden. Dept. Ecology & Environmental Sciences

We are looking for a post-doc to study local adaptation and phenotypic plasticity in isolated populations of sticklebacks in northern Sweden. After the most recent ice age, some stickleback populations became land-locked in ponds in which they are the only fish species, while other populations coexist with predators. This project aims to study the effect of predator pres-

UMichigan MouseSpeciation

Postdoctoral position in genomics of speciation in house mouse

A postdoctoral position is available in the research group of Priscilla Tucker at the University of Michigan Department of Ecology and Evolutionary Biology and Museum of Zoology. The project, NSF funded collaborative research, is focused on finding genes responsible for reproductive isolation between closely related house mouse taxa. The position involves genetic and bioinformatic analyses of a genome-wide sample of SNPs (1 per

2MB) collected from a large number of naturally occurring hybrid mice. Some background on the project can be found in the following publication - Teeter et al., 2008 Genome Research 18:67-76.

Applicants must have demonstrated expertise in the field of bioinformatics, computational biology or genomics and experience in computer programming. The position is available for 1 year with the possibility of renewal. Anticipated start date is between June and September 2009. Salary is \$32,000 plus a benefits package.

Interested applicants should contact Priscilla Tucker ptuck@umich.edu with a cover letter, CV, a one page statement of research interests and the names and contact information of three references.

ptuck@umich.edu ptuck@umich.edu

UMichigan Yeast Evolutionary Genetics

Postdoctoral position in yeast evolutionary genetics/genomics at University of Michigan

A postdoctoral position is available in the lab of Jianzhi George Zhang to use the budding yeast *Saccharomyces cerevisiae* and its relatives as model organisms for the study of evolutionary processes. Potential topics include but are not limited to (1) the molecular basis of adaptation, (2) genic and genomic bases of reproductive isolation, (3) mechanisms of retention and functional divergence of duplicate genes after gene/genome duplication, and (4) driving forces and molecular mechanisms of transcriptome evolution. Potential approaches include experimental evolution and next-generation sequencing, in addition to yeast molecular genetics.

The position requires a motivated individual with an interest in evolutionary genetics and experience in yeast genetics/genomics. Experience in analyzing genome-wide data of DNA sequences, transcriptomes, and/or gene functions will be a plus.

Applicants should email a short statement of research interests, CV, and contact information for three references to jianzhi@umich.edu. The position is available immediately.

For further information about the Zhang lab, see <http://www.umich.edu/~zhanglab/> Jianzhi George Zhang Department of Ecology and Evolutionary Biology Uni-

versity of Michigan 1075 Natural Science Building 830 North University Avenue Ann Arbor, MI 48109, USA Tel: 734-763-0527 Email: Jianzhi@umich.edu <http://www.umich.edu/~zhanglab/> jianzhi@umich.edu jianzhi@umich.edu

UNorthCarolina Chapel Hill Biogeography

Biogeography of climate change Postdoc

A postdoctoral position in mechanistic species range modeling is available in the research group of Lauren Buckley at the *University of North Carolina* at Chapel Hill (www.bio.unc.edu/Faculty/Buckley/Lab/). Lab research combines theory, field and lab ecology and physiology, and informatics to examine how biology (morphology, physiology, and life history) determines an organism's response to environmental change. The researcher will develop a project to advance mechanistic range models, ideally to incorporate evolutionary adaptation or species interactions. While North American lizards will be the default study system, applicants with interest and experience working on any system amenable to developing mechanistic range models are encouraged to apply. Skills in several of the following areas are highly desirable: programming, population or quantitative genetic theory, GIS and spatial analysis, and field and lab physiology. The position is available for 1 year with the possibility for renewal depending on performance. Anticipated start date between June and Sep 2009. Salary range \$36-40K depending upon experience. Application review will begin on April 15 and will continue until the position is filled. Apply by sending curriculum vitae, statement of research interests, and the names and contact information of three references to buckley@bio.unc.edu <<mailto:buckley@bio.unc.edu>>.

Lauren Buckley <Buckley@bio.unc.edu>

UNottingham Molecular Adaptation

University of Nottingham (UK) - Institute of Genetics - School of Biology

Postdoctoral Research Fellow

Applications are invited for the above post to undertake molecular genetics research in livestock and their wild relatives. The research will focus on unravelling both molecular mechanisms of adaption in livestock, including disease resistance traits, and livestock domestication patterns and history. This is a research position which will involve the use of a range of experimental and bioinformatic approaches to undertake internationally competitive research in the field of animal adaptive genetic diversity. The person appointed will also contribute to the day-to-day management of research activities, the day-to-day training and supervision of undergraduate and postgraduate students, and the preparation of research grant proposals and of research articles for publication.

Candidates must possess a PhD in livestock or animal (non-human) molecular genetics and have postdoctoral research experience in livestock genetics, including proven ability to lead research projects. An excellent population genetics background is expected, as well as excellent bioinformatics skills applied to the large scale analysis of DNA sequences and genome wide scanning polymorphisms.

Salary will be within the range £27,183 - £35,469 per annum depending on qualifications and experience (salary can progress to £38,757 per annum, subject to performance). This post is available from 1 May 2009 and will be offered on a fixed-term contract for a period of three years.

Informal enquiries may be addressed to Professor O Hanotte, tel: + 44 (0)115 951 3219 or Email: Olivier.Hanotte@Nottingham.ac.uk, skype: redjunglefowl, WWW: <http://lib.bioinfo.pl/auth:Hanotte,O> . To apply online please go to:

<http://jobs.nottingham.ac.uk/vacancies.aspx?cat=160#j4818>

Olivier Hanotte, PhD Professor of Population and Conservation Genetics Director of the Frozen Ark University of Nottingham School of Biology Nottingham NG7 2RD United Kingdom Tel: 0115 9513256 Fax: 0115 9513251 E-mail: olivier.hanotte@nottingham.ac.uk; frozen.ark@nottingham.ac.uk skype: redjunglefowl <http://www.frozenark.org/> The Frozen Ark Project is a Registered UK Charity (No 1118044). To donate please visit our website www.frozenark.org

Olivier Hanotte <Olivier.Hanotte@nottingham.ac.uk>

UppsalaU EvolutionaryBiol

Postdoc-position available at the Department of Evolutionary biology, Uppsala University

A postdoctoral research position in Evolutionary Genetics/genomics is available at the Department of Evolutionary Biology at Uppsala University. This postdoc will be in the research-group of Dr Hanna Johannesson and offers an opportunity to explore a wide range of evolutionary paradigms, from the genomic consequences of selfing vs outcrossing, to the early steps in the evolution of sex chromosomes.

Our research group uses the filamentous ascomycete genus *Neurospora* as a model system. *Neurospora* is well suited for studies on reproductive systems since its closely related species exhibit a wide spectrum of reproductive behavior. Furthermore, we use the mating-type chromosome of *Neurospora tetrasperma* as a simple, general, model for studies of the early evolution of sex chromosomes from autosomes. It shares features with the complex sex chromosomes found in the animal and plant kingdom, but is not affected by complex sex-biased evolutionary forces such as sexual selection and male biased mutation rate.

The postdoc-project can be developed after the interest of the applicant, but should preferably involve large scale SNP-typing and/ or high throughput sequencing of natural populations of *Neurospora*.

The Program in Evolutionary Biology (<http://www.egs.uu.se/evbiol/index.html>) is situated in the Evolutionary Biology Centre in central Uppsala. The working atmosphere is international with English as working language. The Evolutionary Biology Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, with research programs including ecology, systematics, genetics, genomics, and developmental biology.

Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 40 minutes with train from Stockholm.

Required qualifications for applicants are 1) a PhD in Biology, Genetics, Evolutionary Biology, Microbiology or related field, 2) experience in one or several of the following areas: bioinformatics, population genetics, evolutionary biology, genetics, microbiology, mycology,

and 3) demonstrated communication skills in English.

The position is for two years, and will imply full salary. Start date ASAP. Review of applications will begin immediately and continue until the position is filled.

To apply, send your CV, including contact information for two references, and a cover letter stating your research interest to: Dr Hanna Johannesson, hanna.johannesson@ebc.uu.se. Hanna Johannesson, hanna.johannesson@ebc.uu.se.

UTexasAustin ModelingWildlifeDisease

NSF POSTDOCTORAL POSITION: NETWORK MODELS OF WILDLIFE DISEASE DYNAMICS

One post-doctoral position is available in Professor Lauren Ancel Meyers research group (<http://www.bio.utexas.edu/research/meyers/>) at The University of Texas at Austin in the Section of Integrative Biology. Funding is from an NSF grant held by Professor Meyers. Projects will include developing new network-based mathematical methods for modeling disease transmission through complex wildlife populations, and applying these methods to understanding the ecological and evolutionary dynamics of viruses in Serengeti lion populations.

This position will require a motivated individual who has published in epidemiology, ecology, evolutionary biology, population biology, network modeling, applied mathematics, statistical physics and/or computer science. Mathematical and/or computational modeling skills are essential.

The salary will be \$40,000 to \$45,000 per annum, commensurate with training and experience. Funding is available for two years.

To apply please send CV, brief statement of research interests and contact information for two academic references to laurenmeyers@mail.utexas.edu

Lauren Ancel Meyers Section of Integrative Biology The University of Texas at Austin Ph 512-471-4950 Fax 512-471-3878 laurenmeyers@mail.utexas.edu www.bio.utexas.edu/research/meyers Lauren Meyers <laurenmeyers@mail.utexas.edu>

UTexas YaleSchoolPublicHealth ModelingInfluenza

NIH MIDAS POSTDOCTORAL POSITIONS: MODELING INFLUENZA TRANSMISSION AND INTERVENTION

Two post-doctoral positions are available to join either Professor Galvani's group (<http://info.med.yale.edu/epi/faculty/labs/galvani/>) at Yale Medical School in the Department of Epidemiology and Public Health or Professor Meyers' group (<http://www.bio.utexas.edu/research/meyers/>) at The University of Texas at Austin in the Section of Integrative Biology. Funding is from an NIH MIDAS grant held jointly by Dr Galvani and Dr Meyers, and projects will be pursued in collaboration with both PIs. The focus of the research would be to develop and analyze models of influenza transmission.

This position will require a motivated individual who has published in epidemiology, population biology, network modeling, economics, applied math, statistical physics and/or computer science. Mathematical and/or computational modeling skills are essential.

The salary will be at least according to NIH pay scale, commensurate with experience and expertise. Funding is available for five years.

To apply please send CV, brief statement of research interests and contact information for two academic references to alison.galvani@yale.edu or laurenmeyers@mail.utexas.edu.

Lauren Ancel Meyers Section of Integrative Biology The University of Texas at Austin Ph 512-471-4950 Fax 512-471-3878 laurenmeyers@mail.utexas.edu www.bio.utexas.edu/research/meyers Lauren Meyers <laurenmeyers@mail.utexas.edu>

UToronto EvolutionBiol 2

LAST CALL: Post-Doctoral Fellowships in Ecology and Evolution, broadly defined.

DEADLINE: 3/20/2009

DETAILS:

The Department of Ecology and Evolutionary Biology < www.eeb.utoronto.ca > at the University of Toronto invites applications for Departmental Postdoctoral Fellowships in the areas of Ecology and Evolutionary Biology, broadly defined. One position is available this year, and we expect that another will become available next year through an ongoing EEB Post-Doctoral Fellowship Program. Positions may continue for two years, subject to review after one year, and can begin as early as July 1, 2009. The salary is \$40,000 Canadian per year, with research expenses covered by the Post-Doctoral Advisor.

The Fellow will be a fully participating member in the Department. Candidates must identify and communicate with a potential advisor (or advisors) in advance of the application process. All full-time faculty members at the St. George (downtown) campus of the University of Toronto are eligible to serve as advisors (see < www.eeb.utoronto.ca/postdoc/ > for a list of potential supervisors). Opportunities for teaching in an upper level course may be available.

To apply, applicants should first contact and obtain the agreement of a faculty advisor (or co-advisors). Afterwards, applicants should submit a cover letter clearly indicating the proposed faculty advisor(s), a curriculum vitae, copies of 2 publications, and a short (1-3 pages) description of past research accomplishments and future research plans. Applicants should include names and e-mail addresses for two potential referees. Applicants should also indicate the date they will be available to begin the position. All application materials must be submitted as PDF's in a single email to: Elizabeth Rentzelos <chairsec.eeb@utoronto.ca>.

For more information about the Department, contact your potential supervisor. Queries regarding the fellowship program should be directed to Demetrios Voudouris <demetrios.voudouris@utoronto.ca> Review of applications will begin on March 20, 2009.

Toronto is a vibrant, multicultural city on the shore of Lake Ontario, with rich cultural options in the arts, music and film, ethnic cuisine, and a high quality of life. The EEB department is home to an interactive, collegial group of ecologists, geneticists, and evolutionary biologists, and currently supports a strong group of Post-Doctoral Fellows with diverse research interests.

John Stinchcombe Department of Ecology and Evolutionary Biology University of Toronto, 25 Willcocks St. Toronto, ON Canada M5S 3B2

416-946-5986

<http://labs.eeb.utoronto.ca/stinchcombe/> John Stinchcombe <john.stinchcombe@utoronto.ca>

UVictoria InsectProtistEvolution

Postdoctoral Research Position: Evolution of Associations between Insects and Protists

Institutions: Canadian Institute for Advanced Research, Program in Integrated Microbial Biodiversity; Department of Biology, University of Victoria; Departments of Zoology & Botany, University of British Columbia.

Starting date and duration: The appointment may begin as early as July 15, 2009. The successful applicant will be appointed for 2-years.

Project description V Background

Symbioses between insects and microbes are ubiquitous and far-reaching. Recently there has been enormous interest in the ecology, evolution, and genomics of infectious microbes of insects; this work has focused primarily on inherited bacterial symbionts. There have been comparatively few studies on associations between insects and microbial eukaryotes. We are seeking a CIFAR-Integrated Microbial Biodiversity postdoctoral fellow who will work on highly collaborative research between the labs of Steve Perlman (ecology and evolution of insects and their associates, web.uvic.ca/~stevep/) at U. Victoria, and Patrick Keeling (protist genomics and evolution, www.botany.ubc.ca/keeling/) at U. British Columbia. The goal of this research is to make exciting advances in the area of insect-protist associations.

Possible research avenues:

Molecular approaches to the study of microsporidian male-killers V Diverse inherited microbes of insects increase their transmission by manipulating their hosts reproduction. One common manipulation is to kill male hosts, and this has evolved independently numerous times in bacteria, and at least once in microsporidians infecting mosquitoes. Microsporidian male-killers have received much less attention, and they are unusual in that they kill their hosts late in larval development, just before male mosquitoes pupate and emerge from the water as adults. Male-killing coincides with the release of massive amounts of spores that are infectious to copepods, and thus represents the outcome of a developmental switch V infectious transmission in male

hosts versus maternal transmission in females. Little is known about the mechanism of male-killing, or whether and how microsporidians recognize host sex. This project proposes to address this question by using subtractive hybridization, rtPCR, and ESTs to screen for microsporidian genes with sex-specific expression.

Evolution of Drosophila-protist associations V Surprisingly little is known about microbial eukaryotes infecting Drosophila. This project aims to a) characterize novel infections by screening natural populations of Drosophila for infectious protists, particularly microsporidia, yeasts, trypanosomes, and gregarines; b) measure the effects of infection on host fitness; c) determine how infections alter the expression of immune and stress response genes, and d) test whether inherited bacterial endosymbionts (e.g. Wolbachia) affect resistance to infection. Application package:

A complete application package includes a CV (including list of publications), a brief (1-page) statement of research interests, and the names and e-mail addresses of 3-4 referees (at least 3 of which are not CIFAR program members). Applications must be received by March 31, 2009. Send application to: Dr. Steve Perlman (stevep@uvic.ca)

John Archibald <jmarchib@dal.ca>

UWashington SalmonSNPs

University of Washington Postdoctoral Openings
SNP Discovery and Applications in Pacific Salmon

Position Overview:

Organization: School of Aquatic and Fishery Sciences,
College of Ocean and Fishery Sciences

Title: Research Associate

Position details:

The School of Aquatic and Fishery Sciences (SAFS <<http://fish.washington.edu/>>) at the University of Washington has openings for up to two postdoctoral Research Associates (100% time) to conduct research on SNP discovery using next generation sequencing or possibly SNP applications in Pacific salmon. These are 2-year positions with the possibility to extend depending upon funding. The positions are not eligible for tenure.

The general scope of the appointments may include but

is not limited to:

- * Development SNPs using next generation sequencing and resequencing.
- * Bioinformatics.
- * Original research on salmon population genetics and conservation.
- * Work with regional fisheries managers to apply SNP research to contemporary problems.
- * Formulation of problems, analysis of data, production of scientific papers, and presentation at scientific meetings.
- * Mentor and otherwise assist graduate students who are doing projects in salmon genetics and supervise hourly help involved in data analysis.

Requirements:

- * Ph.D. in genetics, biology, or a related field

The following experience is desired: * DNA sequencing
* Bioinformatics

Positions are located at the University of Washington, Seattle, WA. 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.

“University of Washington faculty engage in teaching, research and service.”

Interested persons should send CV, short letter of intent including names and contact information for three references via email to Dr. Jim Seeb, School of Aquatic and Fishery Sciences, University of Washington (jseeb@u.washington.edu <<mailto:rayh@u.washington.edu>>). Review of applications will start April 24, 2009 and continue until the positions are filled. For successful candidates, a background check for criminal history is required.

Jim Seeb Research Professor International Program for study of Salmon Ecological Genetics School of Aquatic and Fishery Sciences University of Washington 1122 NE Boat Street, Box 355020 Seattle, WA 98105-5020, USA

Phone: 206 685 2097

Jim Seeb <jseeb@u.washington.edu>

UZurich PostDoc GradPositions ModelingGrowth

Post-doctoral Position

Institute of Environmental Sciences, University of Zurich

Modelling Growth of Tropical Tree Seedlings

This project will use modern modelling approaches (mechanistic process models, maximum likelihood and MCMC estimation) to analyse several existing datasets on the growth and survival of tropical tree seedlings from Bornean rainforests. How do plants grow? How do they allocate photosynthate to different structures such as leaves, stems, roots and flowers in different environments, and how do they make such decisions? These are the type of questions we are interested in.

We are looking for an experienced and well-motivated person to join our team of students and post-docs working on plant growth. Applicants need to hold a relevant PhD and be experienced with computer programming and statistical modelling (particularly using C and R). A background in statistics and some knowledge of plant ecology is also desirable. The project is a collaboration between the groups of Andy Hector, Lindsay Turnbull (<http://www.uzh.ch/uwinst/>) and Drew Purves (Microsoft Research, Cambridge, U.K).

Key reference: Turnbull, L. A., Paul-Victor, C., Schmid, B. & Purves, D. W. (2008) *Ecology*, 89, 1352.

Start data: From April 2009.

Working language: English

Salary: Up to approx. 94,000 CHF.

Please send a short relevant electronic CV and application letter to weilen@uwinst.uzh.ch entitled: Your-NameCV.ext.

2 PhD Positions

Institute of Environmental Sciences, University of Zurich

Structure and Functioning of Forest Ecosystems

We are looking for well-motivated candidates for PhD projects on the diversity, stability and functioning of forest ecosystems. The projects will extend work on the relationship between diversity and functioning of ecosystem in grasslands (<http://www.uzh.ch/uwinst/>) to forest ecosystems. One project will be associated with the Sabah Biodiversity Experiment in Malaysian Borneo (experience of tropical would be advantageous) and the other project will work with data from temperate forests.

Applicants need to hold a relevant Honours or (preferably) Masters degree. You should have a good background in ecology and experience of the relevant forest ecosystems would be advantageous. The project will re-

quire knowledge of statistics and programming (particularly using R and C). The projects are collaborations between the groups of Andy Hector, Lindsay Turnbull at the University of Zurich (<http://www.uzh.ch/uwinst/>) and external groups, particularly Drew Purves at Microsoft Research, Cambridge, U.K.

Start data: From April 2009.

Working language: English

Salary: 40 - 45,000 CHF.

Please send a short relevant electronic CV and application letter to weilen@uwinst.uzh.ch entitled: Your-NameCV.ext.

PhD Position

Institute of Environmental Sciences, University of Zurich:

Data-Constrained Plant Growth Modelling

How do plants grow? How do they allocate photosynthate to different structures such as leaves, roots and flowers in different environments, and how do they make such decisions? This project seeks to understand plant growth with the simplest possible assumptions and will use extensive data sets and modelling to approach this problem from an entirely new angle. The project will involve extensive computer modelling including both simulations and fitting models directly to data. The project may also include new data collection depending on the interests and aptitudes of the successful candidate.

We are looking for a well-motivated person to conduct this research, culminating in a PhD from the University of Zurich, Switzerland. Applicants need to hold a good, relevant first degree and have some experience with computer modelling. They must also be able to work in a team with other students and post-docs. A background in statistics and some knowledge of plant ecology is also desirable. The project is funded by Microsoft Research, UK and the successful candidate will receive extensive help and technical support from this source. The project will be based in Zurich, where the successful candidate will be expected to live. The project is co-supervised by Dr. Lindsay Turnbull (University of Zurich) and Dr. Drew Purves (Microsoft Research, UK) and requires an immediate start.

Key reference: Turnbull, L. A., Paul-Victor, C., Schmid, B. & Purves, D. W. (2008) *Ecology*, 89, 1352.

Working language: English

Salary: 40 - 45,000 CHF.

Please send your CV and application to:

sayt@uwinst.uzh.ch. Please label your attached CV file: "CV.applicant.name.doc"

weilen@uwinst.uzh.ch

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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>

WorkshopsCourses

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Bamfield BritishColumbia EvolutionMarineOrganisms Jul6-24

'Evolution & Development of Marine Organisms' is a senior undergraduate and graduate level course that will be an introduction into both comparative and experimental embryology with particular emphasis on early development of marine invertebrates in the vicinity of the Bamfield Marine Sciences Centre. The course will include lectures, field collection, species identification, laboratory observations, embryo and larval rearing, and experimentation. Students will have the opportunity to apply contemporary cellular and molecular marking techniques in their independent projects. Emphasis is placed on seeking both underlying unity as well as diversity in developmental processes and mechanisms.

3 weeks, 6 July - 24 July

INSTRUCTORS: Dr. Cory Bishop, Dalhousie Univer-

sity Dr. Chris Cameron, Université de Montréal

To apply please go to: <http://www.bms.bc.ca/university/courses2009/index.htm>
c.cameron@umontreal.ca c.cameron@umontreal.ca

Dublin MuseumSummerResearch deadline29Mar

Dear all,

There are two weeks until the deadline for organismal biology summer undergraduate research placements in Dublin, with University College Dublin and the National Museum of Ireland.

Research areas include: bio-control, plant genomics, limnology, soil ecology, palaeontology, marine invertebrates, and ecological modelling.

To apply students must submit an application form,

explaining their interest in a specific research topic on offer, and a letter of support to <ureka@ucd.ie>

Full funding will be provided for 10 students, including accommodation in Dublin, living allowance, airfare assistance, and research project expenses. We particularly encourage applications from less developed countries and students from [local] minority groups.

Deadline: 29 March Term dates: June 15 to August 21 2009 Details: <http://www.ucd.ie/ureka> Apologies for cross postings; please bring this to the attention of any eligible students!

Kind regards,

The UREKA Team

Julia Sigwart, CoBiD director Collections-based Biology in Dublin Undergraduate Research Experience & Knowledge Award www.ucd.ie/ureka CoBiD-UREKA <ureka@ucd.ie>

The Summer School course will be held at Eawag Kastanienbaum, near Lucerne, in Switzerland. Eawag is the Swiss Federal Institute of Aquatic Science and Technology, and the Kastanienbaum Centre for Ecology, Evolution and Biogeochemistry (CEEB) is situated at the shores of Lake Lucerne. It offers seminar rooms, laboratories, and on-site housing for students.

For further information and online application, please visit our website: http://www.eawag.ch/programs/-phd_ss_2009/index_EN For questions, please contact us via email: summerschool2009@eawag.ch

Steering committee Dr. Helmut Bürgmann Dr. Blake Matthews Dr. Hitoshi Araki

Eawag, Swiss Federal Institute of Aquatic Science and Technology Center for Ecology, Evolution and Biogeochemistry Seestrasse 79, CH-6047 Kastanienbaum, Switzerland

“Araki, Hitoshi” <Hitoshi.Araki@eawag.ch>

Eawag Switzerland SummerSchool Jul5-18

PhD Summer School 2009

“Interactions between ecological and evolutionary processes in aquatic systems”

will be held in July 5th-18th, 2009, at Eawag Kastanienbaum, Switzerland

Now all 6 invited lecturers are assigned: Prof. James Elser (Arizona State University) Prof. Nelson Hairston (Cornell University) Prof. Eric Triplett (University of Florida) Prof. Andrew Hendry (McGill University) Prof. Elena Litchman (Michigan State University) Prof. Luc De Meester (K. U. Leuven)

The course will confront selected PhD students with the challenge of integrating ecosystems ecology and evolutionary biology, arguably the least well-integrated pair of disciplines in ecology. Some have described this challenge as the last missing synthesis in ecology. We will take a multidisciplinary look at lake ecology, ask how nutrient fluxes shape microbial and algal activity and diversity, how these in turn exert ecological and evolutionary pressure on organisms at higher trophic levels, and lastly, how adaptive evolution at higher trophic levels exerts ecological pressures at lower levels that possibly change ecosystem dynamics. The 2009 course will be built around different aspects of ecological stoichiometry.

Frauenchiemsee Germany HostParasiteCoevolution Sep20-25

The Munich Graduate Program for Evolution, Ecology and Systematics (EES) invites applications for the international EES summer school on Host-Parasite Coevolution held at Frauenchiemsee (80 km east of Munich) from September 20th to September 25th, 2009.

The 5-day summer school will consist of lectures, discussions and exercises organized by the local and invited instructors, as well as oral and/or poster contributions by the students. We will cover theoretical aspects of host-parasite evolution and discuss empirical approaches for studying coevolution. Specific topics will include the evolution of virulence and resistance, local adaptation and spatial structuring in host-parasite systems, and the molecular signature of coevolution.

Instructors (confirmed): Mike Boots, University of Sheffield, UK (theoretical analysis of disease dynamics in humans and wildlife) Jukka Jokela, ETH Zurich, Switzerland (maintenance of sex driven by host-pathogen coevolution) David Nash, University of Copenhagen, Denmark (coevolution on geographical scales) Peter Tiffin, University of Minnesota, USA (molecular coevolution between plants and parasites)

Local Instructors/Organizers at Ludwig-Maximilians-University Munich: Susanne Foitzik, Pleuni Pennings,

Laura Rose, Aurelien Tellier, Volker Witte, and Justyna Wolinska.

The summer school is open to all graduate students (PhD, Masters, Diplom biologists). The summer school will be taught in English. Participants should plan to arrive Sunday, Sept. 20th. The summer school will wrap up on Friday, Sept. 25th in the early afternoon.

Costs: Thanks to support from the Volkswagen Foundation, the University of Munich's EES program will cover housing and meals during the Summer School. Participants are required to cover their own travel expenses and pay a 50 Euro registration fee. A small amount of funding is available to subsidize travel costs for students from the most distant locations.

The Application Procedure: Applicants should submit a single pdf file containing the following: a) a one page CV b) a one page motivation letter for attending the summer school c) a short abstract of your research project (maximum 200 words) Email applications to Dr. Elisabeth Brunner (brunner@biologie.uni-muenchen.de). Application Deadline: June 1st, 2009.

Further information is available at: http://www.eeslmu.de/eeswiki/Summer_school_2009 Dr. Laura Rose Department Biologie - Biozentrum University of Munich Grosshaderner Str. 2 82152 Planegg Germany

Phone: 49 89 2180 74 150 Fax: 49 89 2180 74 104 Email: rose@zi.biologie.uni-muenchen.de Web: www.zi.biologie.uni-muenchen.de/evol/EvoBio rose@zi.biologie.uni-muenchen.de rose@zi.biologie.uni-muenchen.de

Hinxton HumanGenomics Aug16-20

We are pleased to announce the opening of registration for the Wellcome Trust School of Human Genomics 2009 < https://registration.hinxton.wellcome.ac.uk/-display_info.asp?id=139 > , which will be held from the 16th - 20th August 2009, at the Wellcome Trust Conference Centre, Hinxton, Cambridge, UK.

This is an opportunity for current scientific leaders to interact with future stars in the field, and for students to learn and be inspired by those that have shaped human genomics in the last decade.

We would all like to see great students tutored in the great way they deserve, by the best minds in the field. With this aspiration, we are organising the 2nd School

of Human Genomics at the Wellcome Trust Genome Campus from 16 - 20 August 2009. The School of Human Genomics is a 4-day meeting that brings together prominent human geneticists and senior PhD students.

The schedule of this course is designed to be highly interactive with integrated presentations by the tutors and students, discussions about current topics in human genetics, and one-to-one meetings between tutors and students. Organisers:

Leena Peltonen, Wellcome Trust Sanger Institute, UK

Manolis Dermitzakis, Wellcome Trust Sanger Institute, UK

Tutors include:

Stylianos Antonarakis, University of Geneva, Switzerland

Ines Barroso, Wellcome Trust Sanger Institute, UK

Jeffrey Barrett, Wellcome Trust Sanger Institute, UK

Stephan Beck, University College London, UK

Nigel Carter, Wellcome Trust Sanger Institute, UK

Aravinda Chakravarti, Johns Hopkins University, USA

Paolo Gaspirini, IRCCS-Burlo Garofolo/University of Trieste, Italy

Richard Gibbs, Baylor College of Medicine, USA

Harald Göring, Southwest Foundation for Biomedical Research, USA

Matt Hurles, Wellcome Trust Sanger Institute, UK

Nicholas Katsanis, Johns Hopkins University, USA

Augustine Kong, Decode Genetics, Iceland

Kirstin Lindblad-Toh, Uppsala University & Broad Institute of MIT & Harvard

Jim Lupski, Baylor College of Medicine, USA

Mark McCarthy, University of Oxford, UK

Aarno Palotie, Wellcome Trust Sanger Institute, UK

Mike Stratton, Wellcome Trust Sanger Institute, UK

Jussi Taipale, University of Helsinki, Finland

Chris Tyler-Smith, Wellcome Trust Sanger Institute, UK

Gavin Wright, Wellcome Trust Sanger Institute, UK

To register < https://registration.hinxton.wellcome.ac.uk/-display_info.asp?id=139 > and for more information, including speakers, please click Here < <https://registration.hinxton.wellcome.ac.uk/>

display_info.asp?id=139 >

https://registration.hinxton.wellcome.ac.uk/-display_info.asp?id=139 Please ensure that you complete the Application Form < <http://www.wtconference.org.uk/Forms/-WTSHGApplicFormv2.doc> > and attach it in the Abstract Submission section during Registration < <https://registration.hinxton.wellcome.ac.uk/-register.asp?id=139> >

Please forward this email to any of your colleagues who may find the School of interest.

Emmanouil (Manolis) Dermitzakis, PhD Senior Investigator Population and Comparative Genomics The Wellcome Trust Sanger Institute Wellcome Trust Genome Campus Hinxton, Cambridge CB10 1HH UK e-mail: md4@sanger.ac.uk Tel: +44 (0)1223 492322 Fax: +44 (0)1223 494919 URL: <http://www.sanger.ac.uk/Teams/Team16/> < <http://www.sanger.ac.uk/Teams/Team16/> >

md4@sanger.ac.uk md4@sanger.ac.uk

LaFouly Switzerland EvolutionaryBiol Jun20-26 2

Evolutionary Biology Workshop in the Alps

La Fouly, Switzerland, 20-26 June 2009

We are still accepting applications until the end of this week. This is a graduate course based on a concept developed by Steve Stearns and John Maynard Smith. Target participants are advanced master students and students in the first half of their PhD. Taking place in a beautiful small Alpine village (La Fouly), it will allow you to focus while being able to enjoy the landscape and the Alpine flora. The goals are to develop the following skills:

- * developing your scientific ideas through discussions in groups;
- * thinking critically and expressing oneself clearly;
- * turning a general idea into a research project;
- * discovering the many layers of a scientific project: digging deep;
- * writing a grant proposal and defending it;
- * interacting with the faculty in an informal setting

It is you, the students, who will be in charge in this course. You will work with *your* ideas, you will decide yourself what the important questions in broadly defined evolutionary biology are, you will choose one, and propose a research project that will address it. The

faculty will visit the groups during the discussions to answer your questions and provide coaching and they will give you feedback on your proposal, but they will generally take the back seat. Additionally, the faculty will give informal talks about their research and be available for informal discussion. The language of the course is English.

Faculty: Mark Kirkpatrick (University of Texas, Austin), John Taylor (University of California, Berkeley), Ian Sanders and Tad Kawecki (both University of Lausanne, Switzerland).

Costs: there is no tuition fee; the participants will cover the costs of room and board (approximately CHF 420.-).

For more information see <http://www.unil.ch/ee/-page63533.html> To apply, send a single file (pdf or rtf) containing a short motivation letter, a cv and the name of your scientific advisor to to tadeusz.kawecki@unil.ch, with "Evolution Workshop Application" in the subject field. Deadline March 15.

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

tadeusz.kawecki@unil.ch tadeusz.kawecki@unil.ch

LaFouly Switzerland EvolutionaryBiol Jun20-26 correction

Dear Colleagues, our previous mailing about this workshop contained an incorrect URL. The correct one is: http://www.unil.ch/ee/page64465_en.html I apologize for this mistake. Sincerely, Tad Kawecki

Evolutionary Biology Workshop in the Alps

La Fouly, Switzerland, 20-26 June 2009

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in groups; * thinking critically and expressing oneself clearly; * turning a general idea into a research project; * discovering the many layers of a scientific project: digging deep; * writing a grant proposal and defending it; * interacting with the faculty in an informal setting

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For more information see <http://www.unil.ch/ee/-page64465.en.html> To apply, send a single file (pdf or rtf) containing a short motivation letter, a cv and the name of your scientific advisor to tadeusz.kawecki@unil.ch, with "Evolution Workshop Application" in the subject field. Deadline March 15.

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

LakeheadU AncientDNA May11-29

Time is running out! Register now!

Once again, the Paleo-DNA Laboratory at Lakehead University in Thunder Bay, Ontario, Canada is offering students the opportunity to participate in our Ancient DNA Training Program. This year we are delivering the program from May 11-29, 2009.

During the program, students work in small groups (one instructor to 4 students) and are given a project depending upon their interests. This may be genetic anal-

ysis of disease in ancient mummies or forensic profiling of a body or many other such projects. As a student, you will learn different extraction methods to compare and contrast on both your own DNA and other samples. You will generate your own DNA profile, determine your own mitochondrial haplogroup/haplotype, your own STR profile, confirm your own sex genetically and evaluate a great new forensic technique known as DNA Witness or identify your ancestry by DNA.

Students will learn about the different types of DNA that can be analyzed: mitochondrial, nuclear, chloroplast and pathogenic DNA. You will be taught different methods of analysis PCR-RFLP, multiplex PCR, sequencing, regular PCR and electrophoresis. You will learn different methods of sample preparation from a number of different tissue types like bone, teeth, hair, blood residues and mummified tissue.

Students will understand the use of genetic analysis and its potential in archaeozoology, palaeopathology, archaeology, forensic science, palaeobotany and palaeontology. Lectures by professors and experts in the fields of archaeology, genetics, ancient DNA, forensic science, palaeopathology and more are integrated with the laboratory sessions.

Attached to this email is the 2009 Ancient DNA Training Program Poster. We would appreciate it if you would display the poster in a prominent location, targeted specifically at anthropology, biology, bio-molecular and chemistry students. If you would like registration forms or further information, please visit our website at < <http://www.ancientdna.com/> > www.ancientdna.com or feel free to contact me at <<mailto:cjaspers@lakeheadu.ca>> cjaspers@lakeheadu.ca.

With many thanks,

Cheryl Jaspers Administrative Coordinator 2009 Ancient DNA Training Program Paleo-DNA Laboratory Lakehead University Thunder Bay, ON Phone: 1-807-343-8862 Toll Free: 1-866-DNA-LABS cjaspers@lakeheadu.ca

cdmatheson@googlemail.com

NESCENT EvolutionaryMetaAnalysis Jul6-10

AN INTRODUCTION TO META-ANALYSIS IN ECOLOGY AND EVOLUTIONARY BIOLOGY

July 6-10, 2009

A 5-day summer course sponsored by and held at the U.S. National Evolutionary Synthesis Center (NESCent < <http://www.nescent.org/> >) in Durham, North Carolina.

OVERVIEW:

The course will cover with what meta-analysis is, where it comes from, some examples of how it has been used in ecology and evolution, and its major strengths and weaknesses as a tool for the quantitative summary of research results. Students will be introduced to issues and methods for gathering data from the scientific literature and how to organize those data for analysis. Students will be encouraged to produce a preliminary meta-analysis on their own data, and will learn how to interpret, evaluate and critique the results.

INSTRUCTORS

* Jessica Gurevitch, Course Organizer, Professor and Chair, Department of Ecology and Evolution, Stony Brook University * Marc Lajeunesse, Instructor, NESCent postdoctoral fellow * Kerrie Mengersen, Instructor, Professor of Mathematical Sciences, Queensland University of Technology, Brisbane, Australia

APPLICATION DEADLINE:

March 31, 2009. For more information, and to apply, please see: <http://www.nescent.org/courses/-2009/meta.analysis/>

INQUIRIES

Jory Weintraub, NESCent Education and Outreach Program Manager, at jory@nescent.org, or 919-668-4578.

Jory Weintraub <jory@unc.edu>

NESCent GMOD Jul16-19

The application deadline for both GMOD summer schools is April 6, less than a week from now.

GMOD Summer School - Americas will be held 16-19 July at the National Evolutionary Synthesis Center (NESCent), in Durham, NC, USA. Student tuition is free. See http://gmod.org/wiki/-2009_GMOD_Summer_School_-_Americas GMOD Summer School - Europe will be held 3-6 August at the University of Oxford, in Oxford, UK. This is a part of GMOD Europe 2009, which includes the

next GMOD Meeting. Student tuition is £95. See http://gmod.org/wiki/2009_GMOD_Summer_School_-_Europe GMOD (<http://gmod.org/>) is a collection of interoperable open source software components for managing, visualizing, annotating and integrating biological, mostly genomic, data. GMOD is also a community of developers and users dealing with similar problems. GMOD is used in diverse contexts, with both emerging and established model organisms.

The courses includes training on several GMOD components: * GBrowse - the widely used Generic Genome Browser * Chado - a modular and extensible database schema for biological data * Apollo - genome annotation editor * BioMart - biological data warehouse system * GBrowse.syn - a GBrowse based synteny viewer * JBrowse - a brand new Web 2.0 genome browser * Artemis-Chado Integration (Europe only) * MAKER - Genome annotation pipeline (Americas only) * Tripal - Web front end for Chado (Americas only)

Please contact the GMOD Help Desk (help@gmod.org) if you have questions.

We hope to see you in Durham or Oxford,

Dave Clements GMOD Help Desk

Dave Clements <clements@nescent.org>

NESCent-UOxford GMOD Jul16-19-Aug3-6

We are now accepting applications for two GMOD Summer Schools being held in 2009:

Americas, 16-19 July - National Evolutionary Synthesis Center (NESCent), Durham, NC, USA - Student tuition is free, thanks to NIH grant 1R01HG004483-01. - http://gmod.org/wiki/2009_GMOD_Summer_School_-_Americas Europe, 3-6 August - University of Oxford, Oxford, United Kingdom - Part of GMOD Europe 2009, which includes the next GMOD Meeting - Student tuition is £95 - http://gmod.org/wiki/-2009_GMOD_Summer_School_-_Europe GMOD (<http://gmod.org/>) is a collection of interoperable open source software components for managing, visualizing, annotating and integrating biological, mostly genomic, data. GMOD is also a community of developers and users dealing with similar problems. GMOD is used in diverse contexts, with both emerging and established model organisms.

GMOD Summer Schools (http://gmod.org/wiki/-GMOD_Summer_School) introduce new GMOD users to the GMOD project and feature several days of hands-on training on how to install, configure and administer GMOD tools.

The courses includes training on several GMOD components: * GBrowse - the widely used Generic Genome Browser * Chado - a modular and extensible database schema for biological data * Apollo - genome annotation editor * BioMart - biological data warehouse system * GBrowse_syn - a GBrowse based synteny viewer * JBrowse - a brand new Web 2.0 genome browser * Artemis-Chado Integration (Europe only) * MAKER - Genome annotation pipeline (Americas only) * Tripal - Web front end for Chado (Americas only)

***Please submit an application by the end of 6 April 2009, if you are interested in attending. ***

Enrollment is limited to 25 students in each course. If applications exceed capacity (and we expect they will) then applicants will be picked based on the strength of their application. Applicants will be notified of their admission status in mid-April.

Thanks,

Dave Clements GMOD Help Desk help@gmod.org

http://gmod.org/wiki/2009_GMOD_Summer_School_-_Americas http://gmod.org/wiki/2009_GMOD_Summer_School_-_Europe http://gmod.org/wiki/GMOD_Europe.2009

NESCent offers various courses and workshops, as well as funding for post-doctoral and sabbatical positions, working groups and other meetings. For more information about research and training opportunities at NESCent, visit <http://nescent.org>. Sign up for our quarterly electronic newsletter at <http://www.nescent.org/about/contact.php> to automatically receive information about events at NESCent.

clementsnescnet@gmail.com

Portal Arizona Ant Systematics Aug6-16

DEADLINE FOR APPLICATION: April 1, 2009

ANT COURSE 2009 <http://www.antweb.org> Southwestern Research Station (SWRS), Portal, AZ, USA August 6-16, 2009

DEADLINE FOR APPLICATION: April 1, 2009
Application form: http://spreadsheets.google.com/viewform?key=3DpJ5tAoQvdvQ-GA_IFRxxdZA

COURSE OBJECTIVES. - ANT COURSE is designed for systematists, ecologists, behaviorists, conservation biologists, and other biologists whose research responsibilities require a greater understanding of ant taxonomy and field research techniques. Emphasis is on the identification of the ant genera and species occurring in North America. Lectures will include background information on the ecology, life histories and evolution of ants. Field trips are structured to teach collecting and sampling techniques, and associated lab work provides instruction on specimen preparation, sorting and labeling. Information on equipment/supply vendors, literature, and myrmecological contacts are also presented.

COURSE SIGNIFICANCE. - Ant Course is a unique opportunity to acquire training that is unavailable elsewhere. This course will provide students with 1) the confidence and skills to identify the ant genera of North America; 2) an understanding of modern specimen processing and curation techniques; 3) an appreciation for the biological diversity of ants, and 4) experience keying to the species level.

SPONSORS. -California Academy of Sciences and Museum of Comparative Zoology, with funding in part from National Science Foundation.

BACKGROUND INFORMATION. - ANT COURSE will be taught from August 6 - 16, 2009 at the Southwestern Research Station (SWRS) in Portal Arizona (<http://research.amnh.org/swrs/>). The Station is centered amid the richest ant fauna in North America. This is an ongoing course, offered annually.

PARTICIPANT ACCEPTANCE CRITERIA. - ANT COURSE is open to all interested individuals. Priority will be given to those students for whom the course will have a significant impact on their research with ants. An entomological background is not required. We aim to include students with a diverse interest in biology, including ant systematics, ecology, behavioral biology, genetics, and conservation. The high instructor to student ratio will allow students to receive individual attention. ANT COURSE is presented in English and limited to 30 participants

COSTS. - Tuition for the 10-day COURSE is \$475 for current students and \$675 for non-students. In addition, the Southwestern Research Station (SWRS) fee for this period, covering dormitory room and board, is \$600. Transportation costs between home and Tucson (air) or SWRS (auto) are to be borne by all participants.

FELLOWSHIPS. - Four fellowships are available for 2009. Two fellowships cover tuition fees and two fellowships cover station fees. Foreign students may apply for additional fellowships to assist in travel. Those interested in attending the course should seek all possible avenues to secure funding for the course. You should only apply for the Ant Course fellowship if you can not find other support and it is essential for your participation in the course. Beware that if you apply for an ant course fellowship it implies that fellowship funding is essential to your participation in the course. Thus, if you are not selected for a fellowship, you might not be accepted into the course. Please notify the course if your funding request status changes before the application due date.

COURSE APPLICATION. - Application and course information at <http://www.antweb.org> The first step is to fill out a form at: http://spreadsheets.google.com/viewform?key=3DpJ5tAoQvdvQ-GA_IFRxxdZA In addition, you must also submit a CV, personal statement, and letter of reference to 2009AntCourse@gmail.com.

2009 Possible INSTRUCTORS: Brian Fisher (Coordinator), Dept. of Entomology, California Academy of Sciences, San Francisco, CA, bfisher@calacademy.org Stefan Cover (Coordinator), Museum of Comparative Zoology, Harvard University, Cambridge, MA, cover@oeb.harvard.edu Lloyd Davis, Gainesville, FL, ants@gru.net Mark Deyrup, Archbold Biological Station, P.O. Box 2057, Lake Placid, Florida 33862 USA, mdeyrup@archbold-station.org Bob Johnson, Dept. of Biology, Arizona State University, Tempe, Arizona, atraj@imap1.asu.edu Mike Kaspari, Dept. of Zoology, University of Oklahoma, Norman OK, mkaspari@ou.edu Joshua King, Department of Biological Science, Unit 1, Chieftain Way, Florida State University, Tallahassee, FL 32306-4370, jking@bio.fsu.edu Jack Longino, Lab I, The Evergreen State College, Olympia WA, longinoj@evergreen.edu

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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>

**Trento Italy ForestPopGenomics
Jul22-24**

Dear Colleagues,

The INTERNATIONAL WORKSHOP 'Population and Ecological Genomics in Changing Forest Environments' will be held at the Centro di Ecologia Alpina (CEA; <http://www.cealp.it>), Fondazione Edmund Mach, on Monte Bondone, near Trento, Italy, July 22-24, 2009. This workshop will be hosted by CEA, in collaboration with the University of California, Davis, USA (Department of Plant Sciences).

The aim of the workshop is to provide up-to-date knowledge of theoretical and computational approaches to studying adaptation in changing forest environments. The workshop will emphasize the use bioinformatics tools and software packages. Participants must have their own laptop computer and have software applications installed before arriving at the CEA. Information regarding obtaining software and computer hardware requirements will be provided by the organizers in advance of the workshop.

The workshop is primarily intended for young researchers at the doctoral and post-doctoral stages, but is also open to people working outside academic institutions seeking to acquire basic knowledge useful for implementing practical management and conservation plans.

Organizers: David Neale (Dept. of Plant Sciences, UC Davis) Cristiano Vernesi (Centro di Ecologia Alpina, Research and Innovation Centre, Fondazione Edmund Mach) Claudio Varotto (IASMA Research and Innovation Centre, Fondazione Edmund Mach)

Course Instructors: David Neale (UC Davis, USA) , Jill Wegrzyn (UC Davis, USA), Andrew Eckert (UC Davis, USA) and Elena Mosca (UC Davis, USA). Invited speakers: Sally Aitken (University of British Columbia, Canada) and Brad St. Clair (USDA Forest Service, Corvallis, Oregon, USA)

Local committee: Cristiano Vernesi and Floriana Marin (secretary), Fondazione Edmund Mach.

Dates: July 22-24, 2009. Place: Centro di Ecologia Alpina, Viote del Monte Bondone, 38040 Trento, Italy. Registration: Enrollment is limited to 15 participants. Potential participants are kindly requested to submit an e-mail (events@iasma.it) along with a one-page cv and 1-page statement describing why they would like to attend the workshop. Deadline for registration is May 1, 2009. Applicants will be advised of acceptance by May 15, 2009. Fee: 200 includes lunches and dinners (from July 22-24) and the course manual. Contacts: Floriana Marin, Research and Innovation Centre, Fondazione Edmund Mach, (events@iasma.it), phone: +39 0461 615543 - Fax + 39 0461 615183

Cristiano Vernesi Centro di Ecologia Alpina Centro Ricerca e Innovazione, Fondazione Edmund Mach postal address: Viote del Monte Bondone - 38040 Trento - Italy tel +390461939523 - fax +390461948190 - skype name: cvernesi
vernesi@cealp.it vernessi@cealp.it

UAntioquia EMBO Bioinformatics Aug23-30

We are organising an EMBO course: "Advanced bioinformatic methods in the study of gene and genome evolution", at the University of Antioquia, Medellin Colombia. The course will take place from the 23 to the 30 of August 2009, and will cover topics ranging from Gene and Genome evolution to Metagenomics, Database interrogation to Bayesian phylogenetics, practical sessions, and seminars. Registrations are now open, and the deadline is: 31st May 2009. There is no registration fee for the course, EMBO covers the costs of student accommodation and communal meals for the duration of the course only. The students will be responsible to cover the cost of their travel to Colombia or any visa costs.

See the following links for the course programme and to register. Course Home Page: <http://cwp.embo.org/wpc09-04/index.html> Programme: <http://cwp.embo.org/wpc09-04/programme.html> Registration: <http://cwp.embo.org/wpc09-04/application.html>

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UCopenhagen Plant Populations Aug17-21

PhD course in "Molecular marker analysis of plant population structure and processes"

University of Copenhagen 17-08-2009 - 21-08-2009

Our course provides participants with practical and theoretical knowledge on analysis of genetic population structure, mating patterns, and population pro-

cesses in plant populations, using molecular marker data. The course includes theoretical lectures, discussions of student projects, exercises and practicals with various computer programs. The course is taught by staff at University of Copenhagen; this year's guest teacher is Rod Peakall, The Australian National University, one of the developers of GenA1Ex, a widely used software for population genetic analysis.

Course content Estimation of genetic diversity, F-statistics, inbreeding level, gene flow, population and paternity assignment, population admixture, hybridization. Assumptions and limitations of methods, and practical exercises with relevant computer programmes, such as: GenA1Ex, Spagedi, Structure, MLTR, Two-gener, Population Graph, Split tree, New Hybrids, AFLPOP, Famos, Cervus, etc. Discussion of selected student projects.

Course credit 3 ECTS points. Requirement for obtaining credit: approval of a written synopsis of the course content.

Practical information Maximum number of participants is twenty-five. Ph.D. students have preference, remaining *seats* are open to non-PhD students. The course will take place at University of Copenhagen, Frederiksberg Campus (within Copenhagen). Computers with the relevant software will be available for all. Travel, lodging, and accommodation is to be organised and paid by the participants on their own; suggestions for hostels and hotels will be posted on the web. Course fee: To be decided, maximum 70 Euros. All course material will be available through a restricted web site.

Organisers and teachers Thure Hauser, Associate Professor in Plant Ecology, Gunter Backes, Associate Professor in Plant Breeding, Ole Kim Hansen, Assistant Professor in Forest Genetics, Erik D. Kjær, Professor in Forest Genetics, Rod Peakall, Professor in Evolutionary Biology.

Registration and questions Write an e-mail to Thure Hauser, tpha@life.ku.dk, containing the following information: Full name, e-mail address, mobile phone no., institution, full mailing address, country, whether you are a Ph.D. student, title of present research project, education in genetics (courses + experience), and whether you would like to present your project during the course; in that order and on separate lines. Deadline July 1st 2009

Thure P. Hauser, Ph.D., Associate Professor Department of Agriculture and Ecology Faculty of Life Sciences University of Copenhagen Rolighedsvej 21 DK-1958 Frederiksberg Denmark +45 3533 2818 +45 2011 4469 tpha@life.ku.dk www.ecol.life.ku.dk ([http://-](http://www.ecol.life.ku.dk)

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Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification 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 formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting 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.