
E v o l D i r

July 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.



Foreword	1
Conferences	2
GradStudentPositions	16
Jobs	30
Other	43
PostDocs	61
WorkshopsCourses	82
Instructions	85
Afterword	86

Conferences

Bavaria SocialInsectEvolution Oct8-122	Marseilles EvolutionaryBiology Sep22-25 8
Berlin WildlifeGenetics Sep21-24 deadline extended .2	MexicoCity 3rdIntlBarcodeOfLife Nov10-12 8
Budapest RECOMB Comparative Genomics Sep27-29 3	Paris DarwinsLegacy Oct22-23 9
BuenosAires Darwin150 Nov23-25 4	Paris DiseaseEvolution Oct7-9 9
Canberra AustralasianEvolutionSociety Sep29-Oct1 .4	Paris Wollman GeneticTransfer ModernPhylogeny Oct2 10
HarvardU AnolisEvolution Oct2-5 2 5	QueenMaryU DarwinianRenaissance Nov13 10
Ismailia Egypt Adaptation Nov10-11 5	SanDiego ASM EvolutionaryMicrobiol May2010 Sym- posiaCall 11
Leiden Systematics Aug10-14 5	StAndrews BehaviourSpeciation Aug20-22 12
Lisbon PortugueseEvolutionaryBiology Dec21 6	StonyBrook DarwinMeeting Nov4-8 12
Lithuania FishSystematics Sep6-11 6	UGhent EvolutionOfDispersal Sep14-15 14
London SEAsianBiogeography Sept14-17 6	UNebraskaLincoln Bioinformatics Oct9-11 15
Macedonia SpeciationInLakes Sep7-11 7	UParis EuroEvoDevo Jul6-9 15
Marseilles 13thEvolutionaryBiology Sep22-25 3 8	
Marseilles 13thEvolutionaryBiol Sep22-25 2 8	

Bavaria SocialInsectEvolution Oct8-12

1st Central European IUSSI Meeting Registration for oral contributions ends in two weeks (1st of July) The Organizing Committee is happy to invite all social insect researchers to participate in 1st Central European Meeting of the International Union for the Study of Social Insects (IUSSI) and the 3rd Central European Workshop in Myrmecology (CEWiM)

8th- 12th October 2009

Invited speakers Abraham Hefetz, Tel Aviv, Israel
Tom Wenseleers, Leuven, Belgium

Location Abbey Frauenwörth (Lake Chiemsee, Bavaria, Germany)

Registration under: <http://ecology.bio.lmu.de/iussi/-program.html>

Prof. Dr. Susanne Foitzik Department Biologie II Behavioral Ecology (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@biologie.uni-muenchen.de <http://-ecology.bio.lmu.de/etho.e/index.htm> Susanne Foitzik <foitzik@zi.biologie.uni-muenchen.de>

Berlin WildlifeGenetics Sep21-24 deadline extended

7th International Conference on Behaviour, Physiology and Genetics of Wildlife“ between 21st and 24th September 2009 in Berlin, Germany.

As several people have indicated that they need more time, we have decided to extend the deadline to 27th June 2009. For those who have not registered yet, please do so: <http://www.bayceer.uni-bayreuth.de/-izw7/> The main topics of the conference are: - Life History & Maternal Effects (Pat Monaghan, University of Glasgow, UK) - Stress & Disturbance (Marco Apollonio, Università Sassari, Sardinien, 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)

The Conference offers several workshops: 1. Evolutionary Genomics in Conservation (Pierre Taberlet, Université Joseph Fourier, Grenoble, France & Simone Sommer, IZW, Berlin, Germany) Natural populations carry a wealth of molecular variation and there is increasing evidence that a large proportion of it has functionally diverged. Thus, understanding the functional implications of genetic variation provides not only insights into evolutionary processes and selection pressures but also into the adaptive potential of natural populations to a changing environment. Thereby, recent advances in sequencing and genome scan technologies have changed our focus from a few to thousands of genes. Moreover, the fundamental role of gene expression in shaping phenotypes has been recognized. Until recently, mainly sequence variation was taken into account so far disregarding expression differences between alleles. The aim of this workshop is to share information and discuss research applying a genomic approach or investigations of the role of gene expression in wildlife species to gain a more profound understanding of the variation of genes and their function in evolution, ecology and conservation.

2. Communication in Mammals and Birds (Francesco Bonnadonna, Centre d'Ecologie Fonctionnelle et Evolutive, Montpellier, France & Martin Dehnhard, IZW, Berlin, Germany)

3. Welfare and Conservation (Eric Dinerstein, senior scientist WWF-USA, Washington, USA & Marion East, IZW, Berlin, Germany)

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

5. Behavioural Rhythms (Serge Daan, University of Groningen, the Netherlands & Anne Berger, IZW, Berlin, Germany)

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

A practical training workshop on non-invasive monitoring of hormones will also take place at the IZW/Berlin during the week preceding the conference; Martin Dehnhard, IZW.

The conference dinner will take place at a beautiful setting in the city center overlooking the river "Spree".

You will find more information about the conference on our homepage at: [http://www.izw-berlin.de/de/-](http://www.izw-berlin.de/de/)

flink/7thIZW-Conference.html Please do not hesitate to contact us if you require any further information: symposium@izw-berlin.de, IZW, Berlin, Germany.

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>

Budapest RECOMB Comparative Genomics Sep27-29

Dear all,

****THE DEADLINE FOR PAPER SUBMISSION TO RECOMB Comparative Genomics (RECOMB-CG) HAS BEEN EXTENDED TO JUNE 30, 2009.****

The meeting will take place in Budapest in September 27-29 2009.

CONFIRMED INVITED SPEAKERS:

- Richard Durbin (Welcome Trust Sanger institute)
- Jotun Hein (University of Oxford, UK) - Laurence Hurst (University of Bath, UK) - Csaba Pál (Biological Research Center, Szeged, Hungary) - Lisa Stubbs (University of Illinois) - Jeroen Raes (EMBL Heidelberg)

DESCRIPTION OF THE CONFERENCE:

Comparison of related genomes offers enormous inferential power, revealing a wealth of knowledge about genome evolution itself and about genetic function and cellular processes. As the number of fully sequenced genomes grows, so do the opportunities and challenges for computational comparative genomics. This workshop brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and novel experimental results. The program will include a combination of keynote speakers and contributed talks. Topics of interest include, but are not limited to

* Algorithms in comparative genomics * Comparative study of orthologous genes * Gene finding using multi-

ple genomes * Sequence homology * Genome rearrangements * Measures of evolutionary distance * Whole genome phylogeny reconstruction * Sequence assembly using sequence comparison * Multiple genome alignment * Gene and genome duplication * Identification of conserved and fast evolving sequences

MEETING WEBSITE: <http://www.renyi.hu/conferences/recomb-cg2009/>
CONTACT: rcg2009@renyi.hu

CONFERENCE CHAIRS:

István Miklós (Rényi Institute, Budapest) Francesca Ciccarelli (European Institute of Oncology IEO, Milan)

–

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

BuenosAires Darwin150 Nov23-25

Darwin 150. Ist Evolutionary Biology Meeting of the Southern Cone of America. Buenos Aires, Argentina November 23 - 25, 2009 The University of Buenos Aires will celebrate the 150th anniversary of Darwin's "The Origin of Species" by hosting a three-day meeting during which American and European leading scientists will deliver lectures and lead discussions on several topics relevant to Evolutionary research. The third day of the meeting will be devoted to the continuing education of science teachers of all levels of the educational system.

Two poster sessions will be held during the meeting. The specific aims of the meeting are: - Create a forum to discuss recent conceptual and empirical achievements, local and universal, of the sciences dedicated to study different aspects of Evolution. - Generate a space of 'rendez vous' for researchers in the ample field of Evolution, to discuss achievements, concerns and problems in the local and regional areas - Encourage the active participation of undergraduates, graduate students and young scientists interested in the field and the interaction with researchers recognized as local, regional and international leaders in the field - Promote the creation of a Regional Society of Evolutionary Biology with the aim to strengthen the bonds between local, Mercosur and rest of America colleagues and articulate activities

with similar societies like the Society for the Study of Evolution (EEUU) and the European Society of Evolutionary Biology. - Contribute to the continuing education of science teachers of all levels of the national educational system, with the aim to promote the development of innovative strategies for teaching the Evolutionary Theory. All lectures will be in the facilities of Facultad de Ciencias Exactas y Naturales (Universidad de Buenos Aires) located in Ciudad Universitaria in Buenos Aires city. Attendants will find accommodations in the neighborhood of the meeting site or in more centric locations.

For information on registration, accommodations, transportation to the site of the meeting, Organizing Board and scheduled activities please visit our Web site: www.ege.fcen.uba.ar/darwin150 or send an email to 150.darwin.sur@ege.fcen.uba.ar.

Esteban Hasson University of Buenos Aires School of Sciences ehasson@ege.fcen.uba.ar

ehasson@ege.fcen.uba.ar

Canberra AustralasianEvolutionSociety Sep29-Oct1

Dear Evolutionary Biologists!

You are invited to attend Evolution 09 V the 6th Biennial Meeting of the Australasian Evolution Society:

September 29/October 1 at The Australian National University in Canberra.

The AES conference is always a relaxed and enjoyable experience for students and faculty alike, and is open to evolutionary biologists from all around the world.

We have four plenary speakers (Kate Buchanan, Simon Ho, Hanna Kokko, and Daniel Ortiz-Barrientos) and expect regular talks to be of high quality and to reflect the breadth of evolution research.

We have two evening social activities planned and have allowed one evening for you to experience Canberra's culinary delights.

For more information, and to register, please go to our website: <http://aes.eriophora.com.au/events/-Evolution09/index.html> The deadline for submission of abstracts is 31 July 2009.

Spring is a lovely time in Canberra and we look forward

to seeing you here!

(Please help us by advertising this meeting to any friends and colleagues you think may be interested. Thanks!)

Megan Higgie <megan.higgie@anu.edu.au>

HarvardU Anolis Evolution Oct2-5 2

Dear Colleague,

We would like to make a SECOND ANNOUNCEMENT advertising our October 2009 symposium on the biology of Anolis lizards, to be held at Harvard University.

Slots to participate are limited (125 total) and are FILLING UP FAST. If you are interested in attending, we HIGHLY RECOMMEND you register as quickly as possible!

This will be an informal meeting, with events taking place at Harvard's Museum of Comparative Zoology over the weekend of October 2-5. All details, including registration, transportation, meeting schedule, and more may be found on the symposium website:

<http://anolis.oeb.harvard.edu> Please spread the word to anyone who may be interested, and we look forward to seeing you in October.

Sincerely, Luke Mahler, Anthony Herrel, and Jonathan Losos

Luke Mahler <lmahler@oeb.harvard.edu>

Ismailia Egypt Adaptation Nov10-11

I will try to rewrite my advert to indicate why evolutionary biologists specifically are targeted to our conference:

The 4th International Conference is now ample evidence of the ecological impacts of recent climate change from polar terrestrial to tropical marine environments. So on behalf of the Egyptian Society for Environmental Sciences (ESES) it is our pleasure to welcome especially the evolutionary biologists and Ecologists ecologists to the fourth international conference on "Impacts of

Climate Change on Natural Resources" that will take place in Ismailia, Egypt on November 10-11, 2009. As in the past three years, this conference will offer outstanding international speakers. There will be ample time for abstracts, posters, and the many informal discussions that have helped make past meetings successful. Those of you who attended the past conferences of ESES already know that Ismailia is a vibrant modern city, and that Suez Canal University makes an outstanding venue for this meeting.

Evolutionary biologists specifically are targeted to the following Conference Topics

- ï Green-house effect and carbon dioxide emission
- ï Impacts of climate change and Genetic conservation of rarely endangered species
- ï Impacts of climate change on the history and evolution of flora and fauna biodiversity in the arid and semi arid regions.
- ï Climate change in arid lands and desert margins
- ï Climate change and Oceanography
- ï Climate change and water resources management
- ï Biophysical indicators of climate changes
- ï Climate change and Biotechnology
- ï Climate change and risk assessment
- ï Climate change and sustainable development
- ï Climate change and food security
- ï Impact of climate change on the development of rural communities
- ï Socio-economic indicators of climate change

Hassan Mansour Hassan Assistant lecturer Department of Botany Science Faculty Suez Canal University Ismailia, Egypt.

man_griesh@yahoo.com

Leiden Systematics Aug10-14

Approaching deadlines for Systematics 2009 (www.biosyst.eu).

There is just one month left to register at the regular fee for the Systematics 2009 conference, 10-14 August, in Leiden, and one month to submit a presentation. At the moment, there are still slots available for both oral and poster presentation in the open sessions and in some symposia, but availability may be limited to poster presentations for late submissions. Inclusion of submissions received after June 30 cannot be guaranteed.

Please note that also all speakers in symposia and workshops need to register their abstract in order to be included in the abstract book!

Also note that an extra fee of 50 EURO will be enforced for late registrations, irrespective of any reductions that may be applicable!

You can register and submit an abstract through the webpage www.biosyst.eu. If you have problems in accessing this website, please report this to Peter Hovenkamp (hovenkamp@nhn.leidenuniv.nl).

Peter Hovenkamp Nationaal Herbarium Nederland, Leiden branch www.nationaalherbarium.nl

hovenkamp@nhn.leidenuniv.nl
hovenkamp@nhn.leidenuniv.nl

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Lisbon Portuguese Evolutionary Biology Dec21

Dear all,

We are please to announce that the 5th Portuguese Evolutionary Biology Meeting will take place at Instituto Superior de Psicologia Aplicada (ISPA) in Lisbon on December 21st 2009. It is being organized by Unidade de Investigação em Eco-etologia and Centro de Bociências do ISPA (Rua Jardim do Tabaco, 34, Lisbon).

The Portuguese Evolutionary Biology Meetings aim to bring together Portuguese researchers and to promote Evolutionary Biology in Portugal. They are held in late December to allow researchers in foreign institutions to attend, given that many spend their Winter break in Portugal.

To celebrate this special year, we will have Prof. Douglas Futuyma (Stony Brook University, NY, USA) as an invited speaker. The remainder presenters will be either Portuguese or working in Portugal.

Presenters should register by sending a message to biologia.evolutiva@gmail.com with the following information: - Presentation title, - Name and affiliation, - Topic
 Portuguese and English will be the official languages of the meeting.

Also, we are happy to announce that we will discuss the creation of the Portuguese Evolutionary Biology Association. This idea has been on table for some time now and we will decide if this is the time to formalize it.

We will soon have further information. We would appreciate ample distribution of this announcement.

Best regards,

Sara Branco

Sara Branco Committee on Evolutionary Biology University of Chicago 1025 E 57th St Culver Hall 402 Chicago, IL 60637 USA

sara.mayer.branco@gmail.com

Lithuania FishSystematics Sep6-11

13th EUROPEAN CONGRESS OF ICHTHYOLOGY
 Early bird Registration Reminder! DON'T MISS OUT... REGISTER TODAY!

Early bird registration for the XIIIâth ECI closes on 1âst of June.

Click here (<http://www.ku.lt/ECLXIII/-registration.php>) to register at the special discounted rate.

The 13th European Congress of Ichthyology ECI XIII will take place in âKlaipedaâ Hotel, Klaipeda city, Lithuania,

September 6th -11th, 2009

Sessions and symposia include: Taxonomy and Systematics, Zoogeography and Evolution, and Conservation Biology.

Dr Lukas Ruber Department of Zoology The Natural History Museum Cromwell Road London SW7 5BD UK

Tel: +44 (0)20 7942 6208 Fax: +44 (0)20 7942 5054
 e-mail: l.ruber@nhm.ac.uk

www.lukasruber.com www.nhm.ac.uk/zoology Forthcoming meeting: Southeast Asian Gateway Evolution (14-17 September 2009) <http://sage2009.rhul.ac.uk/>
 Lukas Ruber <l.ruber@nhm.ac.uk>

London SEAsianBiogeography Sept14-17

DEADLINE FOR EARLY REGISTRATION EXTENDED TO 14 JUNE!! Provisional list of presenters and titles now available on web page.

Still Possible: Submit Abstract for Poster Presentations

SAGE2009 Conference - "Southeast Asian Gateway Evolution"

14-17 September 2009: Royal Holloway University of London

<http://sage2009.rhul.ac.uk> The Southeast Asian Gateway is the site of the Indonesian Throughflow between the Pacific and Indian Oceans. It is the only low latitude link between the world's oceans, and is increasingly regarded as an important influence on global climate. The throughflow passes through the present zone of collision between Australia and SE Asia. The collision began about 25 million years ago, but SE Asia has a long history of growth by the addition of continental fragments rifted from Gondwana dating back to the Palaeozoic. The fauna and flora display a similar complexity which is partly linked to the geology.

There is a centre of maximum diversity in the marine and terrestrial ecosystems in the Indo-Australian archipelago, and the gateway contains numerous biogeographic boundaries. The centre of the region, known to biologists as Wallacea after Alfred Russel Wallace of Wallace's Line, is an unusual region of high faunal and floral endemism. Plate tectonic reconstructions suggest that geology has played a major role in shaping the distributions of biota and the tectonic development of the region is one key to understanding the links between oceanic circulation, climate and life. However, these links are not well documented and connections between different processes are uncertain. Understanding the geological and biological history of the region, and the evolution of biodiversity, is of considerable importance in managing current and future change.

This will be a three-day multidisciplinary meeting to discuss this important region with an emphasis on reporting new ideas and exchanging views between a wide range of Earth and Life Scientists. It will promote interaction between Earth and Life Scientists working in the region. The programme will include plenary sessions, overview presentations, and breakouts for specialist groups. We seek contributions on all geological and biological aspects of the Southeast Asian Gateway, the region including Indonesia, Malaysia, the Philippines, Indochina, New Guinea and the NW Shelf of Australia.

Details of keynote speakers, accommodation, registration, pre and post conference field trips, abstract submission and important dates are available at: <http://sage2009.rhul.ac.uk/> We look forward to your participation in this meeting.

SAGE2009 Organising Committee Ken Johnson, David Gower, Brian Rosen, Lukas Ruber, Suzanne Williams

Dr Lukas Ruber Department of Zoology The Natural History Museum Cromwell Road London SW7 5BD UK

Tel: +44 (0)20 7942 6208 Fax: +44 (0)20 7942 5054 e-mail: l.ruber@nhm.ac.uk

www.lukasruber.com www.nhm.ac.uk/zoology Forthcoming meeting: Southeast Asian Gateway Evolution (14-17 September 2009) <http://sage2009.rhul.ac.uk/> l.ruber@nhm.ac.uk

Macedonia SpeciationInLakes Sep7-11

This is an announcement for the International Symposium

Speciation in Ancient Lakes 5, SIAL5, September 7-11 2009, Ohrid, Macedonia.

Ancient lakes, that is, extant lakes that have continuously existed throughout the last glaciation or since before the Pleistocene, for example, lakes Baikal, Tanganyika, Malawi, Biwa, and Ohrid, have long been recognized as centres of biodiversity. Moreover, during the past years, speciation in ancient lakes has emerged as an important and fruitful topic in studies of evolutionary biology. The current understanding of a number of key evolutionary concepts, such as sympatric speciation, sexual selection, adaptive radiation, hybridization, and punctuated equilibrium, is in part based on insights from speciation studies in these ancient lakes, and this is evident in the increasing number of citations of articles pertaining to speciation in ancient lakes.

A series of conferences on Speciation In Ancient Lakes (SIAL) was started by a meeting that took place 1993 in Mont-Rigi, Belgium, and was brought together to review the state of art in the field for a first time since the classical seminal review of Brooks (1950). The proceedings of that meeting initiated a wealth of renewed interest in ancient lake issues.

The second SIAL meeting entitled "International Conference on Ancient Lakes: their Biological and Cultural Diversities" was held in 1997 near Lake Biwa in Japan. It focused on the cultural diversity of ancient lakes, as well as on their biodiversity, ecology and evolution. The third conference, SIAL-3, took place in Irkutsk. Naturally, the focus of that conference was the oldest and

arguably most famous of the ancient lakes - Lake Baikal. Finally, the latest meeting SIAL-4 was held September 4-8, 2006, at the Freie Universität Berlin, Germany.

The next SIAL conference is going to take place at Lake Ohrid (Macedonia) on the Balkans. Please find information on registration, fees, excursions, etc. on www.sial-online.org.

Feel free to contact me regarding any request you might have.

ABSTRACT DEADLINE: 30 June 2009

We would highly appreciate if you could forward this announcement to anybody interested in ancient lake issues.

Sincerely yours,

Christian Albrecht, Secretary SIAL5

Dr. Christian Albrecht Department of Animal Ecology and Systematic Zoology Systematics and Biodiversity Group J. Liebig University of Giessen Heinrich-Buff-Ring 26-32 D-35392 Giessen E-Mail: Christian.Albrecht@allzool.bio.uni-giessen.de

Christian Albrecht <Christian.Albrecht@allzool.bio.uni-giessen.de>

Marseilles 13th Evolutionary Biology Sep22-25 3

Dear All,

We are please to inform you that the deadline of the 13th Evolutionary Biology Meeting at Marseilles, 22-25 September, Marseilles, France will be on 30th June.

Do not hesitate to go on our website to see the pre program <http://sites.univ-provence.fr/evol-cgr> Few spots are still available for poster.

Sincerely,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

Marseilles 13th Evolutionary Biol Sep22-25 2

Dear All,

We are pleased to inform you that the 13th Evolutionary Biology Meeting at Marseilles will take place on 22-25 September 2009, Marseilles, France.

Few spots are still available for poster and poster presented.

Do not hesitate to go on our website to see the pre program <http://sites.univ-provence.fr/evol-cgr> Best wishes,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

Marseilles Evolutionary Biology Sep22-25

Dear All,

We are pleased to inform you that the 13th Evolutionary Biology Meeting at Marseilles will take place on 22-25 September 2009 and that you can already register at <http://sites.univ-provence.fr/evol-cgr> The following subjects will be discussed:

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

Few spots are still available for poster and poster presented.

For more information, do not hesitate to go on: <http://sites.univ-provence.fr/evol-cgr> Best wishes,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

MexicoCity 3rd Intl Barcode Of Life Nov10-12

Dear Colleagues,

The Consortium for the Barcode of Life (CBOL; www.barcoding.si.edu) and the Instituto de Biología of the Universidad Nacional Autónoma de México (UNAM) invite you to the Third International Barcode of Life Conference in Mexico City during the week of 7-12 November 2009. The main conference will be Tuesday-Thursday, 10-12 November at the Mexican Academy of Sciences, and there will be three days of pre-conference workshops and a post-conference public event at UNAM's Science Museum.

The conference website is now open at www.dnabarcodes2009.org and the online registration system will be opening next week. Calls for abstracts and applications for travel bursaries (only for participants from developing countries) will also be available through the website in the coming week.

If you would like to be placed on the distribution list to receive future notices about the conference, please send an email to message to inquiries.dnabarcodes2009@si.edu with "MAILING LIST" on the subject line. Please include your name and institutional affiliation in the body of your message.

We look forward to seeing you in Mexico City in November!

Best regards,

David

David E. Schindel, Executive Secretary

Consortium for the Barcode of Life 202/633-0812; fax 202/633-2938; portable 202/557-1149
Email: SchindelD@si.edu <<mailto:SchindelD@si.edu>>
CBOL WEBSITE: <http://www.barcoding.si.edu> <<http://www.barcoding.si.edu/>>

Office and overnight delivery address:

National Museum of Natural History Room CE-119
10th & Constitution Avenue, NW Washington, DC 20560

Postal mailing address:

National Museum of Natural History Smithsonian Institution P.O. Box 37012, MRC-105 Washington, DC 20013-7012

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

Paris DarwinsLegacy Oct22-23

DARWIN'S LEGACY : NEW INSIGHTS INTO HUMAN EVOLUTION

The French Genetics Society (SFG : Société Française de Génétique) and The French Human Genetics Society (SFGH : Société Française de Génétique Humaine) are organizing a two-day meeting at the Buffon building, University Paris-Diderot, October 22-23, 2009 on the topics of : « Darwin's legacy : New Insights into Human Evolution »

This meeting will provide a forum for the presentation of original and up-to-date scientific research in the fields of human population genetics, molecular evolution, comparative genomics, anthropology and paleogenetics. It will bring together leading evolutionary biologists and science historians to commemorate the Darwinian Revolution.

Informations available on : http://www.reaumur.org/-article.php?id_article=737&id_rubriqueB The Buffon Amphitheatre is located in the Bâtiment Buffon of the Paris-Diderot University, 15 rue Hélène Brion, 75013 Paris, close to the Jacques Monod Institute.

Christophe Terzian UMR754 UCBL INRA ENVL EPHE 50, avenue Tony Garnier - 69366 Lyon Cedex 07 France Ph : +33 4 37 28 74 16 fax + 33 4 37 28 76 05 <http://www.ifr128.prd.fr/Terzian.htm> Christophe Terzian <cterzian@univ-lyon1.fr>

Paris DiseaseEvolution Oct7-9

The next EMBO conference on "Host Genetics Control of Infectious Diseases" will be held at Institut Pasteur, Paris, October 7-9, 2009.

Abstract submission, registration and other details are available at the following website:

<http://www.pasteur.fr/ip/easysite/go/03b-00002u-0a0/conferences-and-scientific-congress/conferences-services-colloques/hostgenetics-2009> The program is open to everyone for poster presentations.

Invited Speakers include:

Stylianos Antonarakis, University of Geneva, Switzerland
Rudi Balling, Helmholtz Centre for Infection Research, Braunschweig, Germany
François Barré-Sinoussi, Institut Pasteur, Paris, France
Bruce Beutler, The Scripps Research Institute, La Jolla, USA
Mary Carrington, National Cancer Institute, Freder-

ick, USA Jean-Laurent Casanova, Université Paris V- Necker, Paris, France and The Rockefeller University, New York, USA Andrew G. Clark, Cornell University, Ithaca, USA Michael Emerman, Fred Hutchinson Cancer Research Center, Seattle, USA Claire Fieschi, Université Paris VII-St Antoine, Paris, France Alain Fischer, Université Paris V-Necker, Paris, France David Goldstein, IGSP, Duke University, Durham, USA Adrian V. Hill, Oxford University, Oxford, UK Rolf D. Horstmann, Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany Bruno Lemaitre, EPFL, Lausanne, Switzerland Elena Levashina, CNRS, Strasbourg, France Michael Malim, King's College, London, UK Danielle Malo, McGill University, Montreal, Canada David Modiano, University of Rome "La Sapienza", Italy Etienne Pays, Free University of Brussels, Gosselies, Belgium Jennifer Puck, UCSF, USA Lluís Quintana-Murci, Institut Pasteur, Paris, France Erwin Schurr, McGill University, Montreal, Canada Lennart Svensson, University of Linköping, Sweden Sarah Tishkoff, University of Pennsylvania, Philadelphia, USA Richard Webby, St. Jude Children's Research Hospital, Memphis, USA

Lluís QUINTANA-MURCI <quintana@pasteur.fr>

Paris Wollman Genetic Transfer Modern Phylogeny Oct2

GENETIC TRANSFER and MODERN PHYLOGENY A tribute to Elie Wollman.

Elie Wollman, who died last year, was one of the pioneers who established Molecular Genetics. Together with François Jacob, he made use of the "sexuality of bacteria" to decipher the nature of the conjugation process in bacteria, as well as the basis of prophage induction. He played also a key role in the modernization of the Pasteur Institute. A meeting in his honor will take place at the Institut Pasteur Paris, on October 2. It will encompass the following themes:

Historical accounts: Charles Galperin, Michel Morange. The nature of viruses: Max Gottesman, Patrick Forterre. Horizontal gene transfers and phylogeny in the bacterial kingdoms : Simonetta Gribaldo, Elisabeth Carniel. >From single colonies to single molecules: Jean-François Allemand. Conjugation and recombination. Where do we stand? Miroslav Radman.

Registration is free but, because space is

limited, pre-registration will be required at: Denise.Derhy@pasteur.fr.

The meeting comprises two events: An exhibit. Starting with the day of the meeting, it will describe Wollman's scientific achievements and its administrative career

molecularmicrobiology@yahoo.co.uk

Queen Mary U Darwinian Renaissance Nov13

The Darwinian Renaissance in the Humanities and Social Sciences

Friday 13 November 2009

09:30 - 17:00

The Octagon, Queen Mary University of London

QMUL Mile End Campus

Organizers: Qazi Rahman (QMUL) and Tom Dickins (EHBEA)

This symposium celebrates 200 years of Darwin's birth and 150 years since the publication of *The Origin*. It also coincides with the launch of a new undergraduate degree in Psychology at the School of Biological & Chemical Sciences (QMUL) which is underpinned by an evolutionary framework. We acknowledge the generous support of the European Human Behaviour & Evolution Association (EHBEA), The Galton Institute and the School of Biological & Chemical Sciences (QMUL). Meeting abstract

In the distant future I see open fields of far more important researches. Psychology will be based on a new foundation that of the necessary acquirement of each mental power and capacity by gradation. Light will be thrown on the origin of man and history. (p394, *The Origin*, 1859/1996) Darwin published *The Origin* 150 years ago. From that point on he, and many others, have applied evolutionary theory to behaviour. And from that point on controversy has never been far away. Darwin's own work contributed to the rise of Comparative Psychology in the late nineteenth century, which in turn impacted upon Behaviourism. The 1970s saw the rise of Sociobiology, and much criticism of attempts to apply evolutionary biology to human concerns. Initially these criticisms were grounded in Marxist ideology and set limits to the remit of biological science:

human properties required a different framework. More recently the humanities and social sciences have taken a similar view but with a post-modern twist, actively eschewing scientific, and especially biological understanding, and in so doing forsaking prediction.

In spite of this history of ideological criticism, what might be termed the Human Evolutionary Behavioural Sciences (HEBS) have diversified into Evolutionary Psychology, Human Behavioural Ecology and Cultural Evolution, and in so doing have flourished. In this meeting we hope to showcase new and exciting work from within HEBS, and look at where efforts should be focused in the future. It is our contention that the humanities and social sciences cannot ignore the central place of evolution as a theoretical framework for understanding human affairs. What is more, if we ever hope to practically help others we need to fully understand the nature of the species at hand. Scientific scrutiny is the only option, and evolutionary biology is the unifying framework. Speakers

Alex Bentley (Durham)

Mhairi Gibson (Bristol)

Dominic Johnson (Edinburgh)

Stephen Lycett (Kent)

Alex Mesoudi (QMUL)

Daniel Nettle (Newcastle)

Ian Penton-Voak (Bristol)

Rebecca Sear (LSE)

Costs (includes lunch and wine reception)

EHBEA and Galton Institute members - £20

Non-members - £25

Please make a note of this meeting in your diary and watch this space for registration details.

Contact: http://www.sbcs.qmul.ac.uk/people/qazi_rahman.shtml Alan McElligott
<a.g.mcelligott@qmul.ac.uk>

**SanDiego ASM
EvolutionaryMicrobiol May2010
SymposiaCall**

CALL FOR **SYMPOSIA* *PROPOSALS American Society for Microbiology Division R, Evolutionary

& Genomic Microbiology 2010 General Meeting San Diego, CA May 23-27, 2010*

*ASM **Division R, Evolutionary and Genomic Microbiology*, is now soliciting suggestions for symposia to be presented at the 2010 ASM General Meeting to be held in San Diego in May, 2010.

To propose a symposium that represents a theme of broad interest within Division R, please provide the following:

1. A title for the session.
2. Convenor(s)
3. A description of the session in paragraph format.
4. Speakers with affiliations, titles and topics for the session. List five potential speakers and one or two alternative speakers.
5. Similar sessions in prior years if appropriate.

You may submit your ideas through the following link: http://gm.asm.org/index.php?option=com_content&task=view&id=164&Itemid=162 <<http://mail.asmtusa.org/t/585316/45181548/2933/0/>>.

There is a link on this page so you can check if candidate speakers have presented at a recent symposium. Although past speakers are not barred, the policy of Division R is to encourage alternative speakers where possible. In the interest of promoting the next generation of leaders in our field, organizers are also encouraged to include promising junior faculty in their program.

Note that this is a call for proposals only. Travel arrangements should NOT be made with potential speakers until you are notified that the proposal has been accepted by the ASM General Meeting Planning Committee. Proposals will be reviewed by divisional officers at the 2009 ASM General Meeting in Philadelphia; their recommendations will then be forwarded to the Planning Committee for final approval.

Proposals must be submitted by *July 17, 2009.*

Thanks very much. Sincerely, David Guttman

David S. Guttman Chair, ASM Division R, Evolutionary & Genomic Microbiology Professor Canada Research Chair in Comparative Genomics Director, Centre for the Analysis of Genome Evolution & Function Department of Cell & Systems Biology Department of Ecology & Evolutionary Biology University of Toronto

David Guttman <david.guttman@utoronto.ca>

St Andrews Behaviour Speciation Aug20-22

The Role of Behaviour in Speciation; EU funded workshop at the University of St Andrews, Scotland.

A workshop for early career stage researchers will be held at the University of St Andrews, Scotland on 20-22nd August 2009. This is funded by an EU Initial Training Network grant entitled Speciation awarded to laboratories in the UK, Netherlands and Finland. Space is available for a limited number of external participants. Applications are invited, and delegates are expected to be at the Masters, PhD or early postdoctoral research stage. There are no nationality restrictions.

Speakers and discussion leaders are Mohamed Noor (Duke University, USA), Richard Harrison (Cornell University, USA), Anne Magurran (St Andrews, UK), Nathan Bailey (Riverside, CA, USA), Thomas Schmitt (Freiburg University, Germany) and Constantino Macias Garcia (UNAM, Mexico). The format will include lectures, discussions and some hands-on exercises.

The research programmes funded under the EU award include studies of population genetics and sexual isolation in a range of organisms, several *Drosophila* systems, other insects (orthoptera and *Nasonia*), marine polychaetes and theoretical studies of diversification. Common questions concern genomic studies of behavioural variation, including QTL and candidate gene analyses for song and chemical traits, and studies of population genetics and reproductive isolation. Additional topics to be addressed at the workshop include the role of learning and plasticity in reproductive isolation.

There are a number of bursaries for external participants. Enquiries can be made to Mike Ritchie (mgr@st-and.ac.uk) and application procedures (workshop attendance and bursary) will be posted at <http://speciation.group.shef.ac.uk/> or can be obtained from him. The deadline for the receipt of applications is June 30th.

Exact registration fees will be calculated soon, but will be modest, certainly no more than 100 payable upon attendance.

This meeting immediately follows a three day summer school and one day conference on Comparative

Genomics at the University of St Andrews, organised by the Scottish Bioinformatics Forum, and researchers with overlapping interest may wish to attend either or both of these meetings. Details are available at: http://www.sbforum.org/events.php?e_idp (one-day meeting) and <http://www.genome-bioinformatics.org> (summer school)

Information about St Andrews and the University: <http://www.st-andrews.ac.uk/visiting/> -

Mike Ritchie School of Biology Dyers Brae House University of St Andrews St Andrews, Fife Scotland KY16 9TH

Phone 0 (44 outside UK) 1334 463495 Fax 0 (44 outside UK) 1334 463366

Website: <http://bio.st-andrews.ac.uk/staff/mgr.htm>
PDFs etc: <http://biology.st-and.ac.uk/supplemental/-ritchie/papers.aspx> Mike Ritchie <mgr@st-andrews.ac.uk>

Stony Brook Darwin Meeting Nov4-8

Darwin 2009: 150 Years of Evolutionary Biology

* *

Poster Session Now Added to Meeting:

Log on to darwin.org and click <Meeting and Posters> link on top

On November 4-8 2009, the Department of Ecology & Evolution at Stony Brook

University will celebrate the 150th anniversary of Darwin's *The Origin of Species* by hosting a four-day meeting where leading evolutionary biologists will lecture and help lead discussions on the current status and future of the study evolutionary biology. We will have three stimulating days of keynote addresses, evening panels and discussion groups, and ample opportunity for communication on the important issues of the present and future of evolutionary biology. A poster session will also be included. All lectures will be in modern and pleasant facilities at Stony Brook University, with available nearby lodging and convenient transportation to the meeting site.

To register, secure lodging, and get further information on transportation, our Advisory Board, and other matters, please visit our web site

<http://darwin09.org> Below is our schedule of events

and speakers.

Wednesday, November 4

6:00 â 8:00 Welcoming Reception for Participants

Thursday, November 5

8:45 â 9:00 Welcome from Stony Brook University

9:00 â 9:40 Opening Keynote Address, Douglas J. Futuyma, Stony Brook University

9:40 â 10:00 Q&A

10:00 â 10:30 Coffee Break

10:30 â 11:10 History, Peter Bowler, Queens University, Belfast

11:10 â 11:30 Q&A

11:30 â 12:10 Natural Selection, Mark Kirkpatrick, University of Texas at Austin

12:10 â 12:30 Q&A

12:30 â 2:00 Lunch

2:00 â 2:40 Behavioral Ecology, Hanna Kokko, University of Helsinki

2:40 â 3:00 Q&A

3:00 â 3:40 Evolutionary Ecology, Anurag Agrawal, Cornell University

3:40 â 4:00 Q&A

4:00 â 4:30 Coffee Break

4:30 â 5:10 Organismal Adaptation, May R. Berenbaum, University of Illinois

5:10 â 5:30 Q&A

6:00 â 8:00 Dinner

8:00 â 10:00 Informal Discussions

Friday, November 6

8:45 â 9:00 Welcome and Announcements

9:00 â 9:40 Philosophy, Roberta L. Millstein, University of California, Davis

9:40 â 10:00 Q&A

10:00 â 10:30 Coffee Break

10:30 â 11:10 Evolutionary Genetics, Jianzhi George Zhang, University of Michigan

11:10 â 11:30 Q&A

11:30 â 12:10 Genetics of Population History, John Wakeley, Harvard University

12:10 â 12:30 Q&A

12:30 â 2:00 Lunch

2:00 â 2:40 Genomics, Doris Bachtrog, University of California, Berkeley

2:40 â 3:00 Q&A

3:00 â 3:40 Speciation, Richard G. Harrison, Cornell University

3:40 â 4:00 Q&A

4:00 â 4:30 Coffee Break

4:30 â 5:10 Evolvability, Günter Wagner, Yale University

5:10 â 5:30 Q&A

6:00 â 8:00 Dinner

8:00 â 10:00 Informal Discussions

Saturday, November 7

8:45 â 9:00 Welcome and Announcements

9:00 â 9:40 Ancient Origins, Antonio Lazcano, Universidad Nacional Autónoma de México

9:40 â 10:00 Q&A

10:00 â 10:30 Coffee Break

10:30 â 11:10 Tree of Life, David Hillis, University of Texas at Austin

11:10 â 11:30 Q&A

11:30 â 12:10 Evolution in the Fossil Record, Peter Wagner, Smithsonian

12:10 â 12:30 Q&A

12:30 â 2:00 Lunch

2:00 â 2:40 Evolutionary Developmental Biology, Gregory Wray, Duke University

2:40 â 3:00 Q&A

3:00 â 3:40 The Fossil Record of Diversity, Michael Foote, University of Chicago

3:40 â 4:00 Q&A

4:00 â 4:30 Coffee Break

4:30 â 5:10 Evolutionary Radiations, Jonathan B. Losos, Harvard University

5:10 â 5:30 Q&A

6:00 â 8:00 Dinner

8:00 â 10:00 Informal Discussions

Sunday, November 8

8:45 â 9:00 Welcome and Announcements

9:00 â 9:40 Human Origins, Tim D. White, University of California, Berkeley

9:40 â 10:00 Q&A

10:00 â 10:30 Coffee Break

10:30 â 11:10 Cultural Evolution, Peter J. Richerson,
University of California, Davis

11:10 â 11:30 Q&A

11:30 â 2:30 Lunch

12:30 â 1:10 Applied Evolution, Joanne P. Webster, Im-
perial College London

1:10 â 1:30 Q&A

1:30 â 2:10 Closing Keynote Address, Hopi E. Hoekstra,
Harvard University

Meeting web site address:

<http://darwin09.org> Jeffrey Levinton,

For the Organizing Committee

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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>

UGhent EvolutionOfDispersal Sep14-15

International symposium - University of Ghent, Belgium September 14 and 15, 2009 Dispersal is a central process within metapopulation and metacommunity ecology. Because it has many evolutionary, population dynamical and applied consequences, we aim to bring together international expertise within dispersal ecology by presenting and discussing currently ongoing research themes.

We are happy to invite you to an international symposium with special focus on the ecology and evolution of dispersal that will be held at the University of Ghent in Belgium. The meeting will deal with both conceptual and applied issues, with empirical, experimental and theoretical approaches, and we will present knowledge of dispersal patterns and mechanisms in plants, animals and micro-organisms. The symposium offers a diverse and attractive series of talks including four keynote papers. It is a pleasure to host several international authorities in the field.

We encourage participants, and students in particular, to present their research on any theoretical or applied aspect of dispersal by poster presentations.

The Symposium is sponsored by FWO (Fund of Scientific Research, Flanders, Belgium).

All information on:

<http://www.ecology.ugent.be/terec/events.php?page=ISdispersal&tab=ishome> Program

Monday September 14, 2009 Chairman: Hans Van Dyck 10:00 Registration 10:55 Opening address 11:00 Keynote paper Thomas Hovestadt (University of Würzburg, Germany) - "Unifying dispersal research: information, experience, and movement rules" 11:50 Justin Travis (University of Aberdeen, UK) - "The evolution of movement rules and perceptual range in patchy landscapes" 12:15 Calvin Dytham (University of York, UK) - "Life history strategy and dispersal" 12:40 Marjo Saastamoinen (Leiden University, The Netherlands) - "Condition-dependent life-history responses to flight stress" 13:05 Lunch break 14:30 Keynote paper Hanna Kokko (University of Helsinki, Finland) - "From Individual Dispersal to Species Ranges: Perspectives for a Changing World" 15:20 Annelies De Roissart, Lien Van Oyen, Eduardo de la Peña & Dries Bonte (Ghent University, Belgium) - "Belowground biota affect dispersal decisions of aboveground living herbivores" 15:45 Tim Benton (University Leeds, UK) - "Causes and consequences of dispersal behaviour in mites in microcosm" 16:10 Virginie Stevens & Michel Baguette (CNRS Brunoy Paris, France) - "Filling in the tapestry: a meta-analysis of dispersal in butterflies" 16:35 Nicolas Schtickzelle, Alexis Chaine & Jean Clobert (Biodiversity Research Centre, UCL, Belgium/CNRS Moulis, France) - "Experimental ecology of dispersal in *Tetrahymena* microcosms" 17:00 Reception and extensive poster session

Tuesday September 15, 2009 Chairman: Dries Bonte

09:30 Keynote paper James Bullock (CEH, UK) - "Dispersal and the spatial dynamics of populations" 10:20 Valerie Lehouck, Dries Bonte, Toon Spanhove & Luc Lens (Ghent University, Belgium) - "Recruitment dynamics of an avian dispersed tree in a fragmented landscape" 10:45 Melanie Gibbs & Hans Van Dyck (Biodiversity Research Centre, UCL, Belgium) - "Butterfly flight activity and reproductive plasticity in fragmented landscapes" 11:10 Coffee break 11:35 Sofie Vandewoestijne & Hans Van Dyck (Biodiversity Research Centre, UCL, Belgium) - "Flight morphology and genetics along a latitudinal gradient in the butterfly *Pararge aegeria*: do clines differ between landscape types?" 12:00 Aurélie Coulon, Virginie Stevens

& Michel Baguette (CNRS Brunoy Paris, France) - "Integrating landscape into dispersal studies: state of the art and perspectives" 12:25 Lunch break 14:00 Keynote paper Jean Clobert (CNRS Moulis, France) - "The evolution of immigrant presence-based dispersal" 14:50 Debora Arlt, Hanna Kokko & Tomas Pärt (University of Reading, Great Britain and University of Helsinki, Finland) - "Stay or leave? The role of site availability and intrasexual competition for site choice and breeding dispersal" 15:15 Christoph Meier (Helsinki University, Finland) - "How not to miss the mate as a disperser?" 15:45 Thijs Van Overveld & Erik Matthysen (University of Antwerp, Belgium) - "Dispersal, spatial behaviour and personality in great tits"

Dries Bonte <Dries.Bonte@ugent.be>

UNebraskaLincoln Bioinformatics Oct9-11

Announcing BIOT-2009, the 6th Annual Biotechnology & Bioinformatics Symposium, October 9-11, 2009 at the University of Nebraska, Lincoln, NE.

We invite contributions in any area of Biotechnology and Bioinformatics, theoretical as well as practical. This year the following topics are particularly emphasized: Machine learning application in bioinformatics Distributed database, semantic Web, and ontologies Intelligent user interface and decision support Omics approaches and systems biology High-throughput sequencing technologies and related data analysis RNA interference, microRNA, epigenetics Bioinformatics application in plant science and plant biotechnology Molecular evolution, phylogeny, and phylogenomics Education in computational biology and bioinformatics

For more information on BIOT-2009 see the attached flyer and visit our website at: <http://www.biotconf.org/> Co-Chairs, University of Nebraska: Etsuko Moriyama School of Biological Sciences/Center for Plant Science Innovation emoriyama2@unl.edu

Leen-Kiat Soh Computer Science & Engineering lsoh2@unl.edu

Stephen Scott Computer Science & Engineering sscott2@unl.edu

emoriyama2@unlnotes.unl.edu

UParis EuroEvoDevo Jul6-9

Euro-Evo-Devo Paris, 6-9 July 2010

Dear Evoldir members,

We are pleased to announce the third meeting of the European Society for Evolutionary Developmental Biology (EED). This meeting will be held from 6 to 9 July 2010 at the Université Paris Diderot, Paris 7, along the left bank of the Seine, adjacent to the new library building, the Bibliothèque Nationale de France, François Mitterrand.

We are very pleased that Didier Casane, Michel Vervoort and Patrick Laurenti are willing to be the local organizers at the Université Paris Diderot, Paris 7.

We invite you to SUBMIT PROPOSALS FOR SYMPOSIA.

It is the aim of EED to stimulate the communication between sub-disciplines. We, therefore, particularly encourage submission of symposia on broad and integrative topics of potential interest to researchers from different fields (e.g. developmental biology, genetics, paleontology, genomics, theoretical biology). Symposia that combine animal and plant studies are also welcome.

Symposia should, if possible, accommodate 8 invited speakers and allow 25 minutes for each speaker (20' talk and 5' discussion). A small number of mini-symposia with 3 speakers (also 25') will also be considered.

Please note that invited speakers can only present in a single symposium.

Please include the following information in your proposal for a symposium:

- (1) Title of symposium
- (2) Provisional list of proposed speakers
- (3) Brief (abstract length) description of the symposium, including a short indication of what the different speakers are expected to contribute
- (4) Brief justification of why the symposium is appropriate for an EED meeting (e.g. timeliness, general interest, interdisciplinarity)
- (5) Contact information of all symposium organizers

Please send your proposals to the program officer Gerhard Schlosser (Gerhard.Schlosser@nuigalway.ie) be-

fore June 30th, 2009.

We look forward to seeing you in Paris next year.

The executive committee, Richard Bateman Patricia

Beldade Robert Cerny Frietson Galis Gerhard Schlosser
Michael Schubert

p.beldade@biology.leidenuniv.nl

p.beldade@biology.leidenuniv.nl

GradStudentPositions

EBI Hinxton Bioinformatics	63	UNewBrunswick InsectHostRaceFormation	23
MaxPlanck Ploen HostParasiteCoevolution	17	UNewcastleEngland ParasiteEvolution	23
MichiganTechU PopulationGenomics	17	UniCork Ireland PlantBioinformaticsGenomics	24
NatHistMus UOslo Biosystematics	18	UOxford AntibioticEvolution	25
OhioU Papaveraceae EvoDevo	19	UOxford SocialEvolutionVirulence	25
TexasAMU MosquitoPopulationGenetics	19	UParis13Villetaneuse SocialInsectBehaviour	26
UCollegeCork Bioinformatics	20	USalzburg EvolutionaryBiology	27
UDublin WillowVariation	20	UWindsor EvolutionConservation	28
UGeneva ForaminiferaPhylogenetics	21	UWisconsinMadison MurreletGeneticVariation	28
UHouston 2 EvolutionaryBioinformatics	21	UWisconsinStevens FishPopulationDynamics	29
ULouisiana EvolutionaryBiology	22	UZurich PlantEvolution	29
UNeuchatel ProtistanBiodiversity	22		
UNeuchatel SocialEvolutionTheory	22		

EBI Hinxton Bioinformatics

POST-GRADUATE JOB OPPORTUNITIES IN THE GOLDMAN GROUP, EBI, HINXTON, UK

Positions are currently available in the Goldman Group at the EMBL-European Bioinformatics Institute (EBI) in Hinxton, near Cambridge, UK.

Post-graduate opportunities currently open include:

* software engineering for high-throughput sequencing, with the possibility to contribute scientifically (post-grad or post-doc appointment, depending on experience)

* PhD studentship, potentially in any aspect of theoretical molecular evolution within the group's range of interests

Further details are available via: * [http://-](http://www.ebi.ac.uk/goldman/)

[www.ebi.ac.uk \(EBI\)](http://www.ebi.ac.uk/goldman/) * <http://www.ebi.ac.uk/goldman/>
(Goldman Group) * <http://www.ebi.ac.uk/goldman/-jobs.html> (job details)

Please pass this on to anyone you know who might be interested, or to anyone who might be able to pass it on further.

Mention code EVLDR001 when you refer a prospective candidate to me and you will be eligible for a free gift with a market value in excess of £8.00 (approx. Euro9.00 or \$13.00) if that candidate applies successfully for a position.

I will be at the Evolution meetings in the next few days and then back at EBI, and am happy to meet or correspond with potential applicants.

Please look out for a separate message regarding post-doctoral level positions.

Thanks,

Nick Goldman

Nick Goldman tel: +44-(0)1223-492530 EMBL - Euro-

pean Bioinformatics Institute fax: +44-(0)1223-494468
Wellcome Trust Genome Campus, Hinxton, Cambridge
CB10 1SD, UK

goldman@ebi.ac.uk goldman@ebi.ac.uk

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 to apply for a PhD position in the MPI-Evolutionary Biology. The successful candidate will work on understanding the molecular aspect of the host-parasite co-evolution using our established model system, the three-spined stickleback (*Schistocephalus solidus*) and its specific parasite *Schistocephalus solidus*. This research aims to look for possible molecular evolutionary mechanisms that will explain how these two organisms manage to co-evolve given the pressure exerted by one to the other.

The applicant should have a Diplom/Master in Molecular Biology (or its equivalent) and with a good background in Evolutionary Biology. Knowledge in bioinformatics will be an advantage. The candidate will collaborate with a well-organized team of researchers specializing in immunogenetics, immunology, population genetics, parasitology, and behavioural ecology. English is the working language in the lab so we encourage international 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, located in Plön, Northern Germany, 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 genomics facilities. For more information about the department's research interests you can visit <http://www.evolbio.mpg.de/english/abteilungen/evolutionsoekologie/>. If interested, please submit your CV with a list of your publications, address of three references, and short research statement to milinski@evolbio.mpg.de <<mailto:milinski@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 2 D-24306 Ploen, Germany

direct: +49-(0)4522 763 254 Sec: +49-(0)4522 763 253 Fax: +49-(0)4522 763 310 email: milinski@evolbio.mpg.de* *website: <http://www.evobiol.mpg.de/> "Irene E. Samonte-Padilla" <samonte@evolbio.mpg.de>

MichiganTechU PopulationGenomics

Ph. D. position in Population Genomics Biotechnology Research Center School of Forest Resources and Environmental Science Michigan Technological University, Houghton, MI

A Ph.D. position (3 years) in population and quantitative genetics with a major focus on forest trees is immediately available (see Gailing et al., 2009 in press *Physiologia Plantarum*, Gailing et al. 2008, *Global Change Biology* 14:1934-1946., Curtu et al. 2007, *BMC Evolutionary Biology*. Doi: 10.1186/1471-21-48-7-218.). You will be involved in a project that employs molecular genetic and genomic tools for dissecting the genetic basis of forest trees adaptation to changing and variable environments. You will be part of Michigan Tech's Ph. D. in Forest Molecular Genetics and Biotechnology graduate program and will have ample opportunities to interact with other faculty, research scientists and graduate students (<http://forest.mtu.edu/gradstudies/prospectiv.htm>).

An MS degree earned in the field of plant molecular biology or population genetics is essential. A background in evolutionary biology and population genetics is highly desirable. You should be familiar with molecular genetic techniques, e.g. DNA extraction, PCR, fragment analysis, sequencing and cloning. Selection will be based on academic achievements, reference letters and previous research experience. An on-Campus personal interview may be required. Tuition and fees waiver and a standard stipend package commensurate with your experience will be offered.

Send resume highlighting your experience and interests, GRE scores (TOEFL required for international

students), and names and email addresses of three references to Dr. O. Gailing (ogailing@mtu.edu), Assistant Professor for Ecogenomics, School of Forest Resources and Environmental Science, Michigan Technological University, Houghton, MI 49931. Please visit <http://forest.mtu.edu/faculty/gailing/index.html> for more information on our research programs. Michigan Technological University is an equal opportunity education institution/equal opportunity employer.

Oliver Gailing <ogailing@mtu.edu>

NatHistMus UOslo Biosystematics

PhD Fellows in Biosystematics TWO POSITIONS AS PhD FELLOWS (SKO 1017) IN BIOSYSTEMATICS are available for four years at the Natural History Museum (NHM), National Centre for Biosystematics (NCB).

The Natural History Museum (<http://www.nhm.uio.no>), University of Oslo, has 150 employees engaged in research and education in biological and geological sciences, including the maintenance and development of large scientific collections.

The National Centre for Biosystematics (<http://www.nhm.uio.no/forskning-samlinger/forskning/-forskingsgrupper/ncb/>) is a strategic, interdisciplinary research group which aims to conduct high-quality research and education in the systematics of plants and animals. The research integrates modern tools of molecular genetics with classical taxonomy and tries to reach a deeper understanding of the biodiversity patterns in nature and the evolutionary processes shaping them. NHM has its own multi-user DNA laboratory with all basic equipment, as well as access to a pyrosequencing facility at the Department of Biology at the Blindern campus. NHM also has other relevant research facilities for biosystematic research, such as laboratories for freshwater fish and their parasites, light and scanning electron microscopy, facilities for experimental plant cultures, and a field station in Øvre Heimdalen (near Jotunheimen mountains). NCB currently includes 10 senior scientists and their research groups of postdocs, PhD candidates and Master students, as well as visiting scientists. The NCB thus offers a multidisciplinary and stimulating research environment.

The PhD fellowships announced here may be linked to ongoing research projects on particular taxonomic

groups, but are announced broadly in order to attract the best applicants available with a strong motivation to complete a PhD in biosystematics. One of the fellowships should involve screening of diversity in selected invertebrate groups (e.g. aquatic insects, helminths) using DNA barcoding, while the other one is taxonomically open. The applicants must hold a MSc. degree or equivalent in biology, preferentially in modern biosystematics (or in a related discipline in evolutionary biology), and have experience with molecular methods. The actual research project will be decided and developed by the successful candidates and appropriate members of the NCB staff. The applicant may, however, as part of the application, suggest a biosystematics research project within her/his particular field of interest. The evaluation of applicants will be based on their academic record, relevant experience and past scientific merits. The fellowships require admission to the research training programme at the Faculty of Mathematics and Natural Sciences. An approved plan for the research training, including a project outline, must be submitted no later than one month after taking up the position, and the admission must be approved within three months. Compulsory service (i.e. duty work) shall represent 25% of nominal working time.

A good command of English is required for all students attending the University of Oslo. International students who are not native speakers of English must document their proficiency in English. <http://www.uio.no/english/research/phd/index.html>. UiO has an agreement for all employees, aiming to secure rights to research results a.o.

For more details please contact Professor Jan T. Lifjeld (NCB Deputy Leader), phone (+47)-22851726), email: j.t.lifjeld@nhm.uio.no, Associate professor Arild Johnsen, phone (+47)-22851860), email: arild.johnsen@nhm.uio.no, or Research Director Fridtjof Mehlum, phone (+47) 22851723, email: fridtjof.mehlum@nhm.uio.no

Pay Grade: 45-49 (NOK 353.200-378.300,- pr year, depending on qualifications and seniority)

Application Deadline: 23 June 2009

Ref. No.: 2009/8654

To apply please send three copies of; letter of application, marked with ref. nr., CV, certified copy of the original under- and postgraduate degree certificate, and an original (or certified copy) transcript of marks/grades showing examination in the individual subjects. Names and addresses of two referees, and a covering letter outlining relevant background and work experience, to the following address:

Natural History Museum, University of Oslo, P.O. Box 1172 Blindern, N-0318 Oslo, Norway

An extended applicant form must be completed and submitted together with the application. This form is available at: http://www.admin.uio.no/opa/ledigestillinger/english/sokerskjema_GBR.rtf . Application papers will not be returned.

arild.johnsen@nhm.uio.no arild.johnsen@nhm.uio.no

OhioU Papaveraceae EvoDevo

A teaching assistantship is available in the Department of Environmental and Plant Biology, Ohio University, to study the genetic control of reproductive morphological diversity in Papaveraceae. The project investigates links between inflorescence architecture and flower symmetry in the morphologically diverse Papaveraceae. Poppies and fumitories represent a new model lineage at the base of the eudicots. We have identified homologs of FLORICAULA, FRUITFULL, TERMINAL FLOWER1, and CYCLOIDEA genes in order to study their role in inflorescence determinacy, efflorescence sequence, and flower symmetry in a set of key species.

The project involves (i) cloning and phylogenetic characterization of additional genes from a broader sampling of species, (ii) a comparative morphological study of inflorescence and flower development, (iii) the characterization of gene expression patterns using RT-PCR and in situ hybridization, and (iv) phenotypic analyses of effects of modulated expression using virus-induced gene silencing (VIGS) and Agrobacterium-mediated transformation. As part of this effort, VIGS will be adapted to fumitory species.

Candidates for this position should have a strong interest in plant development and evolution, and demonstrable experience in some of the methods mentioned. The ability to work independently and self-motivated is essential. The student will join a lab with vibrant research spanning from the organismal to the molecular level.

Please send a cover letter, a curriculum vitae, GRE scores, a statement of research experience that also explains what specifically attracts you to this particular project, and the names and contact information of at least two scientists available for reference. Please send your application and informal inquiries to Dr. Stefan

Gleissberg (gleissbe@ohio.edu). Review of applications will start July 31, 2009, and continue until the position is filled. Possible start dates are September 2009 or January 2010.

Dr. Stefan Gleissberg Assistant Professor Plant Development and Evolution Department of Environmental and Plant Biology Ohio University 500 Porter Hall Athens, Ohio 45701, USA Phone: (740) 593 2549 Email: gleissbe@ohio.edu <http://www.plantbio.ohiou.edu/> gleissbe@ohio.edu

TexasAMU Mosquito Population Genetics

A Master of Science graduate student position is available (starting asap) in the laboratory of Michel Slotman in the department of Entomology at Texas A&M University to study the population genetics of the malaria vector *Anopheles melas*.

The Slotman lab is interested in the evolutionary genetics of malaria mosquitoes, with an emphasis on the *Anopheles gambiae* complex. *Anopheles melas* is a saltwater-breeding member of this complex with a patchy distribution along the West Coast of Africa, stretching from Senegal to Angola. This species is a locally important vector on Bioko Island, Equatorial Guinea, and other locations in West Africa. A thorough understanding of the population structure and migration pattern of *An. melas* will allow us to predict the risk and speed of migration from the African mainland to Bioko Island, where an extensive malaria control project has been underway. Additionally, the potential for the spread of insecticide resistance, as well as the effect of habitat fragmentation on this species' population structure are relevant issues.

The successful candidate will use microsatellite markers and mtDNA to study the population structure of *An. melas* across its distribution. This candidate should have an interest in vector biology, and some background in (evolutionary) genetics is preferred.

For further information please contact:

Michel Slotman maslotman@ag.tamu.edu

Office: (979) 845 7556

Information on the Slotman lab can be found at: <http://slotmanlab.tamu.edu/> To be considered for this

position please send a CV, your GRE scores, transcripts, as well as a cover letter explaining your interest in the research to maslotman@ag.tamu.edu maslotman@ag.tamu.edu

UCollegeCork Bioinformatics

PhD Studentship in Bioinformatics/Computational Biology

Title: Understanding Microsatellite Mutation and Evolution - A Bioinformatics Analysis of 1000 Human Genomes

Supervisor: Dr. Avril Coghlan, University College Cork, Ireland.

Application Deadline: 30 August 2009

Funding Details: Science Foundation Ireland - EU students only

Contact: Avril Coghlan, email a.coghlan@ucc.ie

Project Description: A 3-year Science Foundation Ireland PhD studentship is available from October 2009 to work on an internationally collaborative project between Dr Avril Coghlan in University College Cork, Ireland and Dr Richard Durbin at the Wellcome Trust Sanger Institute, Cambridge, U.K. The successful candidate will be based at University College Cork but will visit the Sanger Institute for meetings with collaborators.

The project involves the development of a novel bioinformatics approach for inferring the genotypes of individuals at microsatellite (simple repeat) loci, using data from new DNA sequencing technologies. The novel bioinformatics method will be applied to data from the 1000 Genomes Project, an international project which aims to sequence the whole genomes of 1000 humans from around the world. By inferring genotypes at microsatellite loci in 1000 human individuals, this PhD project aims to investigate important unanswered questions about microsatellite processes and evolution.

The ideal candidate will have an honours B.Sc. or M.Sc. in bioinformatics, computational biology, or a related subject. Candidates with a background in genetics or a related biological subject with strong mathematical skills, or with a background in mathematics or computer science with a strong interest in biology, are also encouraged to apply.

To apply for this position please send a cover letter, copy of B.Sc. transcript and your CV to Dr. Avril Coghlan by email to a.coghlan@ucc.ie

The closing date for applications is August 30th 2009.

Salary/Stipend: The PhD student will have his/her fees paid, and will receive a tax-free stipend of 18500 euro in year 1, 19500 euro in year 2 and 20500 euro in year 3.

A.Coghlan@ucc.ie

UDublin Willow Variation

PhD Graduate Position: Investigating variation of disease resistance and wood formation genes in willow (Teagasc Walsh Fellowship, 3 years, University of Dublin, Trinity College, Ireland)

Willows (*Salix*) are important economically and ecologically. They are a renewable energy source that when grown as an energy crop can mitigate CO₂ emissions. There is increased interest in the use of willow as a source of biomass on Irish farms and production is now grant aided. It is desirable to have varieties with an increased dry matter content and wood density, which would decrease the drying costs and increase the calorific value of the wood. It is also desirable to improve their resistance to biotic agents such as fungal diseases and insect pests. Wild willows in Ireland are well adapted over many generations but their genetic diversity is unknown.

The proposal aims to characterise native species of willow through DNA sequencing to assess the levels and the nature of natural polymorphism within the species and populations studied. Importantly, they will be assessed for variation in specific genes known to confer tolerance to biotic agents (fungi and pests) as well as genes that affect dry matter and wood density. Efforts will concentrate on *Salix viminalis* since commercial varieties are available for this species. Willows and poplars (*Populus*) are closely related (*Salicaceae* family). Several important genes affecting disease resistance and wood formation are well characterized in poplar and will have homologs in willow. We propose to examine these genes in native willows and compare them to commercial cultivars. Material showing greater gene diversity for a target region such as disease resistance will identify germplasm with potential value for further breeding work.

The project is a collaboration between Trinity College Dublin (TCD), Teagasc and the National Botanic Gardens Glasnevin. It will be jointly supervised by Dr Trevor Hodkinson (TCD; www.tcd.ie/Botany/), Dr Gerry Douglas (Teagasc (Kinsealy; www.teagasc.ie) and Dr Colin Kelleher (www.botanicgardens.ie). The researcher will be based at all three institutions. The student will receive an annual tax free stipend of 21,000 Euro for maintenance and to cover university fees. Fees are approximately 5,500 Euro for EU students or 12,000 Euro for non-EU students. There will be opportunities to make more money teaching and demonstrating on undergraduate courses and invigilating examinations.

The ideal candidate will have experience of bioinformatic methods and wet lab experience of PCR and sequencing. They should have an interest in population genetics and evolutionary genetics. Applicants must have a first or second class (preferably upper) Bachelors, or Masters, degree in a biological science or relevant subject. To apply or to obtain further information, please send a CV, contact details of two referees and a letter of motivation to trevor.hodkinson@tcd.ie by July 1st 2009.

– Dr Trevor Hodkinson School of Natural Sciences Botany Building Trinity College Dublin D2, Ireland

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

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Trevor Hodkinson <hodkinst@tcd.ie>

UGeneva ForaminiferaPhylogenetics

PhD position in Phylogenomics of Eukaryotes

A PhD position will be available at the Molecular Systematics Group, Department of Zoology and Animal Biology, University of Geneva, starting in September 2009.

The position will focus on phylogenomics of Foraminifera, one of the most abundant and diverse groups of marine protists. The EST-based phylogenomic approach will be used to examine the higher level phylogeny of Foraminifera, in relation to their morphology and fossil data. The transcriptomic data will also be used to investigate the genes involved in granuloreticulopodial motility, calcification, and denitrification recently discovered in some foraminiferal

species.

The project is a part of the long-term research on foraminifera and other amoeboid protists, supported by the Swiss National Science Foundation. More about this and other our projects can be found at <http://www.unige.ch/sciences/biologie/biani/msg/> The successful candidate is expected to have a diploma/MSc degree in biology or bioinformatics. She/he should have a strong interest in evolutionary biology and genomics and a basic knowledge of systematics and phylogeny of unicellular eukaryotes. A solid experience in using bioinformatic tools is required.

To apply, please send an e-mail with the cover letter, CV, and contact details of two referees to Jan.Pawlowski@unige.ch.

Deadline for applications is 15th June, 2009.

Dr. Jan Pawlowski Dept of zoology and animal biology University of Geneva, Sciences III 30, Quai Ernest Ansermet CH 1211 Genève 4, Switzerland

Phone: 00 41 22 379 30 69 Fax: 00 41 22 379 33 40 E-mail: jan.pawlowski@zoo.unige.ch
<http://www.unige.ch/sciences/biologie/biani/msg/>
Jan.Pawlowski@unige.ch

UHouston 2 EvolutionaryBioinformatics

Ph.D. Scholarships in Evolutionary Bioinformatics at the University of Houston

I am looking forward to recruiting 2-3 graduate students who are interested in pursuing research in evolutionary bioinformatics. Questions that are currently under investigation in my lab are the evolution of compositional heterogeneity in animal genomes, improvement to multiple alignment methodology, and patterns of evolution in overlapping genes. Students are encouraged to identify their own research niche and pursue it. I am particularly interested in students with a bachelor (B.S. or B.Sc.) or a master degree (M.S. or M.Sc.) in Bioinformatics or any other quantitative discipline, such as Computational Biology, Statistics, Computer Sciences, Engineering, Mathematics, or Physics.

The Division of Ecology and Evolutionary Biology is an interactive and dynamic group within the Department of Biology and Biochemistry at the University of Houston (http://bchs.uh.edu/faculty_res_div.php).

Please address inquiries to Dan Graur at dgraur@uh.edu.

Dan Graur John and Rebecca Moores Professor Department of Biology & Biochemistry University of Houston 369 Science & Research Building 2 4800 Calhoun Road Houston, TX 77204-5001 USA

dgraur@gmail.com

ULouisiana EvolutionaryBiology

University Doctoral Fellowships are available for entering Ph.D. students in Environmental and Evolutionary Biology at the University of Louisiana. University of Louisiana Fellowships are funded for 3-4 years at \$15,750 per 9 months (with tuition waiver), and have limited teaching responsibilities. Eligibility requirements include US citizenship (or permanent residency) or degree from a US institution. Rather than replying to this message, potential applicants are strongly encouraged to directly contact prospective advisors. Their contact information and research interests can be found at our departmental web site (<http://biology.louisiana.edu/>). More information is also available at our graduate program web site <http://ulceet.com/site90.php>. The department of Biology has approximately 25 faculty members and 70 graduate students. Areas of strength include ecology, conservation biology, evolution, and marine/coastal biology.

– Paul Leberg Professor and Graduate Coordinator Department of Biology University of Louisiana Lafayette

For more information on my research please visit: <http://ulceet.com/site81.php> For more information about the graduate program please visit: <http://ulceet.com/site90.php> and <http://biology.louisiana.edu/> PO Box 42451 Lafayette, LA 70504 Leberg@Louisiana.edu 337-482-6637 337-482-5660 (Fax)

Paul Leberg <leberg@louisiana.edu>

UNeuchatel ProtistanBiodiversity

PhD Position in Protistan biodiversity

A PhD position will be available at the Laboratory of Soil Biology, Institute of Biology, University of Neuchâtel, starting in August 2009 (at the earliest) or September 2009.

The project will use a combination of morphological (microscopy) and molecular approaches to address questions of phylogeny, systematics and biogeography of free-living microorganisms using testate amoebae as models.

The project is related to several ongoing projects funded by the Swiss National Science Foundation.

The successful candidate should have a M.Sc degree in biology. She/he should have a strong interest in taxonomy, phylogeny and biogeography and the diversity of free-living eukaryotes in general. Good knowledge of molecular phylogeny and/or taxonomy is an advantage.

This position involves some teaching (teaching assistantship for laboratory and/or field courses) at the undergraduate and graduate levels.

To apply or for further information please send an e-mail with cover letter, CV, and contact details of two referees to edward.mitchell@wsl.ch.

Keywords : phylogeny, systematics, protists,

Prof. Edward A. D. Mitchell Swiss Federal Research Institute WSL Research Unit Ecosystem Boundaries Wetlands Research Group Station 2 CH - 1015 Lausanne-Ecublens Switzerland

Phones: office: +41 21 693 57 50; mobile: +41 78 913 15 74; secretary: +41 21 693 39 05; FAX: +41 21 693 39 13 edward.mitchell@wsl.ch <http://www.wsl.ch/personal/homepages/mitchell/> >From August onwards: University of Neuchâtel Institute of Biology Laboratory of Soil Biology

Mitchell Edward <edward.mitchell@epfl.ch>

UNeuchatel SocialEvolutionTheory

Dear colleagues,

Two PhD positions are open under the supervision of Dr. Laurent Lehmann to study social evolution theory at the Laboratory of eco-ethology of the University of Neuchâtel Switzerland (<http://www2.unine.ch/ethol/>). The positions are funded by the Swiss National Science Foundation and are available for three years. Starting date: end of 2009, beginning

of 2010. Salary per annum: 36900 to 45600 CHF.

The focus of the SNF-funded project is to develop gene-culture co-evolutionary models for social interactions, with focus on human evolution. The project will have two different but complementary directions. First, we will seek to develop models, which can explain the evolution of the transition of small-scale egalitarian societies to larger-scale stratified societies. Second, we will seek to develop models aiming at understanding the role of individual and social learning in the expression and dynamics of social behaviours, for example in the context of the usage of adaptive and maladaptive cultural traits. Some related papers on this can be found at <http://www.stanford.edu/~lehmann/>. Depending upon the applicants, the work could be taken in a number of directions.

The Institute of Biology at Neuchatel consists of a dozen groups working in diverse fields of ecology, evolution, physiology and molecular and cell biology. Neuchatel is a University town in the French-speaking part of Switzerland situated between the Jura Mountains and a 40km long lake. The town is well connected with larger centers such as Lausanne, Geneva, Berne, or Zurich by public transportation. For more information, contact Laurent Lehmann (lehmann@stanford.edu).

Applicants must have a university degree that allows entrance to a PhD program. Applicants are required to have good knowledge in mathematics or computer programming. Ideal applicants have a good knowledge of evolutionary biology, behavioural ecology and/or population genetics. A strong interest in understanding the genetic and cultural factors driving social evolution in humans is an asset. Motivated applicants should submit (1) a one-page letter that summarizes interests and relevant experience, (2) a CV, (3) copies of undergraduate and masters/diploma transcripts, and (4) contact information for 2 references (all as PDFs) to lehmann@stanford.edu.

Best wishes, Laurent Lehmann

Laurent Lehmann <lehmann@stanford.edu>

UNewBrunswick
InsectHostRaceFormation

PhD student position, University of New Brunswick:
Plant traits and insect host-race formation

A fully funded position is available for a PhD student

at the University of New Brunswick, Fredericton (laboratory of Dr. Steve Heard), starting in fall 2009 or winter 2010.

The research project involves the study of variation in plant traits, within species and between closely related species, and how they interact with insect preferences to shape the evolution of diet in insect herbivores. We will be particularly interested in trait distributions and preferences that favour the evolution of diet generalism (one insect feeds on several host plants) vs. divergence with the evolution of diet specialization (leading to evolution of a host-race complex with each race feeding on a single host plant). Our model system is the diverse community of insects feeding on the common golden-rods *Solidago altissima* and *Solidago gigantea*. The project will involve both field and laboratory work.

For examples of previous projects/publications in this area, see

<http://www.unb.ca/fredericton/science/biology/-Faculty/Heard.html> To apply, please send (snail mail or e-mail) a letter expressing your interest and summarizing your qualifications, a current CV, undergraduate grades (an informal copy is fine; no need for an official transcript), and names and contact information for at least two references.

Please address your materials to:

Steve Heard Professor and Chair Dept. of Biology University of New Brunswick PO Box 4400 Fredericton, NB E3B 5A3

sheard@unb.ca

UNewcastleEngland
ParasiteEvolution

POST-GRADUATE PHD POSITION IN THE EMBLEY/HIRT GROUP, NEWCASTLE UNIVERSITY, UK

A PhD position is available in our group to work on the evolutionary biology of microsporidian parasites:

Microsporidia, opportunistic intracellular pathogens, cause chronic diarrhoea in children and the elderly, especially in the developing World and frequently infect patients with HIV/AIDS. They are among the simplest eukaryotic cells known, having lost many metabolic pathways common to other eukaryotes and have greatly simplified the structure and functions of

their organelles. As a consequence, Microsporidia are ideal model systems for identifying the truly indispensable features of eukaryotic cells. Recent data from our laboratory suggest that mitosomes, the basic mitochondria found in Microsporidia, house enzymes that are vital for parasite survival (Nature, 452, 624-628; Nature 453, 553-556; Nature, 440: 623-630; Nature, 418: 865-869). The aim of this project is to now fully determine the essential function(s) of these minimal mitochondria. The work has far reaching importance because: (i) it will provide functional data for an organelle that is essential for the survival of major human parasites and (ii) it will challenge the long-held hypothesis that the key function of mitochondria (defined in the broadest sense) in eukaryotic cells is to make ATP.

The successful candidate will join a research group working at the forefront of international efforts to understand the fundamental biology and evolution of Microsporidia and will play a major role in a multidisciplinary international project with similar aims. You will be trained in cell and molecular biology, and in computational analysis, in a laboratory with a strong interest in evolution (Nature, 440: 623-630). You will also have opportunities to work in the laboratories of our leading collaborators in Cambridge and Germany (Nature, 452, 624-628; Nature 453, 553-556).

Person Specification: You should have, or expect to achieve, a first class or upper-second class Honours degree (or European equivalent) or a higher qualification, in a relevant subject.

Eligibility and Value of Award: This Studentship is open to UK and other EU students who have a relevant connection to the UK and meet the BBSRC's eligibility criteria. The award will cover tuition fees and an annual stipend (living allowance) at UK Research Council rates (approximately £13,000 per annum).

Please pass this on to anyone you know who might be interested, or to anyone who might be able to pass it on further.

Thanks,

Martin Embley email: martin.embley@ncl.ac.uk
 Tel: 0044191 222 7702 <http://www.ncl.ac.uk/camb/-staff/profile/martin.embley> http://www.ncl.ac.uk/microbial_eukaryotes/
 Martin.Embley@ncl.ac.uk

UniCork Ireland PlantBioinformaticsGenomics

UniCork.Ireland.PlantBioinformaticsGenomics

PhD Student Position (Plant bioinformatics & genomics)

Genetics & Biotechnology Lab, University College Cork (UCC), Ireland

The Genetics & Biotechnology lab of Dr. Charles Spillane at University College Cork, Ireland is seeking candidates for a PhD in bioinformatics and systems biology of large-genomic datasets. The successful applicant will form part of a team (postdocs, PhD students) in the lab working on a combination of bioinformatic, systems biology and functional wet-lab approaches for understanding gene regulatory systems involving genomic imprinting and gene dosage. The PhD student will also interface extensively with collaborator labs outside Ireland. We are seeking highly motivated applicants with consistently excellent grades (ideally to MSc level), who are eager to develop a long-term career in genome bioinformatics and/or computational systems biology. We are particularly interested in candidates with an excellent grasp of genetics, statistics and computer programming (Python, R, Bioconductor, SQL, UNIX/LINUX), who have bioinformatics research experience (e.g. as RAs, MSc/diploma students, interns, etc) in research lab/institute settings, and are experienced in efficiently handling multiple large datasets.

Applicants should send an e-mail outlining research interest and motivations, including; (a) your C.V. (list grades, interests and experimental skills) & (b) contact details and e-mail addresses for 3 referees to:

Dr. Charlie Spillane, Genetics & Biotechnology Lab, Biochemistry Dept & Biosciences Institute, University College Cork, LM 2.10, Cork, Ireland. E-mail: c.spillane@ucc.ie

The deadline for applications is 10th July 2009 or until suitable candidate is recruited.

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

[T] 00-353-21-4904124 (office) [E] c.spillane@ucc.ie

[W] www.ucc.ie/spillane "Spillane, Charles"
<C.Spillane@ucc.ie>

UOxford AntibioticEvolution

Ph.D Position, Experimental evolution of antibiotic resistance, University of Oxford

Experimental evolution of antibiotic resistance

The evolution of antibiotic resistance in pathogenic bacteria poses a fundamental threat to human, animal, and plant health. Combinatorial drug therapies have been widely advocated as a treatment strategy to prevent resistance from evolving, but the fundamental ecological and evolutionary processes involved in adaptation to multi-drug environments remain poorly understood. The goal of this project will be to address two fundamental questions using experimental evolution in the opportunistic human pathogen *Pseudomonas aeruginosa*: i. Which combinations of antibiotics to use? Population genetic theory predicts that epistasis between resistance mutations can constrain or promote the evolution of multidrug resistance. We will test the ability of metabolic control theory to predict patterns of epistasis between antibiotics based on the functional interactions between their cellular targets. This will involve quantifying the fitness costs of carrying combinations of mutations giving resistance to different antibiotics. ii. How to deploy antibiotics? We will test ability of classical ecological models and novel optimal control models to predict how environmental variation impacts the evolution of resistance. This will involve manipulating the spatial and temporal pattern of antibiotic deployment during long-term experimental evolution of the opportunistic human pathogen *Pseudomonas aeruginosa* in multidrug environments.

APPLICATION DEADLINE: JUNE 19, 2009

To apply please complete the University application form (available from: www.admin.ox.ac.uk/postgraduate/) and include three references from academic referees (follow Notes of Guidance for Applicants to Graduate Study 2009-2010). Please submit two copies of the application forms and all supporting material to the Graduate Administrator, Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS (NOT the address detailed on the application form) and please DO NOT apply online. An application fee of £25 must also be enclosed, please see guidance notes for acceptable methods of payment.

Please quote reference RC06. Further details of this post can be found at the following URL, <http://www.findaphd.com/search/showproject.aspxprojectid=22492> <<http://www.findaphd.com/search/showproject.aspxprojectid=22492&theorder=3&location=&univ=&disc=allsci&searchtype=b&keyword=evolution+antibiotic+resistance&scip=3&scif=0&socp=0&socd=0&socf=0&pd=0&page=1>> or by contacting Craig MacLean (craig.macleaATzoo.ox.ac.uk)

Craig MacLean <craig.maclea@zoo.ox.ac.uk>

UOxford SocialEvolutionVirulence

Oxford.Social_Evolution_Virulence *Social evolution in microorganisms and a Trojan horse approach to medical intervention strategies * Supervisors: Ashleigh Griffin and Sam Brown, Department of Zoology, Oxford http://www.zoo.ox.ac.uk/staff/academics/griffin_as.htm http://www.zoo.ox.ac.uk/staff/academics/brown_s.htm ***Deadline 19 June!***** UK research council funding: Full Stipend for UK students (fees only for EU students)

Medical science is typically pitted against the evolutionary forces acting upon infective populations of bacteria. As an alternative strategy, our growing understanding of population dynamics of social traits in bacteria could be applied to revolutionize the treatment of bacterial disease.

This project will test predictions about the ability of social cheats to invade populations of cooperative strains: public good cheats, cheats carrying beneficial alleles (Trojan horses) and cheats carrying allelopathic traits (anti-competitor chemical bacteriocins). Theory suggests that exploitation of the invasive ability of cheats is a potential new strategy for helping treat bacterial disease (Brown, West, Diggle and Griffin (in press) Phil Trans Roy Soc).

To further develop this idea the student will: a) test relative competitive ability of different kinds of social cheats by experiment in the bacteria *Pseudomonas aeruginosa*, b) test the ability of strains that have been engineered to carry medically beneficial alleles to out-compete wild-type strains. Specifically, we will use cheating strains carrying antibiotic sensitivity alleles and/or a gene for the production of a lethal toxin (under the control of an inducible promoter) which when

activated, would eliminate both cooperators and cheats.
 c) compare antibiotic sensitivity of populations that have been infected with Trojan horse antibiotic sensitive strains, with those that have not.

The integration of theory and experiment is a key goal of this project. The student will receive training in mathematical modelling techniques with SB, and there will be scope for involvement by the student in the construction and analysis of further models inspired by experimental insights. Model development will include extensions to the dynamical ecological models of therapeutic cheat invasion and establishment (extending work in Brown et al in Press), inclusive fitness formalisms to introduce longer-term evolutionary dynamics (e.g. social resistance evolution), and simulations (anchored on the analytical results).

For more info, contact Ashleigh (ashleigh*.griffin@zoo*.ox*.ac*.uk<ashleigh.griffin@zoo.ox.ac.uk>) or Sam (sam.brown@zoo.ox.ac.uk).

To apply please complete the University application form (available from: www.admin.ox.ac.uk/postgraduate/) and include three references from academic referees (follow Notes of Guidance for Applicants to Graduate Study 2009-2010). Please submit two copies of the application forms and all supporting material to the Graduate Administrator, Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS (NOT the address detailed on the application form) and please DO NOT apply online. An application fee of 25 must also be enclosed, please see guidance notes for acceptable methods of payment. Please quote reference RC09. – Sam Brown Wellcome Trust Career Development Fellow Department of Zoology, University of Oxford South Parks Rd, Oxford OX1 3PS, UK +44 (0)1865 281062, www.zoo.ox.ac.uk/staff/academics/brown_s.htm Sam Brown <sam.brown@zoo.ox.ac.uk>

UParis13Villetaneuse SocialInsectBehaviour

Proposition de thèse / PhD opportunity Laboratoire
 Éthologie Expérimentale et Comparée à Université
 Paris XIII

Début de la thèse / Starting date : Automne 2009

Contact : Dr. Nicolas Chaline
 nicolas.chaline@leec.univ-paris13.fr +33 (0) 1 49

40 39 54 <http://www.leec.univ-paris13.fr> A PhD opportunity is available at the Laboratory of Experimental and Comparative Ethology (LEEC) supervised by Nicolas Chaline (Social Hymenoptera Ethology group). The PhD grant is part of the research program SEUILS funded by the French national research agency (ANR) as a project "Jeunes Chercheurs et Jeunes Chercheuses 2009" (see the abstract below). The successful candidate will be involved in one or more of the research axes, according to his experience and interests. More information can be obtained from N. Chaline.

The candidates should have a Master's degree and a solid background in behavioural sciences and will ideally be trained in pharmacology and/or chemical analyses.

Application deadline: 28 June 2009 Please send applications to Nicolas.chaline@leec.univ-paris13.fr with:
 - A detailed CV - Academic records for the Master's degree - A cover letter - At least one personal recommendation sent directly by the referee to nicolas.chaline@leec.univ-paris13.fr Selected candidates will be auditioned by the team members at Paris XIII-Villetaneuse University during the week starting the 6th of July.

Project SEUILS : Modulation of individual behavioral decisions in social contexts

Abstract Individual decision processes have often been overlooked in insect societies. However, investigating the mechanisms underlying these processes allows understanding how individuals adjust to their environment and thereby adaptively satisfy their needs and the colony's. The theoretical framework of our project derives from response-threshold models describing individual decisions as 3-components processes: - Expression: What are the task-related signals? - Perception: What sensory and cognitive processes allow the evaluation of these signals? - Action: How is the decision reached? Each phase will be investigated in three contexts reflecting social complexity: social recognition, task allocation and worker reproductive decisions. We will unravel the role of internal and external factors on social insects' decisions in context. Social recognition, the first aspect, is based in insects on chemical signals. During encounters a phenotype-matching process allows comparison between perceived cues and an internal template acquired through an imprinting-like process and/or self-reference mechanisms. The actual behavioural response (rejection or not) depends on adaptive significance of the discrimination. Interestingly, adult social insects have also been proven able to learn an enemy-specific template from an alien colony,

leading to a modified level of aggression. We aim at (1) characterising the template learning process in adults and (2) elucidating the decisions rules after stimulus assessment. We will assess the influence of bioamines and nutritional status (1) on template learning and (2) on the tolerance threshold value. Task allocation, the second social situation, is characterised by specialisation and behavioural flexibility which permit the workers to respond to colony needs. Among others, larvae may provide information on colony-level attributes and work demands, and adjust individual choices and task performances for both nursing and foraging. After identification of the larval signals, we will characterise the associated response threshold for each age-related task and analyse the effect of individual internal state on the response threshold. Worker reproductive decisions are the third aspect of decision processes studies. In most social insect species, the ability of workers to lay male eggs creates a potential conflict between all colony members for reproduction. The expression of this conflict depends on costs and benefits associated to the decision of reproducing or not. A new strategy has been discovered where workers parasitize conspecific colonies. We will investigate the influence of various factors on the choices available to workers. These choices are to work, to reproduce or to parasitize another colony. Experimental designs will be developed to allow detailed behavioural observations which will be aided by path analyses and behaviour recording software. Signals will be analysed through gas chromatography. Extraction techniques will be developed to test biological activity of signals and to manipulate them, for example by creating fractions or mixed chemical signals to be used in bioassays. We will focus on the influence of two factors on individual decisions in our three social

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USalzburg EvolutionaryBiology

THREE-YEAR PHD POSITION IN PLANT EVOLUTIONARY BIOLOGY

A Ph.D. position in Plant Evolutionary Biology is available at the Dept. of Organismic Biology, Division of

Plant Ecology & Diversity, University of Salzburg, Austria, with Prof. Hans Peter Comes and Dr. Gunter Fischer to study the ecology and evolution of reproductive traits in the orchid genus *Bulbophyllum* from the Southwest Indian Ocean region (Madagascar, Comoros, Mascareignes)

This research project will involve refined molecular-phylogenetic (ITS, cpDNA, single/ low-copy nuclear genes), morphological and pollination-experimental studies in a previously identified clade comprising c. 26 species, mainly distributed in Madagascar, but also occurring in the remote oceanic islands of La Réunion/Mauritius (Mascareignes) and the Comoros, and on the East African continent. These analyses will then be complemented by reconstructions (optimizations) of ancestral reproductive/floral-characters, areas and habitat preferences in conjunction with a molecular dating approach using paleogeological and fossil-based calibrations. Together, this will allow us to infer how mating types (outcrossing vs. auto-pollination), and associated floral traits, have changed within the clade over evolutionary time and under which spatial, temporal and ecological circumstances.

The ideal applicant has a strong interest in plant evolution and a strong background in plant molecular phylogenetics, pollination experimental work, and statistical analyses. As extensive fieldwork in remote places of Madagascar is required, the successful candidate must also have a strong physical fitness and experience in conducting fieldwork under tropical rainforest conditions. A MSc, diploma degree or equivalent in Botany, Ecology, Genetics or Evolutionary Biology is required. Fluent English is a must and French as second language would be an advantage.

Funding is for three years by the Austrian National Science Fund (FWF). The University of Salzburg (<http://www.uni-salzburg.at/>) offers excellent facilities, and a very pleasant working and living environment in one of the most beautiful landscapes in Austria.

Please send a letter of application together with a full CV, a copy (pdf) of your master/diploma certificate and thesis, and the addresses of three referees to:

peter.comes@sbg.ac.at or gunter.fischer@sbg.ac.at

Prof. Hans Peter Comes Department of Organismic Biology Division of Plant Ecology & Diversity Paris-Lodron-University Salzburg Hellbrunnerstr. 34, A-5020 Salzburg Austria Tel.: ++ 43 (0) 662 8044-5505 Fax: ++43 (0) 8044-142

The position will be filled as soon as a suitable applicant is found.

gunter.fischer@sbg.ac.at

UWindsor EvolutionConservation

Graduate student positions available

There are immediate opportunities for qualified graduate students (MSc & PhD) to work in Dan Heath's Evolutionary & Conservation Genetics lab at the Great Lakes Institute for Environmental Research (GLIER) at the University of Windsor (Ontario, Canada).

Projects include; investigating the role of gene transcription evolution in local adaptation in BC salmon, evolutionary ecology and conservation of the Eastern Sand Darter, a threatened species in Ontario, and a population and quantitative genetic analysis of migratory behaviour in salmon and trout.

Students will have opportunities for field and lab work, and will be expected to attend and present at national and international conferences.

Contact Dr. Heath at (519) 253-3000 (ext 3762) dheath@uwindsor.ca www.uwindsor.ca/heathresearchgroup Daniel Heath Great Lakes Institute for Environmental Research University of Windsor 401 Sunset Ave Windsor, Ont, Canada N9B 3P4

E-mail: dheath@uwindsor.ca Phone: (519) 253-3000, Ext 3762 Fax: 971-3616 www.uwindsor.ca/heathresearchgroup/ dheath@uwindsor.ca

UWisconsinMadison MurreletGeneticVariation

MSc position available studying adaptive genetic variation in Marbled Murrelets

I am seeking an outstanding MSc student in the field of conservation genetics in the Department of Forest and Wildlife Ecology at the University of Wisconsin-Madison. Current research in my lab focuses on characterizing demographic history and understanding the effects of habitat fragmentation on the microevolution of threatened species. In doing so, we typically integrate field, genetic, and population modeling ap-

proaches to identify factors limiting populations, understand/predict the genetic and demographic consequences of limiting factors, and provide managers and policy makers with the information needed to make informed management decisions.

The student's thesis will involve characterizing adaptive genetic variation in the Marbled Murrelet, specifically at the major histocompatibility complex (MHC). The Marbled Murrelet is a federally threatened seabird that nests primarily in coastal old-growth forests along the west coast of North America. Fragmentation of old-growth forests and increasing predator populations have resulted in a number of geographically isolated and declining populations. Previous work based on neutral (microsatellite) genetic markers has detected little genetic variation across the species range. Adaptive markers, such as MHC, that are under the influence of natural selection may yield finer-scale among population differentiation and have implications for the current proposal to remove murrelets from the threatened species list. Samples have already been collected and this will primarily be a lab-based project, although opportunities to do field work may develop. This work will be conducted in collaboration with Dr. Vicki Friesen at Queens University. Applicants should possess a B.Sc. in Conservation Biology or closely related field and have a strong background in molecular laboratory techniques, particularly bacterial cloning and DNA sequencing. Funding is in place for two years of graduate student support (\$19,000/year + tuition waiver) and laboratory expenses. Note that 9 months of support will come for teaching assistantships in an introductory conservation biology course.

To be considered for this position, please send a cover letter outlining your interests and research background, a curriculum vitae (including GPA and GRE scores), and contact information for three professional references (name, email, phone, address) as either a PDF or MS Word file to mpeery@wisc.edu with Marbled Murrelet MHC Application in the subject line. The selected student is expected to enroll in the Department of Forest and Wildlife Ecology in January 2010 for the spring semester. Applicants must also apply to the MSc program in the Department of Forest and Wildlife Ecology (<http://forestandwildlifeecology.wisc.edu/grad.htm>) and the UW Graduate School (<http://info.gradsch.wisc.edu/education/admissions/>).

Application materials will be accepted until August 1, 2009 or until a suitable candidate is found.

For more info, contact: Zach Peery Assistant Professor Department of Forest and Wildlife Ecol-

ogy University of Wisconsin, Madison Madison, WI 53706 Phone: 608-890-2766 mpeery@wisc.edu <http://forestandwildlifeecology.wisc.edu/facstaff/peery.html>
M ZACHARIAH PEERY <mpeery@wisc.edu>

UWisconsinStevens FishPopulationDynamics

M.S. Assistantships in Fish Genetics and Aquatic Molecular Ecology

The Wisconsin Cooperative Fisheries Research Unit (WICFRU) and the College of Natural Resources (CNR) at the University of Wisconsin-Stevens Point has openings for M.S. students in Fisheries Science beginning Summer/Fall 2009. Projects include:

- Walleye genetic diversity, population dynamics and habitat
- A multispecies assessment of aquatic genetic structure among watersheds in Wisconsin

The program offers educational opportunities integrating field ecology, resource management, and applied scientific research. Resources available to students include use of the Molecular Conservation Genetics Laboratory, computer and AV equipment, SCUBA equipment, and generous travel support. Successful applicants are expected to have completed a B.S./B.A. in a related biological sciences field (i.e., resource management, biology, zoology, botany, microbiology, etc.) with an undergraduate GPA of 3.0 and minimum GRE scores of 1000 (quantitative and verbal). All Wisconsin Cooperative Fishery Research Unit students are expected to attend and participate in scientific meetings, maintain professional memberships in an appropriate society, and communicate with resource agency personnel regarding their research. Students will be part of a diverse CNR graduate program (www.uwsp.edu/cnr <<http://www.uwsp.edu/cnr>>) aimed at providing superior education, communication, and science-based management professionals.

Research assistants of WICFRU receive funding for 2 years at \$16,000/year and paid tuition. Individuals interested in applying to the program should send a letter of interest, resume, 3 references and photocopies of transcripts and GRE scores to Dr. Brian L. Sloss (Conservation genetics: brian.sloss@uwsp.edu <<mailto:brian.sloss@uwsp.edu>>). Electronic information is preferred.

Wisconsin Cooperative Fishery Research Unit College of Natural Resources University of Wisconsin-Stevens Point

Stevens Point, Wisconsin 54481

Brian L. Sloss, Ph.D. Assistant Unit Leader U.S. Geological Survey Wisconsin Cooperative Fishery Research Unit College of Natural Resources University of Wisconsin-Stevens Point 800 Reserve St. Stevens Point, WI 54481

Office: 715-346-3522 Unit Office: 715-346-2178 Fax: 715-346-3624

“Sloss, Brian” <Brian.Sloss@uwsp.edu>

UZurich PlantEvolution

Two PhD positions funded by the SNF are available from October 2009 at the Institute of Systematic Botany, University of Zürich, to study pollinator mediated selection in orchids with different pollination systems. The project deals with patterns of selection in natural plant populations on a population-specific basis. Additionally, selection dynamics in different pollination systems will be investigated in an experimental approach. You should have a master degree (or equivalent) in any field of biology/ecology and a thorough interest in evolutionary and pollination biology. Further, enthusiasm for field work with plants and insects is required. The two projects are embedded in a larger framework of evolutionary and systematics research at our institute. We are currently a group of 3 professors and 6 academic staff, as well as several PostDocs, PhDs, and Master students investigating mechanisms and patterns of evolution in plants. The institute is located in the pretty botanical gardens and houses modern molecular and chemical ecology labs, including greenhouses and climate chambers for plant cultivation.

Zürich has a large and very active research community at the University of Zürich (www.unizh.ch) and ETH (www.ethz.ch), dealing with various aspects of organismal and molecular biology (www.lifescience-zurich.ch). The city also offers excellent quality of life through active cultural programs and infrastructure, as well as an attractive surrounding including the alps in close proximity.

If you are interested in one of the jobs, please send (preferentially by e-mail) a letter describing your motivation, C.V., copy of degrees, publications (manuscripts) if any,

and e-mail addresses of two academic referees. If you have further question, don't hesitate to contact me.

Prof. Florian Schiestl Institute of Systematic Botany Zollikerstrasse 107 CH-8008 Zürich flo-

rian.schiestl@systbot.uzh.ch

“Florian Schiestl, Inst. f. syst. Botanik (Bot. Garten)”
<florian.schiestl@systbot.uzh.ch>

Jobs

BiK-F Germany Biodiversity	30	SouthAfrica FieldAssist ChatEvolution	37
BroadInstitute ComparativeGenomics	31	UGeorgia ResTech PlantEvolutionaryGenet	38
CSIRO Canberra Phylogenomics	31	UIdaho LabTech ExperimentalEvolution	38
EAWAG Switzerland InvasiveSpeciesEvolution	32	UKansas ResTech DrosophilaVariation	39
KentuckyU GeneticsInstructor	33	ULeeds ResTech HoneyBeeEvolution	40
Kunming 2 EvolutionaryBiology	33	UNamur Belgium 2 TeachingAssistants	40
London ResTech EvolBiol	34	UOulu PopGenetics	41
MaxPlanckInst EvolutionaryBiodemography	36	UPerpignan Epigenetics	41
NatHistMuseum Denmark 2 DNASequencing	36	USDA Maryland PlantEvolution	41
OregonStateU PacificSalmon EvolutionaryGenetics	36	UWindsor InstituteDirector	42
RiceU TeachingEvolution	37		
RoyalHollowayU PopulationGenetics	37		

BiK-F Germany Biodiversity

The Biodiversity and Climate Research Centre (BiK-F) has recently been founded by the Senckenbergische Gesellschaft fuer Naturforschung, the Goethe University in Frankfurt, and additional partners. It is funded by the Hessian State Initiative for the Development of Scientific and Economic Excellence (LOEWE). It has strong interactions with the Goethe University in Frankfurt, the Senckenberg Research Institute and other research institutions in the Rhein-Main area and offers an excellent international and multidisciplinary research environment. The mission of the Centre is to carry out internationally outstanding research on the interactions of biodiversity and climate change at the organismic level. The application deadline for the following position has been postponed to end of July 2009:

Research field C (Biological adaptation and Climate):

Professorship W1/W2 for the Evolutionary Analysis of Biological Archives [Ref. #C02]

The successful candidate is expected to analyse biological archives, such as specimens from museum collections or natural sources, such as sediment cores. Central concept is the interpretation of microevolutionary changes in the past as an explanatory tool for future changes and genetic adaptations. This line of research requires a broad experience and competence in the field of molecular ecology and population genetics with an emphasis on historical and current population and community analyses.

The general conditions include a strong track record in peer-reviewed publications and the demonstration of having acquired substantial external funding for research. Collaborations with other research groups at BiK-F, as well as with its partners at the University of Frankfurt and the Research Institute Senckenberg, are expected. In addition, the applicants will contribute to undergraduate and graduate teaching at the Goethe University in Frankfurt.

The Biodiversity and Climate Research Centre advo-

cates gender equality. Women are therefore strongly encouraged to apply. The Biodiversity and Climate Research Centre is an equal opportunity employer. The position is limited to a three or six years appointment. The place of work will be Frankfurt am Main, Germany.

Applicants must meet the requirements for a university professor at the Goethe University in Frankfurt.

Applications, including a statement of current research achievements (1 page) and future research interests (3 pages), curriculum vitae, list of publications, pdf files of 5 key publications and the names of three academic referees should be sent before 31st of July 2009 to:

Scientific Coordinator, Biodiversity and Climate Research Centre, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany.

E-mail applications to Service & Finances: Anette Ohl, recruiting@senckenberg.de Enquiries: Prof. Dr. Bruno Streit, E-mail: streit@bio.uni-frankfurt.de. For further information, please visit <http://www.bik-f.de> Ursula Maurer <Ursula.Maurer@senckenberg.de>

BroadInstitute ComparativeGenomics

The text for the job posting follows. The ideal candidate for the current job posting would be an evolutionary biologist or population geneticist with a strong computational background.

The following position can be applied for by searching Req Number mit-00006323 at: <http://hrweb.mit.edu/-staffing/index.html> RESEARCH SCIENTIST, Broad Institute of MIT & Harvard (Cambridge, MA), to apply and develop advanced comparative genomic tools to the analysis of large viral genomic datasets comprised of 100s-1000s of genomes. Research will focus on the development of novel approaches and the application of existing phylogenetic and population genetic methodologies to address topics in viral genomics such as the population structure of Dengue, HIV, HCV, and WNV; evolution of these viruses in response to host immune, drug, and vaccine pressures; and identifying genomic correlates of disease. Will implement commercially available software tools, significantly contribute to the design of novel computational tools, and interpret results within a biological context; contribute to the design and maintenance of analysis infrastructure to support such analysis; coordinate large-scale

analyses with collaborators and communicate results to the scientific community through conference presentations, peer-reviewed publications, and project reports; conduct comparative genomic analyses using computational tools and develop appropriate statistical tests; lead design and development of new computational approaches; interpret analytical results; maintain detailed logs of analysis conducted and results obtained; contribute to maintenance of analysis infrastructure supporting the viral analysis team; and perform related tasks.

REQUIREMENTS: a Ph.D. in virology, population genetics, evolutionary biology, mathematics, biostatistics, computer science or relevant scientific discipline; demonstrated experience designing comparative genomic, phylogenetic, or population genetic analyses and interpreting results in biological context; experience with standard phylogenetic tools, e.g., PAUP, BEAST, PAML, and Mr. Bayes; demonstrated knowledge of standard statistical methods and population genetics; initiative; and ability to work in a highly collaborative environment. Experience with relational databases, Perl, Python, Java, UNIX, algorithms, or machine learning a plus. MIT-00006323

Matthew Henn, Ph.D. | Research Scientist II | Director
Viral Genomics Broad Institute of MIT & Harvard

email: mhenn@broad.mit.edu tel: 617.714.7905

Matthew Henn <mhenn@broad.mit.edu>

CSIRO Canberra Phylogenomics

POSTDOCTORAL FELLOWSHIP IN PHYLOGENOMICS

An exciting opportunity to participate in the Cotton Bollworm Genome Project has arisen at CSIRO Entomology, Canberra, ACT, Australia.

CSIRO is Australia's leading research organization with over 6,500 staff located across the country. Its aim is to deliver great science and innovative solutions for industry, society and the environment by igniting the creative spirit of its staff. Much of the Life Sciences-oriented research carried out at CSIRO involves using bioinformatics tools to study genomic data, and as these tools become more sophisticated, so do the scientific questions that are being addressed.

The appointee will be an early career scientist with (i)

good knowledge in genome bioinformatics, phylogenetics and related areas of statistics and computing science; (ii) excellent communication, personal, and interpersonal skills; and (iii) a documented record of publishing papers in international, peer-reviewed journals. Familiarity with bioinformatics tools used in genome-wide comparisons of genomic and proteomic data as well as scripting or programming is also desirable. You will be responsible for assembling and comparing data from a wide range of species. In examining these data, there is an opportunity to use CSIRO¹'s excellent high-performance IT resources. Having analysed your data, you will have the opportunity to relate your discoveries to species-specific life-history traits from the insects compared (e.g., diet, insecticide resistance, etc.). You will be expected to be strongly self-motivated and able to work collaboratively as well as independently on a variety of projects; hence, being able to multitask is highly desirable.

For further details, please go to https://recruitment.csiro.au/asp/job_details.asp?RefNo=-3D2009%2F434 Closing data: 5 July 2009.

– Assoc. Prof. Lars Jermiin Biological Science, Bldg A08 University of Sydney NSW 2006, Australia
+61-2-9351-3717 (phone) +61-2-9351-4119 (Fax)
lars.jermiin[at] usyd.edu.au

As of July 1 2009, my contact details will be

Dr. Lars Jermiin, OCE Science Leader CSIRO - Entomology GPO Box 1700 Canberra, ACT 2601 Australia
lars.jermiin [at] csiro.au

Patience is a priceless commodity...

lars.jermiin@usyd.edu.au

EAWAG Switzerland InvasiveSpeciesEvolution

Eawag is the Swiss Federal Institute of Aquatic Science and Technology, a Swiss-based and internationally-operating aquatic research institute within the ETH domain.

Our Aquatic Ecology Department has a job opening for an

Invasive species biologist (PhD, Tenure Track)

Suitable candidates have an excellent research record in aquatic invasive species research. We are especially in-

terested in candidates who can mix conceptually strong, question-oriented research to relevant problem-oriented applied research. The ideal candidate has post-doctoral research experience and is ready to apply for external research funding.

We are looking for a person who is keen on benefitting from the broad environmental disciplines represented at Eawag. The ideal candidate would be able to develop a strong research program on aquatic invasive species in Switzerland, incorporating the excellent opportunities for inter- and transdisciplinary research at Eawag and engaging stakeholder interests in research. The Department of Aquatic Ecology, where the position is based, can support conceptually and methodologically broad research agendas from field experiments to molecular biology.

The Junior Group Leader is expected to:

* Establish an independent and collaborative research group * Supervise PhD and Masters students * Participate in department activities and administration

The Department of Aquatic Ecology houses 10 research groups in diverse areas of aquatic research, collaborating with other Eawag departments, the ETH-Zurich, and internationally. Our department is connected to the Institute of Integrative Biology, ETH-Zurich (Prof. Jukka Jokela). As a top research institute, Eawag provides excellent support for high-quality research and a stimulating research environment in close vicinity to ETH-Zurich. Eawag has world-class research infrastructure and excellent support for developing research in evolutionary biology, experimental ecology and ecosystem research.

The application deadline is 15.09.2009 with the earliest possible start date of 1.1.2010. The working language in the department is English. Send a CV and application letter (including research interests and names and addresses of 3 references) as a single PDF file to: Eawag, Sandra Isenring, Human Resources, Ueberlandstrasse 133, CH-8600 Duebendorf, Switzerland or by email to recruiting@eawag.ch, indicating reference number 094404. Females are especially encouraged to apply. We are willing to discuss part time employment if it promotes equal opportunity to career development. Visit www.eawag.ch for more information about Eawag. For questions about the position, email Prof. Jukka Jokela (jukka.jokela@eawag.ch).

Jukka.Jokela@eawag.ch Jukka.Jokela@eawag.ch

KentuckyU GeneticsInstructor

A one-year Genetics Instructor position is available in the Biology Department at Western Kentucky University. People with interests in Population or Evolutionary Genetics are especially welcome to apply. Inquiries about the position should be addressed to genetics.search@wku.edu. The full advertisement follows.

Best regards, Jeff Marcus

Dr. Jeffrey M. Marcus Assistant Professor Department of Biology Western Kentucky University 1906 College Heights Boulevard #11080 Bowling Green KY 42101-1080 USA

Office (270) 745-2043 Lab (270) 745-2288 FAX (270) 745-6856

WESTERN KENTUCKY UNIVERSITY DEPARTMENT OF BIOLOGY

GENETICS INSTRUCTOR

Western Kentucky University, Department of Biology is seeking applicants for a temporary, one-year position. The successful candidate will have the background and preparation to teach undergraduate Genetics and Laboratory. Additional teaching assignments may be made according to the candidate's expertise. The Biology Department anticipates searching for a tenure track position in Genetics at the rank of Assistant Professor for the Fall 2010.

The Department of Biology currently has 24 full-time faculty positions and typically employs eight to ten full-time research technicians and post-doctoral researchers. In addition to the main campus in Bowling Green, we employ instructors at several branch campuses throughout the region. Our student body comprises 600+ undergraduates and approximately 60 M.S. students. Potential applicants may discover more about our department at <http://bioweb.wku.edu/faculty/positions/available.asp> Western Kentucky University is a comprehensive university with a vision to become "a leading American university with international reach", a philosophy embodied by the Department of Biology. WKU is located in Bowling Green, Kentucky, a growing city of 60,000+ in a state noted for its high quality of life, modest cost of living, and increasing cultural diversity. With an enrollment of more than 19,000 students in undergraduate and graduate programs, the Univer-

sity has grown 28% in the last ten years and is poised to increase enrollment significantly by 2020.

Responsibilities:

Fall 2009 and Spring 2010 teach an undergraduate genetics lecture with multiple laboratory sections. Laboratory preparation assistance is available.

Teaching duties as assigned totaling 12 contact hours per semester

Required Qualifications:

Ph.D. in the life sciences (or related field)

Able and willing to begin teaching August 17, 2009.

Desired/Preferred Qualifications:

Experience teaching genetics at the undergraduate level.

Post-doctoral experience

Expected Salary Range: \$35K-40K with benefits, depending on experience.

Interested applicants should submit a letter of interest, a current CV, a statement of teaching philosophy, and the names and contact information for three references. Submit applications and nominations to: Genetics Instructor Search, Western Kentucky University, 1906 College Heights Blvd. #11080, Bowling Green, KY 42101-1080 or to genetics.search@wku.edu For further assistance call (270) 745-4856. Review of applications will begin June 22, 2009, and will continue until the position is filled.

All qualified individuals are encouraged to apply including women, minority men and women, persons with disabilities, and veterans. Western Kentucky University is an Affirmative Action/Equal Opportunity Employer.

jeffrey.marcus@wku.edu jeffrey.marcus@wku.edu

Kunming 2 EvolutionaryBiology

Reminder email, review of applications begins 31 July 09

Two PRINCIPAL INVESTIGATOR POSITIONS (Yan2 Jiu1 Yuan2) in ecology, conservation biology, and evolution, at the Chinese Academy of Sciences, based at the Kunming Institute of Zoology (KIZ), Kunming, China.

The Ecology, Conservation, and Environment Cen-

ter (ECEC) at KIZ (www.kiz.ac.cn, English version, ECEC website) invites applications for two full-time PI positions in ecology and evolution, broadly defined. The rank is equivalent to an Assistant or Associate Professor in the US. Senior applicants (those with faculty positions) will also be considered and are eligible for special recruitment packages from the national government.

The ECEC was recently established as a joint center between the Chinese Academy of Sciences and the University of East Anglia (UK). The ECEC's mission is to conduct international-quality research in ecology and conservation biology, to train Chinese and foreign Ph.D. and postdoctoral researchers, to lead the development of ecology and conservation science in China and Southeast Asia, and to provide information necessary for environmental policy-making. The KIZ is one of China's leading scientific research institutes for evolutionary biology, its faculty are internationally recognized, and the institute is building an ecology and conservation group on this foundation.

This is a superb opportunity to pursue an independent research program, backed by a large research team and ample funding. Highly qualified candidates conducting research on any taxa and in all areas of ecology, evolution, and conservation biology are encouraged to apply. We especially encourage applicants with research programs involving molecular ecology and bioinformatics, theory and modeling, conservation planning and economics, and/or climate change. Responsibilities include contributing to the ECEC's mission, obtaining external funding, and publication in top, international journals.

Considerable startup funding is available, generally at levels higher than those offered by European or US universities, and faculty will be members of the KIZ's State Key Laboratory of Genetic Resources and Evolution, led by the director of the KIZ, Prof. Zhang Ya-Ping. Facilities at the KIZ include 454 next-gen sequencing, SNP, and gene-chip facilities in a new, national bar-coding center to be installed this year, extensive internet journal access, a zoological museum with over 600,000 specimens, and access to CAS field stations, datasets, and facilities around the country. In addition to opportunities for collaboration within the ECEC and KIZ, there are ample local opportunities for collaboration with ecologists and evolutionary biologists at the Xishuangbanna Tropical Botanical Garden (xtbg.ac.cn & www.ecologicalrevolution.org) and the Kunming Institute of Botany (www.kib.ac.cn), as well as local universities. In the near future, faculty from the three institutes, including the ECEC, will be combined to establish a new National Laboratory in Biodiversity in

Southwest China.

The working languages at the KIZ are Chinese and English. All nationalities are welcome to apply, and most faculty have had international research experience. It is possible to conduct research outside China with grant monies from China. There is no undergraduate teaching. Starting date is flexible.

Candidates with a strong record of accomplishment (a Ph.D., postdoctoral experience, and published papers in SCI journals) should submit a CV, a statement of research interests and plans, and pdfs of three publications. Please also include the names, addresses, and contact details of three individuals who can provide letters of recommendation. A single, combined PDF or zipped file is preferred and can be emailed to <ECEC.KIZ@gmail.com>. Informal enquiries can be made with the center's director, Dr. Douglas Yu <dougwyu@gmail.com>.

Applications will be reviewed starting 31 July 2009 until the positions are filled. This advert will be repeated over the next months.

Background information:

The Chinese Academy of Sciences (CAS) was established in 1949 and is China's national research organization, funding research and training in basic science and technology across a countrywide network of research institutes. CAS goal is by 2010 to make 30 of its research institutes internationally recognized and 3 to 5 of them world class.

KIZ: Established in 1959. Primary research areas have been evolutionary genetics and developmental biology, animal systematics, and animal and human disease models. There are about 200 staff, including 1 CAS member, and about 50 faculty, of which 7 PIs are supported by a CAS Excellent Young Scientists Program. There are

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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>

London ResTech EvolBiol

Institute of Zoology Zoological Society of London
Research Technician Two year fixed term contract

Starting Salary £22,525 (including London weighting)

ADVERT

The Institute of Zoology, based at Regent's 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 two years, starting as soon as possible, to work with Dr. Trent Garner (IoZ) and Dr. Rob Knell (QMUL) on a Leverhulme Trust funded research project.

The successful candidate will have a BSc focussed on evolutionary biology, with special interest in sexual selection, parasitology, entomology or a related subject. S/he will have the ability to work well in a large institution with people from diverse backgrounds, and will have experience with experimental insect systems, including husbandry and stock maintenance, as well as experience with microsatellite DNA molecular biology

For further information, please see <http://www.zoo.cam.ac.uk/ioz/> or contact HR Dept., ZSL, Regent's Park, London NW1 4RY. Informal enquiries should be directed to Trent.Garner@ioz.ac.uk.

To apply, please send a covering letter and CV, together with the names and addresses of two academic referees, to The Human Resources Department ZSL, (HR@zsl.org). by 18th June 2009.

Institute of Zoology Zoological Society of London

Research Technician Two year fixed term contract
Starting Salary £22,525 (including London weighting)

JOB DESCRIPTION

One of the most fascinating aspects of host-parasite interactions is how behaviour can change when an animal becomes host to a parasite. Often these behavioural changes are purely pathological, but in many cases they appear to have an adaptive function, enhancing the evolutionary fitness of either the host or the parasite. Most attention from biologists interested in this subject has focussed on those cases where behavioural changes in the host appear to arise from manipulation of the host by the parasite in order to increase parasite fitness. Rather less attention has been paid to those behavioural changes that enhance host fitness after infection, but a number of behavioural changes post-infection are now known that can be explained in this way. The two that are best described and most relevant here are terminal investment, when an animal increases its short-term reproductive effort in an attempt to compensate for lost future reproduction, and behavioural fever, which occurs when an ectothermic

organism seeks out hot places in order to increase its own body temperature in order to increase the effectiveness of its immune response.

Arguably the most iconic UK organism used for the study of sexual selection, the yellow dung fly, *Scathophaga stercoraria* has been widely studied since it inspired Parker to develop the paradigm of sperm competition. Easily observed in the field and simple to culture on the laboratory, the sheer wealth of information regarding how selection influences the reproductive biology of yellow dung flies is unrivalled. *Scathophaga stercoraria* is frequently infected with entomopathogenic fungal parasites. The fungus kills the host and then releases infectious conidia from the cadaver, and it appears to change the perching behaviour of infected flies in a number of ways before they die in order to increase the probability of its conidia contacting new hosts. Currently no data exist on fly behaviour post-infection but before the fly becomes moribund. Flies could very well exhibit a variety of different behaviours, with variable effects on their own fitness and on parasite fitness.

We have been awarded two years of funding to address this lack of knowledge and to determine if yellow dung flies exhibit either terminal investment, behavioural fever, or both. The project will involve establishing baseline data on disease progression and, using this information, performing a variety of experiments to assess changes in sex-specific behaviours and reproductive investment after infection has occurred. We seek a self-motivated candidate with a strong interest in evolutionary biology, specifically sexual selection and host/parasite interactions, and experimental biology to fill a two year research technician post.

Job Specification

The successful candidate will provide evidence of the following essential skills: - A BSc focussed on evolutionary biology, with special interest in sexual selection, parasitology, entomology or a related subject, - The ability to work well in large institution with people from diverse backgrounds Additional skills: - Experience with experimental insect systems, including husbandry and stock maintenance, - Experience with microsatellite DNA molecular biology

— / —

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>

MaxPlanckInst EvolutionaryBiodemography

Dear all,

The Max Planck Institute for Demographic Research continues to develop its research activities in the field of Evolutionary Biodemography, and is recruiting to a number of positions. Further details can be found at <http://www.demogr.mpg.de/en/jobs/1484.htm>

Best wishes, David Thomson
<<2009Biodemo.cdr.pdf>>

Dr. David L. Thomson Max Planck Institute for Demographic Research Konrad-Zuse Str. 1 D-18057 ROSTOCK Germany

Tel. +49 (0)381 2081 229 Fax. +49 (0)381 2081 529
Website: www.demogr.mpg.de

NatHistMuseum Denmark 2 DNASequencing

Two Advanced Staff Scientists (AC-TAP)

Two highly motivated and qualified candidates are sought to fill advanced staff scientists positions (AC-TAP) in the newly formed High-Throughput DNA Sequencing Centre, situated at the Natural History Museum of Denmark in Copenhagen.

DNA sequencing technologies have advanced rapidly in recent years, and the successful candidates will be at the core of the implementation of such technologies in Denmark. Located at the Botanical Gardens, in the centre of Copenhagen, the sequencing Centre currently hosts both Roche FLX and Illumina Genomic Analyzer platforms, and over the upcoming years is likely to install the latest sequencers as they appear on the market.

Qualifications Candidates should hold a Master Science degree or equivalent in molecular biology or related fields. Previous molecular biology experience is preferable as is a good level of English, good communication skills and the ability to work in a large dynamic team.

Terms of salary and employment Salary, supplement, pension and terms of employment follow the agreement

between the Ministry of Finance and The Academics Central organization.

The yearly salary begins around 360.000 DKK (= ca. 48.300 Euro) plus pension, and depending on qualifications and experience, a higher salary can be negotiated. Non-Danish and Danish applicants may be eligible for tax reductions, if they have not lived in Denmark the last 3 years.

The position is full time and scheduled to start August 1, 2009 or as soon as possible thereafter.

For further information regarding the position, please contact Prof. Eske Willerslev, Center for GeoGenetics: phone +45 2875 1309, e-mail ewillerslev@bio.ku.dk or Prof. Kristian Helin, BRIC: phone +45 3532 5666, e-mail kristian.helin@bric.ku.dk

Applications should include a short curriculum vitae, a copy of the applicant's diplomas and names of two referees. Applications should be e-mailed to Trine Friis Toldsted (tftoldsted@snm.ku.dk).

Deadline for applications: June 22, 2009 at 12.00pm

We wish to reflect the diversity of society and welcome applications from all qualified candidates regardless of personal background.

Tom Gilbert <mtpgilbert@gmail.com>

OregonStateU PacificSalmon EvolutionaryGenetics

Job: OregonStateU.ResearchAssist.PacificSalmon.EvolutionaryGenetics

Oregon State University is accepting applications for a Faculty Research Assistant at the Hatfield Marine Science Center, Oregon State University, Newport, OR. The individual will work on a long-term study investigating the genetics of migration timing among Chinook salmon populations using candidate genes. This is a full-time, 12-month fixed-term position with renewal at the discretion of the supervisor. A start date of September 1 2009 or a mutually agreeable date in early Fall 2009 is strongly preferred.

APPLICATION: To review the full position announcement and apply, go to <http://oregonstate.edu/jobs> Posting #0004270.

CLOSING DATE: June 30, 2009. OSU/AAEO

Kathleen O'Malley <Kathleen.OMalley@noaa.gov>

RiceU TeachingEvolution

The Department of Ecology and Evolutionary Biology at Rice University, Houston, Texas, is accepting applications for a permanent non-tenure track faculty position to start in the fall semester. The responsibilities of this position include teaching (lecture and lab courses), assisting with undergraduate advising, and coordinating additional educational activities. A PhD in ecology, evolution or a related field is required. Research, particularly involving undergraduates is encouraged but not required.

For informal inquiries or questions regarding this position please feel free to contact Amy E. Duham (aed4@rice.edu) or Michael H. Kohn (hmkohn@rice.edu).

Please see <http://eeb.rice.edu/pdfs/instructor.pdf> for more information

Michael H. Kohn Rice University Department of Ecology & Evolutionary Biology EEB MS-170 130 Anderson Biology P.O. Box 1892 Houston, Texas, 77251-1892 USA

Phone: 713-348-37797 <http://www.ruf.rice.edu/~hmkohn/index.html> hmkohn@rice.edu
hmkohn@rice.edu

RoyalHollowayU PopulationGenetics

Dear Colleagues,

The School of Biological Sciences, Royal Holloway University of London, is recruiting two Lecturers/Senior Lecturers/Readers that may be of interest to evoldir readers. Please see below for details:

ROYAL HOLLOWAY University of London
 School of Biological Sciences

Royal Holloway is one of the four largest multi-faculty Colleges of the University of London. The School of Biological Sciences (<http://www.rhul.ac.uk/biological-sciences>) has 3 Research Centres: Biomedical Sciences, Plant Molecular Sciences; and Ecology, Evolution & Be-

haviour and was ranked joint 3rd in the UK in the 2008 RAE, based upon the proportion of 3* and 4* outputs.

Lectureship in Population Genetics X0609/0750 Salary: £38,666 to £45,756 Applications are welcome from candidates in any field of biology, whose research addresses evolutionary processes.

Senior Lecturer/Reader in Animal Behaviour X0609/0759 Salary: £47,064 to £54,220 Applications are particularly welcome from those who integrate molecular techniques with behavioural ecology.

All positions are available from September 1st 2009. Informal enquiries are welcome to the Head of School, Prof Peter Bramley (tel. +44(0)1784 443555; e mail p.bramley@rhul.ac.uk).

Further details (including the closing dates for receipt of applications) and an application form, are available from <http://www.rhul.ac.uk/personnel/-jobvacancies.htm> or contact Human Resources on tel: 01784 414241 email: recruitment@rhul.ac.uk. Please quote the relevant post reference number.

We positively welcome applications from all sections of the community.

Mark Brown <MARK.BROWN@RHUL.AC.UK>

SouthAfrica FieldAssist ChatEvolution

Job:

Field assistant to study evolution of group living in Ant-eating Chats

Location, Benfontein, Nr Kimberly, South Africa

I am looking for a highly motivated field research assistant to join me working on the behavioural ecology of cooperative breeding in Ant-eating Chat, *Myrmecocichla formicivora*. The study will focus on factors behind the occurrence of delayed dispersal and cooperative breeding in the species. The study site is Benfontein Game Farm (study centre), near Kimberly, Northern Cape, South Africa. Applicants should have a strong interest in bird orientated research, and have suitable banding experience. Field assistants are expected to be fit, able to work in a tough and taxing environment, and be willing to work independently. Field workers should be able to live in close proximity to with a small number of other researchers on site. Responsibilities will include trapping and colour-banding birds both

(largely at night), re-sighting banded birds for territory mapping (using GPS), nest-searching and monitoring, monitoring family groups, behavioural observations and data input (MS Excel). The working conditions will include considerable distances covered on foot in both cold and hot conditions (0 to 40C+) and regular early morning working (whilst cool and the birds are active), and regular work after dark (trapping and banding done at night). Driving experience would be an advantage. The work will be done for 5-6 days per week, and the applicant needs to be willing to work outside normal hours. The position is available from October until mid December 2009. Accommodation (paid for) is provided in the field study centre, and the project will also cover reasonable travel expenses. To apply, please email 1. A short letter stating why you are interested, 2. A copy of your CV, including details of past field experience and bird handling/banding experience, and 3. The contact details for two referees, to Jonathan Barnaby at: Jonathan.Barnaby@ebc.uu.se Please don't hesitate to contact me if you have any questions or for further information. Telephone: +46(0)18 471 26 73 Mobile: +46(0)739 04 46 51 Fax: +46(0)18 471 64 24 Website: www.popbiol.uu.se Evolutionary Biology Centre, Population and Conservation Biology, Department of Ecology and Evolution, Uppsala University in collaboration with the Percy FitzPatrick Institute, UCT, South Africa.

jonathan.barnaby@ebc.uu.se
jonathan.barnaby@ebc.uu.se

UGeorgia ResTech PlantEvolutionaryGenet

The Burke Lab at the University of Georgia in Athens, GA has an opening for a Research Technician. Broadly speaking, our lab studies plant evolutionary genetics. The successful applicant will be involved in various aspects of our research, including DNA/RNA extraction, PCR-based genotyping, sequencing, and data analysis. This individual will also be responsible for general lab management, including ordering supplies, maintaining equipment, supervising undergraduate researchers, and otherwise maintaining an organized lab. This position will also likely involve occasional greenhouse work.

Minimum qualifications are a Bachelor's degree in biology or a related field. Prior laboratory experience is desired, but not necessarily required. While initial

projects will generally be supervised, the ideal candidate will become more independent as they become more experienced. Perhaps the most important requirements are close attention to detail and good organizational skills.

To apply, please send a resume and contact information for three references to John Burke at: jmburke@uga.edu. Informal inquiries are also encouraged.

For details on our research, please visit <http://www.theburkelab.org/> John M. Burke, Ph.D. Tel: 706.583.5511 Fax: 706.542.1805 <http://www.theburkelab.org/> University of Georgia Department of Plant Biology Miller Plant Sciences Athens, GA 30602

jmburke@uga.edu jmburke@uga.edu

UIdaho LabTech ExperimentalEvolution

Lab Technician Position in Experimental Evolution:

A lab technician (scientific aide) position is available starting August 2009 in the laboratory of Professor Steve Krone (<http://www.webpages.uidaho.edu/~krone>) at the University of Idaho (home of Evolution 2009). The technician will work on the adaptive evolution of viruses (bacteriophage) growing in spatially structured environments and subject to fluctuating environmental conditions. Krone's phage lab is one of three in the UI Department of Biological Sciences; the other two (Brown and Wichman) phage labs are in close proximity and help to provide a collaborative and stimulating environment. This is an opportunity to be part of a highly interdisciplinary research project that combines experimental evolution and mathematical modeling. The technician will assist in the day-to-day running of the lab and play an active role (in collaboration with a postdoctoral scientist and undergraduate assistants) in the experimental portion of the project.

This project (Spatial Structure and Adaptive Evolution of Viruses) is one of four supported by the renewal of our NIH Center for Biomedical Research Excellence (COBRE) grant. The technician will be part UI's Initiative for Bioinformatics and Evolutionary Studies

(<http://www.ibest.uidaho.edu/ibest/index.html>), a dynamic and interdisciplinary research group with excellent resources.

The successful candidate should have

1. Bachelors degree (or equivalent years of experience) in Microbiology, Biology, Genetics, or related field.
2. At least one year of experience using contemporary molecular biology methods, such as PCR and sequencing. Some microbiology experience is an asset but not necessary.
3. Knowledge of computer software and scientific principles.
4. A basic understanding of ecological and evolutionary concepts.

Other requirements are listed in the position description posted on the Human Resources website (see below). Salary will be commensurate with the qualifications and experience (in the range \$29K-33K). If you have questions, please write to Steve Krone (krone@uidaho.edu). Qualified candidates should apply no later than July 2, 2009 via the Human Resources website (<http://www.hr.uidaho.edu/default.aspx?pid=35496>). Applications should include an uploaded letter and curriculum vitae. In addition, three letters of recommendation and a copy of academic transcripts should be sent to the address below.

The University of Idaho is an equal opportunity/affirmative action employer.

Dr. Steve Krone

Professor Department of Mathematics Initiative for Bioinformatics and Evolutionary Studies University of Idaho Moscow ID 83844-1103

Phone: 1-208-885-6317 Fax: 1-208-885-5843

“Krone, Stephen” <krone@uidaho.edu>

UKansas ResTech DrosophilaVariation

Quantitative Genetics and Genomics in Drosophila

An NIH-funded Research Technician position is available in Stuart Macdonald’s lab in the Department of Molecular Biosciences at the University of Kansas. The Macdonald lab explores the genetic basis of complex phenotypic variation within and between species using *Drosophila* as a model system. Details of the research can be found at web.ku.edu/sjmac/. We seek an enthusiastic individual to supervise and carry out large-

scale genetics projects and to oversee various lab activities. The responsibilities of the technician will include, but are not limited to, maintaining a large panel of *Drosophila* strains, overseeing/ conducting large quantitative genetic experiments with flies, and carrying out molecular assays (PCR, genotyping, sequencing). The successful candidate should be motivated, organized, and careful, and should have excellent oral and written communication skills. Salary will be commensurate with experience and will include benefits.

Required qualifications are a Bachelors degree in biology or a related field, demonstrable experience conducting research in a (broadly- defined) genetics or molecular biology laboratory, and strong written communication skills as evidenced by the application materials. Preference will be given to candidates with significant experience in the laboratory (including troubleshooting and optimizing protocols), and those who have previously worked with *Drosophila*, and managed large scientific projects.

The University of Kansas (www.ku.edu) has an active academic community in the life sciences. The Macdonald lab is affiliated with the Department of Molecular Biosciences (molecularbiosciences.ku.edu) and works closely with members of the Department of Ecology and Evolutionary Biology (www2.ku.edu/~eeb). The range and number of active research groups presents many opportunities for fostering academic and social interactions. The University of Kansas is in the city of Lawrence (www.visitlawrence.com, www.ci.lawrence.ks.us, www.lawrence.com, en.wikipedia.org/wiki/Lawrence,_Kansas) situated 45 minutes West of Kansas City.

Review of applications will begin Monday, July 13 and continue until the position is filled. Informal inquiries about the position are welcome and can be directed to Stuart Macdonald (sjmac@ku.edu). To apply, complete an online application at <https://jobs.ku.edu> (position number 00206282). Attach a cover letter (describing your interest in the position and any relevant expertise), a full CV, and complete contact information for 3 referees. EO/AA Employer.

Dr. Stuart J. Macdonald Department of Molecular Biosciences 1030 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

tel: 785-864-5362 fax: 785-864-5321 email: sjmac@ku.edu web: <http://web.ku.edu/sjmac/> sjmac@ku.edu sjmac@ku.edu

ULeeds ResTech HoneyBeeEvolution

Job: Research technician in honeybee-parasite evolutionary ecology

Institute of Integrative and Comparative Biology, Faculty of Biological Sciences, University of Leeds

A 36 month fixed-term Research Technician position (University Grade 5) is available in the research group of Dr. William Hughes. You will support a project investigating host-parasite evolutionary ecology in honeybees as well as providing general support and technical management of the research group. You will be responsible for managing an experimental apiary and culturing ant colonies. You will carry out molecular work (DNA extraction, PCR, real-time PCR, sequencing) to diagnose and identify parasite infections, and genotyping to investigate colony genetic diversity.

You will be joining a young and dynamic research group, which will be growing significantly over the course of 2009. The molecular laboratory is well-equipped with a real-time PCR and four conventional PCR machines, while capillary sequencers are provided by a Faculty facility. The experimental apiary is located at the nearby University Farm while ant colonies are maintained in a controlled environment room in the Miall Building.

You should have a first degree in a relevant subject, a driving licence, and experience in beekeeping and with molecular techniques (DNA and RNA extraction, PCR, real-time PCR, sequencing or genotyping). You should be hard working, self-motivated and able to work both independently and as part of a team. Experience with mycology or parasitology would also be useful.

The position is available immediately. Application will be reviewed on 22nd June 2009, but will continue to be considered until the position is filled.

If you are interested in the position, please email Dr. William Hughes (w.o.h.hughes@leeds.ac.uk) with a copy of your CV in the first instance. Formal applications can then be made on line by visiting <http://www.leeds.ac.uk> and clicking on jobs.

w.o.h.hughes@leeds.ac.uk w.o.h.hughes@leeds.ac.uk

UNamur Belgium 2 TeachingAssistants

Two 2-years Academic assistant (teaching assistant) positions are available in the Biology Department at Namur University (Belgium). The full advertisement follows. Speaking French is necessary.

Best regards,

Lise-Marie –

PIGNEUR Lise-Marie PhD student / Academic assistant University of Namur (FUNDP) Lab. of Freshwater Ecology (URBO) rue de Bruxelles, 61 5000 Namur (Belgium)

http://www.fundp.ac.be/universite/personnes/-page_view/01006228/ ———

Deux assistants temps plein (m/f)

Faculté : Faculté des Sciences Département : Département de Biologie - URBO Date d'entrée en fonction : 01/09/2009 Grade : assistant 1 Contrat : durée déterminée renouvelable Catégorie : personnel scientifique Poste : Allocation (au cadre) Référence : Postes 275-05 et 275-07

Tâches

Assurer les travaux pratiques (environ 250 heures de TP/an) et les stages de biologie et d'écologie au sein de l'Unité de Recherche en Biologie des Organismes (URBO) aux FUNDP

Entamer une recherche doctorale au sein de l'URBO. Les doctorants seront associés à des problématiques de recherche en biologie des organismes et écologie aquatique, avec une spécialisation dans une des disciplines suivantes : écophysiologie et écotoxicologie aquatique, écologie aquatique, génétique évolutive. Le sujet de thèse sera en adéquation avec les programmes de recherche de l'URBO (voir site web)

Profil

Le candidat :

sera titulaire d'une licence ou master en sciences biologiques avec une spécialisation en biologie des organismes et écologie ou en biologie moléculaire (génétique) avec un intérêt certain pour la biologie des organismes et l'écologie et/ou l'évolution

aura un intérêt marqué pour la pédagogie et pour la

recherche scientifique (en particulier dans le domaine des sciences environnementales et/ou de la génétique évolutive)

Renseignements complémentaires

Professeur Patrick KESTEMONT - Directeur de l'URBO

Tél.: 081 72 43 63 - E-mail : patrick.kestemont@fundp.ac.be
<mailto:patrick.kestemont@fundp.ac.be>

Professeur Karine VAN DONINCK

Tél.: 081 72 44 07 - E-mail : karine.vandoninck@fundp.ac.be
<mailto:karine.vandoninck@fundp.ac.be>

Remarques

Le contrat est un contrat de travail d'une durée de 2 ans renouvelable deux fois

Les formulaires de candidature doivent être demandés à la Direction du Personnel des Facultés Universitaires Notre-Dame de la Paix, rue de Bruxelles, 61 à 5000 Namur ou peuvent être téléchargés à l'adresse suivante: <http://www.fundp.ac.be/universite/jobs/> et être renvoyés au Rectorat pour le 15/07/2009 au plus tard. lise-marie.pigneur@fundp.ac.be

UOulu PopGenetics

A professorship in evolutionary/or population genetics/genomics will be open at the University of Oulu, Finland. The biology department at the University of Oulu has an emphasis on evolution/ecology, with many active groups in this area, see http://cc.oulu.fi/~biolwww/english/genetics_research.html. The Finnish National Graduate School for Population Genetics is coordinated by the Univ. of Oulu. Teaching can be in English or Finnish. Population genetics and bioinformatics related work at the University also takes place within Biocenter Oulu (<http://www.biocenter.oulu.fi/>).

For further information about the position, please see http://www.lutk.oulu.fi/english/index_english.htm and/or get it touch with Outi.Savolainen@oulu.fi or Pertti.Tikkanen@oulu.fi.

Outi Savolainen Department of Biology PO Box 3000 FIN-90014 University of Oulu Finland

Outi Savolainen <Outi.Savolainen@oulu.fi>

UPerpignan Epigenetics

Two PhD studentships in Epigenetics

Epigenetics and Evolution Infection success and phenotypic variability of the human blood-fluke *Schistosoma mansoni*: elucidation of the involvement of the epigenotype by a whole-genome strategy (Keywords: o ChIP-Seq o epigenetics and evolution o host/parasite relation o *Schistosoma* For details please contact Christoph Grunau (grunau@methdb.net or christoph.grunau@univ-perp.fr) before June 13, 2009.

Epigenetics and oxidative stress: Anthracyclines : antitumoral activity versus cardiotoxicity: the role of reactive oxygen species and relation to epigenetic mechanisms (Keywords: o reactive oxygen species o Cancer o Cardiotoxicity o DNA methylation For details please contact Anne-Cécile Ribou (ribou@univ-perp.fr) before June 13, 2009.

The positions are funded by the French Ministry for Education for a 3 years period (after tax salary 1200 à 1450 Euros / month). Deadline for application is June 22, 2009 but the host laboratory must be contacted before. Qualifying candidates will be selected on merit. Lab language is English and/or French. The goal of the thesis projects is to investigate epigenetic phenomena in research domains, in which epigenetics has so far been neglected. The University of Perpignan is a medium-size state-funded campus university. Roughly 1/3 of the students are from abroad. Perpignan is situated in the south of France, close to the Spanish border, at the Mediterranean coast. There are daily flights to London and Paris, and several train connections to Barcelona and other destinations.

Dr Christoph Grunau University of Perpignan www.methdb.net Klaus Reinhardt <K.Reinhardt@sheffield.ac.uk>

USDA Maryland PlantEvolution

APHIS SCIENCE FELLOW

Position Title: Biotechnologist (with Evolutionary

Ecology/Evolutionary Genetics/Agroecology specialization)

Location: Biotechnology Regulatory Services, Animal and Plant Inspection Service, USDA, Riverdale, MD 20737 (Near University of Maryland, College Park campus)

Salary: \$49,544 to 77,194 (based on work experience and qualifications) with full Federal Employee Benefits

Duration: 1-2 years (Position may lead to permanent employment in one of the federal agencies given the Federal Governments push for green energy)

Qualifications: Ph.D. or equivalent doctoral degree in biological sciences, agriculture, natural resource management, chemistry, or related disciplines appropriate to the position. Accomplished candidates in the areas of plant evolution, genetics, or ecology with research experience in biofuel plant species are encouraged to apply.

Application deadline: Monday, June 29, 2009

Major duties: Incumbent serves as a staff scientist responsible for technical analysis of scientific literature related to the biology and ecology of switchgrass and its relatives in the United States and worldwide, as appropriate. Provides technical and analytical documents on the prospects in the genetic engineering of switchgrass and closely related species. Collaborates and coordinates activities with scientists in BRS' Environmental Risk Assessment Programs and the Office of Science in the area of agricultural or biological sciences, risk assessments, National Environment Policy Act requirements and other informational needs as necessary to successfully accomplish the duties and responsibilities of the position. Prepares a variety of bio environmental engineering documents, reports, and technical analyses on different aspects of biotechnology, including those on biotechnological systems in the protection of the production and processing of foods and fibers as well as the protection of animal and plant life and aids in the preparation of biological, environmental, and ecological studies.

For further details about the position, please visit USAJOBS at <http://jobview.usajobs.gov/-getjob.aspx?JobID=81417636&sort=rv&vw=-d&brd=3876&ss=0&FedEmp=N&FedPub=Y&q=-Biotechnologist+Riverdale%2c+MD+20737&AVSDM=2009-06-08+14%3a41%3a00&rc=4&TabNum=-1>

Subray Hegde Biotechnologist/Ecologist
USDA/APHIS/Biotechnology Regulatory Services
4700 River Road Riverdale, MD 20737

subray@ucr.edu

UWindsor Institute Director

Great Lakes Institute for Environmental Research (GLIER) University of Windsor Executive Director

The Great Lakes Institute for Environmental Research (GLIER) is seeking an exceptional individual with vision and dedication to develop further GLIER as an internationally recognized research institute fulfilling the University's goal of achieving excellence in environmental science.

GLIER is a multi-disciplinary research group that addresses processes and responses related to multiple stressors in large lakes and their watersheds, through the application of environmental tracers. GLIERs faculty specializes in environmental chemistry and chemical tracers, evolutionary and conservation genetics, and biological invasions. To learn more about GLIER, please visit us at www.uwindsor.ca/glier. The Director will provide leadership in developing collaborative research programs and capacity for studies of large lake ecosystems. She/he will also administer the GLIER graduate program and research facilities and will be responsible for implementing GLIERs five year research plan. The appointee will be cross-appointed to a relevant department within the university and shall have access to GLIERs state-of-the-art labs including laboratories for trace organics and metals, environmental isotopes, applied molecular genetics and genomics, toxicology, ecology, GIS, analytical and aquatic geochemistry, and ESEM.

The successful candidate will have a PhD and an exceptional record of scholarship and outstanding skills in facilitating research and scholarship, both basic and applied, and will have the capacity to elicit support for research from private and public sources. In addition, the successful candidate will have the demonstrated ability to work collegially and communicate effectively within GLIER and the University community and with external partners. The initial appointment is for five years and is renewable for a second term. The Director will also hold a regular faculty appointment at an appropriate rank and will be expected to establish a well funded research program at GLIER. The ideal start date is January, 2010.

Candidates are invited to submit a letter of application, a detailed curriculum vitae, a research plan and three current letters of reference, forwarded by the referees.

To ensure full consideration, complete applications and letters of reference should be submitted by August 15, 2009 to:

Dr. M. Cristescu, Chair of the Executive Director Search Committee Great Lakes Institute for Environmental Research University of Windsor Windsor ON N9B 3P4 E-mail: mcris@uwindsor.ca

The University of Windsor is committed to equity and diversity in the workplace and welcomes applications from Aboriginal persons, persons with disabilities, ethnic minorities, women, and others who may contribute to further diversification.

mcris@uwindsor.ca

Other

Alternative to hompart	43	MrBayes Newick trees problem	51
Bioinformatics linux	44	NewJournal EntomologicaAmericana	52
CitizenScienceChallenge Instructions	44	NullAlleleEstimates answers	52
CitizenScienceChallenge Instructions 2	44	Pedigree software answer	53
Comparative analysis	44	Population statistics software	53
DNA recleaning methods	45	Prokaryotic Diversity Database	53
Drosophila species DNA	45	Renaturing Proteins IEF	54
D subobscura lines	45	SAMPL-method	54
Enquiry on FreeNA software	45	Software Crux 1 1 0	54
Enquiry on FreeNA software on Null Allele estimation	46	Software DnaSP PopGenetics	55
Evolution toys	46	Software Multiplex Manager Program	56
Foundations of Evolutionary Biology	46	Software PhyloExplorer	56
Hong Kong Teaching Petition	46	Software RAXML 7 2 0	56
Juniperus seed DNA	47	Software Tandem	57
MBE on Facebook	48	SouthAfrica FieldAssist Chats	58
Merging MrBayes files	48	StKilda volunteer SoaySheepProject	58
Microarray course help 2	49	Storing HumanDNA	59
Micro interpretation	49	TimeTree website	59
Microsatellite cloned sequences	49	Tree construction answers	59
Microsats Stained with EtBr	50	UK research policy	60
Microsats stained with EtBr answers	50		

Alternative to hompart

Dear all

I am using hompart to test for incongruence between sequences. But the algo is time consuming . I will be very interested by un alternative algo

Thank you so much for your help all the best Pierre
Pierre Antoine Pontarotti

Directeur de Recherche CNRS

UMR 6632 Université de Aix Marseille/CNRS .
Equipe Evolution biologique et Modélisation , case
19 3 place Victor Hugo 13331 Marseille Cedex 03
France tel 33491106489 we are organizing the 13th
Evolutionary Biology Meeting at Marseilles [http://-
sites.univ-provence.fr/evol-cgr/](http://sites.univ-provence.fr/evol-cgr/) Pierre PONTAROTTI

<Pierre.Pontarotti@univ-provence.fr>

Bioinformatics linux

Dear Colleagues,

I want to announce the availability of a bioinformatics-centric virtual linux machine for Amazon's Elastic Compute Cloud (EC2). It is public and completely free. It's based on a clean install of Ubuntu 8.04(Hardy) Linux, and has many popular open-source tools preloaded, including BioPerl, blast, hmmer, hyphy, phylip, primer3, clustalw, R, and many others. You can get more details, plus helpful cloud computing links, at

<http://fortinbras.us/bioperl-max> As usual, I make this available purely as a fellow member of the research community. If it works, tell your friends; if you don't, tell me. No salesman will call.

cheers, Mark

Mark A. Jensen, PhD Fortinbras Research

maj@fortinbras.us maj@fortinbras.us

CitizenScienceChallenge Instructions

Greetings everyone,

Here are instructions for participating in the "citizen science on the semantic web" challenge. Please circulate to anyone (anywhere) who you think will want to contribute.

For those in London, here's a preliminary list of places to mini-blitz: <http://spire.umbc.edu/ebio/-Main/London> If you know London, please feel free to add more. (Email me for the edit password.)

See you all soon - Joel.

joel sachs <jsachs@csee.umbc.edu>

CitizenScienceChallenge Instructions 2

Apologies for not including the URL on my last email:

<http://spire.umbc.edu/ebio/> Greetings everyone,

Here are instructions for participating in the "citizen science on the semantic web" challenge. Please circulate to anyone (anywhere) who you think will want to contribute.

For those in London, here's a preliminary list of places to mini-blitz: <http://spire.umbc.edu/ebio/-Main/London> If you know London, please feel free to add more. (Email me for the edit password.)

See you all soon - Joel.

jsachs@csee.umbc.edu

Comparative analysis

Dear Evoldirs,

I am doing a comparative analysis and I want to make a correlation between a few continuous variables. I already have a Bayesian phylogeny that includes all the species I'll use in the analysis. Can someone recommend me a recent and easy program to compare my data by independent contrast?

Best,

Itzel

Itzel Zamora Vilchis PhD student School of Tropical Biology Faculty of Science, Engineering and IT James Cook University Townsville, Qld 4811 AUSTRALIA phone (61 7) 4781 5482 office 029B <http://medusa.jcu.edu.au/crozier/croziergroup/home> itzel.zamoravilchis@jcu.edu.au

DNA recleaning methods

Dear all,

I am having trouble getting PCR amplifications from some of my samples. I have not access to more tissue sample, so I have tried re-cleaning the genomic DNA in solution using different methods with *very* little success, usually losing much of the DNA in the process. I've tried: - Phenol-chlorophorm-isoamyl + chlorophorm-isoamyl + ethanol precipitation; - Heating them in NaOH+SDS for 20 minutes (following Shi et al. 2004) followed by Phenol-chlorophorm-isoamyl + ethanol precipitation; - Promega Wizard Genomic DNA Purification kit; - Qiagen DNeasy Tissue kit; - Qiagen DNeasy Plant kit. I have plenty, long non-degraded DNA in solution (checked on Nanodrop and on agarose gel). I've also tried diluting the samples with no success. When co-amplifying these samples with ones that work, I still get amplifications (that sequence well) which means whatever it is, it's not something in solution but most likely bound/cross-linked to the DNA. I must add that these samples were originally extracted from fish muscle tissue preserved in ethanol or frozen, using an ammonium acetate protocol and isopropanol precipitation. I'd be grateful if you could suggest some alternative method that has worked for you, including modifications of the above (as they are typically meant for extraction from tissue and not from aqueous solution). Thanks! Hugo

Hugo F. Gante Hugo.Gante@asu.edu School of Life Sciences Arizona State University Tempe, AZ85287-4601 and

Museu Nacional de História Natural Rua da Escola Politécnica, 58 Lisboa, Portugal

hgante@asu.edu hgante@asu.edu

Drosophila species DNA

Genomic DNA for the twelve *Drosophila* species with sequenced genomes is available from the *Drosophila* Species Stock Center at UCSD.

<https://stockcenter.ucsd.edu/index.php?table=GenomicDNA> Therese Markow <tmarkow@ucsd.edu>

D subobscura lines

I have ~100 lines of *Drosophila subobscura* collected from a number of locations from around the UK for which I have no use for. If anyone has a use for these flies get in touch and I will be more than happy to send them to you.

Ben Longdon

- Ben Longdon Institute of Evolutionary Biology, Room 112, Ashworth Laboratories, University of Edinburgh, West Mains Road, Edinburgh EH9 3JT Scotland UK

Tel: (0131) 6508659 Email: B.Longdon@ed.ac.uk <http://www.gen.cam.ac.uk/Research/Jiggins/-Ben.html> The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

Ben Longdon <b.longdon@ed.ac.uk>

Enquiry on FreeNA software

Dear all,

I have tried to download FreeNA program from this website <http://www1.montpellier.inra.fr/URLB/> but it appears to be corrupted. Does anyone knows where can I get a copy of it? If anyone can send me one...Ill be grateful.

Sincerely, Carolina

Carolina I. Miño, MSc. Doctoral Student Laboratório de Genética de Aves Departamento de Genética e Evolução Universidade Federal de São Carlos Rodovia Washington Luis km 235 SP-310 CEP: 13565-905 Monjolinho. São Carlos,SP, Brazil. Phone number: +55 16 3351 8391 (Work) Fax: +55 16 3351 8377 Mobile: +55 16 91190380

Carolina Minio <carolinaianido@yahoo.com.ar>

(401) 626-4704 goodman.lawrence@gmail.com

Enquiry on FreeNA software on Null Allele estimation

Dear all,

There are currently several methodologies available to estimate null allele frequencies (and evidence for) when working with microsatellite data. My question is: what is the best method to use? If anyone can shed me a light into it, Ill appreciate it.

Thank you very much, Sincerely, Carolina

Carolina I. Miño, MSc. Doctoral Student Laboratório de Genética de Aves Departamento de Genética e Evolução Universidade Federal de São Carlos Rodovia Washington Luis km 235 SP-310 CEP: 13565-905 Monjolinho. São Carlos,SP, Brazil. Phone number: +55 16 3351 8391 (Work) Fax: +55 16 3351 8377 Mobile: +55 16 91190380

Carolina Minio <carolinaianido@yahoo.com.ar>

Evolution toys

I am writing to let the scientific and educational communities know about a new toy company dedicated to teaching younger kids about evolution, www.charliesplayhouse.com (“Games and Toys Inspired by Darwin”). The first toy is an 18-foot long timeline that introduces kids to over 60 amazing creatures that have sprouted up in the last 600 million years.

The company was founded because there are literally no toys out there focusing on evolution even though the market is replete with toys about chemistry, physics, astronomy, and virtually any other branch of science. The big toy companies also shy away from the subject because of fears of a political backlash from creationists.

Please help me spread the word about this company. It’s not easy to be starting a company right now, but it’s especially hard when so many educators and parents think evolution is a subject little kids can’t handle. Of course, it is, and this company even makes it fun.

www.charliesplayhouse.com Lawrence Goodman w-

Foundations of Evolutionary Biology

Dear colleagues,

In my courses I’ve often used the series by University Of Chicago Press on classic papers in different areas (“Foundations of Ecology”, “Foundation of Biogeography” and “Foundations of Animal Behavior”). I always wondered why don’t we have a similar series on Evolutionary Biology, given that I think it’d be a great teaching tool.

So I decided to contact you and ask for what you think would be the most influential papers in the field of Evolutionary Biology. I’ll compile the list, rank the papers and provide the list back to Evoldir.

Looking forward to your contribution,

Marcio Pie

Marcio R. Pie Departamento de Zoologia Universidade Federal do Paraná C.P. 19020 81531-980 Curitiba, PR Brazil Phone: +55(41)3361-1558

pie@ufpr.br

Hong Kong Teaching Petition

Dear Scientists:

The Hong Kong Education Bureau recently issued a new biology syllabus guideline containing the following statement concerning teaching evolution: “In addition to Darwin’s theory, students are encouraged to explore other explanations for evolution and the origins of life, to help illustrate the dynamic nature of scientific knowledge”.

This statement will open the door for teaching creationism or intelligent design in biology class as “alternative” to the theory of evolution. The South China Morning Post, a leading Hong Kong newspaper, has reported that many Hong Kong middle schools and secondary schools will teach creationism or intelligent design. Some school principals also said they support the idea of teaching creationism/intelligent design as “al-

ternative" to evolution in biology class.

So far, the Education Bureau refuses to review its guidance statement regarding teaching evolution. A letter of support dated May 5, 2009 and signed by 62 people (including principals of schools, teachers, professors, and scientists; among them is a known Intelligent Design advocate) has been submitted to Hong Kong Education Panel of Legislative Council, claiming that there is no problem with the wording in the current biology curriculum guidelines. The arguments presented in the letter are mostly distortions and misunderstandings of evolution. The letter uses the List of Signers from the Scientific Dissent From Darwinism as evidence of scientific authority supporting "alternative explanations to Darwinian macro-evolution", saying that "a growing list of over 750 highly qualified scientists, many from some of the world's most respected academic institutions, have signed a statement which says: "We are skeptical of claims for the ability of random mutation and natural selection to account for the complexity of life. Careful examination of the evidence for Darwinian theory should be encouraged". [<http://www.dissentfromdarwin.org/-index.php>]" A petition is currently being organized by the Concern Group for Hong Kong Science Education [<https://sites.google.com/site/hkscienceeducation/-petition-statement>], asking the Education Bureau to clarify the problematic statement in the upcoming Biology Curriculum for Hong Kong secondary schools. The website <http://www.gopetition.com/online/-28149.html> has more background details. The site contains both Chinese and English versions of the petition. [Sign the Petition] box is located at the bottom of the English version.

Your signature support is very important for promoting evolution education in Hong Kong and preventing creationists from taking over Hong Kong secondary schools.

Please help me forward this email to your fellow scientists for their attention. The petition signing is open until 6/30/2009.

Dr. Mei Sun Associate Professor School of Biological Sciences University of Hong Kong

E-mail: meisun@hku.hk, meihk@yahoo.com

Web site: <http://www.hku.hk/biosch/staff/ms/-index.htm>

"Dr. Mei Sun" <meisun@hkucc.hku.hk>

Juniperus seed DNA

Dear Evoldir members,

We are working with *Juniperus cedrus* (cupressaceae) in population genetics. We have tried to extract DNA from seed (endocarp tissue) using different protocols and commercial kits. However, we haven't obtained DNA enough. *Juniperus* seeds are small and very hard. So, there are anybody that have extracted DNA from similar seeds or woody tissues successfully?

Thank in advance,

Beatriz Rumeu I have received many suggestions that are showed below:

1) I have done quite a bit of work on seeds. With regards to breaking them up...have you thought about just encasing the seed in a couple of layers of tin foil, then giving them a damn good whack with a hammer? Basically flatten them. Then dump them in a tube. Works great on many seeds in my hands, although I haven't tried juniper.

2) It took one year till I got DNA from *Juniperus communis* embryos. It was a hard time, but at the end I succeeded. I used hundreds of extraction protocols but only the Nucleon PhytoPure from Amersham worked. To grind the tissue, I used a Retsch mill. That was all.

3) I have extracted from woody tissues from *Quercus* and also from *avellana* seeds. I always get good results with the qiagen kit DNeasy Plant, but, for PCR, most of the times I worked with only the second elution because the first one got probably more inhibitors of PCR or restriction enzymatic reactions....have you tried a second elution of the column??? Also, for very hard materials I had to use less quantity of material than the one the kit recommends...

4) I extracted DNA from *Arabidopsis* seeds, which are also very small, and fairly hard, especially when frozen. I froze the seeds in liquid nitrogen and ground them in a bead beater (genogrinder 2000). I think I extracted with Qiagen DNeasy Plant. You might want to reduce the amount of elution buffer used in the last step. I think they also have a micro kit, or you could try the puregene kit. Because the seeds are so small, they don't have much DNA. I had to bulk at least 10 seeds to get enough DNA to detect. However, it should be possible to amplify DNA from a single seed, even if you don't

have very much DNA, as long as the fragment you are amplifying is short and the PCR reaction is robust.

5) I have worked with seeds, mostly old and degraded seeds but here are some suggestions. Have you ground them up? This is hard with some of the seeds I have worked with but critical to extracting the DNA. We use a mixer mill to grind them up and get a very fine powder. I know some colleagues who use mortar and pestles with liquid nitrogen, other use pliers cover with plastic to protect from contamination.

The problems we have found is inhibition from;

Phenolics - we remove by precipitating with PVP.

Starch - we remove by treatment with amylase

Humic substances - we remove through chromatography columns

We have extracted with enzymatic extraction methods (proteinase K), and chemical methods (CTAB, GuSCN) and had success with all of these methods.

6) Según mi experiencia con endocarpos de distintas especies, creo que la cantidad de ADN obtenida de un endocarpo depende (además del peso de partida, calidad de muestra, protocolo...) del homogeneizado de éste. Hay que procurar obtener una pulverización total, y para ello necesitas Nitrogeno líquido, bolas (5 mm diámetro) de acero o carburo de tungsteno y un mixer mill (homogeneizador vibratorio). Es lo más eficaz. Si no lo consigues por la dureza del endocarpo, prueba trozándolo con unos alicates antes de molerlo. Los Kits dan menos rendimiento pero ganas en "limpieza" y eso mejora la amplificación posterior. Un protocolo basado en CTAB suele funcionar. En este enlace

[http://ebd10.ebd.csic.es/pdfs/-](http://ebd10.ebd.csic.es/pdfs/-Prunus.Lab.Protocols.pdf)

[Prunus.Lab.Protocols.pdf](http://ebd10.ebd.csic.es/pdfs/-Prunus.Lab.Protocols.pdf) encontrarás uno con CTAB y otro (Cheung) sin CTAB, más rápido pero "menos limpio". Además puedes probar el de Milligan (1998) que a nosotros nos ha dado buen resultado "calidad-tiempo" pero homogeneizando como he comentado antes.

Milligan BG (1998) Total DNA isolation. In: Molecular Genetic Analysis of Populations: A Practical Approach, 2nd edn (ed. Hoelzel AR), pp.

43-44. Oxford University Press, Oxford, UK

Thank you very much to all of you. I have successfully extracted DNA from *J. cedrus* endocarp by using first liquid nitrogen and a mixer mill to obtain a very fine powder. After that, I have used the next protocol: Milligan BG (1998) Total DNA isolation. In: Molec-

ular Genetic Analysis of Populations: A Practical Approach, 2nd edn (ed. Hoelzel AR), pp. 43-44. Oxford University Press, Oxford, UK

The commercial kit Nucleon PhytoPure has worked successfully too, but the best results have been obtained with the Milligan (1998) protocol.

– Beatriz Rumeu Ruiz Island Ecology and Evolution Research Group IPNA, CSIC C/ Astrofísico Fco. Sánchez, n.º 3. 38206, La Laguna, Tenerife,

— / —

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>

MBE on Facebook

evoldir@evol.biology.McMaster.CA 6 June 2009

Dear Folks!

Please check out the Molecular Biology and Evolution (MBE) Facebook group.

Do you have any discussion topics or concerns about the journal to raise? Members include many Associate Editors and Oxford University Press Production.

All the best, Marcy

M. K. Uyenoyama Department of Biology Box 90338 Duke University Durham, NC 27708-0338 USA

Tel: 1-919-660-7350 Fax: 1-919-660-7293 email: marcy@duke.edu

Merging MrBayes files

Dear Evoldir Members, I have been trying to merge both log and tree files from a few runs of MrBayes. I did it in the past in LogCombiner from Beast package, but once I've changed a computer it seems that some regional settings make the tree files illegible to the program. I've been trying to change those settings (which worked perfectly in my previous computer) but now I'm constantly getting following error message:

Exception: 1 java.lang.ArrayIndexOutOfBoundsException not quite satisfactorily explain.

```
1 at dr.app.tools.LogCombiner.<init>(Unknown
Source) at dr.app.tools.LogCombiner.main(Unknown
Source)
```

Does anyone have a good solution to this problem? Maybe another program?

We (Polish) have been on the wrong side of iron curtain, when the fundamentals of computer systems were set.

Many people here would be very grateful if authors of computer programs would keep that fact in mind ;)

Best wishes, Maciek

konopinski@iop.krakow.pl konopinski@iop.krakow.pl

Microarray course help 2

Dear EvoDir Community,

Please note, as of this moment I have not received any response about Microarray-Course help. This course, however, could not be offered during summer, but has been postponed to Fall 2009. I may request Dr. Brian Golding to republish it in the beginning of the Fall semester. Also, if I receive any response in between, I will certainly republish it.

Thanks for reading my request, and that is highly appreciated.

Anand

Anand P. Gupta, Ph.D Johnson C. Smith University
Department of Natural Sciences and Mathematics, SHB
307 100 Beatties Ford Road Charlotte, NC 28216

Voice: (704) 378-3580 e-mail to: agupta@jcsu.edu Web:
<http://sites.google.com/site/geneticsandevolution>
"Gupta, Anand P" <agupta@jcsu.edu>

Micro interpretation

Dear Evoldir,

We would like to draw on your knowledge on microsatellite marker interpretation, as we have some results for the freshwater diatom *Asterionella formosa* that we can

We did a preliminary screen of the *Asterionella* population in Lake Maarsseveen (Netherlands) using ten newly developed microsatellite markers on nine different isolates. The result showed that i) all nine tested isolates showed the same genotype and that ii) all ten tested loci were 100% heterozygous. Although diatoms are assumed to reproduce mainly asexually, this uniformity in the population and the extremely high heterozygote percentage seems a rather farfetched outcome.

Further this result also astonished us, as we have AFLP, allozyme and experimental data that did show high genetic polymorphism in *Asterionella* isolates from the same population. AFLP analysis using four primer combinations produced 116 markers of which 72% were polymorphic. Allozyme analysis using three enzymes yielded one monomorphic and two polymorphic enzymes and showed three genotypes in 24 *Asterionella* isolates. Heterozygosity was estimated at 51.2% based on the two polymorphic enzymes. And last, a reaction norms experiment on the response of seven *Asterionella* isolates to five different temperatures showed significant isolate by temperature interactions. All these data strongly suggest genetic variation in the *Asterionella* population in Lake Maarsseveen.

So we are at loss as to how to interpret the results obtained by the ten microsatellite markers and would be very glad about any ideas or suggestions.

Netherlands Institute of Ecology / Eawag Alena Gsell
Silke van den Wyngaert Bas Ibelings

"Ibelings, Bas" <B.Ibelings@nioo.knaw.nl>

Microsatellite cloned sequences

Dear Evoldir member,

We are working with microsatellite in a plant species. We have found a peak profile that correspond with a triploid species. So, in order to determinate if each peak correspond with a true allele, we have cloned and sequenced PCR product. We have found more than two alleles for the same individual, in fact we have found four and five alleles in the same individual. The bp distance between the true peaks correspond with the bp distance detected between some sequences. On the other hand, the distance between the true alleles and its respective slippage, correspond with the distance in

bp recorded between some sequences. So, could we confirmed the ploidy status (triploid) of this plants in base to these cloned sequences?

Thank in advance,

Miguel Angel

Dr. Miguel Angel González Pérez Departamento de Biología Universidad de Las Palmas de Gran Canaria Campus Universitario de Tafira 35017 Las Palmas de Gran Canaria Canary Islands Spain

Phone: (+34) 928 454 543

Fax: (+34) 928 452 922

canariensis750@hotmail.com

Microsats Stained with EtBr

Dear Colleagues,

I am seeking a low-cost, in-house alternative to sending out microsatellite DNA for genotyping in a capillary array using fluorescent-labelled primers. Ideally, this would be a system that could be handled by undergraduates (including the attendant error rates, safety concerns, and low-technical skills).

I have found some methods from the Ag-science literature that describe a system for staining acrylamide gels using ethidium bromide and visualized using a standard UV-light transilluminator -

<http://crop.sci-journals.org/cgi/content/abstract/43/5/1828> The entire system seems to be commercially available as a custom electrophoresis rig and slab-gel glass plates. This looks like it could be fairly easy, and at ~\$2000 for the gel set-up, the price is right. However, my experience with acrylamide is not something I look back on fondly, and I always prefer non-toxic alternatives when possible.

Has anyone used this system, or something like it? Is the low, low cost worth the predictable hassle?

Christopher Irwin Smith Assistant Professor Department of Biology Willamette University Salem, OR 97301 ph: 503-370-6181 fax: 503-375-5425

www.willamette.edu/~csmith/ChrisSmith.htm

email: csmith@willamette.edu csmith@uidaho.edu chris.smith@post.harvard.edu

Chris Smith <csmith@willamette.edu>

Microsats stained with EtBr answers

Dear Colleagues,

Thanks to the many, many people who replied to my query about using acrylamide and EtBR as an alternative to modern capillary arrays. I apologize for not replying to each of you individually; the number of responses and requests for copies of the answers necessitate a mass-mailing.

It seems that most everyone agrees that analysis in a capillary array using fluorescent-labelled primers is always preferable. However, a number of you suggested alternatives. The most popular were silver-staining of acrylamide gels, and the Elchrom Scientific 'origins' system. My current plan is to try out demo-models of each of these before making a final purchase.

Below, I have posted the responses I received, with identifying information removed out of respect for our colleagues' privacy. If you would like to write directly to any of the respondents, please let me know and I will pass along their contact information.

Best regards, and thanks to all,

Chris.

Christopher Irwin Smith Assistant Professor Department of Biology Willamette University Salem, OR 97301 ph: 503-370-6181 fax: 503-375-5425

www.willamette.edu/~csmith/ChrisSmith.htm

email: csmith@willamette.edu csmith@uidaho.edu chris.smith@post.harvard.edu

—

Elchrom (Switzerland) used to make a system with horizontal agarose gels that may help.

But I think that nothing beats labelled primers and sizing on sequencer.

Dear Chris,

I have been using for this purpose precast gels from Elchrom scientific, which also ship a electrophoresis apparatus. This is in a reasonable price range and staining is easy with Sybergold (or if you want with EtBr). I prefer the Syber as it is more sensitive.

You can check out details on <http://www.elchrom.com/> Cheers

—

Hi Chris,

I don't know anything about the methods you've asked about. But I just wanted to say that genotyping in core facilities using capillary machines isn't expensive. You probably know this already, but here in PA we do multiplex PCRs and send them to Penn state for about \$200 for a 96 well plate. Total cost per locus per individual can be as low as about \$0.50. This is a great and worthy price, given the complication of any alternatives.

Best,

—

hey there, no reason this shouldn't work. your previous experience with acrylamide was tainted by getting the toxic powder into solution, at the right concentration, etc. There are premade solutions available now, so the "toxicity" and difficulty is significantly reduced.

check out biorad, I think they were the ones making this stuff.

best of luck

C

—

Dear Cris,

Just thought I would let you know I have used agarose gels to visualize microsat variation and staining them with EtBr. We used 3 or 5 % agarose gels (which you need to play with to get it right, and must have a degassing step to get rid of many trapped bubbles). We were quite happy with the results. However, I must qualify that we picked and choose microsats where the difference in sizes between the alleles were larger than 15 bp, and we were scoring progeny from a F2 cross (only two alleles present). I don't think it works as well if you have more than 3 alleles segregating, since you may only see a blur.

Best wishes,

—

Dear Chris, There is a system from Elchrom Scientific. The gels are stained with Sybr Gold, it works good but: only 2bp differences can be detected unambiguously, you can do max. 3 loci at once if you have approx. 100bp difference. I have used it some years ago, if you do e.g. paternity analysis using only a few microsatellite loci (3-4) it is ok otherwise you have to run many many gels and the gels are plus minus expensive. Anyway it is very easy and undergrads could easily handle it, you only need a good gel doc system for detection of alleles. The best: you don't have to produce gels, you can just buy them and you don't need fluorescent la-

belling of primers. Just visit their home page (<http://www.elchrom.com/public/index.php>) there is information available and you can ask me for more information. I must say I have a ABI sequencer now and do not use the Elchrom apparatus any more... hope to have helped you. cheers,

—

Dear Christopher

Such staining methods are difficult because if running denaturing gels the 2 DNA strands run differently and there are 2 bands for each allele. If you do non denaturing you get heteroduplex bands as well making it difficult to interpret. I tried the later many years ago with silver staining, colleagues tried silver staining denaturing gels and blotting and probing with biotin labelled probes and gave up for research purposes.

Good luck

—

Hello Chris,

— / —

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>

MrBayes Newick trees problem

When MrBayes makes the Newick tree file, it numbers the samples instead of indicating them by their names in the nexus file. Is there anyway to change that?

Because next I have MEGA display the tree, and I want a tree that lists the names of the samples, and not their order number in the file.

Thanks,

Ms. Addie Evans Mathematics Department, San Francisco State University Cohen Lab, Romberg Tiburon Center for Environmental Studies

Addie Evans <addieevans@gmail.com>

NewJournal EntomologicaAmericana

We would like to announce the first issue of the Journal of the New York Entomological Society under its new name, Entomologica Americana.

Entomologica Americana publishes original research on the taxonomy, classification, phylogeny, biogeography, behavior and natural history of insects and other arthropod taxa primarily from the Americas. Manuscripts are published as research articles, shorter scientific notes or book reviews.

Articles are available on-line to BioOne subscribers at <http://www.bioone.org/loi/nynt.1>.

We accept manuscript submissions electronically through Allen Track.

To submit a manuscript, click <http://nyes.allentrack2.net/cgi-bin/main.plex>. Christine Johnson Managing Editor Entomologica Americana entamer@amnh.org

cjohnson@amnh.org cjohnson@amnh.org

NullAlleleEstimates answers

Dear all,

Many thanks to all of you that have answered my question on null alleles estimates. As required by many of you, below are the answers I have received, together with those of Mike Ritchie, whom had had a similar question and kindly sent to me the answers he has got.

I hope it helps, Best wishes Carolina

Original post:

Dear all,

There are currently several methodologies available to estimate null allele frequencies (and evidence for) when working with microsatellite data. My question is: what is the best method to use? If anyone can shed me a light into it, I'll appreciate it.

Thank you very much, Sincerely, Carolina

Carolina I. Miñero, MSc.

ANSWERS I GET

The routine method is the maximum likelihood method with the EM algorithm. You can use the likelihood ratio test or information theoretic indices for statistical support.

Best Xuhua

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

I use Microchecker and Cervus to check our data sets for the presence and frequencies of null alleles (nf). I generally cull loci with $nf > 0.10$ for population genetic studies and $nf > 0.05$ for parentage analyses.

I hope this helps.

Cheers, Rick

Rick Brenneman, PhD Conservation Geneticist Center for Conservation and Research Omaha's Henry Doorly Zoo 3701 South 10th Street, Omaha, NE 68107 Office: 402-738-6904 Fax: 402-733-0490

Hola Carolina,

I imagine you will receive many replies to your question, as you are correct! There are many methods available to estimate the suspected null allele frequencies. However, perhaps this paper is of interest? We published a paper a few years ago estimating null alleles and mutations as I was dealing with real cases of erroneous estimates of illegitimate offspring in a seabird species we were studying. Perhaps it is useful if you are trying to determine what the case is for specific individuals if you are working on parentage studies. (A formula example is given in the paper. There is a small typo on pg. 213 where it says 'The probability of randomly sampling from the same breeding site a chick and a male that appear by chance to be related was calculated as 1 in 216,000 or less' which should read 'was calculated as 1 in 11111 or less' which corresponds to dividing 1 into the more conservative probability given above in the same paragraph, 9.0×10^{-5}).

Best wishes, Gabriela Ibarguchi

MIKE RITCHIE'S ANSWERS

Good news on null alleles.

Very many thanks to all those who replied to my query about null alleles and population structure. I had around 50 answers, which is testament to the extent of the problem.

Shortly before my submission Chapuis & Estoup published a simulation of the effects of various ways of estimating the frequency of a null allele and adjusting Fst estimates. They have also developed software to do this, which will surely become an essential resource:

Chapuis & Estoup 2007. Microsatellite null alleles and estimation of population differentiation. *Mol. Biol. Evol.* 24: 621-631.

<http://www.montpellier.inra.fr/URLB/>

Van Oosterhout's MICROCHECKER (the current version is a major update from the last time I looked) applies one of these and is available here: <http://www.microchecker.hull.ac.uk/> van Oosterhout, C., D. Weetman, and W. F. Hutchinson. 2006. Estimation and adjustment of microsatellite null alleles in nonequilibrium populations. *Mol Ecol Notes* 6:255-256.

So, if you are prepared to live with the assumptions of these (the main ones being that your problem is due to a single null, and no Wahlund effects) there is great scope for Fst-style analyses.

A nice surprise to me is that an imminent release of STRUCTURE allows treating loci as dominant markers so allowing analyses of potential sub-structure despite nulls. This is not available yet, but is to be released soon on the STRUCTURE website and Daniel Falush and colleagues have a paper just out in *MEN* on this.

<http://www.blackwell-synergy.com/doi/abs/10.1111/j.1471-8286.2007.01758.x> <http://pritch.bsd.uchicago.edu/structure.html> It may be worth mentioning here that there are also methods for relatedness and parentage:

Wagner AP, Creel S, Kalinowski ST (2006) Estimating relatedness and relationships using microsatellite loci with null alleles. *Heredity* 97:336-345.

I will not send all the responses I received out on EvolDir, as these are lengthy and

— / —

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>

Pedigree software answer

Dear all,

Some months ago, I've asked about a place to download PEDIGREE software (Herbinger et al. 2006). I have not received any answers yet, but today I've found a working link for the program's website. Since some of you asked me to post the answers, here is the link I am using:

<http://herbinger.biology.dal.ca:5080/Pedigree/> Best wishes, Carolina

Carolina I. Miño, MSc. Doctoral Student Laboratório de Genética de Aves Departamento de Genética e Evolução Universidade Federal de São Carlos Rodovia Washington Luis km 235 SP-310 CEP: 13565-905 Monjolinho. São Carlos, SP, Brazil. Phone number: +55 16 3351 8391 (Work) Fax: +55 16 3351 8377 Mobile: +55 16 91190380

Carolina Minio <carolinaianido@yahoo.com.ar>

Population statistics software

Does anyone know of a software package that can 1. calculate "within population diversity for chloroplast MSAT (cpSSR's)" data - essentially $D^2(sh)$ of Goldstein et al 1995 but adjusted for plastid genomes, and 2. calculate genetic distances among populations following Goldstein et al 1995? There have been several papers published on these statistics but no references to the programs used. Contacting primary authors have not been successful yet.

Thanks - Erika Hersch-Green

Erika Hersch <erikahersch@gmail.com>

Prokaryotic Diversity Database

We are pleased to announce the availability of envDB, a database that aims to provide the most complete census to-date of the environmental distribution of prokaryotes.

EnvDB connects the environmental characterization of their original samples with the taxonomic identification of 16S rDNA sequences. This is the result of a comprehensive effort to annotate all samplings and sequences stored in the ENV section of GenBank database. Cur-

rently, envDB contains 359.928 sequences belonging to 3.502 samples, classified in 46 different environmental categories and some environmental features.

The user can perform complex queries using all possible combinations of sequences, OTUs, samples and environments, using a user-friendly web interface. The users can also analyze their own data: Given a set of 16S rDNA sequences input by the user, envDB checks for similar sequences and samples in the database. The results include also the environmental distribution of the samples and sequences found.

Examples of questions that envDB can address include: Obtaining all the sequences deposited for a particular taxa; Retrieving all samples and associated sequences for one environment; Finding all taxa present in a given environment; or obtaining the abundance of taxa in environments.

EnvDB is freely accessible at the web address <http://metagenomics.uv.es/envDB>. A paper providing a full description of envDB has been already published: Pignatelli M, Moya A, Tamames J: EnvDB, a database for describing the environmental distribution of prokaryotic taxa. *Environ Microbiol Reports* 1, 191-197 (2009)

For further information, please feel free to contact me: Javier Tamames (tamames.jav@gva.es)

javier.tamames@uv.es

Renaturing Proteins IEF

Dear EvolDirers,

I am trying to adapt immobilized pH gradient (IPG) strips with a basic narrow range (pH 7-10) to screen for presence and activity of S-RNases in *Solanum*. The problem is that the rehydration and sample preparation buffers that the BioRad Protean cells require cause protein denaturing, hence forbidding me from running the RNase activity test. I read somewhere that one can successfully renature the proteins in the IPG strips by rinsing the strip in a particular buffer after the IEF is done and directly test for RNase activity in the strip, but I can't seem to find specific instructions anywhere. Has anyone done this renaturing and testing in these kind of strips? If so, could you share your protocols/recipes? Any insight will be greatly appreciated

Best,

Jorge

Jorge Mena-Ali, PhD Visiting Assistant Professor Dept of Biology, Franklin & Marshall College Lancaster PA 17604

jorge.mena-ali@fandm.edu jorge.mena-ali@fandm.edu

SAMPL-method

Dear EvolDir community,

we are planning some population genetics with several plant species of which no microsatellites are currently available. We therefore were seeking for alternatives and stumbled across a new method with is called SAMPL (selective amplification of microsatellite polymorphic loci). This method allegedly combines the advantages of microsatellites with that of AFLP. However, only few studies have used this method so far, which makes it somehow suspicious. So we would like to know if somebody already has some experiences with this method, if it lives up to its promise and if there are some problems or difficulties one should know about.

Thanks in advance for any suggestions!

Andreas Enßlin (aenssln@uni-potsdam.de) Biodiversity Research and Botany Department of Biology and Biochemistry Potsdam University, Germany

aenssln@uni-potsdam.de

Software Crux 1 1 0

Crux is a recently developed software toolkit for phylogenetic inference that runs on Linux, FreeBSD, and Mac OS X. It is structured as a set of Python modules that exposes all the functionality necessary to conduct sophisticated analyses, including:

- * Metropolis-coupled Markov chain Monte Carlo (MCMCMC) estimation for a broad range of likelihood models, including all specializations of GTR+I+G and mixture models. The 'redpoint' script directly supports all common uses for the MCMCMC functionality.

Note that Crux can use pthreads to concurrently compute tree likelihoods on multi-processor computers, as well as MPI to concurrently run MCMC chains, so it is practical to analyze data sets consisting of hundreds of

taxa and thousands of characters.

* Ubiquitous support for multifurcating trees.

* Sequence simulation under any of the models the likelihood engine is capable of.

* Neighbor joining (NJ) and relaxed neighbor joining (RNJ) tree construction, the implementations of which are extremely fast. Numerous corrected distance computation methods are supported, including par-linear/logDet. The 'MrRogers' script directly supports all common uses for the pairwise distance computation and NJ/RNJ functionality.

* The 'crux' script can be used interactively to browse online documentation and prototype Crux scripts, or it can be used to run scripts non-interactively.

All of Crux's core functionality can be accessed via Python and/or Cython, which makes it extremely flexible as the basis for sophisticated scripts/programs that, for example, require complete control of a capable likelihood computation engine.

To download and install Crux, visit the homepage:

<http://www.canonware.com/Crux/> or download Crux 1.1.0 directly:

<http://www.canonware.com/download/Crux/crux-1.1.0.tar.bz2> Extract the archive, then start by reading the README file, which will direct you to build/installation instructions, documentation, and scripting examples.

You are encouraged to contact the author regarding any questions or comments.

Thank you, Jason Evans

— Jason Evans <jasone@canonware.com>
<jevans@uidaho.edu> Research Assistant University of Idaho

jasone@canonware.com

Software DnaSP PopGenetics

Announcing DnaSP version 5.0

DnaSP, A software for the analysis of DNA Polymorphism data

Pablo Librado and Julio Rozas

DnaSP, DNA Sequence Polymorphism, is a software package for PC-Windows that performs extensive DNA

population genetics analyses.

MAIN NEW FEATURES IN DnaSP V5:

1) Haplotype reconstruction from Unphase/Genotype data (using PHASE, fastPHASE and HAPAR algorithms).

2) Analysis of Insertion/Deletion (InDel) Polymorphisms (DIPs).

3) Characterization of conserved DNA regions.

4) Automatically reading and analyzing multiple data files sequentially (as a batch mode).

5) Possibility to read HapMap3 format files with phased haplotypes.

6) Possibility to define and conduct analysis in functional regions.

7) Possibility to display in the UCSC browser the DNA sequence data and sliding window results integrated with available genome annotations.

... and more other features!

SYSTEM REQUIREMENTS

IBM-Compatible PC

Windows 98, NT, 2000, XP, Vista

Macintosh

Using VirtualBox, VMWare Fusion, Parallels Desktop or Virtual PC

Linux

Using VirtualBox, VMWare or Wine

INPUT Data Files

NBRF/PIR, MEGA, NEXUS, FASTA, PHYLIP and HapMap3 formats

OUTPUT

Windows with text, tables and graphs

AVAILABILITY

The license is distributed free of charge for academic institutions

MORE INFORMATION

<http://www.ub.edu/dnasp>

REFERENCE

Librado, P. and Rozas, J. 2009. DnaSP v5: A software for comprehensive analysis of DNA polymorphism data. *Bioinformatics* 25: 1451-1452.

Julio Rozas

Departament de Genetica Facultat de Biologia Univer-

sitat de Barcelona Barcelona Spain
 jrozas@ub.edu jrozas@ub.edu

Software Multiplex Manager Program

Dear EvolDir subscribers,

It is my pleasure to announce a new free-ware program, that assists researchers to plan and optimize Multiplex PCR reactions. The manuscript is available on the Biotechniques website and the program itself can be downloaded from its own website. Program documentation, including an instructional video is available on the Multiplex Manager website.

Program Download and user guides:
www.multiplexmanager.com Manuscript link:
[http://www.biotechniques.com/biotechniques/BiotechniquesJournal/2009/June/Multiplex-Manager-1.0-a-crossplatform-computer-program-that-plans-and-optimizes-multiplex-PCR/biotechniques-143132.html? autnIDI7547](http://www.biotechniques.com/biotechniques/BiotechniquesJournal/2009/June/Multiplex-Manager-1.0-a-crossplatform-computer-program-that-plans-and-optimizes-multiplex-PCR/biotechniques-143132.html?autnIDI7547)

Manuscript citation details: Multiplex Manager 1.0: a crossplatform computer program that plans and optimizes multiplex PCR. (2009). Biotechniques: Vol. 46, No. 7, pp TBA.

Clare Holleley Laboratory of Genomic Diversity National Cancer Institute-Frederick Frederick MD 21702 Phone: 301-846-7491 E-mail: holleleyce@mail.nih.gov clare@holleley.net

Software PhyloExplorer

Dear EvolDir members,

We are please to announce the release of PhyloExplorer, PhyloExplorer: a web server to validate, explore and query phylogenetic trees according to a reference taxonomy (NCBI or ITIS).

Given an input collection of rooted trees, PhyloExplorer provides facilities for obtaining statistics describing the collection, correcting invalid taxon names, extracting taxonomically relevant parts of the collection using a

dedicated query language, and identifying related trees in the TreeBASE database.

Features provided by PhyloExplorer include:

- Mapping and correcting taxon names according to the NCBI or ITIS reference taxonomy
- Describing, browsing and restricting tree collections
- Performing complex taxonomic queries on tree collections
- Measuring the taxonomic content and coverage of TreeBASE
- Drawing data availability matrices by the scoring the presence/absence of taxa in trees
- Retrieving taxon images from the tree collection for educational purpose

PhyloExplorer is available at: <http://www.ncbi.orthomam.univ-montp2.fr/phyloexplorer/> and the source code can be downloaded from: <http://code.google.com/p/taxomanie/>. The paper describing the software with some biological examples is freely available from BMC Evolutionary Biology:

<http://www.biomedcentral.com/1471-2148/9/108/>
 Ranwez V., Clairon N., Delsuc F., Pourali S., Auberval N., Diser S. & Berry V. (2009). PhyloExplorer: a web server to validate, explore and query phylogenetic trees. BMC Evolutionary Biology 9: 108.

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

Vincent Ranwez, Frederic Delsuc and co-authors

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

Software RAxML 7 2 0

Dear Community,

RAxML has recently been updated and is now available for download as RAxML-7.2.0 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.

To compile:

sequential: "make -f Makefile.gcc" Pthreads: "make -f Makefile.PTHREADS.gcc" sequential-SSE3: "make -f Makefile.SSE3.gcc" pthreads-SSE3: "make Makefile.SSE3.PTHREADS.gcc"

New features:

- The DNA and Protein Likelihood functions have been accelerated using SSE3 vector instructions, this will yield speedups between 10% and 50% compared to the non-vectorized version. If you are experiencing problems compiling the SSE3 code, please ask your local computer nerd for help first.

- Slight improvement of the numerical scaling procedure used to avoid numerical underflow according to a method proposed by BUI Quang Minh, a PostDoc at the CIBIV in Vienna, can yield up to 7% speed improvements on multi-gene datasets.

- Implementation of single-precision versions for DNA and Protein models. While those actually execute 30-50% slower than the standard double-precision implementations they can help to save almost 50% of memory consumption on large alignments which is increasingly becoming an issue. The numerical stability of the single precision version needs further testing though, i.e., usage is currently only recommended when you run out of memory.

- New -F option that stops ML searches under CAT or GAMMA after the specified number of trees has been computed without doing a more thorough search on the best-scoring final tree under GAMMA. If you are experiencing memory shortages you should do ML searches under CAT with -F since RAxML running in this mode will only assign the memory it needs for CAT (4 times less than for GAMMA).

- New -D option: This option further helps to accelerate ML searches on the original tree on datasets with several thousands of taxa. It will stop the ML search much earlier during the "asymptotic convergence phase" of the likelihood score, if the relative RF distance between the trees generated by two successive cycles of Lazy Subtree Rearrangements is smaller than 1%. On datasets with more than 1,000 taxa this yields run-time

improvements of 50%, while returning almost equally good trees.

I have also fixed various bugs from version 7.1.0.

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 Technical University of Munich

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: 01.09.037

stamatak@in.tum.de stamatak@in.tum.de

Software Tandem

Dear EvoDir community,

we have recently released tandem 1.0, a software for the automated binning of microsatellite alleles.

While programs for microsatellite analyses, such as Arlequin, Structure, IM(a) and others expect microsatellite allele sizes to be whole numbers, genotyping generally leads to allele sizes with two decimals. Due to 'allelic drift', binning of allele sizes is a non-trivial problem, and manual rounding to the nearest whole numbers may result in under- or overestimates of allelic richness (besides being tedious and error-prone).

tandem is an easy-to-use program that integrates automated allele binning into population genetics and genomics workflows. It is designed to accept files in MSA and Convert formats, and therefore needs no reformatting of data if one of these two programs is part of the workflow.

The program and a manual are freely available at www.evolution.unibas.ch/salzburger/-software/tandem.htm The article is available on the Bioinformatics website at <http://bioinformatics.oxfordjournals.org/cgi/content/abstract/btp303> Reference: Matschiner M, Salzburger W (2009) TANDEM: integrating automated allele binning into genetics and genomics workflows. Bioinformatics, doi: 10.1093/bioinformatics/btp303 (Advance Access)

Best regards,

Michael

Michael Matschiner

Zoological Institute, University of Basel Vesalgasse 1, 4051 Basel, Switzerland tel. +41 (0) 61 2670302 email michael.matschiner@unibas.ch website www.evolution.unibas.ch/salzburger/-team/mratschiner Michael Matschiner <michaelmatschiner@mac.com>

SouthAfrica FieldAssist Chats

Other: Field assistant to study evolution of group living in Ant-eating Chats

Location, Benfontein, Nr Kimberly, South Africa

I am looking for a highly motivated field research assistant to join me working on the behavioural ecology of cooperative breeding in Ant-eating Chat, *Myrmecocichla formicivora*. The study will focus on factors behind the occurrence of delayed dispersal and cooperative breeding in the species.

The study site is Benfontein Game Farm (study centre), near Kimberly, Northern Cape, South Africa. Applicants should have a strong interest in bird orientated research, and have suitable banding experience. Field assistants are expected to be fit, able to work in a tough and taxing environment, and be willing to work independently. Field workers should be able to live in close proximity to with a small number of other researchers on site.

Responsibilities will include trapping and colour-banding birds both (largely at night), re-sighting banded birds for territory mapping (using GPS), nest-searching and monitoring, monitoring family groups, behavioural observations and data input (MS Excel). The working conditions will include considerable distances covered on foot in both cold and hot conditions (0 to 40C+) and regular early morning working (whilst cool and the birds are active), and regular work after dark (trapping and banding done at night). Driving experience would be an advantage. The work will be done for 5-6 days per week, and the applicant needs to be willing to work outside normal hours.

The position is available from October until mid December 2009.

Accommodation (paid for) is provided in the field study

centre, and the project will also cover reasonable travel expenses.

To apply, please email

1. A short letter stating why you are interested,
2. A copy of your CV, including details of past field experience and bird handling/banding experience, and
3. The contact details for two referees,

to Jonathan Barnaby at: Jonathan.Barnaby@ebc.uu.se

Please don't hesitate to contact me if you have any questions or for further information.

Telephone: +46(0)18 471 26 73 Mobile: +46(0)739 04 46 51 Fax: +46(0)18 471 64 24

Website: www.popbiol.uu.se

Evolutionary Biology Centre, Population and Conservation Biology, Department of Ecology and Evolution, Uppsala University in collaboration with the Percy FitzPatrick Institute, UCT, South Africa.

jonathan.barnaby@ebc.uu.se

jonathan.barnaby@ebc.uu.se

StKilda volunteer SoaySheepProject

Soay Sheep Research - St Kilda

Summer and Rut 2009

Fieldwork Volunteer Assistants

We are currently looking for volunteers for this year's Soay sheep Summer and Rut expeditions to St. Kilda, a group of islands 180 km off the coast of north-west Scotland. The expeditions run from mid July till the end of August and from Mid October until late November 2009.

Activities:

- Population census of sheep using telescopes and hand-held computers
- Mortality searches
- Annual catch up of sheep (August)
- Monitoring of Rut behaviour (November)

Requirements:

- . Must be available for the full period of one of the time periods stated
- . Must be fit, St Kilda has a very demanding terrain;

ability to run essential

. A background in Biological Sciences

Travel to the island will be by helicopter from Benbecula (Outer Hebrides) and the team will stay in cottages built by the original inhabitants of St Kilda (since restored by the National Trust for Scotland). Expenses incurred whilst travelling in Scotland will be reimbursed and food/accommodation on island are provided. This is an ideal opportunity to gain field experience in large mammal research and to visit St Kilda, the remotest of British islands.

If you wish to apply for this work please send: a CV with covering letter, contact phone number and details of two referees that can be contacted immediately by email.

Contact: Jill Pilkington

Email: j.pilkington@ed.ac.uk

The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

Jill Pilkington <j.pilkington@ed.ac.uk>

Storing HumanDNA

Hello

My name is Joana and im working in my master degree. I would like to know if someone can help me in a simple (I guess) question. I need to conserve human blood for a few days before I do the extraction of the DNA, does anyone know whats the ideal temperature for storage in this case?

joana eca <eca.joana@gmail.com>

TimeTree website

TimeTree (www.timetree.org) has been released with more data and options for finding divergence times throughout the tree of life. Times of divergence between pairs of taxa are queried and results are presented after calculating all possible relevant times in the taxonomic hierarchy of life, based on published studies of molecular data.

The site also contains electronic resources, including a 1600-family "timetree of life" poster and open access chapters from the new book "The Timetree of Life" (Oxford U. Press) written by a consortium of 105 authors.

Blair Hedges (Pennsylvania State University) Sudhir Kumar (Arizona State University)

sbh1@psu.edu sbh1@psu.edu

Tree construction answers

This was the original question.

Dear Evoldirs,

Recently, I am trying to identify the best estimated tree using 10 nuclear DNA intronic sequences. As you might know, each nuclear gene might have different evolutionary rate. I've seen many papers dealing constructing tree by combined nuclear DNA dataset. My question is if it is the best to estimate the tree using many nuclear DNA markers which has different evolutionary rate. How about is the case for mitochondrial genome? Some use several mtDNA fragments and other use complete mtDNA. In mt genome, 13 coding genes, several rRNA, tRNA, and control region are present. If you use only 2~3 selected mtDNA markers to draw tree, would it tell you the same tree with the one drawn from complete mtDNA? Are there different evolutionary rate for each genes of mtDNA as well? How different are they? Are there good references to read?

Please let me know.

Best Junghwa AN

1) Hello Jungwha, Mt genes can have different evolutionary rates - we found this out with some of the work we did (papers attached), and Jeff Palmer has found this as well. I'd be curious to hear what kind of responses you get - would you post them on evoldir when they come in? Thanks! Camille

2) Hello Jungwha,

Well, I will start off by saying that I'm not a phylogeneticist. But I was just talking to one last week about using multiple loci for making trees, and he was making it very clear that all genes have independent evolutionary histories, so simply concatenating a handful of genes doesn't necessarily give you a more complete history of the evolutionary history of that organism. I think the way to deal with that is to publish the individual gene

trees along with any concatenated tree. In that light, it shouldn't necessarily matter that much if some of the loci are linked, but you could fairly easily test that presumption by testing for linkage disequilibrium among your loci. As for paralogy, I am not sure of all the ways to test for that, but I do know that if you translate any of the coding portions of the genes you sequenced and find stop codons in the middle of the gene or perhaps high dN/dS ratios, that can indicate a lack of functionality and thus perhaps paralogy. If you are referring to nuclear paralogs of mitochondrial genes, that certainly happens, and there are some known cases of that. Because mutation rates are so different between nuclear and mt genes, you could take a look at your substitution rates and see if they are dramatically lower in any of your suspected paralogs - that could indicate nuclear paralogs.

Camille

3) Hi,

as each dataset is different, you may try at first to do separate analyses for all regions and compare the trees. If they are incongruent to a large degree, it is not a good idea to combine the data.

Best, Judith Dr. Judith Fehrer Institute of Botany
Czech Academy of Sciences Zamek 1 25243 Pruhonice
Czech Republic

4) I can't say I've done this, so I'm sure you'll get more experienced responses, but I doubt that you would see as large of differences with coding regions in mitochondrial DNA as you would in nuclear DNA. The main reason is that mtDNA should really be considered one large linked set of genes (due to size and how quickly it evolves). Using multiple mtDNA coding regions is more like pseudoreplication in statistics than actual replication, whereas if you used several unlinked coding regions of nuclear DNA, you should be getting actual replication.

Julie

5) As to control for mutational variance, long sequence might help, e.g. long segment of mtDNA. However, it only tells you one particular gene history (No recombination inside). However, 10 independent nuclear DNA intronic sequences have different coalescent histories. so best way to do it is not combine them together. Rather, you should use ways that recently burgeoning in this field, like programs BEST, Bucky, things like that.

suggested readings: Maddison&Knowles 2006, Syst. Biol. 55(1):21-30 Edwards, Liu & Perl, 2007, PNAS, 104:5936-5941 Kubatko&Degnan, 2007, Syst.Biol.56(1):17-24 Hope this helps you. Best, Qixin He

6) I good place to start is reading papers by S. V Edwards and his group. A recent one is Edwards S, V. (2009) Is a new and general theory of molecular systematics emerging? Evolution 63, 1-19. They also have a good program to use for multiple genes called BEST. This program gets around problems of simply concatenating the sequences with different rates.

Good luck, Alicia Toon

7) In this case, I'm referring to statistical replication rather than cell or DNA replication. When you are trying to ascertain relationships between species, the reason we want many characters is because we need multiple types of evidence that reflect the same evolutionary pattern. This is why it is so important to use unlinked genes: assuming there is no selection on them and they recombine freely, they should evolve independently. Therefore, if they all give the same relationship

— / —

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>

UK research policy

Dear EvolDir community

Those of you with links to the UK research community may share my concern with the current drastic change in the mission of the UK research councils: they have been strongly directed by the government to fund more commercial-orientated research and research in pre-specified areas (which seem to show little imagination).

This policy hits evolutionary research particularly hard, of course. It is also short-sighted and self-defeating from a wider scientific point of view.

UK citizens and ex-pats may wish to consider signing a petition to the prime minister here:

<http://petitions.number10.gov.uk/honest-discovery/>

For those of you not in this constituency, I hope this movement may spur similar appeals against this trend in other countries too.

Richard Nichols Professor of Evolutionary Genetics
QMUL London Web <http://webspace.qmul.ac.uk/-ranichols/research.htm> Richard Nichols
<r.a.nichols@qmul.ac.uk>

PostDocs

ArizonaStateU 2 ComputationalEvolution	61	UCaliforniaSanDiego EvolutionModels	73
Berlin MateChoice	62	UChicago EvolutionPlantEnemyInteractions	74
DonanaBioStation ViralEvolution	63	UChicago MarineBivalves	74
EBI Hinxton Bioinformatics	63	UColorado ProteinCoevolution	74
ETH Zurich HostParasiteGenomics	64	UGuelph BarcodeOfLifeProject	75
FloridaStateU BivalvePhylogenetics	64	UGuelph Biodiversity	75
Graz CichlidQuantitativeGenetics	65	UGuelph Parasite Vector DNABarcoding	76
HarvardMedSchool EvolutionaryGenomics	65	UHouston 2 Alignment MolEvol BioInfo	76
Ipswich MA ComparativeGenomics	66	UKansas QuantGenetics	77
Italy Modelling	67	UMichigan 2 Phylogenetics	77
LSU AvianSpeciationBiogeography	67	UMichigan EvolutionaryEcol	78
Morocco ReproductiveSenescence	68	UNebraska MolecularEvolution	78
NorthCarolinaStateU EvolutionPlantDefense	68	UOregon FishAnatomicalEvolution	79
OregonStateU Plant Ontology	69	USouthernCalifornia DrosophilaGenotypeToPhenotype	79
PennState FireAntGenomics	70	UUtah PlantSystematics	79
PrincetonU MolPopulationGenetics	70	UVirginia Bioinformatics	80
TrentU EvolutionaryGenetics	71	UVirginia MetagenomicsBioinformatics	80
UCaliforniaBerkeley 2 PopulationGenetics	71	Vienna EvolutionaryEpigenetics	81
UCaliforniaBerkeley EvolutionInsectBehaviour	72		
UCaliforniaDavis PhylogeneticMethods	72		

ArizonaStateU 2 ComputationalEvolution

Postdoctoral Fellows in Computational Evolutionary Bioinformatics

Two NIH-funded postdoctoral positions (2 years) are available in Michael Rosenbergs lab in the Center for Evolutionary Functional Genomics of the Biodesign Institute at Arizona State University.

The funded research is broadly focused on the effects and uses of multiple sequence alignment with respect to phylogeny estimation, ancestral sequence prediction, and gene family identification; opportunities for independent research in the broader area of computational molecular evolution are also available.

The candidate should have a Ph.D. in biology or a related field, with some experience in computer programming and statistics. Familiarity with phylogenetics, sequence alignment, and/or ancestral sequence reconstruction is preferred.

Interested applications should electronically submit a CV, a short statement of research interests, and the names and contact information for two references to Michael Rosenberg at msr@asu.edu.

Michael S. Rosenberg, Ph.D. Associate Professor Center for Evolutionary Functional Genomics / The Biodesign Institute School of Life Sciences / Arizona State University msr@asu.edu <http://www.rosenberglab.net>
msr@asu.edu msr@asu.edu

Berlin MateChoice

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. 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 and is currently expanding its research programme (<http://www.izw-berlin.de>).

The institute has received funding for a major network project on "olfactory mate choice - immune system, olfactory receptors and their adaptive value" under the leadership of Prof Dr Simone Sommer. Olfaction plays a central role for mate choice in mammals, but there is a lack of understanding of the underlying proximate and ultimate aspects of olfactory signal evolution. Recent studies highlighted the importance of the major histocompatibility complex (MHC) for female choice which raises the question how volatiles, olfactory receptors and the MHC co-evolved in mammalian mating systems. The overall project will use a broad genomic and immunological approach to analyse this question, thereby combining state-of-the-art transcriptome analyses with detailed immunological studies and extensive field work in long-term projects on two species with contrasting social and mating systems, the greater sac-winged bat in Costa Rica and the spotted hyena in Tanzania. The network consists of the IZW (olfactory mate choice, Prof Dr Simone Sommer, PD Dr Christian Voigt, Dr Marion East, Prof Dr Heribert Hofer), the Leibniz Institute for Age Research in Jena (transcriptome analysis, PD Dr Matthias Platzer), the Charité in Berlin (immunogenetics, Prof Dr Andreas Ziegler, Dr. Barbara Uchanska-Ziegler) and the University of Geneva, Switzerland (olfactory receptor genes, Prof Dr Michel Milinkovitch). Currently we seek applications for

1 Postdoc: evolutionary immune genetics of mate choice (ref: 13/2009) The postdoc will co-ordinate the network, study the MHC of both study species and co-ordinate lab and field work in Berlin. The successful candidate will have a PhD in evolutionary genetics, zoology or related disciplines, a strong background

in behavioural ecology, genetics and evolution, excellent knowledge of statistics, organisational skills, and a strong publication record. Experience in evolutionary immune genetics, particularly MHC, olfaction, and mammalian mating systems will be an advantage.

1 Phd: mate choice and olfaction in bats (ref: 14/2009) This project will focus on mate choice mechanisms in the harem-polygynous social system of the greater sac-winged bat (*Saccopteryx bilineata*) by combining behavioural, immunological and genetic work. In colonies of *Saccopteryx bilineata* territorial males each defend a group of females, despite their incapability to monopolise the reproductive success with harem females. During courtship, males display scent compounds from pouches in their wing membranes in front of females and females probably base their mate choice decision mostly on volatiles. Field work will include odour collection, tissue collection and behavioural observations including choice experiments. Laboratory work includes chemical, immunological and/or genetic work. The successful candidate will have a diploma or MSc in Biology, Zoology or related disciplines, a strong background in behavioural ecology, genetics and evolution, above average achievements in undergraduate studies, excellent knowledge of statistics, organisational skills, ability to work under difficult conditions in a team and profound knowledge of English (speaking and writing). Experience in field work, immunological or molecular genetic lab work and knowledge of Spanish will be an advantage.

1 Phd: mate choice and olfaction in spotted hyenas (ref: 15/2009) This project will integrate genetic, chemical and behavioural aspects of olfaction to investigate the importance of olfactory cues in mate choice in the spotted hyena (*Crocuta crocuta*); a social carnivore that exhibits strong female mate choice. The candidate will conduct field work for approximately six months per year on a well studied population of individually known spotted hyenas in the Serengeti, Tanzania. Field work will entail both the collection of detailed behaviour data and odour and genetic samples from known individuals. Laboratory work will involve olfactory analyses, immunological and/or genetic work. The successful candidate will have a diploma or MSc in Biology, Zoology or related disciplines, require experience of behavioural research, above average achievements in undergraduate studies, excellent knowledge of statistics, organisational skills, a proven ability in the lab, a driving licence,

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DonanaBioStation ViralEvolution

Postdoctoral Fellowship in EBD-CSIC Flavivirus transmission network in Doñana

Estacion Biológica de Doñana, Department of Wetland Ecology

We have a position available for a postdoctoral scientist to study a bird-mosquito-Flavivirus transmission network, as part of a project funded by the Andalusian Government. This project addresses Flavivirus transmission in Doñana National Park, by combining data on the spatial and temporal distribution of birds and mosquitoes, feeding preferences of mosquitoes and virus prevalence to model the risk of virus transmission. Existing mosquito, bird census and serology and virus prevalence data sets will be used to parameterize models to predict the risk of bird to mammal transmission. There will also be the opportunity for the successful applicant to participate in new field work to inform the modelling approaches, and apply this approach to the study of avian Haematozoa transmission dynamics.

Doñana is one of the main wetlands in western Europe, with a long term monitoring program of biological processes (<http://www-rbd.ebd.csic.es/-Seguimiento/seguimiento.htm>). Main habitats include natural marshes and rice-fields.

The postdoc will be co-advised by Jordi Figuerola (www.ebd.csic.es/jordi), and Ramón Soriguer and work as part of a larger collaborative project with Maria Paz Sánchez Seco and Antonio Tenorio (<http://aevi.isciii.es/>), Javier Bustamante (www.ebd.csic.es/~busta/) and Ciro Rico.

Applicants should have demonstrated interest in ecology and evolutionary biology, and a PhD in landscape ecology, avian pathology, epidemiology, molecular ecology or related field. Preference will be given to young applicants who have experience with molecular methods and/or landscape modelling or demonstrated potential in these areas.

Review of applicants will begin June 20 and continue until the successful applicant is identified. The starting date is flexible but before the end of January 2010. Applications should include a cover letter with a statement of research interests and timing of availability, a CV, and names and contact information for two professional references. Please send your application through

e-mail to jordi@ebd.csic.es.

Estación Biológica de Doñana is a research center of the Spanish Research Council (CSIC, www.csic.es) located in Sevilla (southern Spain). A detailed list of staff and publications can be found at www.ebd.csic.es. Dr. Jordi Figuerola Department of Wetland Ecology Estación Biológica Doñana, CSIC Avda. Americo Vespucio s/n 41092 Sevilla, Spain Telf. (+34) 954 466700 Ext. 1200 <http://www.ebd.csic.es/> <http://www.ebd.csic.es/jordi/> quini@ebd.csic.es

EBI Hinxton Bioinformatics

POST-DOCTORAL JOB OPPORTUNITIES IN THE GOLDMAN GROUP, EBI, HINXTON, UK

Positions are currently available in the Goldman Group at the EMBL-European Bioinformatics Institute (EBI) in Hinxton, near Cambridge, UK.

Post-doctoral opportunities currently open include:

- * high-throughput sequencing analysis
- * software engineering for high-throughput sequencing, with the possibility to contribute scientifically (post-grad or post-doc, depending on experience)
- * short term post-doc fellowships available to anyone with a compelling idea for a project within the group's range of interests

Further details are available via: * <http://www.ebi.ac.uk> (EBI) * <http://www.ebi.ac.uk/goldman> (Goldman Group) * <http://www.ebi.ac.uk/goldman/-jobs.html> (job details)

Please pass this on to anyone you know who might be interested, or to anyone who might be able to pass it on further.

Mention code EVLDR002 when you refer a prospective candidate to me and you will be eligible for a free gift with a market value in excess of £8.00 (approx. Euro9.00 or \$13.00) if that candidate applies successfully for a position.

I will be at the Evolution meetings in the next few days and then back at EBI, and am happy to meet or correspond with potential applicants.

Please look out for a separate message regarding post-graduate level positions.

Thanks,

Nick Goldman

Nick Goldman tel: +44-(0)1223-492530 EMBL - European Bioinformatics Institute fax: +44-(0)1223-494468 Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK

goldman@ebi.ac.uk goldman@ebi.ac.uk

ETH Zurich HostParasiteGenomics

Switzerland.ETH Zurich,

Institute of Integrative Biology (IBZ)

The Experimental Ecology Group (Prof. P. Schmid-Hempel) has an opening:

Post-doctoral Position

(Genomics of a host-parasite system) against the background of studying the ecology and genetics of infectious diseases and their role for host populations or communities. The PostDoc will be part of the team using *Bombus* spp. and their parasites, especially the trypanosome *Crithidia bombi*, as a study system. Currently, the genomic toolbox for this system is rapidly expanding and will allow approaching the basic questions at the genetic level in an unprecedented scale. This will allow tracing changes in gene frequencies or signs of selection in a field-based system. Our broader interests are in the ecology and evolution of this model system with questions about host-parasite co-evolution at different scales, the epidemics of an infection, or variation in the expression of immune defence genes. The ideal candidate has experience in applying molecular tools to such questions, is knowledgeable in the use of gene data banks and familiar with the tools of bioinformatics, e.g. to assemble sequences and doing comparative studies. He/she should have an interest in evolutionary and population biology and - genetics. The position is available for 2-4 years; it is embedded in an active research group with long-term experience with this system and such questions. We offer a stimulating research environment, embedded in the Institute of Integrative Biology (www.ibz.ethz.ch) and ETH at large. Research facilities and support are excellent and the projects have solid funding. Please send applications, with CV, publication list, names of referees, and statement of research interest to Prof. Paul Schmid-Hempel, preferably by email (psh@env.ethz.ch). Please compile the documents to a single pdf file if possible. Screening of applications will start 26 June 2009 or until post

is filled. For more information, check our web page (www.eco.ethz.ch) or contact psh@env.ethz.ch.

Prof. Paul Schmid-Hempel ETH Zurich Institute of Integrative Biology (IBZ) (Experimental Ecology) ETH-Zentrum CHN K11 Universitätsstrasse 16 CH-8092 Zurich

ph: + 41 44 633 6048 / 6033 fax: +41 44 632 1271
psh@env.ethz.ch www.eco.ethz.ch 2009 is Darwin Year!
 see: www.darwinyear09.ch/ in Zurich

paul.schmid-hempel@env.ethz.ch

paul.schmid-hempel@env.ethz.ch

FloridaStateU BivalvePhylogenetics

Post-doctoral position Bivalve molecular phylogenetics and macroevolution

A one to two-year NSF-funded post-doctoral position is available starting as early as August 2009 in the lab of Scott Stepan at Florida State University on the molecular phylogenetics of cardiid and pitarine bivalves. The position is part of a larger project (Bivalves in Time and Space) developing bivalves as a model clade for macroevolutionary studies, taking advantage of their excellent fossil record to test methods of molecular clock dating, ancestral state reconstruction, historical biogeography, and detecting spatial and temporal trends in evolution. The specific responsibilities will involve sequencing 200 species for multiple nuclear genes and conducting phylogenetic analyses. The successful applicant will also participate in semiannual meetings and possible collaborations with other members of the research team who are working on the morphological, paleontological, and computational components.

The Ecology and Evolution program is a highly interactive and supportive environment that works closely with the Computational Evolutionary Biology group in the Dept. of Scientific Computing.

Applicants should have a Ph.D. in evolution, systematics, or related field and be proficient in PCR, DNA sequencing, and phylogenetic analysis. Experience with mollusks preferable. Salary will start at \$38,500 and start date is negotiable. Review of applications will begin June 15. Additional information on the Stepan Lab and more details about the project are available from <http://bio.fsu.edu/~stepan/>, and on the Ecology and Evolution group at <http://www.bio.fsu.edu/-ee/index.html>. Applicants should submit a cover letter,

CV, statement of research interests, and request three letters of recommendation (please include the names and contact information for the three references in the cover letter or CV).

For more information, contact Scott Stepan at: Department of Biological Science Florida State University Tallahassee, FL 32306-4295

e-mail: stepan@bio.fsu.edu phone: (850) 644-6536 fax: (850) 644-9829

I will be happy to discuss the position in person should you be attending the Evolution meetings in Moscow, Idaho June 12-16.

—

Scott Stepan Department of Biological Science Florida State University Tallahassee, FL 32306-4295

stepan@bio.fsu.edu phone: 850.644.6536 fax: 850.644.9829

<http://bio.fsu.edu/~stepan> <http://www.bio.fsu.edu/~faculty-stepan.php> Ecology and Evolution Group at FSU: <http://www.bio.fsu.edu/ee/index.html> Scott Stepan <stepan@bio.fsu.edu>

Graz Cichlid Quantitative Genetics

Research scientist position in Christian Sturmbauer's group in Graz

The Department of Zoology at the Karl-Franzens-University Graz offers the position of a

Post-doctoral scientist (40 hours per week; for an employment of 2 years, starting at 1st July 2009)

Tasks: To join the research group of Christian Sturmbauer for research work on African cichlid fish populations, financed by research grant No. P20994-B03 of the Austrian Science Fund "Natural selection - driving force of adaptive radiation", to carry out quantitative genetic analyses on African cichlid fish populations, and pond-bred offspring. See also <http://www.kfunigraz.ac.at/~zoowww/> Qualification: Ph.D. in Zoology, Genetics or Evolutionary Biology. Experience in quantitative genetics targeting natural populations and breeding experiments, use of ASReml and similar tools, adequate number of scientific publications and conference contributions corresponding to the applicants' experience, team spirit and interest to work in Africa.

Job application: Please apply per e-mail to Prof. Chris-

tian Sturmbauer, christian.sturmbauer@uni-graz.at <<mailto:christian.sturmbauer@uni-graz.at>> with the following documents: CV, letter of research interests, list of publications, contact coordinates of two persons for reference.

Univ. Prof. Dr. Christian Sturmbauer

Department of Zoology University of Graz Universitaet-splatz 2 A-8010 Graz Austria

christian.sturmbauer@uni-graz.at

christian.sturmbauer@uni-graz.at

Harvard Med School Evolutionary Genomics

A postdoctoral position is available at Harvard Medical School and Brigham and Women's Hospital, Boston for Evolutionary Genomic studies in the laboratory of Dr. Charles Lee. Our lab focuses on understanding genomic structural variation particularly pertaining to evolution, population genetics of structural variation and disease associations (<http://www.chromosome.bwh.harvard.edu>). Ongoing research projects utilize array comparative genomic hybridization, DNA sequencing, RT-PCR and fluorescent in situ hybridization techniques, among others, to analyze structural genomic variation (Nature 444:444, 2006; Am J Hum Genet 82:685-695, 2008; Genome Res 18:1698, 2008). We are currently expanding a growing evolutionary group to complement ongoing projects in house and develop novel approaches for data analysis and production. Interested individuals must have or be close to obtaining a Ph.D. degree. In addition, applicants must demonstrate a high level of research productivity and writing proficiency through international, peer-reviewed publications.

The candidate should have a strong background in evolutionary biology and/or population genetics. Bioinformatic approaches relating to molecular biology and/or genetics as well as experience analyzing next generation sequencing or array-CGH data would be desirable. A background in computational and/or statistical methodologies as well as experience in statistical and/or programming languages (PERL, Python) would also be desirable.

Interested applicants should submit current curriculum vitae, statement of research experience and names of three individuals who can provide letters of refer-

ence electronically to: Dr. Omer Gokcumen (ogokcumen@partners.org)

Omer Gokcumen, Ph.D. Postdoctoral Fellow Brigham and Women's Hospital Harvard Medical School 221 Longwood Avenue, EBRC-404 Boston, MA 02115 T: 617-278-0064 | F: 617.264.5176 www.gokcumen.wordpress.com gokcumen@gmail.com

Ipswich MA ComparativeGenomics

Postdoc:

Postdoctoral Research Associate (Job Code: OGL-LC, posted 06/15/09) The Ocean Genome Legacy Laboratory for Marine Genomic Research (www.oglf.org) seeks a postdoctoral research associate to investigate lignocellulose degradation by wood boring marine bivalves of the family Teredinidae (shipworms) and their bacterial endosymbionts. The successful candidate will be knowledgeable and experienced in genomics, proteomics, and bioinformatics and must have excellent laboratory skills in molecular biology and microbiology. Knowledge of microscopy and enzymology of lignocellulose degradation is also desirable. OGL seeks an employee with excellent organizational, communication and laboratory skills, who pays strong attention to detail and has the desire and ability to work well in a collaborative group setting. The position is available immediately and offers exciting opportunities for broad research training, publication, competitive salary and benefits, and the potential for advancement within a new academically oriented non-profit research institution. Applicants should submit a cover letter, resume, list of publications, and contact information for at least three references by email to careers@oglf.org (referencing job code OGL-LC in the subject line) or by regular mail to the address below.

Ocean Genome Legacy, Inc. is a publicly supported non-profit research organization dedicated to exploration, description, documentation, and preservation of the genomic diversity of the oceans. Located on the campus of New England Biolabs in Ipswich, MA, OGL is an equal opportunity employer that receives support from the National Science Foundation, the Department of Energy, and the National Institutes of Health.

Please direct all inquiries to: Daniel L. Distel, Ph.D. Executive Director, Ocean Genome Legacy 240 County Rd., Ipswich, MA 01938 careers@oglf.org

<http://www.oglf.org/> —

Job:

Research Assistants - Full and Part Time (Job Codes: OGL-FTRA09 and OGL-PTRA09, posted 06/23/09) The Ocean Genome Legacy Laboratory for Marine Genomic Research (www.oglf.org) seeks research assistants to aid with all aspects of operation of the Ocean Genome Resource DNA repository and its associated research projects. The successful candidates will have experience and general knowledge of collection management, basic techniques of molecular biology and microbiology (e.g., DNA extraction and handling, gel electrophoresis, PCR amplification, cloning, sterile technique, bacterial cultivation techniques, etc.), and excellent computer and data management skills. Experience and knowledge of protein biochemistry is also desirable. Full- and part-time positions are available immediately.

Applicants should submit a cover letter, resume, list of publications, and contact information for at least three references by email to careers@oglf.org (referencing job code OGL-FTRA09 for full-time or OGL-PTRA09 for part-time in the subject line) or by regular mail to the address below.

Ocean Genome Legacy, Inc. is a publicly supported non-profit research organization dedicated to exploration, description, documentation, and preservation of the genomic diversity of the oceans. Located on the campus of New England Biolabs in Ipswich, MA, OGL is an equal opportunity employer that receives support from the National Science Foundation, the Department of Energy, and the National Institutes of Health.

Please direct all inquiries to: Daniel L. Distel, Ph.D. Executive Director, Ocean Genome Legacy 240 County Rd., Ipswich, MA 01938 careers@oglf.org

<http://www.oglf.org/> —

Job:

Administrative Assistant - Part Time (Job Code: OGL-AA, posted 06/24/09) The Ocean Genome Legacy Laboratory for Marine Genomic Research (www.oglf.org) seeks a part-time administrative assistant to aid in general operations, including editing and formatting an online quarterly newsletter using web forms, summarizing and distributing monthly and quarterly financial reports using QuickBooks and Excel, processing incoming donations and sending out acknowledgements, coordinating shipment and receipt of genomic sample deposits, and assisting with various administrative functions, such as maintaining meeting schedules, entering data, electronic and paper filing, copying, and ordering supplies. The successful candidate will be detail-

oriented, accurate, and efficient with a working knowledge of web forms and the ability to navigate the Web, proficiency in MS Office and QuickBooks, a basic understanding of accounting principles, and 1-2 years administrative experience. This position will start at 5-10 hours a week and is available immediately. Applicants should submit a cover

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Italy Modelling

Title: Post-doc in data analysis and modelling of interaction between ecological, environmental and genetic variables (037_AMB.PDEEGV)

Research Centre: The research carried out at the Environment Department of Edmund Mach Foundation encompasses both ecological and molecular studies. It focuses on the functional integrity and biodiversity of aquatic (mainly plankton, diatoms and salmonid fishes) and land taxa (mainly vertebrate fauna and their parasites, higher plants including annual species and forest trees) that are subject to anthropic pressure and global climate changes. The ACE-SAP (Alpine Ecosystems in a Changing Environment: Biodiversity Sensitivity and Adaptive Potential) Major Proposal is a collaborative project funded by the Autonomous Province of Trento involving three regional institutions (Edmund Mach Foundation, Natural History Museum of Trento, Civic Museum of Rovereto) and one external partner (University of Davis, California).

Description: We are seeking a highly motivated and independent individual to carry out a research project on the Spatial and genetic data management and analysis; application of GIS based statistical methods for identification and estimation of correlations between ecological, environmental and genetic variables at a local scale; use of advance GIS and statistical software packages and development of specific procedure in compatible programming languages; model building, analysis and interpretation, parameter estimation, simulations of different global change scenarios; drafting scientific papers and reports; attending national and international conferences and workshops.

IT knowledge: GIS software (e.g., GRASS GIS, Map-Info, ESRI), Statistical packages (e.g. R, S-Plus); Programming languages (e.g. C, Python); experience in creation of (SQL) databases.

More information and application: http://www.fondazioneedmundmach.it/sperimentazione_context2.jsp?ID_LINK=3418&area=6
Deadline for application: 14th June 2009

Daniele Barbacovi Fondazione Edmund Mach Research Centre - Human Resources Office Via Mach 1, 38010 S. Michele all'Adige (TN) - Italy Phone +39 0461 615542 - Fax + 39 0461 650956 Skype daniele.barbacovi_crfem <http://www.fondazioneedmundmach.eu>
daniele.barbacovi@iasma.it daniele.barbacovi@iasma.it

LSU AvianSpeciationBiogeography

POSTDOCTORAL POSITION IN NEOTROPICAL BIRD SPECIATION

COMPARATIVE PHYLOGEOGRAPHY OF NEOTROPICAL BIRDS WITH CROSS-ANDES DISTRIBUTIONS

A 3-year post-doctoral position is available in the lab of Dr. Robb Brumfield at Louisiana State University. The NSF-funded research project involves a large-scale (in terms of taxa), multi-locus, comparative study of diversification in lowland bird species that occur on both sides of the Andes. The ideal candidate would have expertise in molecular systematics, population genetics, genomics, and GIS. I am particularly interested in the application of next-generation sequencing technologies to this project. The project involves collaborative work with Dr. Alex Aleixo (Emilio Goeldi Museum, Brazil), Dr. Daniel Cadena (University of the Andes, Colombia), and Dr. Jorge Pérez-Emán (Central University of Venezuela). The position could start as early as summer 2009, but the start-date is flexible. Renewal for the second and third years will be contingent on progress and productivity.

Applicants must have a Ph.D. in biology or a related field. Please send a pdf of your CV, a brief statement of research interests, and the names, phone numbers, and email addresses of three references to: Robb T. Brumfield, brumfld@lsu.edu. Review of applications will continue until the position is filled. For additional information about our lab go to <http://www.museum.lsu.edu/>

brumfield.html I will be at the Evolution meetings this month, and would be happy to meet with prospective candidates in person.

Robb Brumfield, PhD Museum of Natural Science & Department of Biological Sciences 119 Foster Hall Louisiana State University Baton Rouge, LA 70803

brumfld@lsu.edu brumfld@lsu.edu

Morocco Reproductive Senescence

*Postdoc position :** Reproductive senescence in the houbara bustard*

* *

A postdoc position is available at the Emirates Center for Wildlife Propagation (Morocco) from September 1st 2009. Although under the supervision of the ECWP, the postdoc will be based in France at the Université de Bourgogne (Biogéosciences, CNRS, Dijon). She/he will work on a collaborative project involving the ECWP (Yves Hingrat), the CNRS/Université de Bourgogne (Gabriele Sorci) and the Museum National d'Histoire Naturelle (Michel Saint Jalme).

The task of the postdoc will be to explore how age shapes the reproductive performance of male and female houbara bustards. The ECWP has started 14 years ago a captive breeding program with the aim to reinforce natural populations of the endangered houbara bustard. They have collected extensive data on the breeding performance of thousands of captive birds, 1 to 22 year old, for many generations. The measured variables involve male secondary sexual traits, characteristics of the ejaculate, clutch size, hatching success, etc.

Applicants for this position are required to have a PhD on ecology/evolutionary biology, a good expertise of the evolutionary theories of senescence and a very good skill for statistical analyses of large database. They should master the use of mixed models.

The position is available for one year, although a renewal for another year can be negotiated. The salary is competitive.**

* *

For further information please contact one of the following persons:

* *

Yves Hingrat, yhingrat@yahoo.com
<mailto:yhingrat@yahoo.com>

Gabriele Sorci, Gabriele.sorci@u-bourgogne.fr
<mailto:Gabriele.sorci@u-bourgogne.fr>

Michel Saint Jalme, mstjalme@mnhn.fr
<mailto:mstjalme@mnhn.fr>**

* *

Applicants should send a full CV and the names of the potential referees to Yves Hingrat and Gabriele Sorci.

* *

Closing date: June 30th 2009.

* *

Stéphane Garnier

Equipe Ecologie Evolutive UMR CNRS 5561
Biogéosciences Université de Bourgogne 6 Bd Gabriel
21000 Dijon - France

stephane.garnier@u-bourgogne.fr

<mailto:stephane.garnier@u-bourgogne.fr>

Tel:

+33 (0) 3 80 39 90 58 Fax: +33 (0) 3 80 39 62 31

stephane.garnier@u-bourgogne.fr

North Carolina State U Evolution Plant Defense

Post-Doctoral Researcher

PROJECT: Plant Sex and the Evolution of Plant Defenses Against Parasites

LOCATION: Department of Plant Biology, North Carolina State University, Raleigh NC, USA

DESCRIPTION: The Johnson Lab (www.evoeco.org) in the Department of Plant Biology at North Carolina State University seeks a Post-Doctoral researcher to work on an NSF funded project examining how a loss of sexual reproduction in plants influences phenotypic and molecular evolution of defenses against plant parasites (insect herbivores and fungal pathogens). This work focuses on the evening primrose genus *Oenothera* which has experienced over 20 independent transitions between sexual and functionally asexual reproduction. We have recently shown that these repeated losses of sex have led to the evolution of increased susceptibility to generalist herbivores and decreased susceptibility to specialist herbivores. We are now testing theoretic

cal predictions about how a loss of sex influences the molecular evolution of plant defense genes as well as the expression of resistance traits functionally related to these genes.

Consistent with the strengths and interests of the successful applicant, there will be the opportunity to contribute to multiple aspects of the project. These include the cloning, sequencing and expression analysis of plant defense genes; field work in North and South America; phytochemical analysis by HPLC-MS, and the use of comparative phylogenetic and population genetic tools for the analysis of various types of molecular and phenotypic data. Consideration will be given to all candidates with expertise in ecology and/or evolution and applicants with experience conducting both molecular and field work are particularly encouraged to apply.

START DATE: September 1st, 2009, but this is negotiable. The position is for 24 months, with a possible extension contingent on funding. Starting salary will be commensurate with experience; the position includes medical insurance and benefits.

APPLICATION: Applicants should send a covering letter, curriculum vitae and contact details for three or more references to Dr. Marc Johnson (marc_johnson@ncsu.edu) in the Department of Plant Biology at North Carolina State University.

North Carolina State University is located in Raleigh, North Carolina's state capital. The university is conveniently located 30 minutes or less from UNC Chapel Hill, Duke University, the National Evolutionary Synthesis Center (NESCent), and the Research Triangle Park. Raleigh is a culturally diverse city with excellent restaurants, parks, museums and theaters. The city is conveniently located 2 hours from both the ocean and the mountains.

Marc Johnson, Ph.D.

Assistant Professor Department of Plant Biology
North Carolina State University Box 7612, Raleigh
NC 27695 U.S.A. Phone: 919-515-0478, Fax:
515-3436 www.evoeco.org marc_johnson@ncsu.edu
marc_johnson@ncsu.edu

OregonStateU Plant Ontology

The Plant Ontology Consortium
(www.plantontology.org) is seeking applicants for

a full-time position of scientific curator who will coordinate the Consortium's efforts. The Plant Ontology Consortium is a collaboration among researchers at Oregon State University, Cornell University and New York Botanical Garden. The project is funded by the National Science Foundation. The Consortium also collaborates with the curators of many model organism databases including rice, Arabidopsis, maize, grasses, legumes, Solanaceae, Bryophytes and plant phylogenomics. The project aims to develop shared vocabularies on plant anatomy and growth and developmental stages, to describe patterns of phenotype(s) and gene expression.

Position Title: Research Associate (Senior Postdoc) / Research Associate (Postdoc)

Working Title: Plant Ontology Project Coordinator

How to Apply:

To review the position description and apply, go to posting #0004322 at <http://oregonstate.edu/jobs>. When applying, you will be required to electronically submit your application, a cover letter citing your interest in the position and your experience, and a CV/resume including 3 references. Closing date 7/15/09.

Duties / Responsibilities:

Develop and refine the ontologies with the PO curators in participating databases and core labs, annotate gene products and stocks with the vocabularies in the ontologies, participate in the development and application of methods to streamline and enhance the quality of annotations, manage website content, set project milestones, organize and moderate project meetings, and work with the project members to deliver the database releases and project reports on strict timelines.

Required qualifications:

Ph.D. in an aspect of plant biology (e.g. Development, Physiology, Biochemistry, Genetics, Plant Pathology, Systematics) and/or genomics, Phylogenomics, Systematics, Plant Biology and Plant Anatomy. Available immediately to start working on the project. Demonstrated ability for independent, critical thinking and excellent communication, networking and teamwork skills. Previous work in any one or more areas of Plant Development, Plant Physiology, Plant Biochemistry, Plant Genetics and/or genomics, Plant Pathology, Museum specimen curation, Phylogenomics, Systematics, Plant Biology and Plant Anatomy. Excellent communication skills in English is a must. Experience in teaching and outreach. Familiarity with Plant Development and Anatomy. Able to travel and attend 3-4

meetings/year of the PO consortium.

In order to be considered for the Research Associate (senior Postdoc) position, the candidate must have 3 or more years of postdoctoral/scientist research experience and supporting publications in peer reviewed international journals. The selection committee will judge the candidate based on the qualifications below; in addition, to showing the ability to lead on a scientific project as an independent researcher.

Preferred qualifications:

Past experience in project coordination, large scale gene expression and phenotype evaluation, familiarity with basic UNIX commands, spreadsheets, and commonly used biological research tools such as BLAST and Literature Database search is desired. A working knowledge of PERL and/or SQL will be considered an asset but not required.

listona@science.oregonstate.edu

lis-

tona@science.oregonstate.edu

PennState FireAntGenomics

Post-doctoral opportunity: Genomic analysis of communication systems in social insects

A post-doctoral position in the Department of Entomology and Center for Chemical Ecology at Pennsylvania State University is available to study the molecular basis of pheromone-mediated behavior in the red imported fire ant (*Solenopsis invicta*). The researcher will interact closely with a dynamic group of colleagues with expertise in behavioral ecology, functional genomics, and bioinformatics, and with collaborators at the USDA-ARS (Gainesville, Florida) and University of Lausanne (Switzerland) to develop genomic tools and resources for this species. The primary focus will be to use microarray analysis to characterize the genes and gene pathways regulated by queen pheromone, and to understand the molecular basis for modulation of behavioral responses to pheromonal cues among individual ants of different castes, genotypes, or social states. A comparative genomics approach will be used to identify conserved socially responsive pathways across multiple social insects, including honey bees, bumble bees and paper wasps. The post-doctoral researcher will be further supported in the development of his/her independent research program. Applicants should have a strong background in behavioral ecology and exper-

tise in molecular techniques. This position is initially funded by a USDA-NRI genomics grant for 2 years and additional support is possible. Salary is \$38,000-\$43,000/year, commensurate with experience. Benefits are included. Start-date is negotiable, but January 2010 is preferred.

Please send your CV, including relevant publications, and contact information for three references by August 1, 2009 to:

Christina M. Grozinger Associate Professor Department of Entomology Center for Chemical Ecology Huck Institutes of the Life Sciences Pennsylvania State University Chemical Ecology Lab 4A University Park, PA 16802 Phone: 814-865-2214 Email: cmgrozinger@psu.edu Webpage: <http://ento.psu.edu/directory/cm25> Christina Grozinger <cmgrozinger@psu.edu>

PrincetonU MolPopulationGenetics

Postdoctoral Position Available

A Postdoctoral position is available in the area of empirical/ functional molecular population genetics in the lab of Peter Andolfatto at Princeton University. This is part of a five-year NIH- funded project to look at the relationship between adaptive evolution of non-coding sequences and gene expression divergence. The project will combine population genetics analyses with genome resequencing, gene expression analyses, and transgenic tools in *Drosophila*. Applicants should have a PhD and experience with standard molecular biology techniques (cloning, expression, etc) and experience with *Drosophila* is an asset (but not required).

The position is available immediately with the expectation of trying to secure a Postdoctoral Fellowship. Applicants should submit a statement of personal research interests, curriculum vitae, publication PDFs, and addresses for references to

pandolfa@princeton.edu

or by mail to Peter Andolfatto, Dept. of Ecology and Evolutionary Biology, 106A Guyot Hall, Princeton University, Princeton, NJ 08544

Peter Andolfatto Assistant Professor Ecology & Evolutionary Biology & the Lewis-Sigler Institute of Integrative Genomics Princeton University pandolfa@princeton.edu

Peter Andolfatto <pandolfa@Princeton.EDU>

TrentU Evolutionary Genetics

Ontario Post-Doctoral Fellowship Trent University

We are seeking a post-doctoral fellow with research interests in the areas of landscape genetics, evolutionary and population ecology, and habitat modeling, to undertake an analysis of broad-scale genetic structuring and evolutionary relationships among lynx in North America. The project will involve an assessment of biological, environmental and/or landscape variables that promote or inhibit effective colonization and dispersal of lynx, especially in the context of source-sink dynamics of boreal vs. southern lynx populations or connectivity between eastern and western populations. Evidence of local adaptation pursuant to the relationship between lynx and their primary prey will be sought.

The focus of the work will be to develop lynx genetic structuring and habitat models using 3000+ fur samples collected from animals harvested in North America. The opportunity to develop an independent research program within the framework of existing funding will be provided.

The successful candidate will work as a member of the Ontario Lynx Research Team (OLRT) at Trent University; the OLRT is a network of university, government, and non-government researchers seeking to understand factors limiting the distribution and abundance of lynx in North America. The successful applicant will have received their PhD in the last 2 years.

Application Procedures

Applicants should hold a PhD in Landscape/Population Ecology, Genetics, or a related area. Priority will be given to candidates with demonstrated expertise in population genetics, landscape ecology, population ecology and spatial modeling. All candidates should submit a letter of application, curriculum vita, and names and contact information for three referees to Dr. Dennis Murray and Dr. Paul Wilson, Department of Biology, Trent University, 1600 West Bank Drive, Peterborough, ON Canada K9J 7B8 (email: dennismurray@trentu.ca, web page: <http://www.people.trentu.ca/dennismurray>; pawilson@trentu.ca, web page: <http://forensics.nrdpfc.ca/-staff/paul-wilson.html>). The position will close on July 30 or as soon as a suitable candidate is found before

that date. The two-year term may start immediately, but no later than December 31, 2009.

The Ontario Post-Doctoral Fellowship Program was developed to recruit and retain outstanding young scientists to spend two years as post-doctoral fellows in an Ontario research institution. The successful Fellow will receive \$50,000 annually.

Dennis L. Murray Associate Professor, Canada Research Chair in Terrestrial Ecology Department of Biology Trent University Peterborough, ON K9J 7B8 tel (w):705-748-1011 x 7078 fax: 705-748-1003 <http://people.trentu.ca/dennismurray> Dennis Murray <dennismurray@trentu.ca>

UCaliforniaBerkeley 2 Population Genetics

Two NIH funded postdoctoral positions will be available in September, 2009, in the laboratory of Montgomery Slatkin at the University of California, Berkeley.

One position is in the area of human evolutionary genetics, with particular emphasis on geographic variation in humans and on the relationship between humans and Neanderthals. Candidates should have training and research experience in theoretical population genetics, statistics and bioinformatics.

The second position is in the area of the population genetics of complex inherited diseases and resistance to infectious diseases. Candidates should have training in human genetics, epidemiology, and statistics and should have some computer programming skills.

Both positions are for 2 years with the possibility of renewal for 2 additional years. The salary for the first 2 years will be \$40,000 per year plus benefits. Applicants should send a letter, cv and names and email addresses of 3 references to Montgomery Slatkin <slatkin@berkeley.edu>. Review of applications will begin June 29, 2009. Information about the evolutionary genomics group in Berkeley is available at <http://fisher.berkeley.edu/cteg/> slatkin@berkeley.edu

UCaliforniaBerkeley
EvolutionInsectBehaviour

Our primary interests are finding someone to study the evolution of and mechanisms underlying insect behavior.

Thanks!

Best,

Neil

Neil D. Tsutsui, Ph. D. Assistant Professor Department of Environmental Science, Policy & Management University of California, Berkeley Berkeley, CA 94720-3114

Mail:137 Mulford Hall, #3114 Office: 326 Hilgard Hall Lab: 3 & 245 Hilgard Hall Email: ntsutsui@nature.berkeley.edu Phone: 510-642-9012 Fax: 510-643-5438

POSTDOCTORAL SCHOLAR

Behavioral Ecology of Social Insects

The UC Berkeley Natural History Museums and Department of Environmental Science, Policy and Management at UC-Berkeley are currently seeking one Postdoctoral Scholar in the laboratory of Dr. Neil Tsutsui.

We are seeking a Postdoctoral Scholar to study the behavioral ecology of social insects. Previous work has focused on the genetics, behavior, and chemical ecology of the invasive, Argentine ant (*Linepithema humile*). In this species, genetic changes during introduction have altered individual behavior and, in turn, the social organization of introduced populations. These changes have contributed to the Argentine ant's invasive success by promoting the formation of massive "supercolonies" in the introduced range. Publications from previous research can be downloaded from: <http://nature.berkeley.edu/tsutsuilab>. Current research topics include the chemical basis of conymate recognition, population genetics of native and introduced populations, and the development of genomic tools for studies of behavior, learning and memory in Argentine ants and other social insects.

The central focus of the Postdoctoral Scholars research will be the structure and function of conymate recognition systems in the Argentine ant. The Scholar will perform manipulative laboratory experiments to ex-

plore the role that social environment and individual experience play in the development of colony identity. The Postdoctoral Scholar will also have opportunities to contribute to ongoing research by using functional genetic, genomic or neurophysiological approaches.

Applicants should have a strong background in one or more of the following areas: behavioral ecology, chemical ecology, population genetics, genomics and gene expression, and genetics of behavior, learning and memory. Previous experience in insect biology is desirable, but not required. The salary range is between \$35,508 - \$41,496 or commensurate with experience; generous benefits are included. A start date during early Fall 2009 is preferable. Applicants must have less than five years of post-doctoral service.

Applicants should submit, by July 15, 2009, a CV, a brief statement of research interests, copies of relevant publications and/or manuscripts, and contact information for two references. Application materials may be submitted by email or postal mail.

Dr. Neil D. Tsutsui Department of Environmental Science, Policy and Management 137 Mulford Hall, #3114 University of California, Berkeley Berkeley, CA 94720-3114 ntsutsui@nature.berkeley.edu

The University of California, Berkeley is an equal opportunity employer committed to excellence through diversity. Applicants should ask referees to review the UC Berkeley Statement of Confidentiality found at: <http://apo.chance.berkeley.edu/evalltr.html>

Neil Tsutsui <ntsutsui@nature.berkeley.edu>

UCaliforniaDavis
PhylogeneticMethods

UC Davis

Postdoctoral Opportunity blending phylogenetic methods with ecological field experiments with Sharon Strauss at UC Davis

The goal of the study is to use experiments to identify the adaptive nature of a number of traits in a suite of related species, and then to examine the sequence of trait evolution and possible trade-offs in the context of the phylogenetic tree. The traits explored are those associated with edaphic (soil) specialization, plant competitive ability and plant resistance to enemies in the clade **Streptanthus** (Brassicaceae). This clade has

about 45 taxa, and about one third are serpentine specialists. There are three taxa that grow both on and off serpentine outcrops, thus allowing both within- and across-species comparisons.

Some expertise in molecular methods and tree building very desirable. Field work in beautiful places in northern California. Must be able to travel out of town for several sequential days at a time.

Other position perks: Great intellectual atmosphere and colleagues at UC Davis Department of Evolution and Ecology and the Center for Population Biology

Start date flexible.

To apply: Please send the following materials to systrauss@ucdavis.edu with the subject "postdoc". (1) a brief cover letter explaining your background, interests, (2) CV (including publications), (3) names and contact information for three references.

Also note the time you'd like to begin working. Thanks.
systrauss@gmail.com

UCaliforniaSanDiego EvolutionModels

Postdoctoral position

STATISTICAL MODELS OF SEQUENCE EVOLUTION

School of Medicine University of California San Diego

DESCRIPTION: An NSF funded postdoctoral position (<http://nsf.gov/awardsearch/showAward.do?AwardNumber=0714991>) is available immediately to work on statistical modeling of sequence evolution. The primary goal of the project is to apply a variety of statistical and computational approaches, such as genetic algorithms, support vector machines, graphical Bayesian models, to describing complex evolutionary processes, inferring their parameters from sequence data and informing hypothesis generation for translational research. Two good examples of such studies can be found in <http://mbe.oxfordjournals.org/cgi/content/full/23/10/1891> and <http://dx.plos.org/10.1371/journal.pcbi.0030231>

The methods will be applied to large collections of viral alignments, including all available HIV-1, Hepatitis C and Influenza A virus sequences, and also deep sequencing data sets of HIV-1 patients. Depending

on the background of the applicant, there are also great opportunities to develop software modules implementing the methodology, as a component of a popular software package HyPhy or its accompanying web server Datamonkey.org.

The position will be for one year, with the possibility of extension for another year, dependent on progress and funding. Salary will be according to recommended pay scales (<http://som.ucsd.edu/articles/downloads/178>), and commensurate with experience

RESEARCH GROUP: The position is based in the UCSD viral evolution group, under the supervision of Dr Sergei Kosakovsky Pond (www.hyphy.org/sergei). The viral evolution group maintains close ties and collaborations with the UCSD Center for AIDS Research (<http://cfar.ucsd.edu>) and the UCSD bioinformatics program (<http://bioinformatics.ucsd.edu/>) There is a potential to develop and co-supervise undergraduate and graduate research projects.

LOCATION: School of Medicine, University of California, San Diego. The position is based at the Antiviral Research Center (<http://www.avrctrials.org>), situated in the Hillcrest area (<http://www.hillquest.com>) near downtown San Diego.

REQUIREMENTS: Applicants must:

- hold a Ph.D. in one of the following disciplines: evolutionary, mathematical or computational biology, statistics, population genetics computer science, bioinformatics (candidates with doctorates in related fields are encouraged to apply as well);
- be knowledgeable about statistical phylogenetics and probabilistic models of sequence evolution
- have programming experience in a high-level programming language (C/C++ preferred) and scripting language such as Python.

A successful applicant should:

- display evidence of research productivity as indicated by peer-reviewed publications and conference presentations;
- have a strong interest in and understanding of molecular evolution;
- have strong communication and teamwork skills.

APPLICATION: Please send letter of interest, C.V., and the names and contact details of three referees to: Postdoctoral Position in Evolutionary Modeling of Sequence Data, Dr Sergei Kosakovsky Pond, UCSD Antiviral Research Center, 150 W. Washington St., San Diego CA 92103, USA. Electronic application materials (PDF, Word) are preferred - please email to spond@ucsd.edu. You can also direct information requests to this e-mail address. Review of applications will begin immediately, and continue until the position

is filled.

spond@ucsd.edu spond@ucsd.edu

UChicago EvolutionPlantEnemyInteractions

POSTDOCTORAL FELLOWSHIP ECOLOGY AND EVOLUTION OF PLANT-ENEMY INTERACTIONS

A two-year V. DROPKIN POSTDOCTORAL FELLOWSHIP is available in the Department of Ecology & Evolution at THE UNIVERSITY OF CHICAGO. One fellow will be selected based on their potential to perform innovative research pertinent to plant pathology and/or sustainable agriculture. The postdoctoral fellow will join a highly interactive group working on the microbial pathogens of *Arabidopsis thaliana* although s/he will have substantial opportunities for independent research. It is hoped that the selected fellow can commence studies no later than Winter 2010. Salaries are competitive; research funds and resources will be provided. Applicants should send a three-page research proposal, curriculum vitae, and have three letters of recommendation sent by 15 August 2009 to Dr. Joy Bergelson, Dept. of Ecol. & Evol, Univ. of Chicago, 1101 East 57th Street, Chicago, IL 60637. The University of Chicago is an Equal Opportunity Employer.

Dan DiLuciano <ddiluciano@uchicago.edu>

UChicago MarineBivalves

POSTDOC IN EVOLUTION/BIOGEOGRAPHY

Seeking a Postdoctoral Scholar to participate in an ongoing collaborative research project (D. Jablonski-K. Roy-J. W. Valentine) on the evolutionary history and future of modern spatial patterns of diversity, particularly the latitudinal gradient. Marine bivalves will be used as a model system due to their excellent fossil record, ecological diversity and highly resolved taxonomy. Research involves quantifying present-day biogeographic patterns, analyzing the Cenozoic spatial and evolutionary dynamics underlying them, and relating these patterns to environmental change. Postdoc will assist in analyses and modeling of diversity dynam-

ics, and take the lead on some new research projects. Experience in modeling, statistical, and/or phylogenetic analyses (and with databases) required. Familiarity with paleontological and/or biogeographic data is preferable. One-year appointment potentially renewable for one or more additional years. Starting date negotiable but prefer September-October 2009. Requires either PhD in hand or dissertation submitted and approved for degree. Please email a letter outlining research interests and experience, a CV, and the email addresses of two references to Dr. Andrew Z. Krug (akrug@uchicago.edu) at the University of Chicago. The University of Chicago is an Affirmative Action/Equal Opportunity Employer.

Andrew Z. Krug University of Chicago Department of Geophysical Sciences 5734 S. Ellis Avenue HGS 285 Chicago, IL 60637 akrug@uchicago.edu

zackumpusu@gmail.com

UColorado ProteinCoevolution

Subject: Molecular Evolution Postdocs in Denver Category: Jobs, Postdocs

Postdoctoral fellowships are available at the University of Colorado School of Medicine to work on evolution and coevolution of protein sequence, structure, and function (with Dr. Pollock), or on evolution of transcription factor binding sites (Drs. Pollock and Kechris). Both of these projects will require considerable strength in computational analysis, and experience with Bayesian phylogenetic techniques and/or mixture models would be a plus. To be eligible for three training grant fellowships

[Www.compbio.uchsc.edu/pages/postdocfellowships.html](http://www.compbio.uchsc.edu/pages/postdocfellowships.html)

applications should be received immediately (by June 15). Other postdoctoral funding sources for these projects (with less immediate deadlines) are available through the NIH and possibly the NSF. Please contact David Pollock (David.Pollock@ucdenver.edu or find him at the Evolution meeting).

“Castoe, Todd” <Todd.Castoe@ucdenver.edu>

gsinger@uoguelph.ca

Greg Singer <gsinger@uoguelph.ca>

UGuelph BarcodeOfLifeProject

Postdoctoral Position at Biodiversity Institute of Ontario

Location: Biodiversity Institute of Ontario, University of Guelph, Guelph, Ontario, Canada.

The Biodiversity Institute of Ontario (BIO) at the University of Guelph in Guelph, Ontario, Canada invites applications for a postdoctoral position to join the International Barcode of Life Project (www.dnabarcoding.org). This postdoc will focus on advancing the global DNA barcoding campaign for pollinators (e.g., bees). The applicant should be a well-rounded individual with a strong molecular evolution and genetics background, and should possess the management and organizational skills necessary for advancing high-throughput protocols and managing the large amount of DNA sequence and taxonomic information required for this campaign. BIO is equipped with state of the art molecular and computational infrastructure and has a dedicated core facility for high-volume production of DNA barcode sequences. The following skills are necessary to carry out the tasks in this project:

- Molecular biology: Well-developed understanding and hands-on experience in basic molecular techniques such as DNA extraction, PCR, QPCR, and DNA sequencing. Occasional use of robotics may be required, but training can be provided. Familiarity with laboratory QA/QC procedures and troubleshooting problems. - Computer work: Hands-on experience with sequence editing and assembly programs (e.g., Sequencher), sequence analysis software (e.g., MEGA, PAUP, or BIOEDIT), and molecular biology software (e.g., primer design, sequence alignment, database searches, etc.).

Qualifications: PhD in the biological sciences, preferably with focus on molecular evolution, molecular ecology, or related fields. Background in entomology (especially prior work on bees) is desired but not essential. The applicant must be eligible to work in Ontario, Canada.

Closing Date: Open until filled. Review of applications will begin on July 01, 2009. Preferred starting date is September 01, 2009.

Contact: e-mail a CV and a cover letter describing your research interests and experience to Dr. Greg Singer,

UGuelph Biodiversity

Postdoctoral Position at Biodiversity Institute of Ontario

Location: Biodiversity Institute of Ontario, University of Guelph, Guelph, Ontario, Canada.

The Biodiversity Institute of Ontario (BIO) at the University of Guelph in Guelph, Ontario, Canada invites applications for a postdoctoral position to join the International Barcode of Life Project (www.dnabarcoding.org). This postdoc will focus on advancing the global DNA barcoding campaign for fishes (FISH-BOL). The applicant should be a well-rounded individual with a strong molecular evolution and genetics background, and should possess the management and organizational skills necessary for advancing high-throughput protocols and managing the large amount of DNA sequence and taxonomic information required for this campaign. BIO is equipped with state of the art molecular and computational infrastructure and has a dedicated core facility for high-volume production of DNA barcode sequences. The following skills are necessary to carry out the tasks in this project:

- Molecular biology: Well-developed understanding and hands-on experience in basic molecular techniques such as DNA extraction, PCR, QPCR, and DNA sequencing. Occasional use of robotics may be required, but training can be provided. Familiarity with laboratory QA/QC procedures and troubleshooting problems. - Computer work: Hands-on experience with sequence editing and assembly programs (e.g., Sequencher), sequence analysis software (e.g., MEGA, PAUP, Mr Bayes), and molecular biology software (e.g., primer design, sequence alignment, database searches, etc.).

Qualifications: PhD in the biological sciences, preferably with focus on molecular systematics and/or molecular ecology, or related fields. Background in fish taxonomy is desired.

Closing Date: Open until filled. Review of applications will begin on July 01, 2009. Preferred starting date is September 01, 2009.

Contact: e-mail a CV and a cover letter describing your research interests and experience to Dr. Robert Han-

ner, rhanner@uoguelph.ca
rhanner@uoguelph.ca

UGuelph Parasite Vector DNABarcoding

A reminder that the application deadline is quickly approaching.

Postdoctoral position in molecular identification (“DNA barcoding”) of pathogens and disease vectors

Outstanding applicants are sought for a two-year post-doctoral position at the University of Guelph, focusing on the development of molecular identification methodology (“DNA barcoding”) for a wide range of pathogens, parasites, and disease vectors. This will include both original research and participation in the assembly and coordination of large-scale international collaborations.

Experience is required in PCR, DNA sequencing, and related analytical approaches, as well as expertise in one or more of protists, nematodes, flatworms, or insect vectors. In addition, applicants must possess excellent written and oral communication skills in English as well as strong leadership qualities.

Salary and benefits will total \$45,000 (CDN) per year, with a further \$5,000 per year in individual research support. The successful candidate will have access to a high-throughput biodiversity genomics facility under the co-supervision of Ryan Gregory (Department of Integrative Biology) and Paul Hebert (Biodiversity Institute of Ontario). The position will be co-funded by the Ministry of Research and Innovation through the Ontario Post-Doctoral Fellowship Program, Round 3.

Candidates must meet the following additional requirements:

- * Have completed their PhD no earlier than June 15, 2007.
- * Be available to begin work no later than Oct. 31, 2009.
- * Be eligible to work in Ontario, Canada.

Applicants should send a CV including a brief overview of experience and research interests to rgregory@uoguelph.ca

Review of applications will commence June 15, 2009.

For more information, visit:

* Canadian Centre for DNA Barcoding: <http://www.dnabarcoding.ca/> * International Barcode of Life (iBOL) project: <http://www.dnabarcoding.org/>
* University of Guelph: <http://www.uoguelph.ca/>
* Gregory Lab: <http://www.gregorylab.org/> Dr. T. Ryan Gregory Assistant Professor Department of Integrative Biology University of Guelph, Guelph, Ontario N1G 2W1 CANADA

<http://www.gregorylab.org/> <http://www.evolverzone.com/> “T. Ryan Gregory”
<rgregory@uoguelph.ca>

UHouston 2 Alignment MolEvol BioInfo

Two Postdoctoral Positions in Evolutionary Bioinformatics

Two NIH-funded postdoctoral position (each for 2 years) are available in Dan Graurs 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 evolutionary reconstructions. Independent research in any other branch of theoretical molecular evolution and bioinformatics is encouraged as well.

Qualifications: a PhD in Biology (or Genetics, Biochemistry, Computational Biology, Physics, Mathematics, or a related field), some 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 of two references. Applications and inquiries should be addressed to Dan Graur at dgraure@uh.edu.

– Giddy Landan, Ph.D. Research Assistant Professor Laboratory of Bioinformatics & Molecular Evolution Department of Biology & Biochemistry University of Houston

E-mail: giddy.landand@gmail.com – Time flies like an arrow. Fruit flies like a banana. - Groucho Marx

giddy.landan@gmail.com

UKansas QuantGenetics

Quantitative Genetics and Genomics in Drosophila

A Postdoctoral Scholar position is available in Stuart Macdonald's lab in the Department of Molecular Biosciences at the University of Kansas. We are interested in understanding the genetic basis of complex trait variation using *Drosophila* as a model system. Details of our research can be found at web.ku.edu/sjmac/. The position is funded as part of our NIH grant to create and test a unique framework for the genetic dissection of complex traits - see the grant abstract on CRISP (http://crisp.cit.nih.gov/crisp/crisp_query.generate_screen and type "Macdonald" and "Stuart" into the PI Name box and hit "Submit Query").

The position will provide an opportunity to develop an independent line of research on a range of problems in quantitative genetics. Potential projects include mapping QTL for drug and stress resistance and characterizing the loci underlying male genital variation. The Postdoctoral Scholar will be able to coordinate experimental work with technicians and undergraduate assistants.

This position requires a Ph.D in evolutionary biology, genetics, molecular biology, or a related field, and a record of published, peer-reviewed research in areas related to population or quantitative genetics. Preference will be given to those candidates with previous experience working with *Drosophila*. Since the projects will involve working with large numbers of fly stocks, and creating and managing large phenotype/genotype datasets, experience with large experimental projects and/or computational analysis (e.g. Unix, Perl, MySQL, R) would be advantageous.

The University of Kansas (www.ku.edu) has an active academic community in the life sciences. The Macdonald lab is affiliated with the Department of Molecular Biosciences (molecularbiosciences.ku.edu) and works closely with members of the Department of Ecology and Evolutionary Biology (www2.ku.edu/~eeb). The range and number of active research groups presents many opportunities for fostering academic and social interactions. The University of Kansas is in the city of Lawrence (www.visitlawrence.com, www.ci.lawrence.ks.us, www.lawrence.com ,

en.wikipedia.org/wiki/Lawrence,_Kansas) situated 45 minutes West of Kansas City.

Review of applications will begin Monday, July 13 and continue until the position is filled. Informal inquiries about the position are welcome and can be directed to Stuart Macdonald (sjmac@ku.edu). To apply, complete an online application at <https://jobs.ku.edu> (position number 00061389). Attach a cover letter (describing your interest in the position and any relevant experience), a full CV, and complete contact information for 3 referees. EO/AA Employer.

Dr. Stuart J. Macdonald Department of Molecular Biosciences 1030 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

tel: 785-864-5362 fax: 785-864-5321 email: sjmac@ku.edu web: <http://web.ku.edu/sjmac/> sjmac@ku.edu

UMichigan 2 Phylogenetics

Two postdoctoral positions in phylogenetics

PIs: Dr. L. Lacey Knowles, University of Michigan; Dr. Laura Kubatko, Ohio State University

Research Project:

Two postdoctoral positions are available to join an NSF-funded project on species-tree estimation - a new and exciting area of phylogenetics that uses population-genetic based approaches for estimating species relationships. Through the combination of empirical investigation, simulation, and theory, the research will examine how accurate estimates of species relationships might be achieved given the messiness of real data (e.g., loci with low levels of variation, missing data, incomplete taxon sampling, and realistic sampling effort). As part of the broader research team, the positions will involve collaborative investigations between the Knowles and Kubatko labs, with each postdoc being based out of the separate labs and focusing on separate but complementary components of the research.

Requirements:

Both desired candidates will possess an interest in / experience with phylogenetics, or coalescent-based approaches for demographic analysis. For the position in the Knowles lab, knowledge of basic programming skills (such as writing PERL scripts), and a familiarity with coalescent-based population genetic simulations,

are desirable, as are basic molecular laboratory skills (such as DNA/RNA extraction and PCR). Experience with next-generation sequencing techniques (e.g., 454 sequencing) would be beneficial, but is not required. For the position in the Kubatko lab, knowledge of scientific programming (preferably in C/C++ or Perl) and familiarity with statistical methodology for phylogenetic estimation are desirable; formal training in statistics would also be beneficial.

The University of Michigan and Ohio State University both have several labs dedicated to the study of phylogenetics, population and evolutionary genetics, and speciation. As such, the postdoctoral fellows will benefit from a rich academic environment, as well as excellent genomic and computational facilities.

The positions can be filled immediately and at least two years of funding are available. To apply, email a statement of research interests and a curriculum vitae to L. Lacey Knowles (knowlesl@umich.edu <mailto:knowlesl@umich.edu>) and Laura Kubatko (lkubatko@stat.osu.edu <mailto:lkubatko@stat.osu.edu>). We will also be at the Evolution meetings and would be happy to meet and discuss the project.

“Knowles, L” <knowlesl@umich.edu>

UMichigan EvolutionaryEcol

Postdoctoral position in evolutionary ecology available in the Department of Ecology and Evolutionary Biology at the University of Michigan. I am searching for a creative and motivated postdoc to particulate in a project examining endocrine-mediated behavioral and physiological plasticity in paper wasps. Independent research related to communication, cooperation, or evolutionary endocrinology is also encouraged. Two years of funding are available. The position is available immediately and the start date is flexible. You must have earned a PhD in a relevant discipline at the time of appointment. To apply: send cover letter summarizing your qualifications and interests, a curriculum vitae, representative reprints or preprints, and the names and contact information for two references. Applications and inquiries should be addressed to Elizabeth Tibbetts, tibbetts@umich.edu. For more details on research conducted in the Tibbetts lab see <http://sitemaker.umich.edu/socialwasps/home>. The University of Michigan is an equal opportunity/affirmative ac-

tion employer.

Elizabeth Tibbetts Assistant Professor Ecology and Evolutionary Biology University of Michigan
tibbetts@umich.edu tibbetts@umich.edu

UNebraska MolecularEvolution

POST-DOCTORAL POSITION in Molecular Evolution University of Nebraska, Lincoln, NE

A post-doctoral position is available in the lab of Dr. Jay Storz at the University of Nebraska. The NIH-funded research project involves a combined evolutionary and functional analysis of molecular adaptation. Specifically, we are investigating mechanisms of hemoglobin adaptation to hypoxia in high-altitude animals. The post-doc will work in collaboration with a team of researchers with disparate backgrounds including population genetics, molecular evolution, functional genomics and proteomics, and structural biology. The project involves collaborative work with Dr. Hideaki Moriyama (University of Nebraska) and Drs. Angela Fago and Roy E. Weber (University of Aarhus, Denmark).

The ideal candidate would have expertise in molecular phylogenetics, molecular evolution, genomics and/or proteomics.

If interested, please send a CV, cover letter, and contact information for three references. The position could start as early as summer 2009, but the start-date is flexible. Funding is potentially available for 3+ years. Salary will be determined by the NIH pay scale and will include full benefits. Please feel free to contact me (jstorz2@unl.edu) with any questions.

I will be at the SMBE and Evolution meetings this month, so I would also be happy to meet with prospective candidates in person.

Jay Storz

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

<http://www.biosci.unl.edu/labs/storz/index.html> jstorz2@unlnotes.unl.edu

UOregon FishAnatomicalEvolution

POSTDOCTORAL POSITION The genetics and evolution of skeletal diversity in fishes

An NSF-funded postdoctoral position is available in the laboratory of Monte Westerfield (University of Oregon Institute of Neuroscience) to study experimentally candidate genes for the diversification of skeletal architecture in fish species related to zebrafish.

The position is available through the Phenoscape project (<http://phenoscape.org>), a collaboration among evolutionary and model organism biologists (including Paula Mabee of the University of South Dakota, Monte Westerfield of the Zebrafish Information Network, and Todd Vision of the National Evolutionary Synthesis Center). The aim of the project is to develop a knowledgebase that can be used to generate hypotheses about the genetic basis of anatomical variation among species. The current version of the knowledgebase combines information from genetically characterized mutant phenotypes in zebrafish and naturally variable phenotypes in the Ostariophysi, with an emphasis on the skeleton. A postdoc is being sought to test experimentally the evolutionary and mechanistic hypotheses that are being generated by the knowledgebase and showcase the utility of the approach.

Applicants should have a Ph.D. in molecular, developmental or evolutionary biology and be proficient in DNA cloning technology and mRNA in situ hybridization. The start date will be at the applicant's earliest convenience. The position is initially for one year with possibility for extension. Salary will be commensurate with experience (Kirschstein NRSA levels).

To apply, please submit a cover letter, CV, statement of research interests, and contact information for three references to Paula Mabee at pmabee@usd.edu. Review of applications will begin immediately and the position will remain open until filled.

For more information, please contact Paula Mabee (pmabee@usd.edu, 605-677-6171).

tjv@bio.unc.edu tjv@bio.unc.edu

USouthernCalifornia DrosophilaGenotypeToPhenotype

We are seeking applications for a post doc, to be supported by the newly funded NIH Center of Excellence in Genome Science (CEGS). The post doc will work in the lab of Sergey Nuzhdin, and experience close collaborations with the labs of Michele Arbeitman, John Tower, Simon Tavare, Magnus Nordborg, and Fengzhu Sun in the section of Molecular and Computational Biology at the University of Southern California, Los Angeles. The intellectual goal of the project is to build a genotype-to-phenotype map in *Drosophila*. We will study natural molecular-genetic variation in the resequenced inbred lines in order to generate predictive models of phenotypic variation, with special focus on life history and behavior. The post doc will experience highly interactive and resource rich environment and full academic freedom. An ideal applicant would be interested in evolution, genetics, genomics, and bioinformatics, as well as self-driven, intellectually independent, and capable of co-supervising a technician and undergraduate students. Please, contact Sergey at snuzhdin@usc.edu for more details.

– Julia Saltz PhD Candidate, University of California Davis Visiting Scholar, University of Southern California

Julia Saltz <jbsaltz@ucdavis.edu>

UUtah PlantSystematics

POSTDOCTORAL POSITION IN PLANT SYSTEMATICS. A postdoctoral position at the University of Utah is available in the area of Solanaceae systematics. Several projects are underway, including one to produce a global monograph of the genus *Solanum* (Solanaceae). *Solanum* includes between 1000 and 2000 species and is one of the largest genera of angiosperms. The species level taxonomy, including images, keys and specimen data, are being made available over the Internet on the Solanaceae Source webpage at <http://www.nhm.ac.uk/solanaceaesource>. Other projects include systematic and phylogenetic studies of other gen-

era in the Solanaceae. Responsibilities include monographic taxonomy of selected groups of Solanaceae; specimen and image databasing and manipulation; field work for the collection of herbarium, seed and silica gel samples; generation of molecular data for phylogeny reconstruction (mainly sequences of chloroplast and nuclear genes); maintenance and analysis of living greenhouse collections of Solanaceae; data analysis, presentation, and publication; training and supervision of undergraduate lab assistants; and oversight of routine lab activities. Candidates should have a Ph.D. and experience in plant systematics, field work and with working in a team; experience with Solanaceae is preferred but not required, as is experience with molecular systematics and a variety of methods of data analysis. The position is available for one year beginning in Aug-Sept 2009 and extendable for up to several years as long as funds are available and satisfactory progress is demonstrated.

Electronic submission of applications is encouraged.

Review of applications will begin immediately and continue until a suitable candidate is chosen. If possible, I would like to interview candidates at the Botany 2009 meeting in Snowbird, Utah in late July, 2009. Applicants should submit a statement of interest and description of past experience, a curriculum vitae, and contact information (names, email addresses, and phone numbers) of three references to:

Lynn Bohs Department of Biology 257 South 1400 East University of Utah Salt Lake City, UT 84112 USA
E-mail: bohs@biology.utah.edu Phone: [1] (801) 585-0380 <http://www.biology.utah.edu/bohs/> Solanaceae Source - <http://www.nhm.ac.uk/solanaceaesource> Information on the Biology Department at the University of Utah is available at www.biology.utah.edu The University of Utah is an Equal Opportunity Employer.

Lynn Bohs Department of Biology 257 South 1400 East University of Utah Salt Lake City, UT 84112 (801) 585-0380 <http://www.biology.utah.edu/bohs/> Solanaceae Source - <http://www.nhm.ac.uk/solanaceaesource>
bohs@biology.utah.edu

UVirginia Bioinformatics

BIOINFORMATICS POSTDOC

Microbes play fundamental roles in all biology-associated processes on the planet. A powerful new tool

in such studies is metagenomics wherein one uses high throughput DNA sequencing methods on DNA isolated directly from environmental samples. Metagenomics has the potential to revolutionize our understanding of the normally hidden yet incredibly important world of microorganisms.

The laboratory of Dr. Martin Wu at the Department of Biology University of Virginia is seeking one postdoctoral scientist to work on methodology for analysis of metagenomic data as part of a collaborative project: Integrating Statistical Evolutionary, and Ecological Approaches to Metagenomics (iSEEM). The iSEEM Project, funded by the Gordon and Betty Moore Foundation, takes an integrated, interdisciplinary approach to metagenomic analysis (<http://openwetware.org/wiki/ISEEM>). Activities will include developing automated large-scale phylogenetic algorithms and other bioinformatics tools to study the phylogenetic diversity and ecological structures of the microbial communities. Candidate can find more information about the PI at <http://wolbachia.biology.virginia.edu>.

Qualifications: Applicants should have a PhD in a biological, computational, mathematical, or statistical field. Programming skills are highly desirable. Applicants should have substantial experience with scripting (e.g. Perl or Python), Linux, SQL, and bioinformatics tools. Experience in phylogenetic analyses is a plus.

Term: Appointments will last 2 years beginning in Summer 2009.

To apply: Please send the following materials to Dr. Martin Wu at mw4yv (at) virginia.edu. (1) a brief cover letter explaining your background, career interests, (2) CV (including publications), (3) names and contact information for three references.

We will evaluate applications as they arrive, until the positions are filled.

mwu2000@gmail.com

UVirginia MetagenomicsBioinformatics

BIOINFORMATICS POSTDOC

Microbes play fundamental roles in all biology-associated processes on the planet. A powerful new tool in such studies is metagenomics wherein one uses high throughput DNA sequencing methods on DNA isolated

directly from environmental samples. Metagenomics has the potential to revolutionize our understanding of the normally hidden yet incredibly important world of microorganisms.

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We will evaluate applications as they arrive, until the positions are filled.

mwu2000@gmail.com

Vienna Evolutionary Epigenetics

1 Career Track Postdoctoral Research Position In Population Genetics of Epigenetic Programming

Research profile:

We are searching for an outstanding candidate with

(i) a strong background in epigenetic modifications in *Drosophila*, who has a keen interest to study epigenetics in an evolutionary context or (ii) an evolutionary geneticist with a strong background in functional *Drosophila* genetics.

Background about the position:

The University of Veterinary Medicine in Vienna (VUW) offers a new funding scheme to attract outstanding postdoctoral researchers to Vienna. The position has two funding phases. In the first phase the candidate is expected to carry out preparatory work for a full research grant application to be submitted to the FWF (Austria's major funding body for basic research). Based on a successful evaluation after two years, the postdoc will be promoted to group leader status with approx. 80k base funding for research/year. After 2-3 years the group leader will be reviewed and upon positive review s/he could be offered a tenured faculty position at the VUW.

The post will be based at the Institute of Population Genetics (<http://i122server.vu-wien.ac.at/pop/index.html>). The Institute hosts research groups in experimental population genetics (C. Schlötterer), functional population genetics/evo-devo (A. McGregor), life history evolution (T. Flatt), conservation genetics (P. Burger), and evolutionary modeling (C. Kosiol). The Vienna research area offers many additional possibilities for collaborations in population genetics: Nick Barton, Reinhard Bürger, Andreas Futschik, Ines Hellmann, Joachim Hermisson, Magnus Nordborg, and Claus Vogl.

Deadline for application:

The official closing date has not yet been announced but is expected after the summer break. In order to ensure full consideration, interested candidates are encouraged to submit their application as soon as possible. Please submit a cover letter, CV, statement of research interests, and the names and contact details of three academic references as a single pdf file by e-mail to Dr. Thomas Flatt: thomas.flatt@vu-wien.ac.at

Dr. Thomas Flatt Veterinärmedizinische Universität Wien Institut für Populationsgenetik Veterinärplatz 1 A-1210 WIEN, Austria

VOX +43(0)1-25077-4334 FAX +43(0)1-25077-4390 E-mail: Thomas.Flatt@vu-wien.ac.at

http://i122server.vu-wien.ac.at/pop/Flatt_website/flatt_home.html flatt.thomas@gmail.com

WorkshopsCourses

London GroupSelection Jul7	82	Naples EvoDevo Oct9-11	83
London Systematics Jul8	82	Piacenza livestock biodiversity conservation Sep8-11	84
Montana PopulationGenetics DataAnalysisCourse		Switzerland MetapopulationEvolution Aug30-Sep2	84
Aug31-Sep4	83		

London GroupSelection Jul7

Over the past few years there has been a resurgence of interest in group/multilevel selection as an explanatory framework, particularly with respect to cooperative behaviour in humans and eusocial animals.

We at the London Evolutionary Research Network think this is a fascinating and timely topic, and we are pleased to announce our forthcoming debate:

'Is natural selection at the group level an important evolutionary force?'

Four eminent speakers in the field will be discussing the motion:

Professor Herbert Gintis (http://www-unix.oit.umass.edu/~gintis/home_index.html)

Emeritus Professor of Economics, University of Massachusetts

Professor Mark Pagel (<http://www.evolution.reading.ac.uk/>)

Professor of Evolutionary Biology, Reading University

Professor Stuart West (http://www.zoo.ox.ac.uk/-staff/academics/west_sa.htm)

Professor of Evolutionary Biology, University of Oxford

Professor Samir Okasha (<http://www.bristol.ac.uk/-philosophy/departement/staff/so.html>) Professor of Philosophy of Science, University of Bristol

Date: 7 July 2009, Tuesday

Time: 15.30 - 18.30

Location: JZ Young Lecture Theatre, Anatomy Building, University College London (http://www.ucl.ac.uk/maps/ucl-maps/map2_hi_res)
SQUARE C3 OF THE MAP, WITH ENTRANCES

IN GOWER STREET OR VIA MALET PLACE.

(Public transport for UCL: <http://www.ucl.ac.uk/-maps/public-transport>)

We would like to ensure that as many students as possible benefit from this debate. Please distribute this email within your departments and to others who you think may find the topic of interest.

Best wishes,

LERN committee

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LERN: the London Evolutionary Research Network. E-mail info@londonevolution.net or visit <http://londonevolution.net> <<http://londonevolution.net/>> for events and further information. New members and suggestions for speakers are always welcome!

If you do not want to receive any more emails from LERN, <http://londonevolution.net/maillinglist/?p=unsubscribe&uid=8d9cce993952a0074a870e7af9e6d4c0>

To update your preferences and to unsubscribe visit <http://londonevolution.net/maillinglist/?p=preferences&uid=8d9cce993952a0074a870e7af9e6d4c0>

Gillian Pepper <ht08ggp1@brunel.ac.uk>

London Systematics Jul8

The Systematics Association Sir Julian Huxley Lecture
Phylogenetic Analysis of Clade Diversification: Is Robust Inference Possible?

Prof. Michael Sanderson - University of Arizona, Tucson

The Linnean Society, Burlington House, Piccadilly, London Wednesday 8th July 2009, 6 pm

The meeting is open to visitors. Wine will be served after the lecture to members and guests

Abstract: Species richness is not distributed evenly across the tree of life. Some clades are exceptionally diverse, others surprisingly species-poor. The reconstruction of phylogenetic trees and their calibration in geologic time has improved our ability to detect these patterns, but by how much? In this talk I review a spectrum of methods for inferring diversification rates and consider their robustness, focusing in particular on the question of whether time calibration is necessary or useful. Several case studies in angiosperm evolution will be highlighted, including Hawaiian silverswords and both recent and old radiations within the large clade Leguminosae. Although research on diversification rates has been dominated by questions of evolutionary success, I will end with a discussion of the "depauperons" of life, those clades with surprisingly little diversity.

W.Baker@kew.org

Montana Population Genetics Data Analysis Course Aug31-Sep4

4th ConGen- Population Genetics Data Analysis Course Recent Approaches for Estimation of Population Size, Structure, Gene flow, Selection Detection focusing on conservation and beyond

31-Aug/4-Sep 2009, Flathead Lake Biological Station, Montana, USA

APPLICATIONS FOR 2009 ARE OPEN!

Objective: To provide training in conceptual and practical aspects of data analysis for the population/conservation genetics of natural populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will

allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics

and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 25 people allowing efficient instruction with hands-on computer exercises during the course.

Deadline for application is 30 June, 2009

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately

following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

For detailed information see <http://popgen.eu/-congen2009/> Instructors: Fred Allendorf, University of Montana, USA Sam Cushman, US Forest Service, Missoula, USA Jonathan Pritchard, The University of Chicago, USA Robert Lacy, Chicago Zoological Society, USA Oscar Gaggiotti, University Joseph Fourier in Grenoble, France Gordon Luikart, CIBIO, Portugal & University of Montana Albano Beja-Pereira, CIBIO, Portugal Tiago Antao, Liverpool School of Tropical Medicine, UK Mike Schwartz, US Forest Service, Missoula, USA David Tallmon, University of Alaska, Juneau, USA Robin Waples, Northwest Fisheries Science Center of the National Marine Fisheries Service, USA

congen@popgen.eu

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

Naples EvoDevo Oct9-11

Dear Colleague,

We would like to draw to your attention and that of your colleagues on the upcoming EMBO Workshop Evo-Devo meets Marine Ecology: New Frontiers in Ocean Science through Integrative Biology that will take place in Sant'Angelo d'Ischia (Naples) from 9 to 11 October 2009 (<http://cwp.embo.org/w09-31/-index.html>).

In addition to 18 invited speakers, there will also be 15 short talks selected among submitted abstracts. We therefore recommend submissions of abstracts by your

young colleagues.

Looking forward to seeing you in Ischia in October.

Best regards,

Maria Ina Arnone and Angela Falciatore Workshop Organizers

gpro@szn.it

Piacenza livestock biodiversity conservation Sep8-11

Dear colleagues,

I am pleased to inform you that application for the GLOBALDIV SUMMER SCHOOL 2009 EDITION is now opened.

Please read the following official announcement:

Globaldiv Summer School 2009: EU invested substantial effort in the investigation of livestock biodiversity, becoming a world leader in this sector. Now, European scientists carry the responsibility of disseminating this knowledge to an international audience.

GLOBALDIV is a 3 years project funded by the European Commission on AGRI-GEN RES Programme that started on March 1st, 2007. It aims at promoting the formation of international interdisciplinary groups of experts in characterization and conservation of Farm Animal Genetic Resources from many different European and non-European countries.

GLOBALDIV Summer Schools are training activities, comprising theoretical and practical lectures, organized by the project on 2008 and 2009, to train PhD students and junior researchers on specific topics related to the use of the new technologies and approaches to characterize and conserve genetic diversity in farm animal species. The 2008 School was dedicated to train students in technologies, statistics and methods for the investigation of animal genomes and the characterization of their diversity. It was held in Piacenza, Italy, from 8th to 11th September, 2008. The 2009 School will be devoted to socio-economic aspects of conservation, to breed prioritisation and conservation strategies, integrating genetics, socio-economics, environmental data and geography. It will be held in Piacenza, Italy, from 7th to 10th September, 2009.

Applications are opened and will close on 25th July

2009. You can find all the information at:

www.globaldiv.eu Best regards.

Licia Colli

Licia Colli, PhD Istituto di Zootecnica - Facoltà di Agraria Università Cattolica del S. Cuore via Emilia Parmense, 84 29122 Piacenza (PC) e-mail: licia.colli@unicatt.it <<mailto:licia.colli@unicatt.it>> skype: liquid-diamond Tel: +39 - 0523599205 Fax: +39 - 0523599276

licia.colli@unicatt.it

Switzerland Metapopulation Evolution Aug30-Sep2

A workshop on "EVOLUTION IN METAPOPOPULATIONS" will be held in La Fouly, Switzerland, from August 30th to September 2nd 2009.

Spatial population structure is both a creative and a constraining force in evolution. On the one hand, it leads to genetic variance among local populations, which may promote local adaptation. On the other hand, it can hinder the spread of favorable alleles and may lead to decreased local genetic diversity and to increased homozygosity and mutation load.

Recent theoretical and empirical developments have been investigating how quantitative traits might be affected by the spatial structure, dispersal and selective pressures. This research has shown that population structure has many important evolutionary consequences, and can affect adaptation to changing environments, the evolution of breeding systems, the structure of quantitative traits, or the evolution of sex.

This summer school will bring together six invited speakers and a number of younger researchers to present and discuss both theoretical and empirical aspects of evolution in spatially structured populations, with special emphasis on quantitative traits. It will take place in La Fouly (VS) where we have already held several highly successful summer schools.

Invited speakers:

- Sergey Gavrilets - Ilka Hanski - Sally Otto - John Pannell - Illik Saccheri - Mike Whitlock

Invited speakers and participants will have the oppor-

tunity to present their own research. Ample time will be allowed for discussions.

Registration fees are CHF 300.-, including local accommodation and food for the whole workshop. Fees are waived for students from Swiss universities affiliated to the CUSO (Geneva, Lausanne, Neuchatel, Fribourg and Berne), which will also be given priority.

Deadline for registration is June 30th 2009.

Please register directly on our web site: <http://www.unil.ch/dee/page62608.html> Note that the workshop is limited to 30-35 participants, and a final selection will be done at the beginning of July.

Organizers : J, Goudet University of Lausanne C. Haag, University of Fribourg L. Excoffier, University of Berne

Workshop location: <http://www.dolent.ch/> A hike to local mountains will end the workshop on Wednesday afternoon.

– 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>

Instructions

Instructions: To be added to the EvoDir 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 EvoDir 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 EvoDir direct them to the email evodir@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.