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# E v o l D i r

March 1, 2006

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

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## Forward

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

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

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



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### ArizonaStateU SMBE2006 May24-28

SMBE 2006 Conference (May 24 - May 28, 2006)  
Genomes, Evolution & Bioinformatics Arizona State  
University, Tempe, Arizona, USA

The conference will open on the evening of Wednesday, May 24 with a Welcome Social and Registration from 7:00 p.m. - 11:00 p.m. The opening symposia and contributed sessions will begin at 8:00 a.m. on May 25. The closing symposia and contributed sessions will take place from 8:00 a.m.- 12:00 noon on Sunday, May 28.

A schedule of events at <http://www.smbe.org/geb/-events.htm> To register visit <http://www.smbe.org/geb/registration.php> (Early registration from Feb 1 - April 1, 2006).

Abstracts submission: <http://www.smbe.org/geb/-abstracts.php> For poster presentations and invited talks, we only require you to provide a title and authors. For contributed talks and for consideration for travel awards, you need to submit a short abstract as well. (Submissions accepted from February 1 - March 15, 2006).

Over 50 leading experts in Genomics, Evolutionary Biology, and Bioinformatics have been invited and confirmed (see a list at <http://www.smbe.org/geb/-speakers>).

Highlights of the scientific program at GEB2006 include: (1) A Keynote Address every morning and over 20 invited symposia (2) "Fitch Legacy" and "Nei Legacy" symposia celebrating the achievements of world-renowned students and academic associates of Walter M. Fitch and Masatoshi Nei, co-founders of the journal MBE. (3) SMBE Awards Banquet for Council Awards for "Life time achievement" (Dr. Tomoko Ohta) and "Service to Evolutionary Biology Community" (Dr. Brian Golding) (4) A NASA Astrobiology Institute symposium on "Discovering the Time-tree of Life" (5) Many Graduate and Undergraduate Student Travel awards sponsored by SMBE (<http://www.smbe.org/geb/awards.htm>).

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### ArizonaStateU SMBE2006 May24-28 StudentTravelAwards

Genomes, Evolution & Bioinformatics (GEB) Meetings Graduate student and postdoctoral fellows are invited to apply for travel awards to attend the SMBE/GEB2006 conference to be held at Arizona State University from May 24-May 28 in Tempe, Arizona, USA.

See website <http://www.smbe.org/geb/awards.htm> for details.

Important deadlines March 15, 2006: Deadline for abstract submission. <http://www.smbe.org/geb/abstracts.php> April 1, 2006: Early registration deadline. <http://www.smbe.org/geb/registration.php> April 7: Announcement of awards.

Fitch Student Prize Members of the SMBE who are either current graduate students or postdoctoral researchers (who received the primary doctoral-level degree no earlier than May 1, 2005). 10 individuals will be selected. <http://www.smbe.org/geb/awards.htm> Graduate Student Travel Award SMBE announces competition for 10 graduate students travel awards. Members of the SMBE who are currently enrolled as graduate students can apply. <http://www.smbe.org/geb/awards.htm> SUDHIR.KUMAR@asu.edu

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## ChicoCA PlantSyst July29-Aug1

Dear Colleagues, The abstract submission for the combined meeting of the Botanical Society of America, the American Bryological and Lichenological Society, the American Society of Plant Taxonomists, and the American Fern Society is now open at: [www.botanyconference.org](http://www.botanyconference.org) <<http://www.botanyconference.org>>

### Conference Overview

The annual Botany Conference brings together a broad spectrum of researchers, professors, educators and motivated students, all focused on what's new and vibrant in plant biology. Botany 2006 promises to be the most stimulating to date as we celebrate one hundred years of promoting and advancing the rich and diverse fields of plant sciences. This centennial celebration brings together our four leading professional societies, namely the Botanical Society of America, the American Bryological and Lichenological Society, the American Society of Plant Taxonomists, and the American Fern Society. The meeting will focus on the important achievements of our members and will highlight

prominent botanists whose contributions have shaped and advanced the varied fields of plant biology.

An anticipated 1000 participants will present over 700 scientific contributions including papers, posters, special lectures and 15 symposia. A full slate of field trips and scientific workshops and social events will round out the program.

Saturday, July 29, will feature the 5th Educational and Outreach Forum. This successful component of the Botany conference is designed to draw educators and researchers involved in the teaching of biology and plant science from kindergarten through college. The day will include a range of engaging interactive sessions, a keynote lecture and a concluding reception that will provide an opportunity for attendees to discuss and network in a social setting. For the first time, teachers will be able to apply for California Continuing Professional Education Credits to participate in Forum activities.

Sunday, July 30th, will be an active day of scientific workshops, and fieldtrips. Sunday evening will open the scientific meeting with the conference-wide Plenary Lecture, followed by an All Society Mixer.

Monday morning, July 31st, kicks off the scientific sessions and symposia. Tuesday afternoon, August 1st, will feature a conference-wide Poster Session, with an expected 400 posters featuring current research and recent topics. Scientific Sessions will conclude on Wednesday, August 2nd. Participating Societies will also hold social events and meetings throughout the week.

Botany 2006 is being held on the campus of Chico State University, Chico, California. Chico State is located 90 miles north of Sacramento and 174 miles northeast of San Francisco. Conference hosts will make available special services to ensure that transportation to and from Sacramento International Airport will be a convenient and enjoyable part of the conference experience. Air service directly into Chico is available when connecting through San Francisco.

Many conference participants will want to drive from the airport of their choice to Chico to take advantage of all the beautiful northern California attractions during their stay.

Chico is a great location for Botany 2006, just a short drive from Mt. Lassen Volcanic National Park to the north and less than three hours away from Lake Tahoe to the east.

Kristina A. Schierenbeck, Ph.D. Associate Professor, Herbarium Director California State University, Chico Department of Biological Sciences Chico, CA 95929-0515 email: [kschierenbeck@csuchico.edu](mailto:kschierenbeck@csuchico.edu)

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“Schierenbeck,  
<KSchierenbeck@csuchico.edu>

Telephone: /www.zbi.ee/Est2006/register.php. Please sign in (by doing this fast you help us to organise the meeting) and distribute the information among your colleagues.  
Kristina”

The next good news is that we have connected the workshop with a doctoral school event (27.06 - 01.07) and therefore the participation of graduate students on the workshop is free of the conference fee (meals, coffee-breaks, excursions and materials). The full programme of the PhD school is available at <http://www.zbi.ee/-Est2006/>. We ask you all to advertise the event among your students.

## Estonia Plant Diversity Jun27-30

### 8th CLONAL PLANT WORKSHOP

Generality, specificity and diversity of clonal growth <http://www.zbi.ee/Est2006/> June 27-30, 2006 Pärnu, Estonia 2nd circular

We are glad to announce that organisation of the 8th Clonal Plant Workshop has proceeded well.

The main focus of the meeting is on the similarities and differences between different taxa and different ecosystems in respect to clonal growth, its heterogeneity and homogeneity. This includes the diversity of processes that regulate clonal growth and serve as factors and mechanisms of diversification or unification of the patterns of clonal growth. Generality and specificity of different clonality related phenomena and functional characteristics of clonal growth will be examined.

The workshop is divided into four sessions as follows:

Evolutionary processes and phylogenetic patterns. Chairman: dr. Josef Stuefer. Invited plenary lecture: prof. dr. Spencer Barrett (University of Toronto, Canada.) “Evolution of mating systems and the possible key-role of plant clonality in this process”.

Genetic variation, plasticity and population dynamics. Chairman: prof. dr. Michael J. Hutchings Invited plenary lecture: dr. Lonnie Aarssen (Queens University, Canada.) “Fitness components in clonal plants”.

Regulatory mechanisms of clonal growth. Chairman: dr. Ariel Novoplansky. Invited plenary lectures: 1) dr. Lawren Sack (University of Hawaii, Manoa) “Physiological coordination and hydraulics in clonal plant”; 2) prof. dr. Rick Grosberg (University of California at Davis, USA) “Clonal organization and regulatory mechanisms in marine invertebrates”.

Biotic interactions and ecosystem function. Chairman: prof. dr. Tomas Herben. Invited plenary lecture: prof. dr. Martin Zobel (Tartu University, Estonia) “Small-scale pattern and dynamics of plant communities - does clonal growth matter?”

The registration to the conference is open at <http://www.zbi.ee/Est2006/register.php>.

We advise you to book your accommodation through travel agent Karin Tamm in HermannReisid Karin.Tamm@hermann.ee as quickly as possible. She can also help you in finding suitable flights. The program will start at 10 on June 27.

The conference fee is 180 EUR that covers all meals, conference dinner, coffee breaks, workshop materials, and two excursions. The deadline for payment is April, 15. For details, please, see the web page.

Abstract submission deadline is March, 1. Abstracts on one page should be sent electronically to Marek Sammul [marek@zbi.ee](mailto:marek@zbi.ee). The preferred file format for abstracts is rtf. Please indicate on the top of the abstract whether you want to give an oral presentation or poster presentation.

Thank you for your patience, and we hope that you can register fluently and arrange your trip without troubles. Hope to see you all in June. If you have questions, please ask immediately.

Best regards,

On behalf of the organising committee,

Marek Sammul

Marek Sammul, PhD Estonian University of Life Sciences Institute of Agricultural and Environmental Sciences Department of Botany E-mail: [marek@zbi.ee](mailto:marek@zbi.ee) Riia str. 181 Fax: 372 7 383 013 51014 Tartu Office phone: 372 7 428 619 ESTONIA Mobile phone: 372 5 276 204

Marek Sammul <[marek@zbi.ee](mailto:marek@zbi.ee)>

## Fribourg EvolBioInvasions Oct2-3

AN EVOLUTIONARY PERSPECTIVE OF BIOLOGICAL INVASIONS

Symposium organised by Heinz Müller-Schärer,

Thomas Steinger, Antoine Guisan, and Luc Gigord 2-3 October 2006, Fribourg/Switzerland

<http://www.unifr.ch/biol/ecology/biolinv> We are organising an international symposium on evolutionary processes of biological invasions. We try to bring together scholars from both ecology and evolution, and from plant and animal biology to discuss concepts and new developments in this greatly expanding research field.

We have invited a number of internationally renowned scientists to give plenary lectures, but we also have time for approximately 18 talks by younger researchers (PhD students & post-docs).

Invited speakers: Spencer C.H. Barrett (Univ. of Toronto, Canada) Ragan M. Callaway (Univ. of Montana, USA) Jes Pedersen (Univ. of Copenhagen, Denmark) Kevin Rice (Univ. of California at Davis, USA) Martin A. Schlaepfer (Univ. of Texas at Austin, USA) Bernhard Schmid (Univ. of Zurich, Switzerland)

The symposium will be free, but registration is necessary.

Deadline for abstract submission: July 21 Deadline for registration: September 1

The symposium is generously funded by the "Troisième Cycle" Program of the Conférence Universitaire de Suisse Occidentale (CUSO).

Best regards,

Heinz Müller-Schärer (heinz.mueller@unifr.ch)  
Thomas Steinger (thomas.steinger@unifr.ch) Antoine Guisan (antoine.guisan@unil.ch) Luc Gigord (luc.gigord@unil.ch)

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### **FtWarden Washington Evo-WIBO Apr21-23**

The 2006 meeting of evolutionary biologists in the Pacific Northwest will take place April 21-23, 2006 at Ft. Warden State Park in Washington. We had about 140 people attend the 2004 meeting and have expanded our capacity for this year, but please register early to make sure that we have a slot for you. We have made every effort to keep costs down (registration covers all housing and food), and a simple goal of the meeting is to have a good time with friends, old and new.

Registration and general information is available at: [http:// www.zoology.ubc.ca/evo-wibo](http://www.zoology.ubc.ca/evo-wibo) The meeting has no concurrent sessions, and talks and posters are presented by faculty, postdocs and students. The slate of talks will be chosen by the organizing committee. We strongly encourage faculty to nominate/encourage outstanding students and postdocs to give platform talks (send an email Patrick Phillips, [pphil@uoregon.edu](mailto:pphil@uoregon.edu), with suggestions).

n.b. Evo-WIBO stands for Evolutionary Biologists from Washington, Idaho, British Columbia and Oregon, although we draw much more widely than that, including California, Alaska, and Montana. As punishment for coming up with this name in the first place, Ray Huey will be giving the plenary talk for the meeting Sunday morning.

Patrick C. Phillips, Associate Professor of Biology Center for Ecology and Evolutionary Biology Email: [pphil@uoregon.edu](mailto:pphil@uoregon.edu) Phone: (541) 346-0916 | FAX (541) 346-2364 Address: 5289 University of Oregon Eugene, OR 97403-5289 USA Web: Lab <http://www.uoregon.edu/~pphil> EvoNet <http://www.EvoNet.org> CEEB <http://evolution.uoregon.edu> IGERT <http://evodevo.uoregon.edu> [pphil@uoregon.edu](mailto:pphil@uoregon.edu)

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### **HalleGermany PlantPopBiol May24-27**

Dear Colleagues,

Herewith we would like to invite you to join the

\*19<sup>th</sup> Annual Meeting of the Plant Population Biology Meeting of the Ecological Society of **Germany**, **Switzerland** and **Austria** (GfÖ),\*

taking place in Halle from 24 May to 27 May 2006 organized jointly by the UFZ-Centre for Environmental Research and the Geobotanical Institute of the University of Halle. Please note that the date differs from the one given in the GfÖe-Letter, the meeting will take place as always it over the Ascension Day.

The annual meeting is being held in English and usually attended by more than one hundred people from all over Europe. Priority is given to young researchers to present results from their PhD theses. The focus of the meeting in 2006 is on interactions of plants with other species, recognizing that plants have to cope with a large number of competitors, herbivores, pathogens

and symbionts. Therefore, to understand the population biology of plants, botanist would have to broaden their scope and incorporate these interactors in their studies. But presentations from the whole field of plant population biology are welcome.

Halle is a small, medieval town approximately 200 km south of Berlin that harbors one of the oldest Universities of Germany. The Institute of Geobotany is one of the largest ecological institutes in Germany with a long lasting history in plant ecology (see <http://www.geobotanik.uni-halle.de/>). The UFZ-Centre for Environmental Research was founded 13 years ago as a competence centre for the heavily contaminated landscape of the former German Democratic Republic. Research in the Department of Community Ecology focuses on biodiversity, population biology of invasive species, species interactions and ecosystem functioning (see <http://www.ufz.de/index.php?en=798>).

Please visit the PopBio2006 - webpage at <http://www.ufz.de/popbio2006> Looking forward seeing you,

Alexandra Erfmeier & Isabell Hensen – University of Halle

Daniel Prati, Harald Auge & Walter Durka – UFZ

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\*\*\* POPBIO2006 <http://www.ufz.de/popbio2006> \*\*\*

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## Harvard BeyondHapMap May8-10

Beyond HapMap - 3rd Annual International HapMap Project Community Analysis Meeting

The Broad Institute of MIT and Harvard, Cambridge, Massachusetts, USA

May 8-10, 2006

PLEASE NOTE: The deadline for submitting abstracts is Friday, March 31.

Abstracts from non-registered persons will NOT be considered.

The conference announcement and details regarding registration follow below for ease of reference.

The deadline for submitting an abstract is Friday, March 31, 2006.

The deadline for registration is Friday, April 14, 2006.

Lecture seating is limited; therefore, early registration is encouraged. Capacity may be met prior to the April 14 deadline.

Complete instructions for abstract submission and registration, and further details of the conference, can be found at the conference Web site: <http://www.broad.mit.edu/events/hapmapmeeting> <http://www.broad.mit.edu/events/hapmapmeeting> The Analysis Committee of the International HapMap Project organized two previous meetings (April 2004 and March 2005) at which investigators from around the world reviewed emerging data from the HapMap Project and related efforts, shared analyses, and debated directions for future research. Phase I of HapMap was published in October 2005, and Phase II is now complete.

This meeting, the third in the series, has as its primary focus the application of the HapMap resource in human disease studies, population genetic and evolutionary insights obtained from the data, and emerging themes that point to new resources (such as knowledge of structural variants) required to perform human genetic research.

“Beyond Hapmap” is an unequalled opportunity for a diverse community of investigators—those involved in the HapMap Project, in population genetic and statistical analysts, and in genetic studies of human diseases—to come together to define and discuss a range of issues related to the use of the HapMap resource, and to identify paths forward to discover genetic contributions to human disease.

We invite participation and registration for this meeting by investigators (both mid-career and trainees) from these and other related fields. We strongly encourage the submission of an abstract from interested scientists, as more than half of the presentation slots at the meeting are reserved for talks selected from the abstracts.

Co-chairs International HapMap Analysis Group: David Altshuler, Broad Institute of Harvard and

MIT Aravinda Chakravarti, Johns Hopkins University  
School of Medicine Peter Donnelly, University of Oxford

#### Travel Awards

Travel awards of \$1000.00 for up to 15 young investigators (students, postdocs, or young investigators) are available for this meeting. Qualified persons requesting consideration for a travel award must be registered for the conference and submit the following items to <mailto:melindaagray@comcast.net>melindaagray@comcast.net no later than March 15:

- 1) current CV
- 2) formatted abstract (please refer to the abstract submission guidelines on the conference Web site)

Awards will be made based on the research submitted in the abstract and the academic promise of the candidate with some priority given to applications from women, underrepresented minorities, and applicants with disabilities. Submitted material will be reviewed, and funding decisions made, by the conference program committee.

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Milka Popov, PhD Assistant Director/Directrice ad-jointe Canadian Institutes of Health Research/Institut de recherche en santé du Canada Institute of Genetics/ Institut de génétique 123 Edward Street, Suite 1211 Toronto, ON M5G 1E2

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Popov <milkaig@sickkids.ca>

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### Innsbruck EvolofFlatworms Jul29-Aug3

International Symposium on Flatworm Biology 2006  
Innsbruck 29.07. - 03.08.2006 Call for Papers and  
Opening of Registration

Dear Friends and Colleagues,

With this email we would like to 1) cordially invite you to submit talks and posters, and 2) officially announce the opening of the registration for the 10th International Symposium on Flatworm Biology that will be held in Innsbruck from Saturday July 29 to Tuesday August 3, 2006.

Registration will be open until April 9, 2006.

For details regarding the Symposium please see the Call for Papers on our meeting home page at:

<[http://www2.uibk.ac.at/zoology/ultra/isfb/-isfb2006\\_call.html](http://www2.uibk.ac.at/zoology/ultra/isfb/-isfb2006_call.html)>[http://www2.uibk.ac.at/zoology/ultra/isfb/isfb2006\\_call.html](http://www2.uibk.ac.at/zoology/ultra/isfb/isfb2006_call.html) In this announcement we have added or updated the following information: Invited Speakers, Call for Papers, Registration and Conference Fees.

Also, we are looking forward to receiving your submissions and registrations. The registration home page can be found at:

<<http://ostom.net/zoology/registr/>><http://ostom.net/zoology/registr/> Finally, please note that the accommodation should be booked directly with the conference center at:

<<http://www.innsbruck-hotels.at/grauerbaer/-index.html>><http://www.innsbruck-hotels.at/grauerbaer/index.html> Please help us in making the meeting known to your colleagues. If you have questions please contact us at ISFB2006@uibk.ac.at.

The organizing Committee,

Reinhard Rieger, Peter Ladurner, Lukas Schärer  
(all University of Innsbruck)

Advisory committee:

Robert Gschwentner (Innsbruck), Bert Hobmayer (Innsbruck), Nico Michiels (Tuebingen), Roland Peter (Salzburg), Gunde Rieger (Innsbruck), Willi Salvemoser (Innsbruck), Wolfgang Schuermann (Salzburg).

International Symposium on Flatworm Biology ISFB  
2006 Institute of Zoology University of Innsbruck Technikerstrasse 25 A-6020 Innsbruck Austria

Fax.: ++43-512-507-2930 Email:  
ISFB2006@uibk.ac.at Web: <[http://zoology.uibk.ac.at/ultra/isfb/-isfb2006\\_home.html](http://zoology.uibk.ac.at/ultra/isfb/-isfb2006_home.html)>[http://zoology.uibk.ac.at/ultra/isfb/isfb2006\\_home.html](http://zoology.uibk.ac.at/ultra/isfb/isfb2006_home.html) lukas.scharer@uibk.ac.at

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### LundU VertEvol June1-3

First announcement- INTERNATIONAL SYMPOSIUM ON THE EVOLUTION OF VERTEBRATE ANIMALS

We are happy to announce the second international

symposium on the evolution of vertebrate animals held at Lund University, Sweden.

The symposium will take place on 1-2 June 2006, with an excursion in Southern Sweden on the 3rd of June.

Currently thirteen distinguished speakers on human evolution, mammalian phylogeny, vertebrate relationships and genome analysis have been invited to give talks. These include: Per Ahlberg, University of Uppsala, Sweden Michael Benton, University of Bristol, UK Giorgio Bernardi, Stazione Zoologica Anton Dohrn Italy Emmanuel Douzery, Université Montpellier 2, France Gaston Gonnet, Institute for Computational Sciences, Switzerland Arndt von Haeseler, Center for Integrative Bioinformatics, Austria Philippe Janvier, Muséum National d'Histoire Naturelle, France Wilfried de Jong, Univ. of Nijmegen, The Netherlands Herve Philippe, Université de Montréal, Canada Martin Pickford, Museum National d'Histoire Naturelle, France Brigitte Senut, Museum National d'Histoire Naturelle, France Cecilia Saccone. CNR - Istituto di Tecnologia Biomedica, Italy

In conjunction with the symposium there will also be a poster session. The registration deadline is 30 April 2006. The symposium carries only a small registration fee of 20 euros.

Please consult the webpage, <http://www.biol.lu.se/isev2006> for information about registration, accommodation and travel.

Axel Janke & Ulfur Arnason

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**MichiganStateU**  
**AnimalFuncGenomics May16-19**

Dear Colleagues:

We are pleased to announce that the Center for Animal

Functional Genomics of Michigan State University will host the 2nd International Symposium on Animal Functional Genomics (ISAFG) on May 16-19, 2006. The Symposium will be held at the Henry Center on the campus of Michigan State University in beautiful East Lansing, Michigan.

The purpose of the 2nd ISAFG is to bring together international researchers, industry representatives, and administrators who seek updated information on the design, analysis, interpretation, integration, and application of high throughput gene expression profiling for the study of cells and organ systems that underlie economically relevant phenotypes in agricultural animals. Featured areas of Symposium guest speakers and international delegates include Statistical Genomics, Bioinformatics and Data Mining, Animal Health, Reproduction, and Growth and Metabolism.

The 2nd ISAFG has been designed around 11 keynote lectures to be delivered by internationally renowned functional genomics scientists. In addition, selected abstracts will be presented orally by Symposium participants. All participants are welcome to bring posters highlighting preliminary or completed studies on gene expression profiling in animal model systems.

This message serves as the formal call for registration (early registration is \$400 if done by March 1, 2006; late registration between March 2-31, 2006 is \$500) and abstracts (deadline March 31, 2006), which must be done on-line at the Symposium web site <http://www.isafg.msu.edu>.

We look forward to greeting you at Michigan State University in May! For more information please contact the 2nd ISAFG co-chairs,

Guilherme Rosa (rosag@msu.edu) Jeanne Burton (burtonj@msu.edu)

–  
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**NewYorkU MolPrimates Mar2-4**



The Center for the Study of Human Origins at New York University is sponsoring a conference entitled “Molecular Primatology: Progress and Promise”, to be held from March 02 to March 04, 2006. The conference will bring together a diverse, international group of leading experts on the application of molecular data in primatology to explore the breadth of current, cutting-edge research in primate evolutionary biology, to provide a prospective view on the field’s future promise, and to forge new collaborative connections among research groups from around the globe.

The conference is organized around four major themes: Molecular Ecology ? the use of molecular techniques for examining kinship, behavior, dispersal patterns, and social organization in wild primates, Conservation Genetics ? the application of molecular techniques to primate conservation biology, Molecular Diversity and Adaptation ? the adaptive significance of patterns of molecular diversity within and between primate taxa, and Behavioral Genetics and Comparative Genomics ? the genetic underpinnings of inter-individual behavioral variation and insights from recent genomic studies into the patterns and functional significance of differences in genome structure across primate taxa.

On the first two days of the conference – which are free and open to the public – these four central themes will be the focus of a series of presentations by four to five invited speakers, followed by an extended discussion involving the speakers, other invited guests, and conference attendees. Poster sessions held on the first two days of the conference, which will showcase research by graduate students and postdoctoral researchers in molecular primatology from the greater New York area and from the laboratories of the invited speakers. Each of the first two days of the conference will close with an evening plenary talk exploring the history and future promise of using molecular data in primate phylogenetic studies, a topic that is not covered explicitly in any of the thematic sessions.

For more information on the conference, please visit the following URL: <http://www.nyu.edu/projects/difiore/-mpconference/mpoverview.html> If you are interested in attending, please send an email to the administrator of the Center for the Study of Human Origins at NYU: [jen.leclair@nyu.edu](mailto:jen.leclair@nyu.edu)

Anthony Di Fiore <[anthony.difiore@nyu.edu](mailto:anthony.difiore@nyu.edu)>

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## Rome EvoLinguisticCommunication Sept30-Oct1

Third Intl. Workshop on the Emergence and Evolution of Linguistic ommunication (EELC III)

<http://bdc.brain.riken.go.jp/eelc2006/> Rome, Italy, 30 Sept. - 1 Oct. 2006.

As part of the Simulation of Adaptive Behavior (SAB) conference <http://www.sab06.org/> Invited Speakers: Peter Gardenfors (Lund University, Sweden), Naoto Iwahashi (ATR, Japan), Elena Lieven (Max Planck Institute, Germany), Eörs Szathmáry (Eötvös Loránd University, Hungary)

Scope of the Workshop Language is generally considered as the hallmark of human intelligence. One important way to study why this is the case, is to investigate how linguistic communication has evolved. In the past decade, this research area has received a lot of attention from the scientific community and could be considered as one of the main areas of Artificial Intelligence and Cognitive Science. The EELC III workshop will focus on empirical and modelling research on the emergence of symbol grounding and other aspects of linguistic communication in language evolution and language acquisition. The key questions relate to how symbolic communication can emerge from interactions of individuals with their environment, including other individuals, and how such communication can become meaningful to the individual or population. Research methods that are used to study these issues include experimental and observational studies on child language acquisition and animal communication; theoretical and computational modelling; and (robotic) simulations of adaptive behaviour. The workshop aims to provide leading scientists in the interdisciplinary area of language evolution and language acquisition a platform to present their latest results and discuss areas of further research.

Until about 15 years ago, there was very little productive research in the study of language evolution. However, with the increased advancements of computational techniques and other empirical methods, the field of language evolution has grown to become one of the major research areas in cognitive science. While the field is largely interdisciplinary with contributions from linguistics, psychology, neuroscience, biology, an-

thropology, philosophy and computer science, the latter has proven to be among the most influential disciplines. A reason for this is that empirical evidence on language evolution is scarce and computer simulations offer a good testbed for investigating hypotheses. One of the major driving forces for language evolution is often considered to be language acquisition. Language can be transmitted over subsequent generations if individuals can learn language. Moreover, it has been claimed that the stages of children's language acquisition mirrors the stages of language evolution. So, the current EELC will not only look at studies on the evolution of language, but also at studies on language acquisition.

Although many computer simulations take the emergence of symbol grounding for granted, recently there has been an increase in studies that focus on issues relating to the emergence of grounded communication systems. The EELC III will therefore have 'adaptive approaches to symbol grounding and beyond' as its central theme, though contributions are not limited to this theme.

**EELC Symposium Series** This workshop is the third edition of the successful workshop on the Emergence and Evolution of Linguistic Communication. The first one was held in 2004 in Kanazawa (Japan) under the auspices of the Japanese Society for Artificial Intelligence (JSAI) and the second one in Hatfield (United Kingdom) under the auspices of the Society for the Study of Artificial Intelligence and Simulation of Behaviour (AISB). Details of the second EELC are found on <http://homepages.feis.herts.ac.uk/comqcln/-EELC05.html>. The Third International Workshop on the Emergence and Evolution of Linguistic Communication will be part of the Simulation of Adaptive Behavior conference. The coincidence with SAB permits a better exchange with other researchers working in the simulation of adaptive behaviour field.

**Submission of Papers** We invite papers of maximum 12 A4 pages that fit within the scope of the workshop. All papers should be submitted electronically in PDF to paulv 'at' ling.ed.ac.uk and formatted according to the instructions given at <http://bdc.brain.riken.go.jp/-eelc2006/>. All submissions will be acknowledged and refereed by the international scientific programme committee. The proceedings will be published as a LNCS/LNAI series by Springer.

**Important Dates** Deadline for submissions: 30 Apr. 2006 Notification of acceptance: 2 Jun. 2006 Camera ready copies: 30 Jun. 2006 Workshop (1st day): 30 Sep. 2006 Workshop (2nd day): 1 Oct. 2006

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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>

## StonyBrookU SSESSB2006 Mentors

DIVERSITY AT SSE/SSB 2006:

Call for applications for undergraduates of diverse backgrounds to attend the 2006 meeting of the Society for the Study of Evolution/Society of Systematic Biologists  
\*\*\* and \*\*\*

Call for volunteer mentors for this program from graduate students, postdocs and faculty.

For the fourth consecutive year, the Undergraduate Diversity at SSE/SSB program, funded by the Undergraduate Mentoring in Environmental Biology (UMEB) program at NSF, will take place again at the 2006 meeting this June in Stony Brook, New York and we are now accepting applications. The program will send 15 undergraduates from the US and Puerto Rico to attend the SSE/SSB meetings to present posters and interact with graduate student, postdoc and faculty mentors. The application deadline is April 1, 2006. Applications will consist of a title, author line and abstract of the poster to be presented by the undergraduate; a one or two paragraph (no more than 1 page) statement of academic interests and career goals and of how attending the Evolution meetings will help meet these goals; and one letter of recommendation from the undergraduate's research advisor. The letter should indicate how inclusion of the student will increase diversity of the group participants and whether or not the student will be attending medical school. All materials should be submitted as pdf files and emailed to Rich Kliman at [rmkliman@cedarcrest.edu](mailto:rmkliman@cedarcrest.edu). Applications will be accepted only from students registered or very recently graduated from U.S. institutions, including Puerto Rico (i.e., having finished classes during the winter or spring semesters before the meeting) and traveling to the meeting from within the US. Students demonstrating a need for funds to attend SSE/SSB will be given preference, and will be selected so that as a group, they will increase cultural diversity among undergraduates at Evolution meetings.

For further information, please see: <http://www.oeb.harvard.edu/faculty/edwards/community/-application.html> In addition to applications from

undergraduates, we hope to receive email notices to [rmkliman@cedarcrest.edu](mailto:rmkliman@cedarcrest.edu) or [edwardsadmin@oeb.harvard.edu](mailto:edwardsadmin@oeb.harvard.edu) from graduate students, post-docs and faculty who wish to serve as undergraduate mentors for the meetings. Duties will include meeting with a pair of undergraduates in the program, attending and demystifying a half-day of talks with them, joining them for a meal, introducing them to colleagues and in general befriending them in ways that make evolutionary biology seem like a welcoming discipline. No costs for travel, housing or registration are covered. Please spread the word about this very rewarding activity.

Contact one of the program organizers for more information:

Scott V. Edwards, Harvard University ([sedwards@fas.harvard.edu](mailto:sedwards@fas.harvard.edu))  
Richard Kliman, Cedar Crest College ([rmkliman@cedarcrest.edu](mailto:rmkliman@cedarcrest.edu))

[Rmkliman@cedarcrest.edu](mailto:Rmkliman@cedarcrest.edu) [Rmkliman@cedarcrest.edu](mailto:Rmkliman@cedarcrest.edu)

Highlights of the scientific program at GEB2006 include: (1) A Keynote Address every morning and over 20 symposia with invited speakers (2) "Fitch Legacy" and "Nei Legacy" symposia celebrating the achievements of world-renowned students and academic associates of Walter Fitch and Masatoshi Nei, co-founders of the journal MBE. (3) SMBE Awards Banquet for Council Awards for "Life time achievement" (Dr. Tomoko Ohta) and "Service to Evolutionary Biology Community" (Dr. Brian Golding) (4) A NASA Astrobiology Institute symposium on "Discovering the Time-tree of Life" (5) Many Graduate and Undergraduate Student Travel awards sponsored by SMBE (<http://www.smbe.org/geb/awards.htm>).

SUDHIR.KUMAR@asu.edu  
SUDHIR.KUMAR@asu.edu

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## Toronto EvolCommunication Mar11

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## TempeAZ SMBE May24-28

The organizing committee for the 2006 Annual SMBE Meetings is pleased to invite you to attend the Genomes, Evolution, & Bioinformatics (GEB2006) conference to be held at Arizona State University from May 24-May 28 in Tempe, Arizona, USA.

The conference will open on the evening of Wednesday, May 24 with a Welcome Social and Registration from 7:00 p.m.-11:00 p.m. The opening symposia and contributed sessions will begin at 8:00 a.m. on May 25. The closing symposia and contributed sessions will take place from 8:00 a.m.-12:00 noon on Sunday, May 28. See a tentative schedule of events at <http://www.smbe.org/geb/events.htm> To register visit <http://www.smbe.org/geb/registration.php> (Early registration from Feb 1 - April 1, 2006). Abstract and title submissions can be made at <http://www.smbe.org/geb/abstracts.php> For poster presentations and invited talks, we only require you to provide a title and authors. For contributed talks and for consideration for travel awards, you need to submit a short abstract as well. (Submissions accepted from February 1 - March 15, 2006). Over 50 leading experts in Genomics, Evolutionary Biology, and Bioinformatics have been invited and confirmed (see a list at <http://www.smbe.org/geb/speakers>).

York University's Association of Graduate Students in the Biological Sciences will hold their 33rd annual biology symposium on

THE ECOLOGY AND EVOLUTION OF COMMUNICATION SYSTEMS

on Saturday, March 11, 2006.

Rm 109 Accolade West Building, Keele Campus (4700 Keele St., North York, Ontario, Canada)

List of speakers:

Dr. Donald Owings (University of California, Davis)

"Animals are self-interested assessors and managers: Communication between ground squirrels and rattlesnakes"

Dr. Kathleen Gilmour (University of Ottawa)

"Bullies in the fish tank: The physiological costs of antagonistic interactions in rainbow trout"

Dr. Winfried Lampert (Max Planck Institute)

"A wet world of smell: The role of kairomones in freshwater communities"

Dr. André Kessler (Cornell University)

"Communicating plants: Ecological consequences of induced responses to herbivory"

Dr. John A. Endler (University of California, Santa Barbara)

“Elaboration and innovation in visual signal design in Australian bowerbirds”

Dr. Thomas Seeley (Cornell University)

“House hunting by honey bees: A study of group decision making”

Registration is free. Please email agsbs@yorku.ca to register.

Please visit <http://www.biol.yorku.ca/grad/-symposium06.htm> for additional information.

Sincerely,

Amro Zayed AGSBS committee Dept. Biology York University

amro@torontodigital.com

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### UAlabama SEEC2006 Mar3-5 LateRegisFeb15

Hello.

This email is to announce that early registration for SEEC 2006 is over, and the final date for late registration is FEB 15. Please see our website [www.seec.ua.edu](http://www.seec.ua.edu) for more details. See you in March!

SEEC 2006 committee

seec2006@gmail.com

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### UBuffalo EGLME May6

Eastern Great Lakes Molecular Evolution Meeting, University at Buffalo, May 6, 2006

The yearly Eastern Great Lakes Molecular Evolution Meeting, will be held at the Center for the Arts, University at Buffalo, on Saturday May 6, immediately after the end of the school year in both the USA and Canada.

This one-day meeting normally attracts around 100 students, postdocs, and faculty from both the US and Canada and has been held ever year in cities surrounding the great lakes. This year's meeting will be held in Buffalo, centrally located between Toronto, Guelph,

McMaster, Waterloo, Cornell, Rochester, and Pittsburgh.

A number of talks will be selected from submitted abstracts, and the remaining abstracts will be presented as posters. The meeting runs all day, with the evening being dedicated to the poster session. Coffee, tea, and lunch will be provided and there will be no registration fee. Dinner is not scheduled but there are a variety of restaurants in close proximity to the meeting venue.

If you want to submit a talk or a poster please send a title and abstract (max 250 words) to one of the meeting organizers:

Dr. Antonia Monteiro ([monteiro@buffalo.edu](mailto:monteiro@buffalo.edu)), Dr. Derek Taylor ([djtaylor@buffalo.edu](mailto:djtaylor@buffalo.edu)), and Dr. William Piel ([wpiel@buffalo.edu](mailto:wpiel@buffalo.edu)).

We look forward to seeing you in Buffalo in May! Antonia, Derek, and Bill

Antónia Monteiro <[monteiro@buffalo.edu](mailto:monteiro@buffalo.edu)>

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### UCaliforniaSantaBarbara EvolLanguages Sept8-10

Conference “Languages and Genes”, University of California Santa Barbara, 2006 September 08-10

Call for abstracts for Poster Session

The University of California Santa Barbara will host an interdisciplinary conference “Languages and Genes” on 2006 September 8-10, which will bring together leading international specialists in the areas of linguistics, genetics, anthropology, and archeology. The aim is to ascertain the state of the art with regard to cooperative research among these disciplines relating to human pre-history, in particular the major population movements that led to the demographic distribution of population groups, and especially to identify the most promising developments for future research on this problem from a multi-disciplinary perspective.

The conference will incorporate a poster session and we invite abstracts for consideration in this session. Abstracts should be a maximum of one page and should be sent no later than 2006 March 10 to Bernard Comrie at the e-mail address <[comrie@eva.mpg.de](mailto:comrie@eva.mpg.de)>. Those submitting abstracts will be informed of the status of their abstract by the end of April.

The conference web site is currently under construction;

further information will be posted when it is ready.

– [I am based in Santa Barbara through 2006 mid-March. From 2006 late March I will be based in Leipzig]

Prof. Dr. Bernard Comrie Director, Department of Linguistics, Max Planck Institute for Evolutionary Anthropology Distinguished Professor of Linguistics, University of California Santa Barbara

E-mail: [comrie@eva.mpg.de](mailto:comrie@eva.mpg.de) Home page: <http://email.eva.mpg.de/~comrie/> Mobile phone: +49 160 9634 2888

Max Planck Institute for Evolutionary Anthropology  
Deutscher Platz 6 D-04103 Leipzig Germany tel. +49 341 35 50 301 tel. secretary +49 341 35 50 315 fax +49 341 35 50 333

Department of Linguistics University of California  
Santa Barbara Santa Barbara, CA 93106-3100 USA tel. +1 805 893 4025 fax +1 805 893 7769

A copy of all incoming e-mail is forwarded to my secretary. If you do not wish your message to be read other than by me, please put "private" in the subject box.

[comrie@eva.mpg.de](mailto:comrie@eva.mpg.de) [comrie@eva.mpg.de](mailto:comrie@eva.mpg.de)

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## UCambridge Palaeobiogeography Apr10-13

Palaeogeography and Palaeobiogeography: Biodiversity in Space and Time April 10-13th April 2006 Hosted by the National Institute for Environmental e-Science

This meeting aims to broaden scientific understanding of the evolution of Earth's biodiversity at a range of spatial and temporal scales by facilitating collaboration among palaeogeographers, palaeobiogeographers, and modern day geographers and biogeographers. The meeting will consist of a day of talks from invited speakers, four workshops, and poster sessions.

The meeting will take place at the Centre for Mathematical Sciences, University of Cambridge. More information and on-line registration can be found at <http://www.tethys.org.uk/biogeography/> The conference organizers can be contacted directly by email. We look forward to a productive and fun meeting in Cambridge.

Dr. Paul Upchurch ([p.upchurch@ucl.ac.uk](mailto:p.upchurch@ucl.ac.uk)) Dr. Alistair McGowan ([a.mcgowan@nhm.ac.uk](mailto:a.mcgowan@nhm.ac.uk)) Claire Slater ([c.slater@nhm.ac.uk](mailto:c.slater@nhm.ac.uk))

Claire Slater <[c.slater@nhm.ac.uk](mailto:c.slater@nhm.ac.uk)>

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## UEdinburgh Symbiosis Apr21

The Evolution of Symbiosis A one day research workshop

April 21st 2006, 9.30am to 6.00pm

Ashworth Laboratories, University of Edinburgh

This workshop will explore all aspects of symbiosis biology from parasitism to mutualism and genomics to behaviour.

Speakers:

Siv Andersson, Uppsala Wolbachia Genomics David Clarke, Bath Photorhabdus-Steinernema symbiosis Isabelle Cote, Vancouver Vertebrate behavioural symbiosis Alistair Darby, Edinburgh Tsetse symbiology Troy Day, Ontario Symbiosis/Parasitism Theory Angela Douglas, York Aphid and coral symbioses Alistair Fitter, York Rhizobial symbioses Andy Gardner, Edinburgh/Ontario Symbiosis Theory Achim Hoerauf, Bonn Wolbachia and filariasis Greg Hurst, London Male-killers and parasitic symbioses Toby Kiers, USA Legume/rhizobial symbiosis Steve Sinkins, Oxford Wolbachia and mosquito control

Website: <http://www.nematodes.org/ResWorkshop/>  
Posters are welcome Lunch and coffee is provided Registration costs £15 payable on the day and is free to students Accommodation can be booked through Edinburgh First (<http://www.edinburghfirst.com/>)

Let us know if you plan to come by e-mailing [Francis.Jiggins@ed.ac.uk](mailto:Francis.Jiggins@ed.ac.uk). Please say if you would like to bring a poster. Directions are available at <http://www.biology.ed.ac.uk/research/institutes/evolution/contacts.php> [Francis.Jiggins@ed.ac.uk](mailto:Francis.Jiggins@ed.ac.uk)  
[Francis.Jiggins@ed.ac.uk](mailto:Francis.Jiggins@ed.ac.uk)

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## UEdinburgh Symbiosis Apr21 2

For clarification, the cost of the Edinburgh Symbiosis Workshop advertised yesterday is just 15 pounds (the pound sign had had been converted to an extra '3').

[Francis.Jiggins@ed.ac.uk](mailto:Francis.Jiggins@ed.ac.uk) [Francis.Jiggins@ed.ac.uk](mailto:Francis.Jiggins@ed.ac.uk)

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## Wageningen LandscapeGenetics 2007 CallForPapers

Dear colleagues,

Landscape genetics is an emerging topic in landscape ecology. Molecular genetic methods allow us to test specific landscape ecological hypotheses concerning the effects of landscape structure on the actual movement of organisms, the connectivity of habitats from an organism's perspective, or the effect of landscape dynamics (natural or anthropogenic changes) on metapopulation dynamics.

At the 2005 US-IALE meeting in Syracuse, we held a first landscape genetics symposium, where primarily geneticists were invited to provide an introduction to landscape genetics for a landscape ecological audience. The collection of papers presented there will be published in *Landscape Ecology* this year.

For the 2007 IALE World congress in Wageningen, we propose a follow-up symposium, specifically welcoming any papers that report applications of molecular methods for testing landscape ecological hypotheses as outlined above. Typically, we expect these studies to address landscape effects beyond isolation-by-distance, e.g. effects of matrix resistance or landscape change on gene flow and population genetic structure.

If you would like to contribute to the planned symposium, please send us the following preliminary information (all this can be updated later if necessary): - Title - Author(s) - Tentative abstract or a few lines describing the study

**IMPORTANT DEADLINE:** Please contact us with the above information before Feb 23, as the deadline for symposia proposals is coming up soon.

Helene Wagner (helene.wagner@wsl.ch) Rolf Holderegger (rolf.holderegger@wsl.ch)

PD Dr. Helene Wagner Senior scientist Swiss Federal Research Institute WSL Zuercherstrasse 111 CH-8903 Birmensdorf

Phone: +41-44-739 25 87 Fax: +41-44-739 22 15 Email: helene.wagner@wsl.ch <http://www.wsl.ch/staff/helene.wagner/> Felix Gugerli Biologist / Senior Scientist Swiss Federal Research Institute WSL Ecological Genetics Zuercherstrasse 111 CH-8903 Birmensdorf

SWITZERLAND

phone: +41-(0)44-739-2590 fax: +41-(0)44-739-2215  
<http://www.wsl.ch/staff/felix.gugerli/>

Felix Gugerli <felix.gugerli@wsl.ch>

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## YaleU PhylogeneticNomenclature Jun28-Jul2

Second Meeting of the International Society for Phylogenetic Nomenclature, Yale University New Haven, June 28 ? July 2, 2006

Second Circular

Dear Colleagues,

The Second Meeting of the International Society for Phylogenetic Nomenclature will be held in New Haven, Connecticut, at Yale University, from June 28 to July 2, 2006. This meeting is an opportunity to discuss topics that pertain directly or indirectly to phylogenetic nomenclature in general and the PhyloCode in particular. In addition to providing a forum to contribute oral and poster presentations, this meeting will also include three symposia with a number of invited guest speakers.

Organizing Committee:

Nico Cellinese, Co-Chair, Yale University; Walter Joyce, Co-Chair, Program Officer, Yale University; Michael Donoghue, Co-Host, Yale University; Jacques Gauthier, Co-Host, Yale University; David Baum, University of Wisconsin, Madison; Philip Cantino, Ohio University; Michel Laurin, CNRS, Paris; Kevin de Queiroz, Smithsonian Institution.

Contact Information

Nico Cellinese (Logistics and general information) and Walter Joyce (Program), Peabody Museum of Natural History, Yale University, 170 Whitney Avenue, PO Box 208118, New Haven, Connecticut, 06511, U.S.A. Email: nico.cellinese@yale.edu or walter.joyce@yale.edu REGISTRATION

To register, please go to [www.phylocode.org](http://www.phylocode.org) and download the meeting second circular. Registration is set at \$165 for regular members and \$70 for students who register by the 1st of May 2006. Late registration is \$190 for regular members and \$75 for students who register by the 9th of June 2006. On-site registration is \$215 for regular members and \$85 for students.

**IMPORTANT DATES**

Arrival and Social Icebreaker: June 28, 2006  
 Conference Dates: June 29? July 2, 2006  
 On-site Registration: June 28 ? July 2, 2006  
 Registration Deadline: May 1, 2006  
 Late Registration Deadline: June 9, 2006  
 Abstract Submission Deadline: April 15, 2006

**OPENING SESSION**

The conference will begin on Thursday, June 29 at 9:00 with introductory comments from the Program Committee followed by a lecture by David Hillis (University of Texas, Austin). **SYMPOSIA**

**Species Symposium**

Organizers: David Baum (University of Wisconsin, Madison) and Benoit Dayrat (University of California, Merced)

Speakers: David Baum (University of Wisconsin, Madison), Julia Clarke (North Carolina State University),

Benoit Dayrat, Matthew Haber (University of California, Davis).

**Implementing Phylogenetic Nomenclature**

Organizer: Philip Cantino (Ohio University)

Speakers: Paul Berry (Washington University), Philip Cantino (Ohio University), David Marjanovic (University of Paris 6), Paul Sereno (University of Chicago)

**Phyloinformatics Symposium**

Organizers: Michael Donoghue (Yale University) and Nico Cellinese (Yale University)

Speakers: Michael Donoghue (Yale University), David Hibbett (Clark University), Mikael Thollessen (Uppsala University). Additional speakers will be announced.

Nico Cellinese, Ph.D. Botany Division Peabody Museum of Natural History Yale University 170 Whitney Avenue P.O. Box 208118 New Haven, CT 06520-8118, U.S.A. Tel. 203-432-3537 Fax 203-432-7907

Nico Cellinese <nico.cellinese@yale.edu>

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**GradStudentPositions**

KansasStateU MolEcolGrouse .....	15	URochester Evolution .....	22
OxfordU GenomeEvol .....	16	USheffield HumanAging .....	22
Trondheim AvianSocialForaging .....	16	USheffield SexualWeapon .....	23
UBasel ParentOffspring Interaction .....	17	USherbrooke EvolEcol .....	23
UEastAnglia InsectAgeing .....	17	UStAndrews Bioinformatics .....	24
UExeterCornwall 4 EvolBiol .....	18	UVictoria EvolEcol .....	24
UFribourg EvolGenetLearning .....	18	UWindsor FishEvol .....	25
UGlasgow BirdColourVariation .....	19	UmeaU SpatialPopEvol .....	26
UJena FloralEvoDevo .....	74	UppsalaU PlantEvol .....	26
ULiverpool Coevolution .....	20	VrijeU MolEcoEvol .....	27
UMelbourne SexualSelection .....	21		
UQueensland EvolGenomics .....	21		

**GRADUATE POSITION IN MOLECULAR ECOLOGY OF GROUSE AT KANSAS STATE UNIVERSITY.** One graduate assistantship is available at Kansas State University to investigate the impacts of wind power development on Greater Prairie-chickens. Field

research will involve live-trapping, behavioral observations, radio-telemetry and molecular ecology of grouse in the Flint Hills region of eastern Kansas. The emphasis of this project will be population genetics and breeding biology based on microsatellite markers. Responsibilities will include: locating suitable study sites, preparing reports, participation and coordination of field research, and working with industry partners. Applications will be accepted at a PhD level; qualified applicants should have a minimum of a Masters of Science in Biology and competitive GPA and GRE scores. Previous experience with avian field research techniques, molecular lab work, statistical software, and organization of field projects is desirable. The annual stipend for graduate positions will be \$21,000 per year including tuition. Information on graduate programs at K-State and current projects is available at [www.ksu.edu/wiselylab](http://www.ksu.edu/wiselylab). The start date will be August 15th, 2006. Interested individuals should send a cover letter outlining experience and research interests, a detailed curriculum vitae, unofficial copies of university transcripts and GRE scores, and contact information for three references to DR. SAMANTHA WISELY, Division of Biology, 232 Ackert Hall, Kansas State University, Manhattan, KS 66506-4901 (PH: 785-532-0978, FX: 785-532-6653, EM: [wisely@ksu.edu](mailto:wisely@ksu.edu)). Applications by e-mail are welcome, and will be accepted until the position is filled.

Dr. Samantha M. Wisely Assistant Professor, Wildlife Biology Division of Biology Ackert Hall Kansas State University Manhattan, KS 66506-4901 Office:785.532.0978, Lab:785.532.6413 Fax:785.532.6653, email: [wisely@ksu.edu](mailto:wisely@ksu.edu) <http://www.ksu.edu/wiselylab> [wisely@ksu.edu](mailto:wisely@ksu.edu)

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## OxfordU GenomeEvol

We are looking for applications to join the graduate programme at the MRC Mammalian Genetics Unit at Harwell, near Oxford UK. We are offering two evolution/bioinformatics projects, one on the evolution of mammalian genomes and one on the use of ontologies to describe mouse phenotypes. Students are generally registered on the Oxford University DPhil (PhD) programme.

Possible applicants should check <http://www.mgu.har.mrc.ac.uk/aboutus/jobs&study/study/> or

<http://www.findaphd.com/search/-showproject.asp?projectid=8918>

<http://www.findaphd.com/search/-showproject.asp?projectid=8917>

The deadline for applications is 28th February 2006.

John Hancock

Dr John M. Hancock Head of Bioinformatics, MRC Mammalian Genetics Unit, Harwell, Oxfordshire OX11 0RD, U.K.

E-mail: [J.Hancock@har.mrc.ac.uk](mailto:J.Hancock@har.mrc.ac.uk) Telephone: +44 (0)1235 84 1014 Fax: +44 (0) 1235 84 1210 WWW: <http://informatics.har.mrc.ac.uk/> Personal Page: <http://informatics.har.mrc.ac.uk/jmhwww/-johnhancock.html> [j.hancock@har.mrc.ac.uk](mailto:j.hancock@har.mrc.ac.uk)

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## Trondheim AvianSocialForaging

Ph.D. Project: 'Social foraging in cooperative birds'

We are seeking a PhD candidate to undertake detailed behavioural observations and experiments to explore the foraging strategies of wild cooperative birds, specifically concerning state-dependence, risk-sensitivity and cooperation. In the past, such experiments have almost exclusively been conducted on socially isolated birds held under laboratory conditions. However, habituated populations of wild Siberian jays (*Arvidsjaur*, northern Sweden) and apostlebirds (UNSW Fowlers Gap, Australia) make it possible to carry out more appropriate tests of evolutionary predictions within a natural ecological and social context. The starting point for understanding behavioural decision-making in these systems will be one based around individual 'state' (variation in body mass). Diurnal and seasonal variation in social foraging strategies will be explored, including comparisons during periods of food-caching and helping-at-the-nest. Quantitative comparisons will be made between observational data on natural foraging and the results of experimental tests using artificial feeders in the field. This position is fully funded for 4 years, and includes research expenses. The position carries a 25% teaching responsibility, contributing toward the Department's courses in animal behaviour. Application Deadline: 10th March 2006.

Contact: Prof. Jonathan Wright, Department of Biology, NTNU, 7491 Trondheim, Norway. Phone: +47 735 96070 Fax: +47 735 96100 E-mail: [jonathan.wright@bio.ntnu.no](mailto:jonathan.wright@bio.ntnu.no)



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## UBasel ParentOffspring Interaction

Ph.D.-position: Evolution and genetics of parental supply and offspring demand

We are seeking a motivated Ph.D.-candidate with keen interest in evolutionary and behavioral ecology, the genetics underlying behaviors, and the performance of experimental research.

In our group, we are studying the evolution of interactions/communication among family members using both theoretical and experimental approaches. Of particular interest are the provisioning of care by parents, and the demand for care by offspring. Such social interactions can create evolutionary complexities by inducing the potential for conflicts of interest (supply and demand need not coincide) and affecting the genetic trait architecture due to indirect genetic effects (IGE). Both factors can have profound effects on the evolution of interactions and communication among family members.

A major aim of our research is to experimentally disentangle genetic and environmental components underlying parent-offspring interactions and communication (including behavioral and chemosensory aspects), and investigate patterns of parent-offspring coadaptation as test of recent indirect genetic effects models (Kölliker et al. 2005. *Am. Nat.* 166, 506-516). Our experimental system is the European earwig (*Forficula auricularia*), a sub-social insect species where females tend eggs, and care for the first larval instars by provisioning them with food. We are maintaining a newly founded lab population of this species. The successful candidate will carry out breeding experiments and behavioral and chemosensory experiments to investigate the nature, functional significance and genetic architecture of maternal and offspring traits (e.g., "solicitation pheromones"; Kölliker et al. 2005. *Anim. Behav.* 69, 959-966).

Our research group is situated at the Zoological Institute of the University of Basel, and part of the larger group in Evolutionary Biology lead by Prof. Dieter Ebert. Additional groups at the institute and in the area of evolutionary biology will be established in the nearby future.

The successful candidate should have a Diploma/Master degree (or equivalent) in biology

/ natural sciences. Statistical skills will be an advantage, an interest in acquiring advanced statistical knowledge a prerequisite. Earliest possible starting date is April 1st, 2006.

For more details, please visit our website at [www.evolution.unibas.ch/koelliker](http://www.evolution.unibas.ch/koelliker), or mail to [mathias.koelliker@unibas.ch](mailto:mathias.koelliker@unibas.ch).

To apply, please send a CV / resume, a copy of your MSc.-thesis and contact details of two referees by March 15th 2006 to: [mathias.koelliker@unibas.ch](mailto:mathias.koelliker@unibas.ch); Dr. Mathias Kölliker, Zoological Institute, Evolutionary Biology, University of Basel, Vesalgasse 1, 4051 Basel, Switzerland (application by e-mail preferred).

[Mathias.Koelliker@unibas.ch](mailto:Mathias.Koelliker@unibas.ch)  
[mathias.koelliker@unibas.ch](mailto:mathias.koelliker@unibas.ch)

Mathias

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## UEastAnglia InsectAgeing

HOW DOES AGEING AND INBREEDING INFLUENCE SPERM QUALITY AND MALE FERTILITY IN INSECTS?

Starting October 2006. Supervised by Matt Gage, Brent Emerson and Tracey Chapman, School of Biological Sciences, University of East Anglia, NORWICH NR47TJ <http://www.uea.ac.uk/bio/> Widespread evidence shows that male ageing is associated with declines in sperm quality and fertility. Similarly, reproductive compromise occurs under inbreeding. This NERC-funded Ph.D. project (<http://www.nerc.ac.uk/funding/students/>) project will determine how ageing and inbreeding influence spermatozoal competence using insect models. Spermatozoa are generated continuously from dividing stem cells and mutations in the male germline may accumulate as individuals age or are inbred, while pathologies in the ageing/inbred testis may disrupt normal spermatogenesis. The project will seek to identify whether fertility in old and/or inbred males is reduced because of haploid damage, or diploid-derived compromises to sperm form and function.

The research models will be laboratory strains of the cricket *Gryllus bimaculatus*, and the flour beetle *Tribolium castaneum*. Both present excellent attributes for this work, and are familiar subjects in our laboratory for investigating sperm competition and sexual selection. Selective breeding can easily generate differential levels of inbreeding in laboratory strains. Repeated measures of either individuals through time (G.

bimaculatus), or different-aged cohorts (*T. castaneum*) will allow direct tests using representative sample sizes. *G. bimaculatus* adult males live for ~6 months in the laboratory. Sperm are transferred via an externally-attached spermatophore, so that sperm can be recovered from individuals repeatedly through time without harm to the male. Histological changes in the testis will also be screened. *T. castaneum* is exceptionally long-lived (up to 4 years) for its size and ecotype, allowing measures of Senescence in a domesticated species with an unnaturally long lifespan. For both species, females continuously oviposit and egg development can be tracked to assess fertilization and embryogenesis success. Phenotypic and genotypic spermatozoal compromise will be determined by a range of in vitro and in vivo histological and molecular approaches. In addition to measuring the consequences for fertility per se, the influence of male age and inbreeding in sperm competition will be measured.

Applicants should have at least a 2:1 degree in biological sciences and a strong interest in evolutionary biology. The student will join an active research group at UEA containing a number of Ph.D. students and postdoctoral researchers exploring sexual selection, sexual conflict, reproductive genetics and speciation. The School of Biological Sciences at UEA (<http://www.uea.ac.uk/bio/>) provides an excellent Ph.D. research and training environment in a Grade 5 department; details at [http://www.uea.ac.uk/menu/-study\\_and\\_research/grad/pgprospectus/schools/-biological\\_sciences.html](http://www.uea.ac.uk/menu/-study_and_research/grad/pgprospectus/schools/-biological_sciences.html) For more details on this project contact Matt Gage (m.gage@uea.ac.uk). For formal application, go to <http://www.uea.ac.uk/bio/-studentships/studentships/download.htm> -

Brent Emerson Lecturer in Evolutionary Biology Centre for Ecology, Evolution and Conservation School of Biological Sciences e-mail: b.emerson@uea.ac.uk University of East Anglia ph: (44) 01603 592237 Norwich NR4 7TJ fax: (44) 01603 592250 ENGLAND mob: (44) 0795 121 8827

b.emerson@uea.ac.uk

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### UExeterCornwall 4 EvolBiol

Four PhD positions are available at the University of Exeter's Cornwall Campus in the School of Biosciences Centre for Conservation and Ecology. The positions are: Genetic Integration and Constraints on the Evo-

lution of Complex Phenotypes - Dr J. Hunt and Dr T. Tregenza Sex peptide evolution in insects - Dr N. Wedell and Dr D. Hosken Antioxidants and the Cost of Egg production: Studies in Green Turtle - Dr J. Blount and Dr A. Broderick Molecular genetics of timekeeping and temporal kin recognition - Prof. A. Moore

These are research council funded positions are only open to UK/EU residents. Other positions are also available at the School's Streatham Campus. Further information can be found by visiting the School of Biosciences web site:

<http://www.biosciences.ex.ac.uk/postgraduate/-phd.php> Dr DJ Hosken Centre for Ecology & Conservation School of Biosciences University of Exeter, Cornwall Campus Tremough, Penryn, Cornwall TR10 9EZ UK

Tel: +44 (0) 1326 371843 D.J.Hosken@exeter.ac.uk

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### UFribourg EvolGenetLearning

PhD position (with funding) Evolutionary Genetics of Learning and Memory in *Drosophila* Tad Kawecki's group, University of Fribourg, Switzerland

In my research group we use experimental evolution and genetic approaches, and *Drosophila* as the study system, to address questions such as: -What environmental circumstances favor the evolution of improved learning ability? -What are the fitness costs of learning (trade-offs between learning ability and other fitness components)? -What is the genetic basis of heritable variation that evolution could use to produce improvements in learning and memory?

I am looking for a PhD student to work on the genetic basis of improved learning ability and memory in *Drosophila melanogaster*. The position is funded by the Swiss National Science Foundation (initial salary CHF 32,800 per year), and is for three years, with a possibility of extension for another year. Preferable starting date between May and September 2006. For more details on our research see our website ([www.unifr.ch/-biol/ecology/kawecki](http://www.unifr.ch/-biol/ecology/kawecki)).

The successful candidate should be highly motivated and able to work independently in the lab. Background in animal behavior and/or some experience with *Drosophila* genetics and molecular methods would help but are not required. The application is open to all nationalities. The research group functions in English; no

preexisting knowledge of French or German is required, although some knowledge of one of them makes living in Fribourg easier. Fribourg is a small bilingual university town in western Switzerland, 20 min by train from Bern and 45 min from Lausanne.

To apply, send your CV and a letter describing your research interests and experience to [tadeusz.kawecki@unifr.ch](mailto:tadeusz.kawecki@unifr.ch), with "Learning PhD" in the subject line (text of pdf files). Arrange for one or two letters of recommendation to be sent to the same address. The review of applications will begin on March 20, 2006.

Tad Kawecki

Tadeusz Kawecki Unit for Ecology and Evolution, Department of Biology University of Fribourg Chemin du Musee 10, CH-1700 Fribourg, Switzerland [www.unifr.ch/biol/ecology/kawecki](http://www.unifr.ch/biol/ecology/kawecki) phone +41 26 300 88 71 fax +41 26 300 96 98 e-mail [tadeusz.kawecki@unifr.ch](mailto:tadeusz.kawecki@unifr.ch)

[tadeusz.kawecki@unifr.ch](mailto:tadeusz.kawecki@unifr.ch)

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## UGlasgow BirdColourVariation

BBSRC Industrial CASE Ph. D. Studentship, University of Glasgow, UK Colour preferences in birds: species variation, associative learning & foraging decisions

Birds perceive colour differently to humans. In addition, to possessing a fourth retinal cone allowing them to see into the UV, birds perceive a greater diversity of colours than do humans. This project will use comparative analyses, as well as experiments in the lab and field to investigate the evolution of visual signals in foraging, and the role of colour preferences in learning and memory.

The project will be jointly supervised by Dr Kathryn Arnold (<http://www.gla.ac.uk:443/ibls/staff/staff.php?who=PGe~Pn>) <http://www.gla.ac.uk:443/ibls/staff/staff.php?who=PGe~Pn>) at the University of Glasgow where the project will be based and Dr Lucille Alexander at the WALTHAM Centre for Pet Nutrition.

For further details on the project please contact K. Arnold, Division of Environmental and Evolutionary Biology, Graham Kerr Building, University of Glasgow G12 8QQ ([K.Arnold@bio.gla.ac.uk](mailto:K.Arnold@bio.gla.ac.uk)). See also the University of Glasgow studentship website <http://www.gla.ac.uk/ibls/GradSchool>.

The closing date for applications is the 27th February 2006 and interviews will take place soon afterwards. The start date is 1st October 2006 and the duration of the project is 3 years. The maintenance grant in the first year (2006/7) will be £15,500. Non-EU students are not eligible for this studentship.

Dr. Kathryn Arnold

Royal Society University Research Fellow

Division of Environmental & Evolutionary Biology, Graham Kerr Building, University of Glasgow, Glasgow G12 8QQ

Tel. + 44 141 3302898 Fax. + 44 141 3305971 <http://www.gla.ac.uk:443/ibls/staff/staff.php?who=PGe~Pn>  
Kathryn Arnold <[K.Arnold@bio.gla.ac.uk](mailto:K.Arnold@bio.gla.ac.uk)>

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## UJena FloralEvoDevo

2 PhD positions or 1 Postdoc position

In our group we have openings for two graduate students or one Postdoc with strong interest in the evolutionary developmental biology of plants. The project focuses on the evolution of the interaction of floral homeotic proteins (MADS-domain proteins) by integrating experimental and bioinformatic approaches.

Floral homeotic proteins of higher eudicotyledonous flowering plants are key determinants of floral organ identity. They exert their function by constituting multimeric complexes that bind to cis-regulatory DNA sites in their target genes. We wonder how this situation originated during evolution by studying evolutionary informative taxa such as gymnosperms and basal flowering plants. Given the enormous importance of floral homeotic proteins and their interaction behaviour for flower development in eudicots, unraveling the evolutionary trajectories that led to the present day interaction network may help to elucidate the origin of the angiosperm flower - still one of the most enigmatic questions in biology.

In the experimental part of the project, interactions of floral homeotic proteins are studied by "wet lab techniques" such as gel retardation assays, the yeast-2/3/4-hybrid system and co-immunoprecipitation assays. Candidates applying for this part of the project should have a Diploma or Master degree in Biology, Biochemistry or related fields. Experience in the tech-

niques mentioned above is of advantage, but not absolutely required. Demonstrable practical experience in standard molecular biology techniques, including molecular cloning is essential, however.

In the bioinformatics part of the project, the question is addressed as to whether protein-protein interactions affect the rates of protein evolution. Candidates applying for this part of the project should have a Diploma or Master degree in Bioinformatics, Biochemistry, Biology or related fields, and should have demonstrable experience with methods of phylogeny reconstruction (e.g. Neighbor Joining, Maximum Likelihood, Maximum Parsimony) using sequence data, and profound knowledge of Molecular Evolution methods.

Postdocs applying for the position should be prepared to work in both parts of the project. Candidates will be considered on a competitive basis and only applications containing all the required documents will be reviewed. Applicants will be considered from 1st of March 2006 until the positions are filled. Interested candidates should send the following, preferably as PDF files via e-mail:

1. A statement detailing your research experience and scientific interests.
2. An updated Curriculum Vitae (including a complete list of publications).
3. The names and contact information of at least two scientists available for reference.

Please send your application or informal inquiries to Prof. Günter Theißen, Friedrich-Schiller-Universität Jena, Lehrstuhl für Genetik, Philosophenweg 12, D-07743 Jena, Germany; E-mail: guenter.theissen@uni-jena.de; Tel.: +49-3641-949550.

Introductory literature: Kaufmann et al. (2005). *Gene* 347, 183-198. Becker, A., Theißen, G. (2003). *Mol. Phyl. Evol.* 29, 464-489. De Bodt et al. (2003). *Trends Plant Sci.* 8, 475-483. Theißen, G., Saedler, H. (2001). *Nature* 409, 469-471.

mariana.mondragon@uni-jena.de

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## ULiverpool Coevolution

Experimental coevolution with multiple parasites

Dr. M.A. Brockhurst  
(michael.brockhurst@liverpool.ac.uk), Dr. A. Fen-

ton (a.fenton@liverpool.ac.uk)

Antagonistic coevolution between hosts and parasites, the reciprocal evolution of host defence and parasite counter-defence, is ubiquitous and there is a considerable body of work exploring this issue in simple one-host-one-parasite systems (e.g., Sasaki 2000; Restif & Koella 2003). However, coevolution with multiple parasite species is likely to be a major selection pressure for host organisms in nature? there may be various positive and negative interactions, each modifying the optimal strategies of the component species, affecting the evolutionary dynamics of the community. While exposure to multiple parasites is likely to have far reaching ecological, evolutionary and health implications no experimental studies (and few theoretical ones) have looked at coevolution between a host species and multiple parasite species.

An experimental evolution approach using populations of bacteria and their viral parasites (bacteriophage) is ideal for studying host-parasite coevolution, due to the rapid generation time of hosts and parasites, and the ease of experimental manipulation. We have previously demonstrated rapid coevolution between *Pseudomonas fluorescens* and phage phi2 (Brockhurst et al. 2003). This project will extend previous findings using a mixture of experimentation and theory to investigate the effect of exposure to multiple parasite species on: i) coevolutionary dynamics; ii) resistance evolution including costs and epistasis; iii) host and parasite local adaptation. As such, this project brings together ideas concerning host-parasite coevolution, the evolution of life history strategies and community ecology and will appeal to anyone interested in testing evolutionary theory.

References 1 Brockhurst MA, Morgan AD, Rainey PB and Buckling A (2003) Population mixing accelerates coevolution. *Ecology Letters* 6, 975-979. 2 Restif O and Koella JC (2003) Shared control of epidemiological traits in a coevolutionary model of host-parasite interactions. *American Naturalist* 161, 827-836. 3 Sasaki A (2000) Host-parasite coevolution in a multilocus gene-for-gene system. *Proc R Soc Lond B Biol Sci* 267, 2183-8.

Application by letter, indicating the project(s) of interest, giving the reasons for this, together with a c.v. including the names of two academic referees, should be sent as soon as possible to: Mrs. Linda J. Marsh, Research Support Office, School of Biological Sciences, The Life Sciences Building, Crown Street, Liverpool L69 7ZB (Fax: 0151 795 5122, email: bilores@liverpool.ac.uk). Review of applications begins from 1st March, 2006. Please indicate where you first saw the project(s) advertised.

Other projects advertised on the university website:

<http://www.liv.ac.uk/bio/postgrad/-studentships/uk/index.html> Mike Brockhurst  
<michael.brockhurst@liverpool.ac.uk>

Dr Raoul Mulder Senior Lecturer Department of Zoology University of Melbourne VIC 3010, Australia

Tel: + 61 3 8344 6245 Fax: + 61 3 8344 7909 Mobile: 0410 412 825

email. r.mulder@unimelb.edu.au homepage:  
[www.zoology.unimelb.edu.au/staff/mulder.htm](http://www.zoology.unimelb.edu.au/staff/mulder.htm)  
r.mulder@unimelb.edu.au

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## UMelbourne SexualSelection

PhD Scholarship opportunity in the Dept of Zoology, University of Melbourne

An exciting opportunity exists for a student to undertake a PhD study on Mutual sexual selection and sperm competition in the Black Swan.

We are seeking a highly motivated student to undertake a PhD study as part of a research project investigating pre- and post-copulatory sexual selection in this iconic bird.

Both male and female black swans have ornamental wing feathers that have a variety of complex social and sexual functions. This project will investigate the evolutionary significance of these mutual ornaments. It will involve field experiments (performed in conjunction with the deployment of an innovative transponder-based system to detect and record copulations) as well as laboratory-based paternity analysis, and participation in the management of a captive colony of swans.

The prospective student should have, or expect to obtain, a first- class or upper second-class honours degree or equivalent. Field experience, previous experience in a molecular laboratory, and technical talent with electronics are not essential but would be an advantage.

Stipend: \$22,000 per annum (plus full fee remission for international students)

Applications close 31 March 2006.

Please send applications, including the names and contact details of two referees and evidence of academic results to:

Dr Raoul Mulder Dept of Zoology University of Melbourne VIC 3010

For further information, contact:

Dr Raoul Mulder email: r.mulder@unimelb.edu.au phone: (03) 8344 6245 fax: (03) 8344 7909

or

Prof Mark Elgar email: m.elgar@unimelb.edu.au phone: (03) 8344 4338 fax: (03) 8344 7909

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## UQueensland EvolGenomics

PhD - EXPERIMENTAL ECOLOGICAL AND EVOLUTIONARY GENOMICS

School of Integrative Biology University of Queensland, Australia

I have a PhD scholarship available in my new lab in sunny Queensland. The PhD candidate will use a combination of molecular genetics, experimental evolution and field work to dissect the molecular genetic basis of adaptation in a mate recognition system. Students with broad interests in evolution, genetics and animal behaviour are encouraged to apply. An understanding of either population or quantitative genetics is essential and candidates with technical skills in molecular genetics (SNPs, microsatellites, microarrays) will be held in high regard.

If you are interested please email a CV and a short description of your research interests. Applications will be considered until a suitable candidate is found.

Contact: Steve Chenoweth on 07-3365-2188 or s.chenoweth@uq.edu.au

Non-Residents: Please note the scholarship is open to residents and non-residents alike and includes tax-free living expenses. However, tuition fees may not be covered in all cases for non-residents, although avenues do exist for their waiver.

Steve Chenoweth ARC Australian Research Fellow School of Integrative Biology University of Queensland, 4072 Australia

[http: www.sib.uq.edu.au](http://www.sib.uq.edu.au) ph: +61-7-3365-2188 fax: +61-7-3365-1655 email: s.chenoweth@uq.edu.au

Steve Chenoweth <s.chenoweth@uq.edu.au>

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## URochester Evolution

The Department of Biology at the University of Rochester is seeking applicants for graduate fellowships in Evolutionary Biology. The University of Rochester's nine evolution labs offer diverse research opportunities for Ph.D. students; the group is particularly strong in the areas of speciation and adaptation. For those broadly interested in evolution, a rotation program permits entering graduate students to explore their interests across several labs. Moreover, Rochester's Department of Biology is truly integrated with daily interactions among evolutionary, cellular, molecular, and developmental biologists. The Department is also in the midst of an exciting period of expansion with three new faculty having joined the evolution program over as many years. Financial support for Ph.D. students is excellent (\$22,000 U.S., health benefits, tuition remission), while teaching commitments are minimal (typically one semester or less per year). The University of Rochester is a mid-sized, private institution with a historic campus on the banks of the Genesee River north of New York State's beautiful Finger Lakes region. The deadline for applications is February 15th, 2006. More information may be found at "<http://www.rochester.edu/College/BIO/-graduate/EEBgradrecruit.html>" . reglor@ucdavis.edu

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## USheffield HumanAging

PhD Studentship

Reproduction, senescence and longevity in humans

Supervisor: Dr Virpi Lummaa ([www.sheffield.ac.uk/-aps/contacts/acadstaff/lummaa.html](http://www.sheffield.ac.uk/-aps/contacts/acadstaff/lummaa.html))

Department of Animal & Plant Sciences, University of Sheffield, U.K.

Whereas most animals reproduce until they die, in humans, females can survive long after being unable to reproduce themselves. This represents an enigma for current evolutionary thinking, for there should be no selection for living beyond one's reproductive capacity, but instead surplus resources should be allocated earlier

to reproduction to maximise fitness. One explanation is that, if mothers can increase the reproductive success of their adult offspring by helping with childcare, then a woman with genes for living beyond fertility may forward more copies of their genes to following generations than women dying early. Indeed, our previous research has shown that human females gain significant increments to their fitness by surviving beyond their reproductive potential, as for every 10 years that women survived beyond the age 50 in historical Finland, two extra grandchildren were produced.

That female humans accrue fitness during both reproductive and post-reproductive years indicates that the reproductive success gained prior to menopause represents only a fraction of total fitness. This has important implications for estimates of fitness, life-history trait optimisation and rates of senescence in humans that have typically been limited to analyses during reproductive phases. Consequently, it now appears that investment during reproduction is likely to trade off with fitness gains during post-reproduction, and that fitness in humans is governed by optimisation of trade-offs during both reproductive and post-reproductive phases. This leads to the intriguing possibility that humans suffer from both reproductive and post-reproductive senescence, with the relative importance of fitness accrued during each phase determining the ultimate lifespan.

This PhD project will determine the evolutionary and ecological causes and consequences of cooperative breeding and prolonged post-reproductive lifespan in humans. As the model system, we use extensive pre-collected, demographic pedigree datasets from several pre-industrial human populations. The data includes all basic life-history information as well as a range of ecological variables (social class, weather, harvest quality, famine, war, disease). The project will address the following questions;

1. How does reproductive timing and investment influence rates of reproductive and post-reproductive senescence?
2. How are rates of senescence influenced by interactions between reproductive timing/investment and maternal characteristics, ecology and demography?
3. How do patterns of fitness acquisition account for menopause, prolonged post-reproductive lifespan and ultimately the age of death?

The PhD project will be part of a long-term research project on life-history strategies in human populations. The student will join the large and lively Evolution and Behaviour research group in the Department of Animal and Plant Sciences in Sheffield. Students with a good first degree or Masters degree in areas such as Evolution, Behaviour, or Biological Sciences are encouraged

to apply. The position is equally open to all EU nationals.

Informal enquiries about this studentship should be addressed to Dr Virpi Lummaa (email [v.lummaa@sheffield.ac.uk](mailto:v.lummaa@sheffield.ac.uk)). More information is available at our website <http://www.huli.group.shef.ac.uk/-index.html> Interested applicants should send a full CV and covering letter including the names of two academic referees to:

Mrs Sue Carter Department of Animal and Plant Sciences, University of Sheffield, Sheffield. S10 2TN. UK.

Tel: +44 (0)114 222 4376, Fax: +44 (0)114 222 0002, email : [s.a.carter@sheffield.ac.uk](mailto:s.a.carter@sheffield.ac.uk)

Applications should be sent by Friday 3rd March 2006.

Relevant references include: Lahdenperä M, Lummaa V, Helle, Tremblay & Russell AF 2004 Fitness benefits of prolonged post-reproductive life span in women. *Nature* 428: 178-181.

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## USheffield SexualWeapon

### PhD Studentship

#### Genetic Basis of a Sexual Weapon

Supervisor: Dr Jon Slate (<http://www.jon-slate.staff.shef.ac.uk/>)

Department of Animal & Plant Sciences, University of Sheffield

The Soay sheep of St Kilda, a remote group of Scottish Islands, are one of the most-intensively-studied vertebrate populations in the world. From an evolutionary genetic viewpoint the population is interesting because several phenotypic polymorphisms are present, of which the most striking is presence/absence of horns. Males are either normal horned or have scurs (very small horns, that cannot be used as weapons). Females are either normal horned, scurred, or polled (a complete absence of horns). Given that scurred males cannot win aggressive interactions with normal-horned males it is surprising that scurred genes persist in the population. We have recently mapped the horns gene to sheep chromosome 10, but we do not yet know what the gene is. In this project the student will attempt to fine-map and identify the horns locus by studying pedigrees of Soay sheep and two domestic breeds - Merinos and Dorsets. The project involves collaboration with Professor Josephine Pemberton at Edinburgh Uni-

versity, and is jointly funded by the BBSRC and an Edinburgh-based CASE partner, Catapult. CASE studentships offer an additional £2500 p.a. above standard studentships. The project will involve visits to Edinburgh, and possibly New Zealand, as well as an opportunity to carry out field work on St Kilda. St Kilda is a world heritage site, and one of the most spectacular archipelagoes in the UK (<http://www.kilda.org.uk>). The Department of Animal & Plant Sciences has a dynamic and very well equipped Molecular Ecology laboratory and was awarded the maximum possible grade, 5\*, in the last Research Assessment Exercise. Applicants should have an interest in one or more of the following: evolutionary genetics, gene mapping, comparative genomics, molecular ecology.

Background material:

J Slate (2005). QTL mapping in natural populations: progress, caveats and future directions. *Molecular Ecology* 14:363-379

TH Clutton-Brock & JM Pemberton (editors) (2004) *Soay Sheep: Dynamics and Selection in an Island Population*. Cambridge University Press.

Informal enquiries to Jon Slate ([j.slate@shef.ac.uk](mailto:j.slate@shef.ac.uk))

Interested applicants should send a full CV and covering letter including the names of two academic referees to:

Mrs Sue Carter, Department of Animal and Plant Sciences, University of Sheffield, Sheffield. S10 2TN, UK. Tel: +44 (0)114 222 4376, Fax: +44 (0)114 222 0002, email : [s.a.carter@sheffield.ac.uk](mailto:s.a.carter@sheffield.ac.uk)

Applications should be sent by Friday 3rd March 2006

Jon Slate <[j.slate@sheffield.ac.uk](mailto:j.slate@sheffield.ac.uk)>

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## USherbrooke EvoEcol

### Graduate Student - Research Opportunity

I am looking for students at either the MSc or PhD level in the field of Evolutionary Ecology in the Département de Biologie at the Université de Sherbrooke, Québec, Canada (<http://www.usherbrooke.ca/biologie/>), to start as soon as May 2006.

Research in my lab aims at determining the impact of environmental change on evolutionary processes in wild animal populations by combining molecular ecology,

quantitative genetics, population dynamics and habitat modelling approaches.

The following are some potential projects, to be conducted in a Tree swallow (*T.bicolor*) population.

-Quantifying the stability of the population genetic structure across habitats

-Establishing the genetic determinants of survival across an environmental continuum

-Assessing the impacts of the environment on the paternal and maternal genetic contribution

Interested candidates should send a cover letter describing their research interests, a complete CV and names of two references at: [Dany.Garant@USherbrooke.ca](mailto:Dany.Garant@USherbrooke.ca)

Dany Garant Assistant Professor Département de Biologie Faculté des Sciences Université de Sherbrooke Sherbrooke, QC J1K 2R1, Canada  
Tel: (819) 821-8000 ext.3198 Fax: (819) 821-8049  
<http://www.usherbrooke.ca/biologie/recherche/-ecologie/garant.html> [Dany.Garant@USherbrooke.ca](mailto:Dany.Garant@USherbrooke.ca)

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## UStAndrews Bioinformatics

Dear All,

Applications are sought for a PhD studentship, "Gene function and genome evolution in eukaryotes", in the research group of Dr Daniel Barker (email [db60@st-andrews.ac.uk](mailto:db60@st-andrews.ac.uk)), School of Biology, University of St Andrews, with funding from the Biotechnology and Biological Sciences Research Council, UK (BBSRC).

Prospective applicants should first check they meet the eligibility requirements for residence and qualifications for the studentship.

### 1. ELIGIBILITY - RESIDENCE

NO FUNDING IS AVAILABLE FOR NATIONALS OF COUNTRIES OUTSIDE THE EU. Such nationals are not eligible for fees or stipend on this project.

FULL FUNDING IS ONLY AVAILABLE FOR BRITISH NATIONALS, covering tuition fees and a stipend paid to the student. Candidates who are British nationals and who have lived all their lives in the UK will automatically satisfy residence criteria.

Reduced funding (covering tuition fees only, with no stipend) may be available for non-British EU nation-

als.

Full details on eligibility are given in the document "Guide to studentship eligibility" on the BBSRC Web site (<http://www.bbsrc.ac.uk>).

### 2. ELIGIBILITY - QUALIFICATIONS

Candidates must normally hold a first or upper second class UK honours degree, or the equivalent qualifications gained outside the UK, in an appropriate subject.

### 3. FURTHER DETAILS

For informal enquiries, please contact Dr Daniel Barker, email:

[db60@st-andrews.ac.uk](mailto:db60@st-andrews.ac.uk)

For details of the project, please see:

[http://biology.st-and.ac.uk/postgrad/-PHDprojects.php?co=detail&iA\[2\]\[0\]=81&iA\[0\]\[0\]=-refID](http://biology.st-and.ac.uk/postgrad/-PHDprojects.php?co=detail&iA[2][0]=81&iA[0][0]=-refID)

For details of Daniel Barker's research, please see:

<http://biology.st-andrews.ac.uk/staff/barker-d.html>

For general information on postgraduate studies in the School of Biology at the University of St Andrews, including applications procedure, please see:

<http://biology.st-and.ac.uk/postgrad/index.php> Best regards,

Daniel Barker [db60@st-andrews.ac.uk](mailto:db60@st-andrews.ac.uk)

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## UVictoria EvolEcol

Two graduate student positions (Masters or Ph.D. level) at the University of Victoria, British Columbia.

I am seeking graduate students who are interested in insect evolutionary ecology and/or host-parasite interactions.

One position will be to work on an NSF funded project in collaboration with Martha Hunter (U. of Arizona) examining interactions between the reproductive parasites *Wolbachia* and *Cardinium* and their parasitoid wasp host *Encarsia inaron*. *Wolbachia* and *Cardinium* are bacterial endosymbionts of insects that manipulate host reproduction in diverse ways. In *Encarsia inaron*, symbiont infection causes reproductive incompatibilities, such that uninfected female hosts produce virtually no offspring when mating with infected male hosts. The goals of this project are to compare the incompatibilities induced by these unrelated symbionts, and to



understand how symbionts interact in their shared host, using differential antibiotic curing experiments, genetic crosses, and quantitative PCR measures of symbiont density. While this project will be based in Victoria, students will undertake a significant portion of the research at the U. of Arizona.

The second position is to work on an NSERC funded project on evolution and ecology of associations between *Drosophila* and their parasitic nematodes. Mushroom-breeding *Drosophila* are commonly infected with parasitic nematodes with strong effects on host fitness, including sterility. Possible projects include examining the role of parasitism in shaping differentiation of closely related *Drosophila* species, and testing for recent host range expansions using a combination of phylogeography and experimental infections. This project will involve laboratory work in Victoria and fieldwork in western Canada.

Information about the U. of Victoria graduate program can be found at <http://web.uvic.ca/biology/Grad.Progs/Grad.htm> If interested, please send a CV and short statement of research interests, and/or for further information, please contact me at [stevep@uvic.ca](mailto:stevep@uvic.ca)

Steve Perlman Department of Biology University of Victoria PO Box 3020, Stn CSC Victoria, BC, Canada V8W 3N5 email: [stevep@uvic.ca](mailto:stevep@uvic.ca) phone: 250-721-6319 <http://web.uvic.ca/biology/People/perlman/perlman.htm> [stevep@uvic.ca](mailto:stevep@uvic.ca) [stevep@uvic.ca](mailto:stevep@uvic.ca)

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## UWindsor FishEvol

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). Available projects include;

1) BC rainbow trout conservation genetics (MSc): The project will include field sampling and molecular genetic lab analysis of the Babine Lake rainbow trout, one of the few large-body morph populations in British Columbia, Canada. Working with BC Provincial and First Nations fisheries technicians, the student will collect DNA samples from adult and juvenile rainbow trout in Babine Lake as well as from tributary spawning populations. Microsatellite and mtDNA analysis of the

samples will be performed in the Conservation Genetics and Environmental Genomics Facilities at the GLIER. The goal will be to identify the stock composition in the lake and assign sport and food-fishery captures to specific source populations.

2) Feeding ecology of Lake Erie yellow perch predators (PhD): The project will include developing molecular genetic methods to determine gut contents to species level, validating the approach with captive yellow perch predators, and applying the technique to wild-caught yellow perch predators. The student will apply quantitative real-time PCR techniques with species-diagnostic mtDNA fragments to quantitatively determine the species present in digested gut content matter taken from field-caught piscivorous fish. The goal of the project is to determine the relative role of predation on Lake Erie yellow perch population structure and dynamics.

3) Mate choice in Chinook salmon: effects on fitness (PhD): The student will work as part of a team investigating the relative fitness of artificially-bred versus naturally-bred Chinook salmon. Adult Chinook salmon will be provided with the opportunity for mate choice, while fish from the same stock will be bred artificially as a control group. Behavioural, immunological, physiological and genetic analyses will be used to partition differences in performance of the offspring into additive genetic, environmental and genotype-by-environmental interaction components, and ultimately to assess the economics of the breeding strategies for aquaculture and conservation production. The student will focus on using molecular and quantitative genetics to partition offspring trait variance into genetic, environmental and interaction components. The student will also have the opportunity to assess gene expression patterns using both Q-RT-PCR and DNA microarray approaches.

Contact Dr. Heath at (519) 253-3000 (ext 3762) [dheath@uwindsor.ca](mailto:dheath@uwindsor.ca)

Daniel Heath Great Lakes Institute for Environmental Research University of Windsor 401 Sunset Ave Windsor, Ont, Canada N9B 3P4

E-mail: [dheath@uwindsor.ca](mailto:dheath@uwindsor.ca) Phone: (519) 253-3000, Ext 3762 Fax: 971-3616

[dheath@uwindsor.ca](mailto:dheath@uwindsor.ca)

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## UmeaU SpatialPopEvol

PhD position in spatial population ecology I am looking for a PhD-student to participate in the “Spatial heterogeneity, functional responses and predator-prey dynamics”, financially supported by the Swedish Research Council.

Why are there so many species? This question is motivated by the finding that simple models and model systems are fragile - species extinctions are ubiquitous- and increasing the realism by including more species tend to make systems even more unstable. Many ecologists believe that the answer is that spatial heterogeneity stabilizes ecological systems. The objective of the project is therefore to increase our understanding of how spatial heterogeneity affects predator-prey dynamics. This is done by applying and developing a new theoretical tool, moment approximation, which can be used to investigate how population dynamics are influenced by spatial heterogeneity. The project includes testing a predator-prey model based on moment approximation, developing empirical models of the relationship between predator-prey covariance and population densities, and studying the relationship between covariance and density dynamics in published models and empirical data sets. The project has an emphasis on mathematical and statistical models but will also include predator-prey experiments in the lab. The project is intellectually challenging but will likely yield publications in top-ranked journals.

More information at my webpage: [www.emg.umu.se/~personal/goran\\_englund.htm](http://www.emg.umu.se/~personal/goran_englund.htm) The application should include a short description of your research interests and why you are interested in the position, CV, copies of certificates from higher education, copies of publications including Bachelors/Masters thesis, and updated contact information for reference persons. Further information can be obtained from Dr. Göran Englund email: <mailto:goran.englund@emg.umu.se> goran.englund@emg.umu.se. Send your application, quoting appropriate reg.no 313 4666-05, to Umeå University, The Registrar, SE-901 87, Umeå, Sweden, no later than February 20, 2006.

\* Göran Englund \* Department of Ecology and Environmental Science \* Umeå Marine Sciences Centre \* Umeå University, 901 87 Umeå, Sweden \* Phone: +46 90 786 9728, FAX: +46 90 786 6705 \* E-mail: Goran.Englund@emg.umu.se \* Homepage: [http://www.emg.umu.se/sve/personal/goran\\_englund.htm](http://www.emg.umu.se/sve/personal/goran_englund.htm) \*

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## UppsalaU PlantEvol

PhD student position in Plant Ecology at the Evolutionary Biology Centre, Uppsala University, Sweden

We seek a PhD candidate with a keen interest in population biology and the ecology and evolution of local adaptation in plants. The PhD student will join the research group of prof. Jon Agren and will work in a project exploring the functional and genetic basis of local adaptation in the outcrossing model plant *Arabidopsis lyrata*. The project is based on a combination of field experiments designed to identify the targets and agents of selection on morphology and phenology, and quantitative and molecular genetic approaches to identify the genetic basis of adaptive differentiation. It focuses on potentially adaptive characters such as resistance to herbivory, flowering time, and flower morphology. Problems addressed include (a) to what extent is population differentiation maintained by selection? (b) to what extent can selection on morphological and phenological characters be attributed to variation in the abiotic and biotic environment, respectively? (c) What is the genetic basis of plant adaptation? The exact profile of the PhD project will be settled together with the supervisor.

The successful candidate should have a masters or honors thesis in ecology or a related field. Experience from work in population ecology or population genetics is an advantage. Proficiency in English is a requirement.

Applications should include a brief description of undergraduate training, research interests and research experience, and a motivation of why the position is of interest. It should further include Curriculum vitae, an authorized copy of the undergraduate degree, and the names and contact information (address, email address, and phone number) of two-three referees. Relevant publications (including BSc/MSc thesis) should be enclosed.

The candidate will receive her/his postgraduate training within the postgraduate school at the Evolutionary Biology Centre (see [http://www.ebc.uu.se/-index\\_eng.htm](http://www.ebc.uu.se/-index_eng.htm)). The postgraduate training comprises four years of full time studies. The successful candidate will receive a postgraduate fellowship the first year (14400 SEK/month) and a postgraduate position year 2-4 (18700-20900 SEK/month). The position can be combined with up to 20% of teaching assistantship,

which will then prolong the position accordingly. Tentative starting date: 1 April 2006.

Please, feel free to contact Prof. Jon Agren (phone +46 18 471 2860, jon.agren@ebc.uu.se) for more information.

Applications, quoting the reference number UFV-PA 2006/197 should arrive no later than February 15, 2006 at the Registrars office, Uppsala University, Box 256, SE-751 05 Uppsala, Sweden.

Jon Agren Dept. of Plant Ecology Evolutionary Biology Centre Uppsala University Villavagen 14, SE-752 36 Uppsala, Sweden Phone: +46-18-471 2860 Fax: +46-18-55 34 19

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## VrijeU MolEcoEvol

Graduate position Molecular Ecotoxicology (f/m) Full working hours

Vacancy number: 1.2005.00247

The department of Animal Ecology, which is part of the Faculty of Earth and Life Sciences, Vrije Universiteit Amsterdam (The Netherlands), has a vacancy for a PhD student.

### Job description

The student will conduct a research project entitled: Stress-based expression profiles in soil arthropods, which is part of the program Assessing the living soil. An ecogenomics approach to explore and unlock sustainable life support functions of soils. Genomic tools will be used to characterize and evaluate biological functions of the living soil. The aim is to link expression profiles with characteristics of the soil, in particular with the degree and type of pollution. Eventually this will lead to the development of a rapid microarray-based method of soil diagnosis. The aim of this Ph.D. project is to provide an understanding at the gene expression level of inhibition of *Folsomia candida* reproduction, growth and survival by soil contaminants. Firstly, the invertebrate soil quality chip will be used to study transcription profiles of springtails exposed to clean soils from different environments to create a normal operating range (NOR) of the *F. candida* transcriptome. Subsequently, effects of soil contaminants (metals, PAHs, oil) on the *F. candida* NOR will

be investigated. The data will give more insight in the molecular consequences of sub lethal effects and will contribute to the development of a new framework for the diagnosis of ecological quality of soils.

### Requirements

Molecular biologist with an interest in ecotoxicology;

Experience in statistical analysis of gene expression data is an advantage;

Good social skills necessary for working in the laboratory with colleagues.

### Particularities

The appointment will be fulltime for an initial duration of 12 months. After satisfactory completion the appointment will be extended to a total duration of 4 years. Visit our website <<http://www.vu.nl/-vacatures>>[www.vu.nl/-vacatures](http://www.vu.nl/-vacatures) for a review of working conditions at the VU.

### Salary

The gross salary will be 1.877 Euro a month (first year) gradually increasing to -2.407, -*amonth(fourthyear)*.

### Additional information

About 75% of the time is devoted to research, the remaining 25% to education and assistance in courses. The education program is organized by the national research school on Environmental Science (SENSE). Applicants may request the complete project description from Désirée Hoonhout, tel +31-20 59 87004. Further information can be obtained from Dr. D. Roelofs, tel +31-20 59 87078, e-mail: <[mailto: dick.roelofs@ecology.falw.vu.nl](mailto:dick.roelofs@ecology.falw.vu.nl)> [dick.roelofs@ecology.falw.vu.nl](mailto:dick.roelofs@ecology.falw.vu.nl), or Prof.dr. N.M. van Straalen, tel: +31-20 59 87070. The project will start by March 1st 2006.

### Applications

Written applications should be addressed before February 1st to the Vrije Universiteit, Dr. J.M.R.M. Neutelings, Managing Director, Faculty of Earth and Life Sciences, De Boelelaan 1085, 1081 HV Amsterdam, The Netherlands (the vacancy number should be mentioned on the letter and on the envelop) or e-mail to: <[mailto: %20falw-vacature@falw.vu.nl](mailto:%20falw-vacature@falw.vu.nl)> [falw-vacature@falw.vu.nl](mailto:falw-vacature@falw.vu.nl).

### Dick Roelofs

Vrije Universiteit, Animal Ecology Room H-147 Phone: +31-20-5987078

[dick.roelofs@ecology.falw.vu.nl](mailto:dick.roelofs@ecology.falw.vu.nl)

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### ChicagoBotanicGarden SummerField

Summer Field Research for undergrads or recent graduates

Are you interested in gaining field research experience and learning about the ecology and evolution of plants and plant-animal interactions in fragmented prairie? We are looking for field assistants (2-4 undergraduates and one recent grad) for an NSF-funded research project on habitat fragmentation of the tallgrass prairie. We are investigating how small plant population sizes influence inbreeding, demography, pollination, and herbivory in the purple coneflower (*Echinacea angustifolia*).

No experience is necessary, but you must be enthusiastic and hard-working. You will survey natural plant populations, measure fitness and floral traits in experimental plots, hand-pollinate plants, observe & collect insects, and assist in all aspects of research. Housing is included and there is a stipend. There are opportunities for doing an independent project.

If you want more information or wish to apply, please look here <http://echinacea.umn.edu/> or contact Stuart Wagenius. Applications due 16 March 2006.

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Stuart Wagenius, Ph.D. Institute for Plant Conservation Chicago Botanic Garden 1000 Lake Cook Road Glencoe, IL 60022

phone: 847 835 6978 fax: 847 835 5484

email: [swagenius@chicagobotanic.org](mailto:swagenius@chicagobotanic.org)

[SWagenius@chicagobotanic.org](mailto:SWagenius@chicagobotanic.org)

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### CityUNewYork EvolGenetics

ASSISTANT PROFESSOR EVOLUTIONARY GENETICS Queens College of the City University of New York

The Department of Biology at Queens College of the City University of New York seeks a tenure-track Assistant Professor to begin September 1, 2006. We seek candidates with a doctoral degree, postdoctoral experience,

rience, and a record of research accomplishment in the area of evolutionary genetics. Suitable research areas include population genetics, comparative genomics, and molecular ecology, and related fields. Successful candidates will be expected to establish an externally funded research program and teach at the undergraduate and graduate (M.A./Ph.D.) levels. Please submit a cover letter, a CV, a two- to three three-page research plan, a statement of teaching interest, and arrange for submission of three current letters of recommendation. Candidates must submit materials by March 27, 2006 to: Dr. Stephane Boissinot, Chair, Evolutionary Genetics Search Committee, Department of Biology, Queens College of CUNY, 65-30 Kissena Blvd., Flushing, NY 11367-1597. An equal opportunity/affirmative action/IRCA/Americans with Disabilities Act Employer

Stephane Boissinot, Ph.D. Department of Biology Queens College, CUNY 65-30 Kissena Boulevard Flushing, NY 11367 Tel: 718 997 3437 email: stephane\_boissinot@hotmail.com

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### CornellU LabTech

Technician Position Available in Quantitative and Evolutionary Genomics Laboratory at Cornell University.

Seeking qualified applicants for a laboratory technician position with Jason Mezey at Cornell University. The lab focuses on addressing fundamental questions about the genetics and evolution of complex phenotypic traits. The successful candidate will provide technical assistance for molecular biology research. Candidates should have a working knowledge or direct experience with DNA and RNA extractions and manipulations, PCR, DNA cloning, rtPCR. The ideal candidate will also have experience in bioinformatics research, statistical analysis of large data sets, or computational work and a strong interest in devoting time to computational projects that are being conducted in the lab. The amount of time devoted to molecular lab versus bioinformatics projects will depend on the strengths of the applicant.

About the Group:

Jason Mezey is an Assistant Professor of Biological Statistics and Computational Biology (BSCB). Mezey's lab is closely associated with the labs of BSCB faculty Carlos Bustamante and Adam Siepel, and also has close ties with the labs of Molecular Biology and Genetics

faculty Andy Clark and Chip Aquadro and is part of a larger computational biology and genomics community at Cornell. For more information see:

[http://www.bscb.cornell.edu/Homepages/-Jason\\_Mezey/](http://www.bscb.cornell.edu/Homepages/-Jason_Mezey/) [http://www.genomics.cornell.edu/About\\_Cornell\\_and\\_Ithaca/](http://www.genomics.cornell.edu/About_Cornell_and_Ithaca/)

Cornell is a top-ranked research university with particular strengths in the life sciences. It is located in Ithaca, NY, the cultural center of the scenic Finger Lakes region of central New York, which is known for its spectacular gorges and waterfalls, lake-side wineries, and rolling farmland. Ithaca has been called the "best emerging city" in the US (Cities Ranked and Rated, 2004). It is about a 4-hour drive from New York City.

To Apply:

Apply through the Cornell University Office of Human Resources:

<http://www.ohr.cornell.edu/jobs/index.html> and search under Job Number: 05023 (Staff, non-academic, Technician III). Informal inquiries to [jgm45@cornell.edu](mailto:jgm45@cornell.edu) are welcome.

Jason Mezey Department of Biological Statistics and Computational Biology 169 Biotechnology Building Cornell University Ithaca, NY 14853

Cornell University is an affirmative action/equal opportunity employer.

[jgm45@cornell.edu](mailto:jgm45@cornell.edu) [jgm45@cornell.edu](mailto:jgm45@cornell.edu)

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### DurhamNC NESCent AssistDirector

Assistant Director of Informatics National Evolutionary Synthesis Center

The National Evolutionary Synthesis Center (NESCent) is an NSF-funded center in Durham, North Carolina jointly managed by Duke University, North Carolina State University, and the University of North Carolina at Chapel Hill.

NESCent seeks a senior bioinformaticist to create and lead a team in developing and deploying software/database tools for evolutionary biology. The incumbent will lead the conception, design, and deployment of software/database tools to meet the needs of developers and end users in the community (the global community of evolutionary biology researchers and educators). The incumbent will report to NESCent's As-

sociate Director of Informatics and will supervise various system and database administrators, application developers and bioinformatics specialists. The incumbent will collaborate with the Center directors in assessing user requirements for software/database tools of use to the evolutionary biology user community and seeking external financial support for major informatics initiatives. The position requires close collaboration with domain scientist/developers to gather user requirements and translate those requirements into software/database tools. The incumbent will contribute directly to software projects within his/her area of expertise.

#### Duties and Responsibilities:

1. Provide technical leadership: Provide advice and technical guidance to the Associate Director for Informatics. Collaborate with NESCent senior scientists, fellows and visitors to articulate their software/database needs into requirements documents. Assist the Associate Director for Informatics in setting priorities and goals for scientific software support. Adapt and structure development with respect to specific timelines and milestones. Make decisions required to create and deploy software/database applications, including decisions regarding hardware systems and personnel. Supervise implementation and maintenance of software modules for automated building and testing of code. Guide the preparation of software releases, and create policies and strategies for orderly scheduled releases.
2. Contribute to software development: Contribute directly to the development of applications deemed to be of high priority to NESCent.
3. Supervision of informatics staff: Supervise various system and database administrators, application developers and bioinformatics specialists. Develop positions and work plans, employ and supervise staff, determine salaries, and perform evaluations.
4. Proposal preparation: Prepare proposals that seek external financial support for major informatics initiatives.
5. Communication and training: Inform/instruct NESCent staff, partner developers, and scientists of new techniques in software/database development. Communicate NESCent informatics activities to the scientific community through presentations at meetings. Provide reports on informatics activities to the Associate Director for Informatics. Serve as an expert resource for developers or scientists collaborating with the Center.

Education/Training: Advanced degree in biology, com-

puter science or related field. Proven ability to design and implement complex software usable by and useful to life scientists. Proven technical leadership and team orientation. Outstanding interpersonal and communication skills.

Experience: Five or more years of computing experience.

Technical Skills: Major operating systems, programming languages, database systems, and communication protocols.

Minimum Salary: \$ 74654

To apply, please send a CV and contact information for 3 references to Karen Henry (khenry@nescent.org) or specify position number CAM318370-021706 at the following URL: <https://apprefp.hr.duke.edu/JP/>. For inquiries, please contact Associate Director for Informatics Todd Vision at [tjv@bio.unc.edu](mailto:tjv@bio.unc.edu).

[tjv@bio.unc.edu](mailto:tjv@bio.unc.edu)

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### ElmhurstCollege EvolBiol

Assistant Professor Biology Description: The Department of Biology at Elmhurst College invites applications for a tenure-track position in cell biology at the Assistant Professor level to begin Fall 2006. The successful candidate will be expected to teach principles of Biology, genetics and develop an upper level cell biology/immunology course. Opportunities exist to develop classes in the area of the candidate's expertise. The successful candidate is expected to establish a productive, externally funded research program utilizing undergraduate biology majors. The Biology Department has six full-time faculty members, a secretary, lab coordinator and a number of student teaching assistants. Faculty members teach both the lecture and laboratory sections of each course. Our biology majors often enter professional schools in the areas of medicine, allied health or basic research. We have a strong group of secondary education majors as well as affiliations with neighboring hospitals where our students can complete tracks in Nuclear Medical Technology and Clinical Laboratory Science. The Department of Biology has four excellent teaching laboratories, a greenhouse, smaller research labs associated with each office, a student laboratory and other amenities. Applicants must demonstrate a strong commitment to undergraduate teaching and research. Scholarly activity that is appro-

appropriate to a Liberal Arts setting is also required. Submit a letter of application, curriculum vitae, graduate and undergraduate transcripts, statements of teaching interest and research plans, and three letters of reference to: Dr. Tamara Marsh, Search Committee Chair, Biology Department, Elmhurst College, 190 Prospect Ave., Box 145, Elmhurst, IL 60126 Elmhurst College is an equal opportunity employer fully committed to achieving a diverse workforce.

Qualifications: A Ph.D. is required and teaching experience preferred.

Application Deadline: Until position is filled.

Contact Person: Dr. Tamara Marsh

Contact Address: Search Committee Chair Biology Dept. Elmhurst College Box 145 190 Prospect Ave. Elmhurst, IL 60126t

paula@elmhurst.edu

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### European FieldAssist

#### PLANT EVOLUTIONARY ECOLOGY IN FRANCE & PORTUGAL VOLUNTEER FIELD ASSISTANTS NEEDED

We (collaborators at Indiana University) are looking for enthusiastic field assistants to participate in a project on the conflict between natural and sexual selection in a European wildflower, *Silene latifolia*. This summer we are examining whether populations from Portugal and France are locally adapted to their home sites. Field assistants would measure morphological, floral and fitness traits in our European experimental plots as well as conducting surveys of the natural populations.

Field work extends from early May through August; field assistants should be available for at least two months during this period. Experience is not necessary but enthusiasm and commitment to field work are essential. Developing independent project is a possibility for experienced and highly motivated and individuals. A stipend for housing expenses may be available if needed.

Applications (letter of motivation, name and email addresses of two references, and your curriculum vitae or resume) should be sent via email to danlb@indiana.edu

If you want more information please consult the fol-

lowing webpage, <http://mypage.iu.edu/~danlb/summer.htm> You can also contact Dr. Daniela L. Bell via email (danlb@indiana.edu) or phone +1 812-355-0820.

danlb@indiana.edu danlb@indiana.edu

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### IPK Germany PlantGeneFlow

Hi,

I have a six month internship position from the "The International Association for the Exchange of Students for Technical Experience"

<http://www.iaeste.org/network/index.html> The position will begin in April/May 2006, and will involve both flow cytometric analyses of apomictic (asexual reproduction through seed) seed production, and molecular genetic analyses (microsatellite) of plants in the North American genus *Boechera* (wild relative of *Arabidopsis*). I am looking for someone who has basic molecular biology skills who also likes to work with computers, since many of our analyses are automated. Knowledge of German would be helpful, but is not required.

The candidate must be registered at a university, but you should also contact your local IAESTE office for more details on any restrictions (see above link).

The IPK is a large and well-endowed research center located about 2 hours southwest of Berlin, in the foothills of the beautiful Harz Mountains.

Please don't hesitate to contact me if you have any questions, or would like to apply.

Best wishes, Tim

Dr. Tim Sharbel Apomixis Research Group Dept. of Cytogenetics Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstraße 3, D-06466 Gatersleben Germany Email: sharbel@ipk-gatersleben.de

Apomixis Group Webpage <http://www.ipk-gatersleben.de/en/02/04/05/index.html> IPK Webpage [www.ipk-gatersleben.de](http://www.ipk-gatersleben.de) tel: +049 (0)39482 5608 fax: +049 (0)39482 5137

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## KansasStateU EcologicalGenomics

The Ecological Genomics Visiting Scholar Program provides sabbatical opportunities at Kansas State University for researchers interested in Ecological Genomics. Applicants should contact the PI of a potential host laboratory ( <<http://www.k-state.edu/ecogen/resgroup.html>> <http://www.k-state.edu/ecogen/resgroup.html>) to explore space availability and overlap in research interests. The start-date and duration of appointments are flexible. Visiting scholars will have full access to several excellent university resources including the KSU Gene Expression Facility ( <<http://www.k-state.edu/gene-exp/>> <http://www.k-state.edu/gene-exp/>) and the nearby Konza Prairie Biological Station ( <<http://climate.konza.ksu.edu/>> <http://climate.konza.ksu.edu/>).

Recipients of this award will receive a generous stipend and a substantial monetary supplement to support research endeavors. Review of applications will begin March 25, 2006, and will continue quarterly until program resources are committed. Visiting scholars will be expected to present a research seminar of their work. The Visiting Scholar Program is sponsored by a Kansas State University Targeted Excellence Award in Ecological Genomics. More information on the Ecological Genomics Program at KSU can be found at: <<http://www.k-state.edu/ecogen/>> <http://www.k-state.edu/ecogen/>> Full applications consist of a description of proposed research\*, C.V., and a letter of support from the host PI at KSU. A cover letter also should be included indicating a proposed start date. Electronic applications can be sent to <<mailto:dmerrill@ksu.edu>> dmerrill@ksu.edu. Paper applications should be mailed to Ecological Genomics, Visiting Scholar Program, Kansas State University, Division of Biology, 231 Ackert Hall, Manhattan KS 66506-4901. Questions can be directed to Doris Merrill, 785-532-3482.

\*Descriptions of proposed research are not to exceed 5 numbered pages, single-spaced, 11 point font or larger (not more than 16 characters/inch) with one inch margins. Proposals must be fully referenced (references are not included in the five page limit). Sections of the proposal should include Specific Aims, Background and Significance, Preliminary data (if any), and Research Plan. An abstract of 200 words or less should appear

on page one.

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4th Annual Ecological Genomics Symposium: Plan now to attend the 2006 Ecological Genomics Symposium in Kansas City on November 3, 4, and 5. Details will be available soon on our website, <<http://www.ksu.edu/ecogen>> [www.ksu.edu/ecogen](http://www.ksu.edu/ecogen)!

dmerrill@ksu.edu

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## LeibnizInst FishPopulations

The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) in Berlin, Germany invites 6 applications for an interdisciplinary project on understanding the dynamics of recreational fishing.

The IGB is a member of the Research Society "Wilhelm Gottfried Leibniz" (WGL) comprising 84 independent, non-governmentally based, basic research institutes. IGB is devoted to study spatio-temporal dynamics, structures and functions of freshwater ecosystems. From an applied research perspective, the IGB has a major commitment to study fish and fisheries systems including aquaculture and to develop scientifically based principles for sustainable management. Two of the five departments are exclusively dealing with fish and fisheries. The IGB has an annual budget of more than 8 million , hosts 65 full time scientists from various scientific disciplines such as fish ecologists, fisheries scientists, hydrologists, chemists, microbiologists, limnologists, 20 Ph.D. students depending on external funding and about 60 administrative and technical employees. Several experimental lakes, extensive laboratory facilities practicing cutting edge molecular genetics and physiological methods are available including a brand new wet lab constructed in 2005. About 20 earthen ponds and several tanks and raceways are also available together with a several field stations for aquatic research. The institute is located in a water-rich landscape in the highly vibrant German capital Berlin, next to the 700 ha Lake Mueggelsee, and is in its form unique in central Europe. The institute has close collaborations with all three Berlin universities and runs a Masters Programme entitled "Fishery Science and Aquaculture" at Humboldt-University of Berlin ([http://www.agrar.hu-berlin.de/studium/index\\_st\\_en.html](http://www.agrar.hu-berlin.de/studium/index_st_en.html)). Therefore, scientific work conducted at IGB can be submitted as a doctoral dissertation to one of the Berlin universities.



Heads of Departments typically are also university professors. Within IGB, the research group dealing with “Sustainable Recreational Fisheries Management” lead by Dr. Robert Arlinghaus, has recently been awarded a prestigious grant for the period 2006-2008/2009 entitled “Adaptive Dynamics and Management of Coupled Social-Ecological Recreational Fisheries (ADAPTFISH)”. Within this program one post doc position and five PhD student positions are now open.

6 research positions All positions start as soon as possible and are limited to three years.

1 Post doc position (Ref. nr. ADAPTFISH-1) Integrative modelling of fish-angler interactions at the landscape level.

1 PhD student position (Ref. nr. ADAPTFISH-2) Institutional conditions for sustainable governance of a transforming inland fisheries sector.

1 PhD student position (Ref. nr. ADAPTFISH-3) The complexity of angler behaviour constraint by fishing quality and fishing regulations.

1 PhD student position (Ref. nr. ADAPTFISH-4) Modelling the ecological and evolutionary impact of size-selective recreational fishing.

1 PhD student position (Ref. nr. ADAPTFISH-5) Inducing phenotypic and genetic changes in an experimentally harvested fish stock.

1 PhD student position (Ref. nr. ADAPTFISH-6) Effects of angling on reproductive output and fitness in fish.

ADAPTFISH aims at analysing recreational fisheries from both a social scientific and biological perspective including development of integrative models investigating the interaction between anglers and the ecological systems. The ultimate goals of ADAPTFISH are to facilitate understanding of the complexity of fish-angler-interactions, the angler behaviour per se and the potential biological impacts of angling and to derive management implications than can improve fisheries management in the future. PhD students and the post doc will in principle be based in Berlin (Germany). However, several national and international partners are part of the program and students and the post doc will be working closely with these partners in their home institutes depending on the specific project’s aims. Therefore, international applications are highly welcome to this truly interdisciplinary and international opportunity. This will ensure that the idea of interdisciplinary and internationality will flourish for the benefits of the students’ work and the advancement of recreational fisheries science. It is also possible, depending on the

student’s background and network, to establish new collaborations and host the people at least temporarily outside Berlin. It is also conceivable that students attend a Ph.D. programme at an international university, but answer research questions from Germany. In this case, significant travelling will be involved, for which some funds are available as well. The current partners of ADAPTFISH that serve as supervisor of the students

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## Lucerne EcolModeller

Eawag (Swiss Federal Institute for Aquatic Science and Technology) is a Swiss-based, internationally-operating aquatic research institute committed to ecological, economical and socially-responsible management of water resources. The Department “Surface Waters Research and Applications” is offering a tenure track position for interdisciplinary research in

Aquatic Ecological System Analysis and Modelling (Ph.D. degree)

Location: EAWAG Limnological Research Centre Kastanienbaum (near Lucerne)

We are seeking an innovative person with an excellent track record in science and new ideas for future interdisciplinary projects. She/he should be familiar with the general tools of system analysis and physical / biogeochemical as well as population biological and genetic modelling, be interested in biogeochemical processes in aquatic systems, and in how they link to ecological processes at population and ecosystem level. He/she should be interested in collaboration with scientists of other disciplines in interdisciplinary projects and ready for external and internal consulting on modelling questions to non-specialists. A strong background in math or numerics as well as in aquatic physics, aquatic ecology, environmental engineering or biogeochemistry is required. The successful candidate is expected to build up a small research group and interact intensively and in an interdisciplinary fashion with the local laboratory in Kastanienbaum (80 persons), and with the departments System Analysis / Modelling, Limnology, Fish ecology & Evolution and other research groups at Eawag. Teaching at ETH is envisaged in the long-term.

“Surface Waters Research and Applications” consists of six research groups involved in the entire setting of aquatic research from microbiology, geochemistry and isotope analysis to physics. A special focus is the interdisciplinary approach to mass fluxes and cycling in aquatic ecosystems. Our facilities include besides a fully equipped laboratory on molecular biology, analytical chemistry and stable isotopes, as well as excellent facilities for field work.

Please send your application to Personnel Department, Eawag, Ueberlandstrasse 133, CH-8600 Duebendorf. For additional information please consult our homepage <<http://www.eawag.ch/->www.eawag.ch> or contact Alfred J. Wüest (<<mailto:alfred.wueest@eawag.ch>>alfred.wueest@eawag.ch). E-mail applications will be deleted and not considered. Application deadline: March 15, 2005.

[ole.seehausen@eawag.ch](mailto:ole.seehausen@eawag.ch) [ole.seehausen@eawag.ch](mailto:ole.seehausen@eawag.ch)

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## MichiganStateU EvoDevo

### Research Assistant Job

I am looking for an active and well-organized person with relevant research experience to work as a laboratory manager and research assistant in the laboratory of Alexander Shingleton in the Department of Zoology at Michigan State University. My research involves the nutritional regulation of size, and the mechanism and evolution of allometry in *Drosophila*. The successful applicant will be helping establish a new laboratory and research program, so will have considerable influence over the future direction of their work.

The precise details are:

**REQUIRED:** Bachelor's degree in genetics, developmental biology, molecular biology or related field; one to three years of related and progressively more responsible or expansive work in area of genetics or developmental/molecular biology; experience planning research methodology and developing, adapting, and updating research procedure.

**DESIRED:** Good understanding of *Drosophila* genetics; experience in a *Drosophila* development laboratory; experience with basic microscopy (dissecting, compound and confocal) and staining techniques (anti-body, in situ hybridization); experience with microscope imaging- software and statistical packages; good basic molecular biology skills (e.g. PCR, West-

ern/Southern/Northern blotting).

**BASIC FUNCTION:** Assists in coordinating laboratory research activities; helps plan, design and execute experiments on *Drosophila* development; uses various molecular and microscopy techniques to obtain research data; analyzes results using imaging and statistical packages; researches current literature to determine most economical, efficient and productive research methods.

**CONDITIONS:** Pay >\$35,042 p.a..This is a 12-month position, renewable for several years subject to funding.

Please apply by email with a letter expressing interest, your CV and names of three references to Alex Shingleton ([shingle9@msu.edu](mailto:shingle9@msu.edu)). Applications should be received by February 31, 2006. Start date is expected to be April 1, 2006.

See [www.msu.edu/~shingle9](http://www.msu.edu/~shingle9) for more details.

Alexander W. Shingleton Assistant Professor Ecology, Evolutionary Biology & Behavior Program Genetics Program

Department of Zoology Natural Sciences Building  
Michigan State University East Lansing, MI 48824 Tel:  
517-353-2253

[shingle9@msu.edu](mailto:shingle9@msu.edu) [shingle9@msu.edu](mailto:shingle9@msu.edu)

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## NCStateU StatGenetBioinformatics

### Position 1:

Assistant Professor in Computational Biology and Bioinformatics

The North Carolina State University Bioinformatics Research Center (BRC) seeks highly qualified candidates for a tenure-track Assistant Professor with a research emphasis in one or more of the following areas: genomics, proteomics, networks and population genetics.

The successful applicant will have a demonstrated record of excellence in research and good communication and teaching skills. This appointment will be in either the Department of Genetics or the Department of Statistics, with primary teaching responsibilities in the Bioinformatics Program.

North Carolina State University is a leading center of activity in genomic sciences, with substantial strength in bioinformatics and statistical genetics (please see

<http://bioinformatics.ncsu.edu>). The NCSU Graduate Program in Bioinformatics was established in 1999 and has produced 13 Ph.D. and 28 Master of Bioinformatics graduates. There are 53 students currently in the program, supported by NIH Training Grant funds, University Fellowships, teaching and research assistantships and industry internships. The Bioinformatics Research Center was established in 2000 to work collaboratively with genomic scientists on campus, as well as in the nearby Research Triangle Park and beyond.

North Carolina State University is located in Raleigh, one of the vertices of the Research Triangle Park (RTP), a conglomerate of university and industrial research institutions, including Duke University, the University of North Carolina at Chapel Hill, the National Institute of Environmental Health Sciences (NIEHS), SAS Institute and Glaxo SmithKline. Thus, faculty enjoy highly productive and synergistic interactions with numerous academic and industrial scientists in the area.

All applicants must have a Ph.D. in genetics, statistics, or a related field. Postdoctoral research experience in computational biology and bioinformatics is preferred. To apply for this position, please visit our website at <http://jobs.ncsu.edu> and provide a letter of application, curriculum vitae, concise description of research interests and goals with emphasis in your interdisciplinary expertise. Also candidates should email, fax or mail representative preprints or reprints and arrange to have at least three letters of recommendation sent electronically to [cb\\_search@statgen.ncsu.edu](mailto:cb_search@statgen.ncsu.edu), by fax to 919-515-7315, or by mail to

Professor Zhao-Bang Zeng, Chair Computational Biology Search Committee Bioinformatics Research Center, Box 7566 North Carolina State University Raleigh, NC 27695-7566

Processing of applications will begin March 1, 2006 and continue until the position is filled. Women and members of other underrepresented groups are especially encouraged to apply. AA/EOE. In addition, NC State University welcomes all persons without regard to sexual orientation. ADA call 919-515-3148.

Position 2:

Associate/Full Professor in Statistical Genetics and Bioinformatics

The Department of Statistics at North Carolina State University invites applications for a senior position (Associate/Full Professor) for its statistical genetics and bioinformatics programs. The appointee will be a tenured member of the Department of Statistics, will be housed in the Bioinformatics Research Center, and will have teaching responsibilities for the bioinformatics

and statistics programs. As a senior scientist, responsibilities also include methodological and collaborative research as well as mentoring students and junior faculty.

North Carolina State University is a leading center of activity in genomic sciences, with substantial strength in bioinformatics and statistical genetics (<http://bioinformatics.ncsu.edu>). Its bioinformatics graduate program was established in 1999 and has now produced 13 Ph.D. and 28 Master of Bioinformatics graduates. There are 53 students currently in the program, supported by NSF-VIGRE and NIH Training Grant funds as well as by University Fellowships and industry internships.

The Bioinformatics Research Center was established in 2000 to work collaboratively with genomic scientists on campus as well as in the nearby Research Triangle Park and beyond. The Department of Statistics at the university has housed an internationally acclaimed program in statistical genetics since its founding in 1941, and it is now also a key contributor to the bioinformatics activity on campus. The Department of Statistics belongs to both the College of Agriculture and Life Sciences and the College of Physical and Mathematical Sciences.

The Department's location in the Research Triangle provides rich opportunities for interactions with industry; other universities, including Duke University and the University of North Carolina at Chapel Hill; and government agencies, including NIEHS. Faculty enjoy

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## NorthCarolinaStateU ResTech PopGenet

A full-time research technician job is available in a laboratory of population and evolutionary genetics at the Department of Entomology at North Carolina State University. In this laboratory research is focused on interspecific and intraspecific variation in the sexual communication of two heliothine moth species (Lepidoptera, Noctuidae).

The responsibilities include breeding lines from differ-

ent regions, green house experiments, and possibly field work. The successful candidate will have a minimum of a bachelors degree in biology or related field and some laboratory research experience.

Anticipated starting date: March 15, 2006. To apply, please send your resume and a list of three references including telephone number and email address to: Scott Bowdridge, [scott\\_bowdridge@ncsu.edu](mailto:scott_bowdridge@ncsu.edu)

[astrid\\_groot@ncsu.edu](mailto:astrid_groot@ncsu.edu)

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### PacificU TeachingEvol

Pacific University (Forest Grove, Oregon) has a one-year full-time teaching position available for 2006-2007. Teaching responsibilities include introductory biology, physiology labs, and an upper division course in ecology/evolution/animal behavior (e.g., population genetics) that complements current course offerings.

Complete job listing is at: <http://www.pacificu.edu/as/biology/ONE-YEARTERMposition.cfm> Stacey Halpern, Assistant Professor Biology Department Pacific University Forest Grove, OR 97116

503-352-3109 (tel) 503-352-2933 (fax)

[shalpern@pacificu.edu](mailto:shalpern@pacificu.edu) <http://www.pacificu.edu/as/biology/faculty/halpern.cfm>

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### QueensU EvolAquaticBiol

QUEEN'S UNIVERSITY - The Department of Biology invites applications for an Aquatic Biologist at the level of Assistant Professor. We seek an outstanding individual with a demonstrated commitment to excellence in research and teaching, and with an interest in developing a vigorous research program in any area of freshwater aquatic sciences, preferably at the Queen's University Biological Station. Minimum requirements for hire include a Ph.D. and postdoctoral and/or field experience. The Queen's University Biological Station (<http://biology.queensu.ca/~qubs/> <http://biology.queensu.ca/~qubs/>) is an excellent field facility with a wide range of freshwater habitats and around 2,800 hectares of property, located

50 km north of the main campus in Kingston, Ontario. The main campus of Queen's University is situated on the shores of Lake Ontario and provides many additional opportunities for research in aquatic sciences. The successful candidate will join an expanding group in freshwater fisheries and aquatic sciences in the Department of Biology (<http://biology.queensu.ca/~quffas/> <http://biology.queensu.ca/~quffas/>). Expected date of appointment is July 1, 2006, subject to negotiation. Review of applications will begin February 17, 2006 and will continue until the position is filled. Applicants are required to submit a curriculum vitae, statement of current and prospective research interests, statement of teaching interests, and arrange to have three letters of reference submitted directly to: Dr. R.M. Robertson, Head, Department of Biology, Queen's University, Kingston, Ontario, Canada K7L 3N6 (Web: [biology.queensu.ca](http://biology.queensu.ca), E-mail: <mailto:biohead@biology.queensu.ca> biohead@biology.queensu.ca, Fax: (613-533-6617). Academic staff at Queen's University are governed by a collective agreement between QUFA and the University which is posted at <http://www.queensu.ca/qufa>. The University invites applications from all qualified individuals. Queen's is committed to employment equity and diversity in the workplace and welcomes applications from women, visible minorities, aboriginal people, persons with disabilities and persons of any sexual orientation or gender identity. All qualified candidates are encouraged to apply; however Canadian citizens and permanent residents will be given priority.

[friesenv@biology.queensu.ca](mailto:friesenv@biology.queensu.ca)  
[friesenv@biology.queensu.ca](mailto:friesenv@biology.queensu.ca)

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### Sulawesi Macaque FieldAssist

Field assistant positions available

The Sulawesi Macaque Project

We are looking for field assistants supporting a project investigating male and female sexual signals in Sulawesi crested black macaques (*Macaca nigra*). The study will be conducted in the Tangkoko-Batuangus-Dua Saudara Nature Reserve in North Sulawesi, Indonesia. It will be carried out in tight collaboration with our Indonesian counterparts. Assistants will be expected to follow habituated groups to:

-record behaviour, -collect and pre-process faecal samples, -take pictures of visual signals, -record vocalisa-

tions, -assist in playback experiments and body weight measurements, -pre-process data

This is a great opportunity for someone wishing to gain valuable experience with various techniques of field research and get acquainted with the life in South-East Asia.

Ideally, you should have prior experience with living, working or at least travelling in a developing country in the tropics. Some background in biology or anthropology is preferred. Furthermore, you should have a strong interest in primates. In general, applicants should:

-be physically fit and mentally strong with very good social skills, -be able to work independently within our team -feel comfortable living under basic conditions and being far away from family/ friends, -be willing to adapt to a foreign culture -be emotionally mature, friendly, energetic, and very patient, -be able to maintain a positive attitude towards hard and tiring work.

Ability to get along with others is important! Previous field experience and computer skills are welcome, but not required. The language of our team is English.

This is a volunteer position so the assistants will need to cover all costs for airfare and transportation, health insurance, vaccination, medicine, personal equipment such as headlamps, field clothes, shoes, backpacks etc., as well as visa fees. Meals and lodging in the field will be provided. Furthermore, depending on funding, there will be a small monthly stipend.

The project should start no later than May 1st 2006 and is planned to finish approximately April 2007. Applicants can join the project for either 6 or 12 months.

Applicants should send a CV, a letter describing research interests and experiences, graduate certification (if available), and contact information for 2-3 references. Please send only e-mail applications to:

Dr. Antje Engelhardt Dep. of Reproductive Biology  
German Primate Centre aengelhardt@dpz.gwdg.de  
antje@interjam.de antje@interjam.de

through comparative genomics of closely related species. The bioinformatics engineer is responsible for a wide range of technical tasks involving the creation and use of software for the display and manipulation of biological data, database mining, and implementation of methods to improve gene annotation based on comparative methods. Minimum requirements include a Bachelor's or Master's degree in the biological sciences or computer science, with at least one year experience in bioinformatics software development, and solid knowledge of Perl, SQL, CGI, relational databases, and C/C++ and/or Java. Interest in the fields of comparative genomics and molecular evolution is a plus. Details on current research are available at <http://www.tigr.org/faculty/Silva-Joana/>. TIGR has a highly interactive research group, with world-renowned expertise in organismal and evolutionary biology and bioinformatics, and provides ample opportunities for career advancement, a competitive pay scale and a very attractive benefits package. TIGR's 17-acre campus is located in the Shady Grove Life Sciences Center in Rockville, MD, in the greater Washington, D.C. metropolitan area, and close to the National Institutes of Health (NIH). Among TIGR's neighbors are satellite campuses of Johns Hopkins University and the University of Maryland, as well as other research institutes and biotechnology companies located within Maryland's biotech corridor. More details about research at TIGR can be found at <http://www.tigr.org/>. Interested applicants should apply through the <sup>3</sup>Careers<sup>1</sup> link on TIGR's website (<https://www.tigr.apply2jobs.com/>). Applications will be reviewed as they are received and the position will remain open until filled. Informal inquiries are welcome (contact jsilva@tigr.org)!

Joana C. Silva, Ph.D. Assistant Investigator

The Institute for Genomic Research 9712 Medical Center Drive Rockville MD 20850

jsilva@tigr.org voice:301.795.7896 fax:301.838.0208

jsilva@tigr.ORG

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## TIGR Bioinformatics

A Bioinformatics Engineer position is available in the group of Joana Silva at The Institute for Genomic Research, TIGR, located in Rockville, MD.

The project aims at studying genome evolution,

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## UAlberta EvoDevo

Would you kindly circulate the position announcement below? Applicants using molecular genetic tools to study evo-devo would be welcomed. Regards, Rich Palmer

— Assistant or Associate Professor in Molecular Ge-

netics

UNIVERSITY OF ALBERTA - We invite applications for a tenure-track position at the Assistant or Associate Professor level in research areas related to molecular genetics. The candidate should have a strong record of research using genetic tools to address a basic problem in molecular, cellular and/or developmental biology. The candidate should also have the potential for excellence in teaching within our undergraduate and graduate programs in Molecular Genetics. The successful candidate will interact with a dynamic group of colleagues with expertise in molecular, cellular and/or developmental genetics. The candidate must have a PhD and two or more years of postdoctoral research experience. The University of Alberta offers a competitive salary commensurate with experience and an excellent benefits plan. The Dept. of Biological Sciences (<http://www.biology.ualberta.ca/>), with 70 faculty members and 275 graduate students, offers an exciting environment for collaborative research. Exceptional infrastructure includes a microarray and proteomics facilities, molecular biology and advanced microscopy service units, and aquatic and terrestrial animal care and plant growth facilities. Candidates should submit a curriculum vitae, a one-page summary of research plans, a statement of teaching interests and reprints of their three most significant publications electronically to [positions@biology.ualberta.ca](mailto:positions@biology.ualberta.ca) or by mail to Dr. L. S. Frost, Chair, Department of Biological Sciences, CW 405 Biological Sciences Bldg, University of Alberta, Edmonton, Alberta, Canada T6G 2E9. Applicants must also arrange for three confidential letters of reference to be sent to the Chair. Closing Date: February 15, 2006. The effective date of employment will be on or after July 1, 2006. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. The University of Alberta hires on the basis of merit. We are committed to the principle of equity in employment. We welcome diversity and encourage applications from all qualified women and men, including persons with disabilities, members of visible minorities, and Aboriginal persons. –

A. Richard Palmer Systematics and Evolution Group  
Department of Biological Sciences University of Alberta  
Edmonton, Alberta T6G 2E9 CANADA phone: (780) 492-3633 message: (780) 492-3308 FAX: (780) 492-9234

<http://www2.biology.ualberta.ca/palmer/palmer.html>  
(biological asymmetries, software, course notes)  
Chair, Comparative Morphology & Development section,  
Canadian Society of Zoologists. For info. see: <http://www.biology.ualberta.ca/CMD/home.htm>  
[rich.palmer@ualberta.ca](mailto:rich.palmer@ualberta.ca)

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## UFribourg Evol

Junior Group Leader (“Maître-assistant”) in Ecology or Evolution

The Unit of Ecology & Evolution of the Department of Biology at Fribourg University, Switzerland, invites applications for a junior group leader position (“Maître-assistant”) in the field of Ecology and/or Evolution. We are seeking a highly motivated young scientist with a post-doctoral experience, a strong publication record, and the will to develop an independent research group within the Unit. We are open to any area of Ecology and/or Evolution. Applicants will be expected to develop an externally funded and internationally recognized research program. The position comes with funding for one PhD student or 50% lab technician. Teaching duties include participation in undergraduate courses, and an advanced Master-level course in the applicant’s research area. Undergraduate teaching is usually done in German or French, but English is also possible. Master-level teaching is in English.

The Department of Biology comprises 14 research groups organized in three Units. The Unit of Ecology & Evolution consists of five groups studying plant population ecology and genetics, invasive plant species, behavioral ecology of birds, community ecology in agricultural landscapes, and evolutionary biology of learning (<http://www.unifr.ch/biol/ecology>).

The University of Fribourg is a bilingual University (French and German). It provides excellent facilities, and a stimulating intellectual and social environment. Fribourg is a very pleasant and lively medium-sized town located between Lausanne, Bern and Neuchâtel. Students account for more than one fourth of the total population of Fribourg. The old town is charming and holds one of the finest remnant of medieval architecture in Europe.

The position is open starting January 2007 (if necessary, a few months earlier), and is for a maximum of five years.

Annual salary starts at about CHF 90'000 (~ 56'000). The evaluation of applications will start in April 2006.

To apply for the position, send a CV with a list of publications, a summary of current and planned research, as well as the name of two referees by email (as pdf attachments) to Catherine Cuennet: [catherine](mailto:catherine)

ine.cuennet@unifr.ch.

For further information contact Prof. Louis-Félix Bersier, Unit of Ecology and Evolution, Ch. du Musée 10, CH-1700 Fribourg, Switzerland tel +41 26 300 8869; fax +41 26 300 9698; louis-felix.bersier@unifr.ch

Tadeusz Kawecki Unit for Ecology and Evolution, Department of Biology University of Fribourg Chemin du Musée 10, CH-1700 Fribourg, Switzerland [www.unifr.ch/biol/ecology/kawecki](http://www.unifr.ch/biol/ecology/kawecki) phone +41 26 300 88 71 fax +41 26 300 96 98 e-mail tadeusz.kawecki@unifr.ch

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## UManchester 5 Fellowships

As seen in the 9 February issue of Nature:

FIVE INTERNATIONAL FELLOWSHIPS IN THE LIFE SCIENCES University of Manchester

Five University of Manchester funded fellowships are available immediately with a 10 March 2006 deadline. Two posts are 5-year positions open to all, and three posts are 5-year positions for those with a background in Physical Sciences working in the Life Sciences. Evolutionary, theoretical and computational biologists are also encouraged to apply for the Physical Sciences/Life Sciences Interface Fellowships. Research in the Faculty of Life Sciences spans twenty research themes ranging from evolutionary and computational biology, through cellular function, to whole organismal biology <[http:// www.ls.manchester.ac.uk/research/themes/](http://www.ls.manchester.ac.uk/research/themes/)> . Successful applicants will be able to lead independent groups, supervise PhD students, apply for external funding, and will be reviewed no less than a year before the end of their fellowship for the possibility of securing a permanent position in the Faculty. See further details below and at <<http://www.man.ac.uk/news/vacancies/>> . The University of Manchester was formed on October 1st 2004 by the fusion of the University Of Manchester Institute of Science and Technology and the Victoria University of Manchester. The resulting institution is the biggest university in the UK and one of Europe's leading higher education institutions with an unrivalled quality, breadth and volume of research activity. Historically, no fewer than 23 former staff and students have gone on to become Nobel Prize winners. There are a large number of specialist research centres and groups at the University, each undertaking pioneering research into areas ranging from hypertension, neurodegeneration and diabetes

to artificial intelligence and aeronautics. In November, the University was named 'Higher Education Institution of the Year' at the Times High Education Supplement Awards 2005. Further information about the University and its faculties may be found on the University's website <[www.manchester.ac.uk](http://www.manchester.ac.uk)> . Casey Bergman, Ph.D. Faculty of Life Sciences University of Manchester Michael Smith Building Oxford Road, M13 9PT Manchester, UK <http://umber.sbs.man.ac.uk/-bergman/> MANCHESTER FELLOWSHIPS IN THE LIFE SCIENCES (ref. LS/013/06)

Applications are invited for two prestigious research fellowships within the Faculty of Life Sciences (UK RAE 2001 5\*). We seek exceptional candidates, with outstanding potential as independent scientists, working in any area of the Life Sciences. Both posts are available immediately.

Appointment to these positions will present the successful candidates with a unique opportunity to develop their research in one of the largest and most successful Life Sciences Faculties in Europe. The absence of independent departments within Life Sciences encourages a strong culture of interdisciplinary collaboration both within the Faculty and with groups in the physical and medical sciences and applications from individuals prosecuting interdisciplinary research programmes are particularly welcome. These fellowships are integral to the Faculty's strategic aim to attract the highest quality young researchers to Manchester, and each will cover salary and running costs (one staff position, consumables and equipment) for 5 years. Each Fellow will be expected to attract external funding during the tenure of the fellowship.

Salary: Circa £35,000 - £42,000 p.a. Informal enquiries: Professor Martin Humphries [Research Dean] Email: [martin.humphries@manchester.ac.uk](mailto:martin.humphries@manchester.ac.uk) Tel: +44-(0)161-275-5071 Professor Alan North [Dean] Email: [r.a.north@manchester.ac.uk](mailto:r.a.north@manchester.ac.uk) Tel: +44-(0)161-275-1499

Further particulars can be found on the web at: <<http://www.man.ac.uk/news/vacancies/research.html#ls013>>

If you are unable to download the details you can request a hard copy from: Tel: +44-(0)-161-275-8836 Email: [Lifesciences-hr@manchester.ac.uk](mailto:Lifesciences-hr@manchester.ac.uk) Please quote reference: LS/013/06

Closing date: 10 March 2006

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FELLOWSHIPS AT THE LIFE SCIENCES/PHYSICAL SCIENCES INTERFACE (ref LS/ 012/06)

Applications are invited for 3 innovative, 5-year, research fellowships within the Faculty of Life Sciences. In recognition of the importance of cross-disciplinary approaches across the Life Sciences, the Faculty wishes to appoint exceptional researchers with a proven background in mathematics, computer science, chemistry, physics, or engineering whom have successfully applied these skills to address a biological problem. We seek individuals who have clearly-

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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>

### UStellenbosch PlantMolSyst

A full-time lectureship is available at the Department of Botany & Zoology, University of Stellenbosch, Cape Town, South Africa from March 2006.

We are looking for a plant molecular systematist, preferably with focus at the population level, to complement existing departmental strengths in Cape Flora research. Current interests include the radiation of the Cape Flora and the processes that underpin this differentiation.

The successful candidate will teach at first year level, as well as in the appointee's speciality at more senior undergraduate and Honours levels. Although generous institutional start-up funding will be provided, the incumbent will be expected to obtain extramural grant support, train postgraduate students, and develop their own research speciality.

Interested candidates should submit a comprehensive Curriculum Vitae and statement of research interests, together with the names of two academic references, by email or post to the address given below.

The closing date for applications is 15 February 2006.

Professor Terence J. Robinson Executive Head: Department of Botany & Zoology University of Stellenbosch Private Bag X1 Matieland 7602 South Africa

E-mail: [lwillems@sun.ac.za](mailto:lwillems@sun.ac.za) Tel: +27 21 808 3236 Fax: +27 21 808 24 05

[apauw@sun.ac.za](mailto:apauw@sun.ac.za)

### UWestAustralia EvolBiol

LECTURER (REF: 1203) Evolutionary Biology/Behavioural Ecology SCHOOL OF ANIMAL BIOLOGY

5 year appointment Salary range: Lecturer Level B \$62,119 - \$73,768 p.a. Closing date: Friday, 17 March 2006

The appointee will develop an internationally competitive research program in evolutionary biology, teach undergraduate courses in behavioural ecology and/or conservation biology and attract and supervise postgraduate research students. The position complements existing staff in the Centre for Evolutionary Biology led by Professor Leigh Simmons recently appointed as a Federation Fellow for a period of five years (<http://www.lwsimmons.org>). Applicants must have a PhD in a relevant discipline and postdoctoral research experience. Applicants with teaching experience are requested to submit a teaching portfolio as part of their application. For further information regarding the position please contact Professor L W Simmons on 61 8 6488 222 or email [lsimmons@cyllene.uwa.edu.au](mailto:lsimmons@cyllene.uwa.edu.au) or Head of School, Associate Professor J D Roberts on 61 8 6488 2237 or email [droberts@cyllene.uwa.edu.au](mailto:droberts@cyllene.uwa.edu.au).

Application Details: For copies of the selection criteria please access the website <http://jobs.uwa.edu.au/>. Applicants must address the prerequisites and selection criteria. Written applications quoting the reference number, personal contact details, qualifications and experience, along with contact details of three referees should be sent to Director, Human Resources, The University of Western Australia, M350, 35 Stirling Highway, Crawley WA 6009 or emailed to [jobs@uwa.edu.au](mailto:jobs@uwa.edu.au) by the closing date.

Committed to international excellence

—

Professor Leigh W Simmons Center for Evolutionary Biology School of Animal Biology (M092) The University of Western Australia Crawley WA 6009 Australia

Tel: +61 8 6488 2221 Fax: +61 8 6488 1029

<http://www.lwsimmons.org>  
[lsimmons@cyllene.uwa.edu.au](mailto:lsimmons@cyllene.uwa.edu.au)

lsim-



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**WoodsHoleMA ResAssist**

POSITION: Research Assistant I Josephine Bay Paul Center Marine Biological Laboratory Woods Hole, MA 02536 Full-Time

Position Description: A full-time Research Assistant I position is available in the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution at the Marine Biological Laboratory. This position is part of an evolutionary genomics research program and will involve interconnections among parasitology, genomics, evolutionary biology, and phylogenetics. The successful candidate could start as early as March 2006. Questions can be addressed to [sbordenstein@mbl.edu](mailto:sbordenstein@mbl.edu) and additional information about the Center or Bordenstein lab can be found at: <http://jbpc.mbl.edu/bordenstein>. Duties/Responsibilities: Wolbachia are a genus of obligate intracellular bacteria that span the spectrum of symbiotic associations from parasitism in arthropods, mutualism in nematodes, and pathogenesis in humans. Primary research projects will focus on, but are not limited to, the molecular evolution of Wolbachia genes and the purification of symbiont genomic DNA from insect hosts. Primary responsibilities comprise molecular biology activities such as preparation of large scale infected insect homogenates, purification of symbiont DNA, insect rearing, primer design, PCR, southern hybridizations, high-throughput DNA sequencing, phylogenetic analysis and genetic database searching. Skills in some of these duties are required and should be highlighted in your cover letter.

Conditions: Position is available as early as March 2006. Continuation is contingent on performance and

available funds. The position includes generous benefits and coauthorship.

Educational/Experience/Skills: B.A./B.S. degree and experience in Microbiology, Molecular Biology, Evolution, Genetics, or a related field. Training in some molecular biology techniques required, including polymerase chain reaction, gel electrophoresis, sequence alignments, phylogenetics, or genomics. Familiarity with computational skills, GenBank, Mac OS, Windows, and Linux/Unix a plus. The successful applicant is expected to have good team skills, but work with a high level of independence under broad supervision. Candidates with interest and experience in Molecular Biology, Parasitology, Evolution, Genetics, or Comparative Genomics may find this position particularly rewarding.

Instructions: Applicants should submit a cover letter, curriculum vitae or resume, transcripts, and list of three references including telephone numbers and email address. Please see the Marine Biological Laboratory Employment Website for full instructions: [http://www.mbl.edu/inside/what/-human\\_resources/employment.html](http://www.mbl.edu/inside/what/-human_resources/employment.html). The MBL is an Equal Opportunity/Affirmative Action Employer/Non-smoking workplace. Contact Dr. Seth Bordenstein ([sbordenstein@mbl.edu](mailto:sbordenstein@mbl.edu)) with specific questions.

Application Deadline: Until a suitable candidate is identified.

– Seth Bordenstein Assistant Scientist Global Infectious Disease Program Josephine Bay Paul Center for Comparative Molecular Biology and Evolution The Marine Biological Laboratory 7 MBL Street Woods Hole, MA 02543

phone: 1-508-289-7220 fax: 1-508-457-4727 email: [sbordenstein@mbl.edu](mailto:sbordenstein@mbl.edu) <http://jbpc.mbl.edu/-bordenstein> [sbordenstein@mbl.edu](mailto:sbordenstein@mbl.edu) [sbordenstein@mbl.edu](mailto:sbordenstein@mbl.edu)

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## AmSocMam Student Honoraria

The American Society of Mammalogists (ASM) encourages graduate students to submit a manuscript to their competition for three student honoraria, the Anna M. Jackson, Elmer C. Birney, and A. Brazier Howell awards, to be awarded at the 2006 annual meeting of the Society in Boston, MA, USA. The competition is open to all student members of the American Society of Mammalogists, a long standing society organized to promote the study of mammals. ASM has an international membership and encourages students internationally to join the Society and enter the competition. To become a member of the Society visit the ASM membership page at <http://www.mammalsociety.org/membership/index.html> Participants must not have received their Ph.D. before September 2006 and must not have received a previous honorarium from ASM. Each award carries an honoraria of \$750. Honoraria will be awarded based on originality, quality, and written presentation of the research. Applicants should submit a manuscript on their current research written in the format of an article for the Journal of Mammalogy (please consult the journal webpage for style: <http://www.asmjournals.org/perlserv/?request=index-html>). Manuscripts must be single-

authored and should not exceed 12 double spaced pages of text in length (not including figures, tables, and references). Authors must submit either pdf or Word files. No other formats will be accepted. Electronic submissions should be sent to [vhayssen@science.smith.edu](mailto:vhayssen@science.smith.edu) before 10 March 2006. Questions should be directed to Virginia Hayssen, Biology Department, Smith College, Northampton, MA 01063 [413 585 3856]. Papers that do not meet the above requirements or are received after the deadline will not be considered. Applicants will be notified of award recipients around 31 March 2006. Winners of honoraria will be invited to present their research at the Plenary Session of the ASM annual meeting. These platform presentations will be 15 min in length (12 min for the presentation, 3 min for questions). Regardless of the outcome of the competition, applicants intending to present a paper at the meeting must submit the usual abstract and pre-registration material to the local committee before their deadline.

Sacha Vignieri, PhD Centre for the Study of Evolution School of Life Sciences University of Sussex Brighton, BN1 9QG [sv43@sussex.ac.uk](mailto:sv43@sussex.ac.uk)

[sv43@sussex.ac.uk](mailto:sv43@sussex.ac.uk)

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## Anchovies samples

Dear all,

Our group is looking for tissue samples from anchovies, *Engraulis australis* and *Engraulis capensis*, from, respectively, Australia and South Africa locations. If you can help us, please e-mail at marc.jerome@ifremer.fr. Thanks a lot in advance for any assistance,

Véronique Verrez-Bagnis

– Véronique Verrez-Bagnis Ifremer Département Sciences & Techniques Alimentaires Marines Rue de l'Île d'Yeu, B.P. 22105 44311 Nantes Cedex 3 - France

Tél. : +33 (0)2 40 37 40 81 Fax : +33 (0)2 40 37 40 71  
E-mail : vverrez@ifremer.fr

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## Brycinus macrolepidotus Markers

Dear Evoldir members,

Does anybody know of a species-specific genetic marker(set) to distinguish *Brycinus macrolepidotus* from other (congenic) species?

Thanks, Dieter

Dieter.Anseeuw@kuleuven-kortrijk.be

---

## Coalescent Theory DNA Polymorphism

Dear Evoldir Members,

I am analyzing mitochondrial DNA polymorphism in a bivalve mollusk showing Doubly Uniparental Inheritance (i.e. transmission to progeny of two different mtDNAs, one by females and the other by males).

I need to analyze levels of polymorphism within the two groups (male-type mtDNAs and female-type mtDNAs) and see if there is any significant difference between the

two. I made this using a basic ANOVA on p-distances (and it turned out to be significant), but I wonder if it is possible to apply Coalescent Theory and related equations to my problem, to incorporate in my tests stochastic and drift errors.

Does anyone have suggestions on the best statistic approach should I use? Is any software available for this sort of analysis. Any help will be super-welcome!

Best wishes,

Marco Passamonti

Dr. Marco Passamonti, PhD Dipartimento di Biologia Evoluzionistica Sperimentale via Selmi 3 I-40126 Bologna (Italy) tel. +39/0512094162 fax +39/0512094286 email mpassa@alma.unibo.it

mpassa@alma.unibo.it

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## Control region amplification answers

Dear Colleagues,

About 2 weeks ago I sent an email asking for suggestion about how to amplify the difficult control region. I post the replies here (see below) since many people sent me emails asking for that. Thanks to all who sent comments.

Best,

Joan

Dr. Joan Pons Unitat de Biologia Evolutiva, Facultat de Ciències de la Salut i de la Vida, Universitat Pompeu Fabra C/ Dr. Aiguader 80, 08003 Barcelona, Catalonia, SPAIN Telephone: +34 93 5422947 Fax: +34 93 5422802 Email: joan.pons@upf.edu

---

Hi,

Try lowering the extension temperature to between 65 C and 68 C and using a high quality polymerase suitable for long PCR. Many polymerases fall off after processing just a few dozen residues. To continue extension, another molecule has to bind. At the typical extension temperature (72 C) the nascent strand can melt off the template before another polymerase molecule can bind. The long PCR polymerases are less likely to fall off.

I use a primer in tRNA-Met, TM-N201 5' ACCTT-TATAARTGGGGTATGARCC and one in 12S, such as SR-J14610: 5' ATAATAGGGTATCTAATCCTAGT

These give enough coding sequence to determine whether you are actually amplifying the control region.

Good luck, Andy Beckenbach

---

just a few suggestions: - Are you sure that your primers fit 100%? Do you have already a sequence from your special beetle or only from related species? Just a few mismatches in the hypervariable region could stop your primers work. Don't feel shy to use degenerate primers if nothing else works - the control region is extremely AT rich; not a good place for amplifications in general. Try to slow down the reaction to improve conditions for the Taq (low enzyme concentration, high dNTPs, optimize Mg concentration between 1-10 mM) - check out the AT content of your amplicon and make a dNTP mix where A+T are overrepresented in the same relation; otherwise your mix may be depleted on free nucleotides in the last cycles - make sure that your primers are rather long (>22 to 24 nt), with no secondary structures and try to include a GC clamp at the 3' end. FastPCR program may help to find suitable primers - anneal long at rather low temp - maybe add a bit (1:10 to 1:40) of a proofreading polymerase (Pwo, Pfu) to the Taq. In this case use the buffer of the proofreading enzyme for reaction

Good luck, Wolfgang

---

The control region can be very long in beetles (up to 13kb in bark weevils), due in part to the presence of a highly repetitive region. This may explain the problems you have to amplify this region. If this is the problem, you cannot just use a standard PCR protocol. You need a PCR protocol designed specifically to amplify long fragments. Some kits are available. I have successfully used the Long Expand PCR system from Roche to amplify fragments of 5 to 9 kb, including the control region of some leaf beetles species (see the attached PDF). Note also that the presence of a repetitive region makes it very difficult to design primers to sequence the control region (due to the fact that a primer designed within this repetitive region will anneal in different places). One way to get around the problem is described in the attached article.

Patrick Mardulyn

---

Hello Joan. Just a wild guess (sorry, I know nothing of beetle genetics), but if your DNA preparation and primers are both good then you may have a gene rearrangement on your hands (control regions sometimes do this, for example in birds). Try longer PCRs span-

ning where you think the control region is, then size the fragment directly from on agarose gel. If the fragment is much smaller than expected, your control has likely migrated somewhere else in the genome. If the size is what you expected, then I guess your control region primers are not so good after all. Good luck. Joseph.

---

Hi Joan

You say that you have 100% matching, so presumably you have something sequenced from a clone? I imagine that you are using tRNA primers spanning Dloop, and that there may have been a rearrangement and/or inversion of the tRNA genes involved, precluding amplification. The solution may be as simple as reversing a primer- you need a map. Alternatively, you could have large insertions and/or secondary structures that the polymerase cannot cross.

good luck,

graham

---

Are you sure of the gene order for mtDNA in Pimelia? Generally control region primers are anchored in the transfer RNA sequences that bracket the control region - if there's been a rearrangement those tRNA sequences may no longer be bracketing the control region as you expect. If you're reasonably confident of the correct gene order, you might use primers based on the bracketing coding genes such as cyt-b. Just a thought.

-Chris Wilson

---

Dear Joan I had the same problem with my butterflies because it is an extremely AT rich region in insects.

— / —

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

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## Creationism texts answers

Dear all,

A huge thanks to all those who responded to my request for creationism texts a few weeks ago. I was quite overwhelmed and very grateful, sincere thanks to all I am

sorry I couldn't respond to each email individually.

The most votes were for Michael Behe's Black Box and the talk origins web site.

There is a lot out there. A (not entirely comprehensive) summary is below (numbers in brackets are number of people who recommended it).

Sincere thanks again, what a superb community.

Domino.

Authors Title Michael Behe Darwins black box (8) Massimo Pigliucci Denying Evolution: Creationism, Scientism, and the Nature of Science (4) Barbara Forrest & Paul R. Gross Creationism's Trojan Horse: The Wedge of Intelligent Design (3) Jonathan Wells Icons of Evolution (3) Henry Morris Scientific Creationism (2) Kenneth Miller Finding Darwin's God: A Scientist's Search for Common Ground Between God and Evolution (2) Phillip Johnson Darwin on Trial (2) Robert Pennock Tower of Babel: The Evidence Against the New Creationism (2) William A. Dembski Intelligent Design: The Bridge Between Science & Theology (2) Arthur Strahler Science and Earth History D. Dennett Darwin's Dangerous Idea Duane Gish The Fossils Still Say No Duane Gish Evolution: The Challenge of the Fossil Record Eugenie Scott Evolution vs. Creationism Fazale Rana Origins of Life: Biblical and Evolutionary Models Face Off Fazale Rana & Hugh Ross Who Was Adam?: A Creation Model Approach to the Origin of Man Hugh Ross The Genesis Question: Scientific Advances and the Accuracy of Genesis Ken Miller Finding Darwin's God Mariano Artigas The Mind of the Universe. Understanding science and religion. Mariano Artigas The Frontiers of Evolutionism Mark Isaak The Counter-Creation Handbook Matt Young & Taner Edis (eds) Why Intelligent Design Fails: A Scientific Critique of the New Creationism Michael Denton Evolution: A Theory in Crisis Michael Ruse Can a Darwinian Be a Christian? Michael Ruse Darwin and Design: Does Evolution Have a Purpose Niall Shanks God, the Devil, and Darwin: A Critique of Intelligent Design Theory Percival Davis & Dean H. Kenyon Of Pandas and People Robert Pennock Intelligent Design Creationism and Its Critics Ronald Numbers The Creationists William A. Dembski No Free Lunch

<http://www.talkorigins.org> (7) <http://www.creationresearch.org/crsq.html> <http://www.harunyahya.com> <http://www.ncseweb.org/> <http://evolution.berkeley.edu/> <http://www.reasons.org> <http://www.answersingenesis.org/museum/> Domino Joyce Evolutionary Ecology and Biodiversity Group School of Biological Sciences, University of Hull, Cottingham Rd, Hull HU6 7RX

Tel: 00 44 (0)1482 465542 Fax: 00 44 (0)1482 465458  
E-mail: D.Joyce@hull.ac.uk

and sometimes: EAWAG, Limnological Research Center Seestrasse 79 6047 Kastanienbaum, Switzerland

Tel: 00 41 (0)41 3492200

D.Joyce@hull.ac.uk D.Joyce@hull.ac.uk

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## Dobzhansky Award

FINAL NOTICE !

Call for applications for the 2006 Theodosius Dobzhansky Prize

The Theodosius Dobzhansky Prize is awarded annually by the Society for the Study of Evolution to recognize the accomplishments and future promise of an outstanding young evolutionary biologist. The prize was established in memory of Professor Dobzhansky by his friends and colleagues, and reflects his lifelong commitment to fostering the research careers of young scientists.

Eligibility The candidate must have a Ph.D. (or equivalent) awarded no earlier than June 2003 and no later than 1st February 2006, and must be actively involved in research in the field of evolutionary biology. There are no other restrictions. Applicants do not have to be members of the Society for the Study of Evolution, but such membership is encouraged. Nomination/Application.- Candidates may apply directly or may be nominated. Established researchers are encouraged to nominate outstanding young scientists who may be unaware of the existence and prestige of this prize. Each candidacy must be supported by the following materials detailing the candidate's career to date: (1) a curriculum vitae, (2) a summary of research accomplishments, (3) a statement of research plans for the next 5 years, (4) pdf copies of three recent publications, (5) names and addresses of the three referees (including the nominating scientist where applicable) who have sent supporting letters. N.B.: THE THREE LETTERS OF REFERENCE ARE SENT SEPARATELY, but no application will be considered without these letters. All application/nomination materials and letters of reference must be sent as PDF e-mail attachments. No file type other than PDF will be accepted. The deadline for receipt of all materials, including letters of reference, is 1 March 2006. All materials should be sent to the secretary of SSE (Dale H. Clayton) at the

following email address:

careymadsen@bioscience.utah.edu

Award.- The Dobzhansky Prize is accompanied by a check for U.S. \$5000, and will be awarded at the annual meeting of the Society for the Study of Evolution, 23-27 June 2006, in Stony Brook, New York. The recipient is expected to be present to receive the award and to give an oral presentation about his/her research. To facilitate attendance, the SSE provides funds to cover the costs of conference registration, accommodation during the conference, and expenses for travel to and from the conference. The recipient will be notified of the award by early May 2006.

Carey Madsen <careymadsen@bioscience.utah.edu>

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### ESF ConGen GrantsScienceMeetings

The ESF Programme on Integrating population genetics and conservation biology: Merging theoretical, experimental and applied approaches (ConGen) announces a Call for Workshops and for Applications for Exchange Grants, deadline 15 May 2006.

ConGen invites proposals from potential organisers of Workshops to be held in 2006 on topics with a clear connection to the core of the ConGen Programme. We would particularly welcome proposals that integrate the different scientific topics as outlined in the scope of the Programme (<http://www.esf.org/congen>). Priority will be given to workshops taking place in countries that financially support the Programme.

ConGen is offering funding for a number of Exchange Grants (visits from 15 days to 6 months) related to the scientific objectives of the Programme. Priority will be given to applicants who come from or intend to visit countries that financially support the programme, particularly if both criteria are fulfilled.

ConGen also offers a limited number of Short Visit Grants (visits up to 15 days). There is no fixed deadline for the submission of applications. Applicants should ensure that there is at least 3 months between the date of submission and the proposed starting date of the visit.

Further information, including access to the online application forms, at <http://www.esf.org/congen> Joanne Goetz Life, Earth and Environmental Sciences (LESC)

European Science Foundation (ESF) BP 90015 1 quai  
Lezay-Marnésia 67080 Strasbourg Cedex France

Tel: +33 3 88 76 71 22 (Direct Line) Fax: +33 3 88 37  
05 32

Email: [jgoetz@esf.org](mailto:jgoetz@esf.org) <<mailto:jgoetz@esf.org>> <http://www.esf.org> <<http://www.esf.org>>

Joanne Goetz <[jgoetz@esf.org](mailto:jgoetz@esf.org)>

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### Eppendorf Heat Sealer

Hi,

Has anyone had any experience with Eppendorf heat sealers ([http://www.eppendorfn.com/products/-pqr\\_heatsealer.de.asp](http://www.eppendorfn.com/products/-pqr_heatsealer.de.asp))? Our lab is thinking of buying one, but we like to hear from people with experience of using it. Have you experienced leakage during PCR or storage of plates sealed with the heat sealer? Which type of heat seal and plates could you recommend?

I would be most grateful for any comments

Thanks

Jens

Dr. Jens Carlsson Population Geneticist

Virginia Institute of Marine Science P.O. Box 1346 (for mail) Route 1208 Greate Road (for FedEx, UPS) College of William and Mary Gloucester Point, VA 23062-1346, USA

[jc@vims.edu](mailto:jc@vims.edu)

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### Eppendorf Heat Sealer repost

As the fonts were messed up in my previous email, I've reposted it.

Hi,

Has anyone had any experience with Eppendorf heat sealers ([http://www.eppendorfn.com/products/-pqr\\_heatsealer.de.asp](http://www.eppendorfn.com/products/-pqr_heatsealer.de.asp))? Our lab is thinking of buying one, but we like to hear from people with experience of using it. Have you experienced leakage during PCR or storage of plates sealed with the heat sealer? Which type of heat seal and plates could you recommend?

I would be most grateful for any comments

Thanks

Jens –

Dr. Jens Carlsson

Population Geneticist Virginia Institute of Marine Science P.O. Box 1346 (for mail) Route 1208 Great Road (for FedEx, UPS) College of William and Mary Gloucester Point, VA 23062-1346, USA [jc@vims.edu](mailto:jc@vims.edu)

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## EvolBioinformatics journal

Dear colleagues,

I am pleased to announce that the open-access journal, Evolutionary Bioinformatics Online\* (<http://www.la-press.com/ebo.htm>), will be indexed by PubMed. The inaugural issue of Evolutionary Bioinformatics Online is available at

<http://www.la-press.com/evolbio05.htm> With an international editorial board of leading scientists, EBO publishes peer-reviewed papers in any area of computational evolutionary biology. We invite authors to submit manuscripts to EBO.

- Author Guidelines - <http://www.la-press.com/Instructions.htm> - Article processing fee applies to accepted papers only - <http://www.la-press.com/article-processing.htm> - Copyright - <http://www.la-press.com/copyright.htm> - Honorary Editorial Board - <http://www.la-press.com/EBO-edboard.htm> Evolutionary Bioinformatics Online 2005

Application Notes

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MySSP: non-stationary evolutionary sequence simulation, including indels - Michael S Rosenberg

Arlequin (version 3.0): an integrated software package for population genetics data analysis - Laurent Excoffier, Guillaume Laval, Stefan Schneider

ALFRED: An Allele Frequency Database for Microevolutionary Studies Haseena Rajeevan, Kei-Hoi Cheung, Rohit Gadagkar, Shannon Stein, - Usha Soundararajan, Judith R Kidd, Andrew J Pakstis, Perry Miller, and - Kenneth Kidd

Original Research

=

Phylogenetic biodiversity assessment based on systematic nomenclature - Ross H Crozier, Lisa J Dunnett,

Paul-Michael Agapow

Fast Structural Search in Phylogenetic Databases - Jason T. L. Wang, Huiyuan Shan, Dennis Shasha and William H. Piel

Functionality and the evolution of marginal stability in proteins: inferences from lattice simulations - Paul D Williams, David D Pollock, Richard A Goldstein

Estimation of phylogeny using a general Markov model - Vivek Jayaswal, Lars S Jermini, John Robinson

The identification of functional motifs in temporal gene expression analysis - Jiuzhou Song, Jaime Bjarnason, Michael G Surette

Evolution of proteins and proteomes: a phylogenetics approach - Toni Gabaldón

\*Evolutionary Bioinformatics Online is the official journal of The Bioinformatics Institute (New Zealand).

Mark Pagel Editor-in-Chief Evolutionary Bioinformatics Online

[sas98mp@reading.ac.uk](mailto:sas98mp@reading.ac.uk) [sas98mp@reading.ac.uk](mailto:sas98mp@reading.ac.uk)

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## Fecal DNA extraction kits

Dear EvolDir members,

I am trying to make a list of the “best” fecal DNA extraction kits and protocols that people use for their target non-human organisms. While it’s easy to extract DNA from fresh feces (up to 2 days old), older feces tend to yield low-quality DNA, which is almost impossible to amplify in some cases.

I am aware of phenol/CHCl<sub>3</sub>, Qiagen QIAamp Stool Kit, and Epicentre ExtractMaster. Is there something else or a combination/modification of kits/methods people use? For instance, different kits/methods may be suitable for elephant “leafy” dung or lagomorph or goat dry pellets.

The compiled list will posted on EvolDir ASAP.

Thank you in advance for your time. Cheers, sergios-orestis kolokotronis

sergios-orestis kolokotronis molecular systematics labs american museum of natural history central park west @ 79th street new york, ny 10024 -usa-tel (+1)2123137648 \*\* [koloko@amnh.org](mailto:koloko@amnh.org) <http://research.amnh.org/users/koloko> [koloko@amnh.org](mailto:koloko@amnh.org)

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### FreqDep Selection

Dear Evoldir members, Does anybody knows if an excess of nonsynonymous polymorphism is expected under frequency-dependant selection or endocycling selection? Ill appreciate if you could recomend me literature dealing with this point. Thank you very much. Kind regards, Romina

rpicci@ege.fcen.uba.ar

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### GilaMonsterLizard samples

I wanted to thank the community for the strong response we had for our request for salmonid tissue and DNA samples. On a completely different project, we are looking for genomic DNA, blood, or tissue from both the gila monster and Mexican bearded lizard. We would be very thankful to anyone who can help us.

David Liberles Department of Molecular Biology University of Wyoming

“David A. Liberles” <Liberles@uwyo.edu>

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### FstPHIst question

Dear all,

I was wondering if anyone knows the difference between of fixation coeffienct Fst and PHIst? I found in some reference, Fst and PHIst were used for mtDNA and microsatellite data, respectively.

Could you give any answer or reference for this question? Thank you all in advance.

Vivian Zhongshan University, China

vivian\_ysj@yahoo.com

---

### Good Micro companies

I would be most grateful to hear about any reasonably priced commercial microsatellite genotyping companies which people have actually used and were satisfied with.

Please supply contact email address etc.. for your recommendation.

I will post a summary of replies to EvolDir

Cheers,

Per

NB: New email spam filters at Berkeley may result in emails bouncing back. If so, please advise me by fax (510-643-5098, Attn.: Per Palsboll)

Per J. Palsboll Assistant Professor of Conservation Genetics

Mail address: Ecosystem Science Division Department of Environmental Science, Policy & Management University of California at Berkeley 137 Mulford Hall #3114 Berkeley, CA 94720-3114, USA

Web-sites: Department <http://cnr.berkeley.edu/-espm/index.html> Faculty page [http://www.cnr.berkeley.edu/espm/directory/fac/-palsboll\\_p.html](http://www.cnr.berkeley.edu/espm/directory/fac/-palsboll_p.html) Phone nos: Office (326 Hilgard Hall), phone +1 510.643.8225 Main laboratory (245 Hilgard Hall), +1 510.643.0956 Student & Post doc office (3 Hilgard Hall), +1 510.643.5142 Department fax; +1 510.643.5438

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### GPSDB

### GeneProteinSynonymsDataBase

Hi,

We have just launched a new database: GPSDB, the Gene and Protein Synonyms DataBase. It is freely accessible online.

The URL is <http://biomint.pharmadm.com> kind regards, kurt.

– ir. Kurt De Grave <http://www.PharmaDM.com> PharmaDM nv. phone: +32-16-298494 Kapeldreef 60, B-3001 Leuven, Belgium fax: +32-16-298490

discovery@pharmadm.com.



Per J Palsboll <palsboll@berkeley.edu>

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## ModelTest web server

Dear all,

ModelTest is available for execution online at the software section at

<http://darwin.uvigo.es> All the best,

David.

– David Posada Facultad de Biología Campus Universitario 36310 Vigo

Phone: +34 986 812038 Fax: +34 986 812556 Email: [dposada@uvigo.es](mailto:dposada@uvigo.es) Web: [darwin.uvigo.es](http://darwin.uvigo.es)

[dposada@uvigo.es](mailto:dposada@uvigo.es)

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## NED Dye Substitution answers

Hi, here is the list of all replies I got on my question about the NED dye substitution. I am truly grateful for all the answers - they were really helpful. It seems that it is possible to substitute NED with some other dye..I will try it out soon.

best regards tomasz

– Tomasz Wilk Institute of Environmental Sciences Jagiellonian University Gronostajowa 7 30-387 Krakow, Poland

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the question was:

> Hi, >does anyone know whether it is possible to substitute NED with some other >dye when doing fragments analysis on ABI? I've read that it may work with >TAMRA. Did anyone try such substitution? >Any comments will be very helpful... > >thank you in advance >tomasz

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...and the answers are:

Hi Tomasz,

The short answer is that the dyes you should choose

depend on what sequencing machine and filter set you are using.

The ABI 3730 comes with a pre-installed filter called the G5 Filter Set, which is set up for 6FAM (blue), VIC (green), NED (yellow), PET (red) and LIZ (orange, size standard). The ABI 3100 is similar, but is set up with the D Filter Set which is FAM (blue), HEX (green), NED (yellow) and ROX (red, size standard). The filter sets are pieces of software that the instrument writes during a calibration process - the emission spectra of the dyes overlap quite a lot so the 3730 tries to choose a wavelength to read each dye that minimizes the 'background' from the other dyes.

For the G5 filter set VIC, NED and PET are all proprietary dyes so are only available from ABI (they are quite expensive). It is possible to substitute VIC with the much cheaper HEX but if you do this you won't be able to use NED. This is because HEX has a slightly higher max emission than VIC, which causes HEX to have spectral overlap with NED, so if you run HEX and NED together with the G5 filter you will contaminate your NED signal with signal from HEX - called "spectral bleeding" or "pull-up" (we found this out the hard way!).

Of course other filter sets may exist, and it is possible to make a customized filter set, i.e. program the sequencer to read the different dyes (such as what you suggested, replacing NED with TAMRA - although we have heard that TAMRA is a particularly bad dye) at the most appropriate wavelengths for those dyes, which is something you also could try. In the end, we stuck with the dyes recommended by ABI for the G5 filter set for use on the 3730 for our own AFLP studies. We would probably recommend you do the same - the ABI dyes may be more expensive but you could potentially waste a lot of time and money trying to get the sequencer set up with different dyes (and ABI warned us that they might only be able to provide limited support if we got ourselves into that situation).

Here are some links you might find useful:  
<http://www.sigmaaldrich.com/sigma/general%20information/oligo-brochure.pdf> [http://www.cstl.nist.gov/div831/strbase/pub\\_pres/-NEAFS\\_CEintro.pdf](http://www.cstl.nist.gov/div831/strbase/pub_pres/-NEAFS_CEintro.pdf) p. 18 <http://stokes.chop.edu/-action.lasso?-database=wr&-response=intranet/-cores/napcore/3730FragmentAnalysis.html> Heidi Meudt & Andrew Clarke

Dear Tomasz, yes, you are right. It is possible to take TAMRA instead of NED. NED is something like a improved form of TAMRA. We are working on an

ABI 377 and never experienced problems, when using the same matrix for both dyes. Hope this helps. If you have further questions, please do not hesitate to contact me again! Good luck and best regards, Cornelya Dipl. Biol. Cornelya Kluetsch Zoologisches Forschungsinstitut und Museum Alexander Koenig (ZFMK) Adenauerallee 160 53113 Bonn Germany Tel.: ++49-+228-9122-242 Fax: ++49-+228-9122-202 E-mail: c.kluetsch.zfmk@uni-bonn.de

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Hi Tomasz, we have been dealing with the same issue with a new ABI 3130xl. Several of the dyes we use on the 310 are not supported by ABI for their new machines. Their application specialist says that TAMRA labeled samples should be run separately from other dyes because of spectral overlap and possible peak "pull-up" problems. However, we have recently been running multiple dyes (HEX, 6-FAM, and Promega's CRX size standard - similar to ROX) with TAMRA and have not had any problems. You might just give it a go and see how the data look. Best regards, Rich

---

Hi Tomasz, Various combinations of fluorescent dyes can be used with the different filter sets available on ABI sequencers. I have attached a Excel table (excerpted from ABI literature) that we use to keep track of such things - any of the dyes with a color indicated under a filter set can be

— / —

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

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## PopGenet PopDynamics

Dear All,

I face to questions which involve population genetics and population dynamics.

It is assumed that only few migrants per generation between two populations allow the homogenization of their genetic pools so that no genetic difference is revealed.

My questions are:

What these "few migrants" mean from a population

dynamic point of view?

Are they sufficient to influence significantly the populations' growth rates?

In broader view, is it justified to consider the definition of a population (and so its conservation/management) only from a genetic point of view?

I am conscious that my question is somewhat wide, but I failed to find relevant articles.

I would appreciate any comments, references, papers, point of view.

Thanks

Best wishes,

Nicolas

Nicolas Poulet <poulet@cict.fr>

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## PopGenet PopDynamics answers

Dear All,

I wish to thank all the people who reply to my request: this was very interesting and I really enjoy.

I add the replies and some references below.

Best wishes,

Nicolas Poulet

## Some references ##

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## The replies ##

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>From Jeff Markert

Dear Nicolas,

I think you ask some excellent questions in your evoldir post, I'll fill you in on my conclusions from my struggles with the same issue. I'm not sure I have a definite view yet, and I would be interested to see what you learn from your evoldir post.

First, the idea about homogenization of is an important one. I believe there is a 1980's paper by Slatkin that suggests even one migrant every second generation is sufficient to prevent populations from diverging through genetic drift alone. There are at least two important caveats:

One is that selection could act differently in the two populations, and could lead to divergence in both phe-

notypes and marker loci even with low or moderate levels of gene flow. It's basically a balancing act between the homogenizing effects of gene exchange and the differentiating effects of selection.

The second is that if two populations start out as separate gene pools and then for some reason start exchanging migrants, then they will become homogeneous. However the time it takes for them to become the same (expressed in generations) is proportional to the number of individuals. For insects or other animals with very high population sizes, the effects of moderate levels of gene flow can be insignificant because it would take so long for homogeneity to be restored that the biogeographic scenario would often be quite likely to change over that time period.

The effect of migration on population dynamics is an important one. A

good place to start exploring this might be a paper by Westemeier et al (*Science* 282 pp 1695) on the genetic rescue of some genetically depauperate populations. We discussed this paper in a course last year, and I came away wondering whether the "rescue" effect was entirely due to a change in the genetics, or due to a change in the demographics because additional individuals were added to the population. It's likely both, but since you can't do controlled experiments on endangered populations it would be difficult to disentangle the genetic effects from population dynamics outside of the laboratory. I wonder whether there might be an experimental conservation genetics literature on this. The obvious experiment to do would be to set up several genetically impoverished populations. To some you add genetic diversity by putting in an unrelated individual and removing one of the individuals from the impoverished population. You also add impoverished

— / —

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

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## PopGenetics software

Dear evoldir members,

I will teach a computer lab course about population genetics. To introduce the standard models I need software to run some simulations. Do you know of any

numerical software that

- can find solutions to differential equations - can draw random numbers - is programmable - is free

Former teachers have used Berkeley Madonna (similar to the program Stella) that can do all of the above but is not free.

Any help is much appreciated! Peter Pfaffelhuber

- Peter Pfaffelhuber University of Munich Department Biology II Großhaderner Straße 2 D-82152 Planegg-Martinsried Tel.: 089 2180 74 108 email: p.p@lmu.de

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### Rt testing answers

Thanks to everyone for their rapid response to my question. As requested by quite a few people, here are the responses.

Regards,

Tim

— Original Message —

> > Does anyone know of software for testing difference in allelic richness between two samples, preferably with a permutation test that resamples individuals as opposed to populations within sample (ie FSTAT)? > >

Tim, I don't have software or know of anything particular, though there is probably something in the Ecological arena, where they have the "species richness" analogue to contend with. There are, as far as I can see, two aspects to the problem. The first is whether what we see in two samples is comparable or really different. The second is how well the two measures capture what is really there. The second problem is probably the more challenging and interesting,

but the first is fairly easy to attack. Imagine a pair of populations of sizes  $N_1$  and  $N_2$ , respectively, preferably but not necessarily the same. In the first population, allelic richness is  $K$  alleles, with counts of  $n_{11}, n_{12}, \dots, n_{1K}$ , summing to  $N_1$ . In the second population, we see  $L$  alleles, with counts of  $n_{21}, n_{22}, \dots, n_{2L}$ , summing to  $N_2$ . Now, the question is whether  $K$  and  $L$  are really different, or whether the apparent difference is just a consequence of drawing two samples, of sizes  $N_1$  and  $N_2$  from the same "pool".

If we take the view that "the data are the data, and anything else is extrapolation," then we might be inclined to conduct a resampling exercise, using only the data at hand, randomly shuffling the  $N = N_1 + N_2$  alleles between the two populations, without replacement, and in numbers  $N_1$  and  $N_2$  allocated to the two pseudo-populations, on the null premise that both populations are drawing from the same pool. We simply count  $K$  and  $L$  from the two (constructed) pseudo-populations, or perhaps  $(K/N_1)$  and  $(L/N_2)$ , if  $N_1$  and  $N_2$  are very different, and compute the difference (or some derivative translation of that difference), and tally it. We then shuffle again, record the criterion of interest, and do it again. With (say) 999 random trials, to which we add the observed data outcome (on the premise that it too is the result of a random draw from a common pool), we have constructed a null distribution of our chosen criterion, against which to compare the actual result. The whole thing is conditioned on the data we actually have, and never mind what we have not seen.

I suspect, on the basis of accumulated experience, that the common alleles will be recovered in both populations, and that the precise allocation of the rarer alleles will be unpredictable. Typical sampling stuff. You may find a program that does this, but my guess would be that you could set it up as an Excel routine. Many years ago, the Michigan team published a paper on thousands of genetic samples from Hiroshima and Nagasaki,

Neel JV, Satoh C, Smouse PE, Asakawa J, Takahashi N, Goriki K, Fujita M, Kageoka T and Hazama R. 1988. Protein variants in Hiroshima and Nagasaki: Tales of two cities. *Am. J. Hum. Genet.* 43:870-893,

the point of which was not "allelic richness" per se, but the samples were so large that they were instructive about the sampling aspects of the problem. The common alleles were shared, but the really rare alleles, say those in frequencies  $< 0.001$ , were virtually unique to the two cities. Of course, with our more typical sample sizes of (say) 50-100 individuals, we would never have seen these alleles at all. When we subsampled, the relatively common alleles survived, but the really rare alleles ( $p < 0.001$ ) and most of the unusual alleles (say  $p < 0.01$ ) dropped out of the sample. Typical rarification result.

Several years later, working with colleagues on mtDNA haplotypes from marine fish, we encountered a similar problem, but there the sample sizes were (for single populations) on the order of  $N = 100$  per population, and the total ( $N_1 + N_2 + \dots + N_{17}$ ) was on the order of 1000 or so. There, haplotypic richness was at least part of the issue,

Brown BL, Epifanio JM, Smouse PE and Kobak CJ. 1996. Temporal stability of mtDNA haplotype frequencies in American shad stocks: to pool or not to pool

across years? *Can. J. Fish. Aquat. Sci.* 53:2274-2283, and we discovered that by doubling the total sample size, we added large numbers of rare haplotypes, the majority of which had not been seen in the previous sample. The common haplotypes were recovered again, and in roughly the same frequencies. Some of the uncommon haplotypes, seen perhaps once or twice in the first sample, showed up again (once or twice) in the second sample.

Today, this is well-traveled territory. There are standard measures of expected allelic richness, with increasing sample size, but they usually require some way to determine the parametric frequencies of the

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## Rt testing answers 2

Another reply to my question regarding significance testing of allelic richness:

Doing a straightforward permutation test by randomising alleles among samples is not useful when you want to test a diversity index such as the allelic richness. The reason for that is that the alleles may or may not be comparable between populations, and this influences the test. A test between populations with richnesses 10 and 20 that share a lot of the alleles, will likely give a different result than a test between populations with richnesses 10 and 20 that have no alleles in common. In the latter case, the average richness after randomisation is likely to be even higher than 20, the maximum of the two populations.

It is however possible to do a bootstrap test, though this also has some (smaller) complications. See Thomas MG, Weale ME, Jones AL, et al. (2002) Founding mothers of Jewish communities: Geographically separated Jewish groups were independently founded by very few female ancestors. *American Journal of Human Genetics* 70, 1411-1420.

I wrote a small app (GenoDive) to test for differences in diversity between pairs of populations, it does not calculate allelic richness (though that probably depends on your definition of allelic richness) but some other indices

of diversity like Nei's (=Simpson's) index and the Shannon (=Wiener/Weiner) index. The program was not made for allelic data, but for clonal genotypes, though it can handle alleles if you just code every allele as a genotype (with an added assumption of HW-equilibrium as that breaks down the connection between the two alleles at a locus).

My program can be found at <http://staff.science.uva.nl/~meirmans/> Good luck with your analysis!

Patrick Meirmans: [meirmans@science.uva.nl](mailto:meirmans@science.uva.nl)

Tim Jones <[tjones@utas.edu.au](mailto:tjones@utas.edu.au)>

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## SMBE Abstracts Titles Deadlines

Genomes, Evolution & Bioinformatics (GEB) Conference May 24-May 28, 2006 Arizona State University, Tempe, Arizona, USA [www.smbe.org/geb](http://www.smbe.org/geb) Deadlines for title submissions (for poster presentations) and abstracts (for contributed talks) is fast approaching.

Abstract Submission Deadline: March 15, 2006. (Go to [www.smbe.org/geb/abstracts.php](http://www.smbe.org/geb/abstracts.php))

The SMBE/GEB conference will open on the evening of Wednesday, May 24 with a Welcome Social and Registration from 7:00 p.m. - 11:00 p.m. The opening symposia and contributed sessions will begin at 8:00 a.m. on May 25. The closing symposia and contributed sessions will take place from 8:00 a.m.- 12:00 noon on Sunday, May 28.

A schedule of events at <http://www.smbe.org/geb/events.htm> To register visit <http://www.smbe.org/geb/registration.php> (Early registration from Feb 1 - April 1, 2006).

[s.kumar@asu.edu](mailto:s.kumar@asu.edu) [s.kumar@asu.edu](mailto:s.kumar@asu.edu)

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## SMBE FitchPrizeCompetition

Fitch Prize Competition Genomes, Evolution, and Bioinformatics Conference [www.smbe.org/geb](http://www.smbe.org/geb) (May 24-28, 2006)

Beginning with the first annual meeting of the Society for Molecular Biology & Evolution (SMBE) in 1993, the

Walter M. Fitch Symposium has provided a forum for young investigators (students and Postdocs) to showcase their exemplary research.

The selection committee will nominate 8-10 individuals to enter the competition on the basis of the abstracts submitted.

This year, the winner will receive a US \$1,000 gift check. In addition, all selected contestants will receive a travel award to cover the cost of airfare, accommodations, and meeting registration expenses. The travel award amount will not exceed US \$1,000 for each domestic US contestant and \$1,500 for each international contestant.

Each selected participant will also receive an online student/postdoc MBE membership for the year of 2007.

Important Date: March 15, 2006 is the abstract submission deadline. (Go to [www.smbe.org/geb/awards](http://www.smbe.org/geb/awards))

Eligibility: Student and Postdoc Members of the SMBE who are either current graduate students or postdoctoral researchers (who received the primary doctoral-level degree no earlier than May 1, 2005).

Presentation: Each contestant will make a 20-minute platform presentation in the Fitch Award Competition Symposium on May 25, 2006. The winner will be chosen based on these presentations.

REQUEST: please distribute this advertisement to your students, colleagues, and department to make them aware of this opportunity.

s.kumar@asu.edu

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### SMBE GradTravelAwards

Graduate Student Travel Awards Genomes, Evolution, and Bioinformatics Conference [www.smbe.org/geb](http://www.smbe.org/geb) (May 24 - 28, 2006)

The Society for Molecular Biology & Evolution (SMBE) announces a competition for 10 graduate student travel awards, which will be given on the basis of the abstracts submitted.

Each awardee will receive funds to cover the cost of airfare, accommodations, and meeting registration expenses for the 2006 meetings at ASU. The travel award amounts are US \$1,000 for each US contestant and US \$1,500 for each international contestant. Each awardee will also receive an online student MBE membership for

the year of 2007.

Important Date: March 15, 2006 is the abstract submission deadline. A graduate student can enter the Walter M. Fitch Prize and the Graduate Travel Award competitions at the same time. (Go to [www.smbe.org/geb/awards](http://www.smbe.org/geb/awards))

Eligibility: Student Members of the SMBE.

Presentation: Each awardee will be given an opportunity to make a 15-minute platform presentation in a symposium. The symposium will be assigned based on the awardees' research description.

REQUEST: please distribute this advertisement to your students, colleagues, and department to make them aware of this opportunity.

s.kumar@asu.edu

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### SMBE UndergradTravelAwards

Undergraduate Student Travel Awards for minority and underrepresented groups

Genomes, Evolution, and Bioinformatics Conference [www.smbe.org/geb](http://www.smbe.org/geb) (May 24 - 28, 2006)

The Society for Molecular Biology & Evolution (SMBE) is pleased to make available 10 travel awards for undergraduate students from under-represented and minority groups, on the basis of the abstracts submitted.

Each awardee will receive funds to cover the cost of airfare, accommodations, and meeting registration expenses for the 2006 meetings at ASU. The travel award amounts are US \$1,000 for each US awardee and US \$1,500 for each international awardee. Each awardee will also receive an online student MBE membership for the year of 2007.

Important Date: March 15, 2006 is the abstract submission deadline. (Go to [www.smbe.org/geb/awards](http://www.smbe.org/geb/awards))

Eligibility: Applicants must be currently enrolled as undergraduate students (Bachelor's level degree) at the time of application and be from under-represented groups (e.g., minority groups and women).

Presentation: Each awardee will be required to make either a platform or a poster presentation. The assignments of symposium and poster sessions will be based on the awardees' research description.

REQUEST: please distribute this advertisement to

your students, colleagues, and department to make them aware of this opportunity.

s.kumar@asu.edu

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## SSB ErnstMayr Award

### Ernst Mayr Award

**General Information.** The Ernst Mayr Award is given to the presenter of the outstanding student paper in the field of systematics at the annual meetings of the Society of Systematic Biologists, as judged by the Ernst Mayr Award Committee. The award consists of \$1000.00 and a set of a set of available back issues of *Systematic Zoology/Systematic Biology*.

**Who is Eligible.** Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible. In addition to submitting their titles for the SSB Meeting in Stony Brook, New York, students should submit a 400-word abstract of their talk to the current awards chair (Kelly Zamudio, krz2@cornell.edu). Please include your abstract in the text of your e-mail, and include your name and complete contact information. Based on the submitted abstracts, the Mayr Awards committee (appointed by the Awards Chair) will select the best 15 for inclusion in the actual competition at the meetings, which will be held at a single venue in a separate session. Previous winners are not eligible. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: <http://systbiol.org/join.html>).

**Judging.** Papers will be judged on creativity, quality, excellence of research, and quality of presentation. Abstracts should clearly indicate methods used, the relevance to systematics and the conclusions. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible.

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

**Notification of Winner.** The winner of the award will be announced at the SSB business meeting at Stony Brook, during the banquet at the annual meetings, and

an announcement will be published in *Systematic Biology*.

Application submission and confirmation

Applications should be sent to Dr. Kelly R. Zamudio, SSB Award Committee Chair, at krz2@cornell.edu E-mail submissions are required.

Application deadline is March 31, 2006.

To ensure that applications are not lost in electronic transfer, the awards chair will send each applicant a confirmation e-mail. If you do not receive this confirmation within 3 days of your submission, please contact the awards chair to arrange for re-submission.

—  
Kelly R. Zamudio Associate Professor Faculty Curator of Herpetology Dept. of Ecology and Evolutionary Biology E209 Corson Hall Cornell University Ithaca NY - 14853-2701

phone: (607) 254 4212 FAX: (607) 255 8088

<http://www.eeb.cornell.edu/zamudio/KZhome.html>  
krz2@cornell.edu krz2@cornell.edu

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## SSB GraduateStudent ResearchAwards

### Awards for Graduate Student Research

The Society of Systematic Biologists (SSB) announces its fifth annual Graduate Student Research Award competition. The purpose of these awards is to assist students in the initiation (first two years) of their systematics projects and in the collection of preliminary data needed by them to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: <http://systbiol.org/join.html>). Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply. Awards will range between \$1,000 and \$2,000 and up to six awards will be made.

All applications materials this year must be in electronic format. Applicants and their recommenders are strongly encouraged to use pdf format, rather than

Word or some other application, to minimize difficulties in file transfer. We strongly recommend that applicants send all materials (except letters of reference) in a single pdf file. Letters of recommendation should be sent separately by the referees in pdf format or in the text of an e-mail; please include the full name of applicant in letters of recommendation.

Applicants must submit 1) a curriculum vitae (one page) 2) brief research proposal including objectives, methods, significance, and schedule (max. three single-spaced pages including literature cited and any figures and tables) 3) budget and budget justification (1 page) 4) and arrange for two letters of recommendation; one letter must be from the student's current graduate advisor.

The research proposal must clearly state the current stage of the proposed research and the current year and status of the student. Please include e-mail contacts for the applicant in the application itself. Both Masters and Ph.D. students are eligible. Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work.

Please email all application materials and queries to Dr. Kelly Zamudio at krz2@cornell.edu

To be considered for this year's award, application materials, including letters of recommendation, must be received electronically no later than March 31, 2006.

To ensure that applications are not lost in electronic transfer, the awards chair will send each applicant a confirmation e-mail. If you do not receive this confirmation within 3 days of your submission, please contact the awards chair to arrange for re-submission.

—

Kelly R. Zamudio Associate Professor Faculty Curator of Herpetology Dept. of Ecology and Evolutionary Biology E209 Corson Hall Cornell University Ithaca NY - 14853-2701

phone: (607) 254 4212 FAX: (607) 255 8088

<http://www.eeb.cornell.edu/zamudio/KZhome.html>  
krz2@cornell.edu krz2@cornell.edu

Society of Systematic Biologists Mini-PEET awards to enhance transfer of taxonomic knowledge

SSB is pleased to announce the availability of awards to enhance the transfer of taxonomic expertise, modeled after the highly successful PEET program at NSF. Unlike the NSF PEET program, awards will not be limited to taxonomically understudied taxa; the primary purpose of this program is to pass on taxonomic expertise in general. The awards are designed to allow SSB members (students, post-docs, and faculty) to spend a summer or semester apprenticed to an expert in a particular taxonomic group. This would support the PEET goal of passing on taxonomic expertise before it is lost. Activities can include a trip to the taxonomists' laboratory, or pay for the taxonomist to visit the applicants' laboratory for a period of time. Requests for support may be in any amount up to \$4,000.

Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: <http://systbiol.org/join.html>).

A complete application includes a brief description of the project, justification of the importance of the taxon, an itemized budget, the applicant's CV, and a letter of support from the taxonomic expert. If the applicant is a student or post-doc, please also include a letter of recommendation. The total request application should be no more than two pages long, not including the curriculum vitae and letters of support.

Requests should be sent to Dr. Kelly R. Zamudio, SSB Award Committee Chair, at krz2@cornell.edu

E-mail submissions are required, and applicants are encouraged to use pdf format for all documents.

Application deadline is March 31, 2006.

To ensure that applications are not lost in electronic transfer, the awards chair will send each applicant a confirmation e-mail. If you do not receive this confirmation within 3 days of your submission, please contact the awards chair to arrange for re-submission.

—

Kelly R. Zamudio Associate Professor Faculty Curator of Herpetology Dept. of Ecology and Evolutionary Biology E209 Corson Hall Cornell University Ithaca NY - 14853-2701

phone: (607) 254 4212 FAX: (607) 255 8088

<http://www.eeb.cornell.edu/zamudio/KZhome.html>

krz2@cornell.edu krz2@cornell.edu



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## SSB TravelAwards IntlScholars

Scholarships and travel awards for scientists from developing countries to obtain modern systematics training in the United States

SSB is pleased to announce the availability of scholarships for scholars from developing countries to attend workshops and courses in systematics, or to visit a lab engaged in systematic research for training. The emphasis of this program is the transfer of knowledge to the scholar's home country. Therefore, applicants should currently be in their home country or have definite plans to return in the near future. Courses such as the Molecular Evolution Workshop at Woods Hole and the applied Systematics Course at Bodega Bay are examples of courses that are appropriate for this funding, in addition to other equivalent opportunities. Support for attending a course will be contingent on admission to the course through the normal admissions process.

Applicants should submit a CV, and a letter detailing how the knowledge acquired will be transferred to their country of origin, a justification of the course or lab visit as providing appropriate training, and one letter of recommendation from a researcher familiar with the scholar's work.

Applications should be sent to Dr. Kelly R. Zamudio, SSB Award Committee Chair, at [krz2@cornell.edu](mailto:krz2@cornell.edu)

E-mail submissions are required, and applicants are encouraged to use pdf format for all documents.

Application deadline is March 31, 2006

To ensure that applications are not lost in electronic transfer, the awards chair will send each applicant a confirmation e-mail. If you do not receive this confirmation within 3 days of your submission, please contact the awards chair to arrange for re-submission.

–

[krz2@cornell.edu](mailto:krz2@cornell.edu) [krz2@cornell.edu](mailto:krz2@cornell.edu)

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## Software Geneious

SOFTWARE: for organizing sequences, alignments,

phylogenetics trees and abstracts

We have recently released a new software system (Geneious version 0.9e) which allows evolutionary biologists to easily manage their data and access web-based databases such as NCBI. It also integrates several core tasks that are essential for evolutionary biologists to perform quickly, often and easily, including

- \* phylogenetic reconstruction (NJ with bootstrapping)
- \* tree viewing
- \* pairwise sequence alignment
- \* multiple sequence alignment
- \* dot plots
- \* sequence viewing, including sequence annotations from NCBI database
- \* translating from DNA to amino acids
- \* export to Endnote, Nexus, Newick, Fasta
- \* import trees, sequences alignments and bibliographies in a variety of formats
- \* adding user information and notes to sequences, alignments and trees

The novel thing about this software is that for the first time these tasks can now be done in an integrated way using a tool that also allows local database storage and retrieval of all sequences, proteins, and research publications in formats including PDF. The result is that much of the drudgery of downloading, sorting and analysing sequences is now streamlined, so that you can spend more time on genuine research. The other major innovation is that any existing bioinformatics applications that you are using can be rapidly integrated into the product so that your workflow becomes even faster.

- Significantly increases your chance of finding the research paper you are looking for - in minutes, not hours
- and being automatically told when new ones come in
- Organise, search, and perform non-exact searches through all PDF-format research publications for keywords
- By creating a well-organised searchable, continuously updating local database of sequences, you can perform much more complicated searches and analyses much quicker than if you had to search from scratch on the whole of NCBI and/or EBI each time

You can download Geneious without charge at [www.geneious.com](http://www.geneious.com). Versions for Mac OS X, Windows and Linux are available.

Geneious will grow as we continue to build new tools through open-source upgrades and new features. We will plan to focus special attention on developing analysis tools for sequence alignment and phylogenetics and welcome any and all feedback on current and future features in the product.

Biomatters plans to release version 1.0 of Geneious in Q2 2006.

Inquiries

Dr Alexei Drummond Chief Scientist Biomatters Ltd

(Auckland, New Zealand) 64 9 3737599 ext 88298 or 021 1601959 alexei@biomatters.com

Dr Daniel Batten Chief Executive Officer Biomatters Ltd (Auckland, New Zealand) 64 9 3795064 or 021 747131 daniel@biomatters.com

alexei@cs.auckland.ac.nz

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## Software Geneious 2

**SOFTWARE:** for organizing sequences, alignments, phylogenetics trees and abstracts

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- \* import trees, sequences alignments and bibliographies in a variety of formats
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- Significantly increases your chance of finding the research paper you are looking for - in minutes, not hours
- and being automatically told when new ones come in
- Organise, search, and perform non-exact searches through all PDF- format research publications for keywords
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Dr Alexei Drummond Chief Scientist Biomatters Ltd (Auckland, New Zealand) 64 9 3737599 ext 88298 or 021 1601959 alexei@biomatters.com

Dr Daniel Batten Chief Executive Officer Biomatters Ltd (Auckland, New Zealand) 64 9 3795064 or 021 747131 daniel@biomatters.com

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## Software LVB release2 2

Dear all,

I would like to announce the release of LVB version 2.2.

LVB uses parsimony to reconstruct phylogeny, with a fast (simulated annealing) heuristic search. LVB 2.2 is significantly faster than LVB 2.1.

LVB is free and is available for Windows, Mac OS X, Linux and as source code for other systems. Please see the LVB Web page:

<http://biology.st-andrews.ac.uk/cegg/lvb.htm> Thank you and best regards,

Daniel Barker db60@st-andrews.ac.uk

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## Software Notung 2 1

Dear Colleagues,

It is our pleasure to announce the release of Notung 2.1, a software tool that provides a unified framework for incorporating duplication/loss parsimony in phylogenetic tasks. Notung can be obtained at <http://->

[www.cs.cmu.edu/~durand/Notung/](http://www.cs.cmu.edu/~durand/Notung/) Given a gene tree and a species tree as input, Notung can

- Reconcile a gene tree with a species tree,
- Estimate upper and lower bounds on gene duplication times in terms of speciation events,
- Root an unrooted tree by minimizing gene duplications and losses,
- Rearrange regions of a gene tree with weak support in the sequence data to obtain alternate hypotheses. The structure of regions with strong support remains unchanged.

Notung's graphical user interface supports exploratory data analysis of very large trees and rapid review of a large number of alternate hypotheses. Notung also provides a command-line interface for automated analysis of many trees in high-throughput genomic studies.

URL: <http://www.cs.cmu.edu/~durand/Notung/> DISTRIBUTION: Notung is freely available and runs on Mac OS X, Windows and Linux. The distribution includes the Notung executable, a manual in PDF format with worked examples, sample gene and species trees, and sample scripts for automated analysis of trees.

PLATFORMS: Mac OS X 10.3 and above; Windows 2000 and Windows XP; Linux. Java 1.4 or higher must be installed.

FILE FORMATS: Notung can read and save trees in Newick, NHX, or Notung file format. Notung can also output images in PNG format for use as figures in publications.

AUTHORS: Notung was written by Benjamin Vernot, Aiton Goldman, and Dannie Durand. It uses a novel, fast algorithm by Durand, Halldorsson, and Vernot [1], and is based on an approach first presented in Chen, Durand, and Farach-Colton [2]. Notung is implemented in Java and makes use of the tree visualization library provided by FORESTER (version 1.92) [3].

#### REFERENCES:

[1] "A Hybrid Micro-Macroevoolutionary Approach to Gene Tree Reconstruction." D. Durand, B. V. Halldorsson, B. Vernot, *Journal of Computational Biology*, in press. A preliminary version appeared in *Recomb 2005*, LNBI 3500, Springer Verlag, 250-264.

[2] "Notung: A Program for Dating Gene Duplications and Optimizing Gene Family Trees." K. Chen, D. Durand, M. Farach-Colton, 2000. *Journal of Computational Biology*, 7 (3/4), 429-447.

[3] "ATV: Display and Manipulation of Annotated Phylogenetic Trees." C.M. Zmasek & S.R. Eddy, 2001.

*Bioinformatics*, 17:383-384.

[durand+@motif.compbio.cs.cmu.edu](mailto:durand+@motif.compbio.cs.cmu.edu)

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## Software Selection server

It is our pleasure to announce the release of version 2.0 of the Selection server, at <http://selecton.bioinfo.tau.ac.il>.

The Selection server is a server for the identification of selection forces acting upon proteins [1]. This is done by estimating the degree of positive Darwinian selection and purifying selection at each site. Positively selected sites may be interpreted as being a consequence of molecular adaptation, which confers an evolutionary advantage to the organism

Given a file of coding sequences, Selecton can:

- compute Ka/Ks scores - project the score on the linear sequence. This enables the detection of blocks of similarly evolving sites
- project the scores on the 3-dimensional structure (if available). This enables the detection of patches of similarly evolving sites

AVAILABILITY The server is freely available at <http://selecton.bioinfo.tau.ac.il> <<http://selecton.bioinfo.tau.ac.il/>> .

METHOD (in brief): The server implements both a Bayesian [2] as well as a Maximum likelihood [3] approach. The user may choose between the two methods. Both methods explicitly take into account the phylogenetic relations among the sequences and the underlying stochastic process of evolution.

INPUT: (1) The input may consist of a file of coding sequences, either non-aligned, or codon-aligned. (2) PDB ID or PDB file (if available)

OUTPUT: (1) Projection of the color-coded Ka/Ks scores on the linear sequence (and 3D if available) (2) Actual Ka/Ks scores of each site (3) Amino acid multiple sequence alignment (4) Codon multiple sequence alignment (5) Phylogenetic tree

#### REFERENCES:

1. Doron-Faigenboim, A., et al., Selecton: a server for detecting evolutionary forces at a single amino-acid site. *Bioinformatics*, 2005. 21(9): p. 2101-3.
2. Yang, Z., et al., Codon-substitution models for heterogeneous selection pressure at amino acid sites. *Genetics*, 2000. 155(1): p. 431-49.
3. Goldman, N. and

Z. Yang, A codon-based model of nucleotide substitution for protein-coding DNA sequences. *Mol Biol Evol*, 1994. 11(5): p. 725-36.

Adi Stern Department of Cell Biology and Immunology  
Tel-Aviv University

adi.stern <sternadi@post.tau.ac.il>

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## Squirrel samples

Dear colleagues,

for a project studying the effects of the range expansion of the American grey squirrel, *Sciurus carolinensis* on the genetic identity of the European squirrel, *Sciurus vulgaris*, in Italy, we are looking for samples of *S. carolinensis* from America, and *S. vulgaris* from European locations, preferentially from south-eastern Europe.

Hairs with bulbs plucked from the tail and/or dorsal area and stored in pure ethanol or tissue samples, as well as museum specimens are welcome. In exchange, we can provide samples from our geographic area. All contributors will be acknowledged by name in eventual outcoming publications of this project.

Contact:

Andrea Grill Istituto Nazionale per la Fauna Selvatica  
Dipartimento di Genetica Via Cà Fornacetta, 9 40064  
Ozzano Emilia (BO) Italy e-mail: grill@science.uva.nl

With best regards,

Andrea Grill.

Andrea Grill <grill@science.uva.nl>

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## Storing DNA

Hello,

I have extracted DNA from fishscales using the method described in Elphinstone et al. (2004) (\*\*and below). I have encountered a problem where the extracted DNA (dissolved in water) apparently degrades after being stored (+4 and -20) for about 12-15 months. I was wondering if any of you might have good tips and information how to prolong the preservation time of DNA.

How long can I expect the DNA to preserve in +4, -20 or -80? Should I use buffer like 0,2M TE instead of water to dissolve the DNA in or perhaps some other buffer or concentration?

\*\*The method is based on the binding of DNA to silica beads under chaotropic salt conditions, vacuum is applied to remove unwanted liquids, few washing steps with some solvents and finally the DNA is detached from silica beads and eluted with water.

Thanks Juha-Pekka

Juha-Pekka Vähä <juha-pekka.vaha@utu.fi>

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## Used sequencer

My startup lab at Simmons College is looking for a used sequencer. Anybody have one collecting dust that they would let go for a reasonable price? (all models considered)

Thanks

Vlad

Vladimir Douhovnikoff Assistant Professor Biology Department Simmons College

Vladimir Douhovnikoff <vlad@nature.berkeley.edu>

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## WikipediaResources EvolBiolTeaching

Dear All,

Many of you may know Wikipedia, the free on-line encyclopedia. You may also know that anyone can edit and add to it.

This is just what a number of us (mostly grad students, postdocs and assistant professors) have done for a few months, or in some cases longer. Specifically, we have recently created a number of navigation templates that are like tables of content for mini-textbooks.

The following evolution-related templates are available so far. The topics are not yet covered exhaustively or with complete intellectual rigour (if you find any lack of precision or detail, please fix it!), but you may want

to judge for yourselves whether you find any of the below useful as supplementary resources for first year students.

Evolution <http://en.wikipedia.org/wiki/Template:Evolution> Population genetics <http://en.wikipedia.org/wiki/Template:Popgen> Development of phenotype (or “genetic architecture”, its original name) <http://en.wikipedia.org/wiki/Template:Genarch> Phylogenetics <http://en.wikipedia.org/wiki/Template:Phylo> Quantitative genetics <http://en.wikipedia.org/wiki/Template:Qg> Speciation <http://en.wikipedia.org/wiki/Template:Speciation> Evolution of chromosomes <http://en.wikipedia.org/wiki/Template:Chromo>  
Origin of life [http://en.wikipedia.org/wiki/Template:Origin\\_of\\_life](http://en.wikipedia.org/wiki/Template:Origin_of_life) == For those concerned about vandalism =

Vandalism or intellectual distortion of established Wikipedia content is a well-studied problem with a few well-established solutions. Generally, a defacing edit of a page will not last more than five minutes - at any time of day or night, there will be many wikipedians active in checking any recent changes, and undoing any changes that seem incorrect.

There are, however, some pages that are so zealously protected that it is difficult to make a contribution.

A Wikipedia stable version, or Wikipedia 1.0, is also being prepared. I expect it may get finished within the next three years.

== For those concerned about copyright =

Quoting from wikipedia.org:

“Wikipedia contributions are voluntarily given under the GNU Free Documentation License (GFDL), which applies the legal principle known as copyleft, a way of using the copyright process to prevent information being controlled by any one person, to ensure it remains freely accessible forever.

All of the information in Wikipedia is free for anyone to copy, modify for their own purposes, and redistribute or use as they see fit, as long as the new version grants the same freedoms to others and acknowledges the authors of the Wikipedia article used (a credit or backlink to the original article is sufficient for this). For full information see the copyright page or the text of the GNU

Free Documentation License.”

For further details, see: <http://en.wikipedia.org/wiki/Wikipedia:Copyright> So finally, I would like to invite you all to see wikipedia as what it is and use it for what it can do.

Best wishes,

Philipp

– Philipp Wesche Institute of Evolutionary Biology University of Edinburgh Tel.: 0131 650 8657 (office) <http://www.philippwesche.org/> philipp.wesche@ed.ac.uk philipp.wesche@ed.ac.uk

## WintoMac conversion software ABI

dear all,

does anyone happen to have the software to convert ABI 310-Genescan files generated on a Windows-system (\*.fsa) into Mac-files ? I once had two little programs (named win\_to\_mac and mac\_to\_win or something similar), but I do not find them anymore...

thanks Walter

– \*\*\*\* Register for “Plant Population Biology” <<http://www.ufz.de/PopBio2006>> \*\*\* A conference from 24.05.-27.05.2006 in Halle, Germany \*

Dr. Walter Durka Dr. Walter Durka UFZ - Centre for Environmental Research Leipzig-Halle UFZ - Umweltforschungszentrum Leipzig-Halle Dept. Community Ecology Department Biozönoseforschung Theodor-Lieser-Strasse 4 Theodor-Lieser-Str. 4 06120 Halle 06120 Halle Germany Deutschland Tel.: (+49)345/558-5314 Tel.: 0345/558-5314 Fax: (+49)345/558-5329 Fax: 0345/558-5329

email: [walter.durka@ufz.de](mailto:walter.durka@ufz.de)  
<<mailto:walter.durka@ufz.de>>

INVASIONS: <http://www.ufz.de/index.php?en=2773> <<http://www.ufz.de/index.php?en=73>> Home: <http://www.ufz.de/index.php?en=798> <<http://www.ufz.de/index.php?eny8>>

[walter.durka@ufz.de](mailto:walter.durka@ufz.de)

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## PostDocs

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### Canberra ComputationalGenomics

JOHN CURTIN SCHOOL OF MEDICAL RESEARCH DIVISION OF IMMUNOLOGY and GENETICS POST DOCTORAL FELLOW or RESEARCH FELLOW Academic Level A or B

Fixed Term - Up to 3 years

Salary Range: AUD\$49,690 - AUD\$74,313 pa plus 17% superannuation

Reference: JC 3290

Applications are invited for a position as Post Doctoral Fellow in the Computational Genomics laboratory at the John Curtin School of Medical Research, Australian National University. The position is funded by a NHMRC grant awarded to Dr Gavin Huttley and Prof. Simon Easteal.

The successful applicant will work on a project aimed at exploiting comparative genomic sequence data to assess the influence of biological processes affecting germline mutagenesis. The work will build on PyEvolve, a sophisticated software toolkit for statistical modelling of molecular evolution developed in Dr Huttley's lab.

A strong track record in numerical computation is

essential, and experience in mathematical statistics and/or molecular evolution are desirable.

Level of appointment will be according to experience and qualifications.

Selection Criteria: <http://info.anu.edu.au/hr/jobs/> or contact HR Management Section, JCSMR, T: 6125 2580 or E: [hr.jcsmr@anu.edu.au](mailto:hr.jcsmr@anu.edu.au)

Enquiries: If you wish to discuss the position after obtaining the selection criteria please contact Dr Gavin Huttley, email [Gavin.Huttley@anu.edu.au](mailto:Gavin.Huttley@anu.edu.au) tel: +61 2 6125 7961

Closing Date: 14 April 2006

Information for applicants: [http://info.anu.edu.au/hr/Jobs/How\\_to\\_Apply/index.asp](http://info.anu.edu.au/hr/Jobs/How_to_Apply/index.asp) Job Application Cover sheet: [http://info.anu.edu.au/policies/forms/human\\_resources/recruitment/hr86.asp](http://info.anu.edu.au/policies/forms/human_resources/recruitment/hr86.asp)

Dr Gavin Huttley, Head, Computational Genomics Laboratory, John Curtin School of Medical Research, Building 54 The Australian National University Canberra ACT 0200 Australia

T: 61 2 6125 7961 F: 61 2 6125 2595 M: 61 404 004 919  
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CRICOS Provider Number: 00120C

[Gavin.Huttley@anu.edu.au](mailto:Gavin.Huttley@anu.edu.au)

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## CollegeWilliamMary EvolPhysiology

Postdoctoral Position, Evolutionary Physiology, College of William and Mary. A postdoctoral position will be available beginning August of 2006, renewable through May 2009, to investigate the evolution of complex neuroendocrine pathways. Applicants should have a PhD prior to May 2006 and experience in one or more of these areas: physiological ecology, neuroendocrinology, behavior, evolutionary biology, physiology, or cell and molecular biology. The research focus is on the contribution of genetic variation and phenotypic plasticity to the evolution of the photoneuroendocrine pathway in mammals. This pathway integrates photoperiod and other environmental information to regulate reproductive, physiological and behavioral responses to seasons. The model system is a wild-derived laboratory colony of white-footed mice (*Peromyscus leucopus*). The successful candidate will conduct collaborative research, supervise undergraduate students in the research laboratory, and teach a one semester course in animal physiology during the spring. More details on the research are available at: <<http://faculty.wm.edu/-pdheid>><http://faculty.wm.edu/pdheid>. The College of William and Mary is a "Public Ivy" with 5500 undergraduate enrollment, an excellent undergraduate program, and a strong research tradition. Starting salary is \$35,000 plus benefits. Please send curriculum vita, a brief description of research interests/experience, and the names and contact information of three references to: Dr. Paul Heideman, Chair, Department of Biology, P.O. Box 8795, College of William and Mary, Williamsburg, VA 23187-8795; e-mail: [pdheid@wm.edu](mailto:pdheid@wm.edu). Review of applications begins March 1st and continues until the position is filled. The College of William and Mary is an Affirmative Action/Equal Opportunity Employer.

David Broussard Visiting Assistant Professor Department of Biology College of William and Mary Williamsburg, VA 23187 e-mail: [drbrou@wm.edu](mailto:drbrou@wm.edu) Phone: 757-221-2238 <http://drbrou.people.wm.edu> [drbrou@wm.edu](mailto:drbrou@wm.edu)

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## DukeU coloniality

Could you please post the following on evoldir:

Post-doctoral Fellowship. Applications are invited from biologists (with a strong interest in philosophy) or philosophers (with training in biology) for a two-year post-doctoral position leading a study of possible universal principles of coloniality/sociality. The empirical component of the study is a search for the morphological, physiological, and behavioral correlates of the emergence of colonial associations generally (from bryozoans to bees to buffalo). The philosophical component is an analytical study of the possible correlates, leading to methods for operationalizing them. For a more detailed description of the project, see: [www.biology.duke.edu/mcshealab](http://www.biology.duke.edu/mcshealab). Funding for the position is expected but pending. Opportunity to join Duke Biology Dept, which has exceptional strength in evolutionary studies. Applicants should submit a CV, short statement of research interests, one or two sample papers, and names and e-mail addresses of three references. Electronic submission of documents is encouraged. Consideration of candidates will begin on 15 February. Start date is 1 July. Send materials to: Dan McShea, [dmc Shea@duke.edu](mailto:dmc Shea@duke.edu), Dept. of Biology, Duke University, Box 90338, Durham, NC 27708.

Thanks! Dan McShea

Dan McShea Dept. of Biology Duke University Box 90338 Durham, NC 27708-0338

Office phone: 919-660-7342 E-mail: [dmc Shea@duke.edu](mailto:dmc Shea@duke.edu)  
FAX: 919-660-7293

[dmc Shea@duke.edu](mailto:dmc Shea@duke.edu)

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## EcoleNormaleSuperieureLyon EvoDevo

Postdoctoral Research in Comparative Developmental Biology

Laboratory of Molecular and Cellular Biology

Ecole Normale Supérieure in Lyon, France

A postdoctoral position is available in a research group studying the roles of retinoic acid signaling during development. The successful applicant will work on a project designed to decipher the molecular hierarchy of the retinoic acid signaling pathway using chordate model systems, such as zebrafish, lampreys and the invertebrate amphioxus. The position is offered for an initial period of 2 years. The project will focus on the

study of retinoic acid signaling activity during development and on the characterization of direct retinoic acid signaling targets using cutting edge approaches in developmental and molecular biology. A background and previous experience in both developmental and molecular biology are thus desirable. Recent publications of the research team related to the project: Schubert et al (2005) Retinoic acid signaling acts via Hox1 to establish the posterior limit of the pharynx in the chordate amphioxus. *Development* 132:61-73

Bardet et al (2005) The ERRA orphan nuclear receptor controls morphogenetic movements during zebrafish gastrulation. *Dev Biol* 281:102-111

Schubert et al (2004) Retinoic acid influences antero-posterior positioning of epidermal sensory neurons and their gene expression in a developing chordate (amphioxus). *Proc Natl Acad Sci USA* 101:10320-10325

Escriva et al (2002) The retinoic acid signaling pathway regulates anterior/posterior patterning in the nerve cord and pharynx of amphioxus, a chordate lacking neural crest. *Development* 129:2905-2916

Delaunay et al (2000) An inherited functional circadian clock in zebrafish embryos. *Science* 289:297-300

Interested candidates should submit a CV to:

Vincent Laudet

Laboratoire de Biologie Moléculaire de la Cellule, Ecole Normale Supérieure de Lyon

46, allée d'Italie, 69364 Lyon cedex 07, France

E-mail: Vincent.Laudet@ens-lyon.fr

Tel: +33 (0)4 72 72 81 90 - Fax: +33 (0)4 72 72 80 80

Frederic Brunet <Frederic.Brunet@ens-lyon.fr>

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## EwhaWomaniU Korea EvolPrimates

Postdoctoral Research Associate in Primatology

Applications are invited for a postdoctoral research associate position in behavioral and ecological research of primates. The Ewha Womans University of Korea seeks a primatologist with expertise in field studies of free-ranging primates, preferably with additional experience with captive primates. The position can begin as early as March 2006 or any time thereafter for 2 years, renewable for the following years. Activities shall be divided into field research in Southeast Asia and laboratory

work in Seoul, Korea. The research program is a newly founded one and thus s/he will be responsible for helping to develop the project for the years to come. Areas of interests include, in addition to cognition, foraging strategy, habitat use, anti-predation behavior, and movement ecology. Suitable candidates should have experience with ecological/behavioral methodologies and be willing to work with graduate and undergraduate students. Stipend commensurate with experience and personal needs (\$32,000~36,000). To apply, please send resume and a list of references to Professor Jae C. Choe, jaechoe@ewha.ac.kr. All applications must be submitted by e-mail. Applications will be reviewed individually as they come in and the position will be open until filled.

sanhakim@hotmail.com

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## France 12 EvolBiol

Dear colleagues,

I would like to draw your attention on the possibility of 12-months post-docs in France (for people aged less than 35) funded by the French Ministry for Research. The procedure is as follows: candidates should build a project in connection with a French laboratory (the scientific part of the project should be 3 to 5 pages) and submit it to the Ministry (deadline: March 11 2006). Evaluation will be based on the quality of the project, the candidate and the host research group. Given the limited number of fellowships (100, covering all scientific fields), very good projects only will be retained.

The net salary will be 1830 euros (about 2300 - 2400 US \$) per month, and social insurance will be paid by the Ministry.

More details (in French) at <http://www.recherche.gouv.fr/appe/2006/acpostdoc.htm>

. All the best,

P. Jarne

Philippe Jarne CEFÉ - CNRS 1919 route de Mende  
34293 Montpellier cedex 5 France Tél / phone (0)4 67  
61 32 27 Fax (0)4 67 41 21 38

- passerelle antivirus du campus CNRS de Montpellier

-

Philippe JARNE <philippe.jarne@cefe.cnrs.fr>



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**GifsurYvette EvolGenetics**

A post-doctoral position is available in our group 'Génétique Evolutive: Adaptation et Redondance' (Evolutionary Genetics: Adaptation and Redundancy), UMR de Génétique Végétale, Ferme du Moulon, 91190 Gif sur Yvette, FRANCE.

The project deals with the proteomic and molecular characterization of gene expression and its regulation following allopolyploidy events. Our plant model is oilseed rape (*B. napus*, AACCC) of which we dispose of newly synthesized amphiploids resulting from independent AA (*B. rapa*) × CC (*B. oleracea*) crosses (INRA Rennes). Comparative proteomics performed on early generations of these synthetic lines led to the observation of numerous non-additive patterns. Identifications of the corresponding proteins are in progress, using mass spectrometry. The applicant will have to: 1/ determine, using quantitative PCR, at which level (during or after transcription) the modifications of gene expression occur; 2/ study the origins of various isoforms (gene family products? post-translational modifications?); 3/ evaluate the implication of epigenetic mechanisms (methylation, transposable elements) in the observed regulation.

Candidates should have a PhD degree with a strong background in plant molecular biology (including quantitative PCR) and proteomics. Taste for evolutionary genetics is welcome.

Applications should comprise a curriculum vitae including a brief statement of previous research experience, and names and e-mail addresses of 2 referees. The post-doctoral position, funded by the French National Agency for Research (ANR), is available for 18 months, starting by April 2006. Salary will be of approximately 2000 euros per month. Applications should be sent by e-mail to Hervé Thiellement (thiellement@moulon.inra.fr <mailto:thiellement@moulon.inra.fr>)

and/or Karine Alix (alix@moulon.inra.fr <mailto:alix@moulon.inra.fr>). Closing date: 3 March 2006.

Hervé THIELLEMENT, Philippe BRABANT, Karine ALIX. <http://moulon.inra.fr/> alix@moulon.inra.fr

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**INRA France MolPopGenet**

POSTDOCTORAL POSITION: MOLECULAR EVOLUTION; DOMESTICATION; MAIZE

We are seeking a motivated postdoctoral fellow to conduct lab experiments and analyses on the molecular population genetics of maize and its wild ancestors. The research is designed to better understand patterns of genetic variation to increase our understanding of the domestication process. The successful applicant must have a strong background in population genetics with lab experience in molecular methods (e.g., PCR, cloning, sequencing). Programming ability and interest for theoretical developments is also desirable. Candidates with less optimal profiles will be considered providing that their motivation and past experience allow them to adapt rapidly to the project. Applications will be reviewed until the position is filled. Postdoc annual salary is approximately 25.000 euros and includes medical benefits. The initial appointment is for one year and is renewable for a second year.

Applicants should submit their cv, a summary of research interests and contact information of two references (either Electronically or via post) to:

Dr. Maud Tenaillon, Department of Plant Genetics, UMR8120, Ferme du Moulon, 91190, France

tenaillon@moulon.inra.fr <mailto:tenaillon@moulon.inra.fr>

For more information, please visit our web site at <http://moulon.inra.fr/SGV/GEAR/geargb.html>

– Maud Tenaillon, CNRS

UMR8120 CNRS-INRA-UPS-INA PG Ferme du Moulon 91190 Gif-sur-Yvette France

Phone: +33 1 69-33-2377 Fax: +33 1 69-33-2340 [http://moulon.inra.fr/pages\\_pers/tenaillon/-index.html](http://moulon.inra.fr/pages_pers/tenaillon/-index.html) tenaillon@moulon.inra.fr

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**ImperialCollegeLondon  
PopulationBiology**

Postdoctoral Research Associates in Population Biol-

ogy/Ecology

NERC Centre for Population Biology

The NERC Centre for Population Biology is a centre hosted by Imperial College London, which is funded by NERC to carry out research in all areas of population biology.

We seek to recruit two post doctoral research associates with a strong background in population biology or related subjects. Your work should complement current research at the CPB (see <http://www.cpb.bio.ic.ac.uk/>) and may be theoretical, lab or field based. As part of the application procedure we request that, in addition to your CV and references, you also send a brief description of possible research projects.

The three-year appointments will be on the Imperial College scale R&E B (£22,870 - £33330) depending on qualifications and experience.

For further details and an application form contact: Sarah Snellin, NERC CPB, Imperial College London, Silwood Park Campus, Ascot, Berks, SL5 7PY. Tel: 020 7594 2346. e-mail: [s.snellin@imperial.ac.uk](mailto:s.snellin@imperial.ac.uk) .

Applications to be received by Friday 3rd March 5.00 pm.

– Prof. Ian P.F. Owens Division of Biology & NERC Centre for Population Biology Imperial College London Silwood Park Ascot, Berkshire SL5 7PY, UK

<http://www.imperial.ac.uk/people/i.owens> Ian Owens <[i.owens@imperial.ac.uk](mailto:i.owens@imperial.ac.uk)>

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## InstZooLondon PopGenet

POSTDOCTORAL POSITION IN POPULATION GENETICS

Three years fixed term contract Starting salary GBP 26,470plus GBP 3,051 London weighting

We would like to appoint a PDRA in population genetics, starting 1st July 2006, on a BBSRC funded project 'Inference of genealogical relationships among individuals from genetic markers'. The appointee will work in Dr. Jinliang Wang's lab and with collaborators (Drs. W. C. Jordan and A. F. G. Bourke) to develop statistical methodologies inferring genealogical relationships and relatedness between individuals from marker information, and to test the methodologies using empirical

and simulated datasets.

The starting salary for this position has been enhanced by two spine points, by the BBSRC, to help improve selection and retention of staff in this area of research.

The candidate should have a doctorate in biology (population genetics; statistical genetics; computational biology) or other related fields (statistics, applied mathematics or physics, bioinformatics), demonstrated knowledge of population genetics and/or statistics, excellent programming experience and a good record of scientific publication.

Please see our website for further information at <http://www.zoo.cam.ac.uk/ioz/>

Informal enquiries can be directed to [jinliang.wang@ioz.ac.uk](mailto:jinliang.wang@ioz.ac.uk).

Full applications (including a cover letter outlining research interests, complete CV, publication list and contact details for three referees) should be sent to the HR Department, Zoological Society of London, Regent's Park, London NW1 4RY, UK ([hr@zsl.org](mailto:hr@zsl.org)) by 31st March 2006.

Dr. Jinliang Wang Institute of Zoology Regent's Park London NW1 4RY Phone: +44 20 74496620 Fax: +44 20 75862870 <http://www.zoo.cam.ac.uk/ioz/index.htm> [Jinliang.Wang@ioz.ac.uk](mailto:Jinliang.Wang@ioz.ac.uk)

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## KansasStateU PhloxEvol

POSTDOCTORAL POSITION DIVERSIFICATION AND CHARACTER EVOLUTION IN THE PLANT GENUS PHLOX KANSAS STATE UNIVERSITY

A Postdoctoral Research Associate position is available to explore diversification and character evolution in the plant genus Phlox (Polemoniaceae). The aim of this project is to elucidate fine-scale relationships within a species complex including diploids and tetraploids, examine floral phenotypic variation in light of relationships, and apply molecular ecological tools (particularly microsatellites) under development for Phlox. Candidates should have experience in phylogeography and phylogenetics and/or population genetics.

This position is funded by the KSU Center for the Understanding of Origins, which is a broad interdisciplinary initiative at Kansas State promoting research and education on origins and evolution in the broad sense (cosmology to evolutionary biology; <http://www.k-state.edu/origins/>)

/www.phys.ksu.edu/origins). Through this initiative, the post doc will also collaborate with workers in the humanities through a short internship focused on communicating research in evolutionary biology to a general audience.

The post doc will greatly benefit from the recently formed Ecological Genomics Institute at KSU (<http://www.ksu.edu/ecogen>). Researchers at KSU form a strong program in ecology and evolutionary biology, and enjoy resources including the KSU Herbarium (<http://www.ksu.edu/fergusonlab/herbarium>) and the Konza Prairie Biological Station (an NSF-LTER site; <http://www.ksu.edu/konza>). Manhattan is a pleasant university community located two hours west of Kansas City in the Flint Hills (<http://www.manhattan.org>).

The position is available beginning 1 July 2006. This is a one year appointment with the possibility of reappointment for a second year.

To apply, submit a cover letter, curriculum vitae and up to three reprints, and have three letters of recommendation sent to Carolyn J. Ferguson by mail (Division of Biology, 313 Ackert Hall, Kansas State University, Manhattan, KS, 66506-4901) or email ([ferg@ksu.edu](mailto:ferg@ksu.edu)). Review of applications will begin 15 March 2006 and continue until the position is filled. For further information about this position, contact Carolyn Ferguson ([ferg@ksu.edu](mailto:ferg@ksu.edu); 785-532-3166).

Kansas State University is an Equal Opportunity Employer, and actively seeks diversity among its employees.

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

office ph: 785-532-3166 herbarium ph: 785-532-6619  
fax: 785-532-6653

[ferg@ksu.edu](mailto:ferg@ksu.edu) [ferg@ksu.edu](mailto:ferg@ksu.edu)

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## KenyaILRI MolGenet

INTERNATIONAL LIVESTOCK RESEARCH INSTITUTE

POSITION ANNOUNCEMENT

POST-DOCTORAL SCIENTIST - MOLECULAR GENETICIST

REF: PD/MG/T4/02/2006

General: The Africa-based, globally networked International Livestock Research Institute (ILRI) helps reduce poverty, hunger and environmental degradation by enhancing animal agriculture in developing countries. ILRI positions its work at the dynamic interface of poverty alleviation and sustainable livestock livelihoods. Our staff work in partnerships and alliances with hundreds of organisations in developed and developing countries, including some of the finest universities and research institutions in the world. ILRI's headquarters are in Nairobi, Kenya, with a second principal campus in Addis Ababa, Ethiopia. Our staff are also based in 7 partner institutions in other parts of Africa, in Asia and Latin America. We employ more than 700 staff from about 40 countries and are one of 15 centres around the world sponsored by the Consultative Group of International Agricultural Research (CGIAR).

The position: ILRI seeks to recruit a Post-Doctoral Molecular Geneticist to join its genetic research projects (Theme 4 Biotechnology) on "Improving Characterization of Animal Genetic Resource (Biodiversity mapping and gene discovery) that seeks to improve the understanding of the genetic diversity in, and enhanced utilization of, indigenous animal genetic resources.

Specific Duties include: Contribute to an extensive ongoing research portfolio of research projects on characterization, utilisation and improvement of livestock genetic resources, with projects including the development, and application of genetic markers for molecular characterisation of livestock genetic resources, the identification and characterization of molecular signatures of selection for diseases resistance/tolerance (cattle, small ruminant and chicken) QTL mapping and study of gene expression in relation to disease resistance in livestock and model organisms. Assist with supervision of a research team including graduate students, technicians and visiting scientists. Develop collaborative research projects with Advanced Research Institutes and National Research Institutes in the developing and developed world.

Location: ILRI - Nairobi, Kenya.

ILRI laboratories are hosting BecA, a NEPAD center of excellence in biosciences for East and Central Africa. Our joint laboratories are equipped with the state of the art molecular genetics tools including automated DNA sequencers (ABI 3730, ABI 3100), micro-array and gene expression facilities and a strong bioinformatics platform. Small and large animal research facilities are available on site.

The successful candidate will have: A PhD degree obtained no more than 5 years ago in molecular genetics Good population genetics, quantitative genetics and

bioinformatics skills. Excellent communication and interpersonal skills and the ability to perform in a multi-disciplinary and multi-cultural research environment. Fluency in spoken and written English essential.

Terms of appointment: Initial appointment is for three years with the possibility of renewal, contingent upon individual performance and the availability of funding. ILRI offers a competitive remuneration package paid in US dollars.

Applications: Applicants should send a cover letter, curriculum vitae and the names and addresses (including telephone, fax and email) of three referees who are knowledgeable about the candidate's professional qualifications and work experience to the Human Resources Manager, ILRI, P.O. Box 30709-00100, Nairobi Kenya; Telephone 254-20-4223000; Fax 254-20-4223001; email: [recruit-ilri@cgiar.org](mailto:recruit-ilri@cgiar.org). The name and reference number of the position for which the application is made should be clearly marked on the envelopes of mailed, or on the fax or email applications. Screening of applications will begin immediately and will continue until the post is filled. For further information regarding the ongoing molecular genetics research projects please contact: Dr. Olivier Hanotte [o.hanotte@cgiar.org](mailto:o.hanotte@cgiar.org) or Professor Steve Kemp [s.kemp@cgiar.org](mailto:s.kemp@cgiar.org).

To find more about ILRI, visit our Website at <http://www.cgiar.org/ilri/> ILRI is an equal opportunity employer and is keen to further diversify its staff in terms of both gender and nationality. Qualified women and professionals from developing countries are particularly encouraged to apply.

Olivier Hanotte, PhD Project Leader Improving Animal Genetic Resources Characterization International Livestock Research Institute (ILRI) P.O. Box 30709 Nairobi 00100 Kenya Tel + 254 20 4223466 (office) + 254 20 4223140 (home) Fax +254 20 4223001 Mobile + 254 (0)734 333071 E-mail [o.hanotte@cgiar.org](mailto:o.hanotte@cgiar.org) <http://www.ilri.cgiar.org/> ILRI via USA-Direct Tel + 1 650 8336660, Fax 1 650 833 666

[o.hanotte@cgiar.org](mailto:o.hanotte@cgiar.org)

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## KenyaILRI QuantGenet

POST-DOCTORAL SCIENTIST - QUANTITATIVE GENETICIST/ANIMAL BREEDER

REF: PD/QG/T4/02/2006

General: The Africa-based, globally networked International Livestock Research Institute (ILRI) helps reduce poverty, hunger and environmental degradation by enhancing animal agriculture in developing countries. ILRI positions its work at the dynamic interface of poverty alleviation and sustainable livestock livelihoods. Our staff work in partnerships and alliances with hundreds of organisations in developed and developing countries, including some of the finest universities and research institutions in the world. ILRI's headquarters are in Nairobi, Kenya, with a second principal campus in Addis Ababa, Ethiopia. Our staffs are also based in 7 partner institutions in other parts of Africa, in Asia and Latin America. We employ more than 700 staff from about 40 countries and are one of 15 centres around the world sponsored by the Consultative Group on International Agricultural Research (CGIAR).

The Position: ILRI seeks to recruit a Post-doctoral quantitative geneticist/animal breeder to join its genetics research projects (Theme 4 Biotechnology), focusing on improving understanding and utilization of Animal Genetic Resources in developing countries.

Specific Duties include: Assist with the development of a portfolio of research projects on utilisation and improvement of livestock genetic resources, with projects ranging from the development of in situ breeding strategies suitable for resource poor farmers, through to developing breeding programmes for delivery to smallholder livestock keepers in tropical developing countries. Genetic improvement options under consideration include marker-assisted breeding strategies for these low-input production systems and the need to test innovative ways to deliver genetic change in smallholder livestock herds/flocks in ways that are sustainable and address poverty. Approaches will of necessity need to include conventional breeding including crossbreeding and, where appropriate, marker/QTL technologies. Development of effective and sustainable institutional arrangements as well as considerations of market issues will be important elements in the research portfolio. Thus, links to other ILRI Themes and Projects will be essential. Assist with supervision of graduate students, technicians and short-term visiting scientists. Develop collaborative research projects with Advanced Research Institutes and National Research Institutes in the developing and developed world.

Location: ILRI - Nairobi, Kenya.

ILRI laboratories are hosting BecA, a NEPAD center of excellence in biosciences for East and Central Africa. Our joint laboratories are equipped with the state of the art molecular genetics tools including automated DNA sequences (ABI 3730, ABI 3100), micro-array and

gene expression facilities and a strong bioinformatics platform. Small and large animal research facilities are available on site.

The successful candidate will have: A PhD degree obtained no more than 5 years ago in quantitative genetics/animal breeding, with high level competency in quantitative methods and good understanding of production systems in developing countries. Knowledge of bioinformatics and quantitative techniques applied in animal breeding will be a definite advantage. Excellent communication and interpersonal skills and the ability to perform in a multi-disciplinary and multi-cultural research environment are essential. Fluency in spoken and written English essential.

Terms of appointment: Initial appointment is for three years with the possibility of renewal, contingent upon individual performance and the availability of funding. ILRI offers a competitive remuneration package paid in US Dollars.

Applications: Applicants should send a cover letter, curriculum vitae and the names and addresses (including telephone, fax and email) of three referees who are knowledgeable about the candidate's professional qualifications and work experience to the Human Resources Manager, ILRI, P.O. Box 30709-00100, Nairobi, Kenya; Telephone: 254-20-4223000; Fax: 254-2-4223001; e-mail: [recruit-ilri@cgiar.org](mailto:recruit-ilri@cgiar.org). The name and reference number of the position for which the application is made should be clearly marked on the envelopes of mailed, or on the fax or e-mail applications. Screening of applications will begin immediately and will continue until the post is filled. For further information regarding the ongoing research projects please contact: Dr. Leyden Baker, [l.baker@cgiar.org](mailto:l.baker@cgiar.org).

To find more about ILRI, visit our Website at <http://www.cgiar.org/ilri/> ILRI is an equal opportunity employer and is keen to further diversify its staff in terms of both gender and nationality. Qualified women and professionals from developing countries are particularly encouraged to apply.

Olivier Hanotte, PhD Project Leader Improving Animal Genetic Resources Characterization

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## MichiganStateU BioinformaticBactGenomics

Bioinformatics and Bacterial Genomics Postdoctoral Research Position

A postdoctoral position is available immediately in the Microbial Evolution Laboratory at the National Food Safety & Toxicology Center at Michigan State University. The research involves the analysis of genome level data derived from related NIH projects studying the population genetics and molecular epidemiology of infectious disease agents. The postdoctoral researcher will (1) analyze genomic and multilocus sequence data of several bacterial pathogens, including pathogenic *E. coli* and *Shigella*, *Mycobacterium tuberculosis*, and group B *Streptococcus*; (2) maintain and enhance existing in-house sequence databases, analysis tools, and websites; and (3) provide help and support in data mining, sequence comparisons, standalone BLAST, and analysis of microarray data for ongoing projects. Michigan State University has exceptional strength in microbiology, molecular genetics, and microbial ecology, and the National Food Safety & Toxicology Center provides an outstanding facility and interdisciplinary research environment.

The Applicant should have a Ph.D. in bioinformatics, molecular evolution or related field and have a working knowledge of scripting and databases. Please contact Dr. Thomas S. Whittam ([whittam@msu.edu](mailto:whittam@msu.edu)) for more information.

Michigan State University is an Affirmative Action/Equal Opportunity Employer

Thomas S. Whittam, Ph.D. National Food Safety & Toxicology Center 165 Food Safety & Toxicology Building Michigan State University East Lansing, MI 48824-1314 Phone: 517-432-3100 ext 178 Fax: 517-432-2310 Website: <http://www.foodsafe.msu.edu/whittam/> "Thomas S. Whittam" <[whittam@msu.edu](mailto:whittam@msu.edu)>

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## Smithsonian Gulls

Post-doc: Multi-locus identification of gulls.

Post-doctoral position in molecular systematics at the Smithsonian Institution, National Museum of Natural

History (NMNH), Division of Birds. Seeking qualified applicants for post-doctoral position in molecular study of multi-locus species discrimination of ?white-headed? gulls (Larus).

Goals for this study are to assess the genetic variation in the ?white-headed? gulls in an effort to improve techniques of species identification with molecular methods. Mitochondrial DNA data have been unable to distinguish many of the species within this group. We propose to use a combination of nuclear markers, including microsatellites, AFLPs, SNPs and sequencing of nuclear introns, to develop methods to discriminate among species. Additional goals include developing multi-locus approaches for studying recently diverged species.

Research/Experience in any or all of the following: DNA sequencing, population genetics, coalescent methods, avian systematics, DNA sequence analysis. Specimen collecting and preparation a plus but not required.

Qualifications include A Ph.D. in related areas of biology including evolution, systematics or molecular biology. Analytical as well as molecular technique oriented. Background in ornithology preferred but not required.

Position term is two years, full time. Proposed start date June 2006. Stipend is \$35K per year with additional lab and travel support. Position is based at the Smithsonian Institution, NMNH in Washington, DC with extensive work at the Smithsonian molecular lab in nearby Suitland, MD. Some travel and specimen collection may be required.

Research Group includes: Carla Dove and Marcy Heacker, NMNH; Terry Chessler, USGS, NMNH, Division of Birds; Amy Driskell and Lee Weigt, NMNH Laboratories of Analytical Biology (LAB), and Kevin Omland, University of MD, UMBC

To apply: Submit a CV, 2-3 reprints or manuscripts, and three references. A brief description of research experience is encouraged. Review of applications will begin immediately with a target deadline for applications of 15 March 2006.

Contact: Carla Dove NMNH Div of Birds E600 MRC 116 P.O. Box 37012 Washington, DC 20013-7012 dove@c@si.edu phone: 202-633-0787; fax 202-633-0801

– Kevin Omland, Ph.D. Assistant Professor Dept. of Biological Sciences University of Maryland, Baltimore County 1000 Hilltop Circle Baltimore, MD 21250 410-455-2243 (phone) 410-455-3875 (fax) <http://www.umbc.edu/biosci/Faculty/omland.html> Kevin Omland <omland@umbc.edu>

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## Smithsonian MarineBiol

Can you please post this to EvolDir:

Deadline Extended until March 10th.

New Fellowships Opportunities Marine Postdoctoral Fellowship For comparative research of the Atlantic and Pacific coasts of the Republic of Panama. Preference will be given to projects using STRI's research station in Bocas del Toro. Applications should include detailed research proposal with budget, CV, two letters of reference, names and telephone numbers of three additional references. Applicants should consult with STRI scientists who will serve as advisors before submitting final application. Send inquiries and application to STRI/Office of Academic Programs, Unit 0948, APO AA 34002-0948 / fellows@si.edu.

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Dra. Rachel Collin Director, Bocas Research Station Smithsonian Tropical Research Institute Apartado Postal 0843-03092 Balboa, Ancon, Republic of Panama collinr@si.edu <http://striweb.si.edu/collinlab/> Phone: +507-212-8766

Bocas del Toro Research Station <http://www.stri.org/-bocas> Rachel Collin <collinr@si.edu>

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## TexasAMUniv GenomeEvol

POSTDOCTORAL POSITION: GENOME EVOLUTION; COMPARATIVE / FUNCTIONAL GENOMICS

POSITION DESCRIPTION:–An NIH-funded Postdoctoral Position is available immediately in the area of comparative genomic analysis with emphasis on the structural and functional characteristics of the newly sequenced genome of the gray, short-tailed opossum, *Monodelphis domestica*, a key laboratory marsupial model for genomic, biomedical, and evolutionary research. Research will center on development and analysis of an EST database, genome annotation, microarray development, and application of these and other tools (e.g., BAC libraries, linkage map) in comparative

(evolutionary) genomic analyses of interest to the successful candidate (negotiable; to be determined). Applicants must have a Ph.D. (or equivalent), with emphasis in genetics, genomics, computational biology, or related disciplines, and possess strong computational skills. A background in bioinformatic analysis, evolutionary genomics, molecular evolution, statistical genetics, or functional genomics would be desirable, and proficiency with basic molecular biology/genetics laboratory skills would be a definite advantage. The project is centered in the laboratory of Dr. Paul B. Samollow, Department of Veterinary Integrative Biosciences, Texas A&M University (TAMU), with collaborative aspects at the University of Pittsburgh (UPG).

**RESEARCH OPPORTUNITIES:**—Specific objectives of the supporting grant are to establish an EST database for use in empirical annotation of the *M. domestica* genome sequence, designing of a set of cDNA-based oligonucleotide microarrays for expression-profiling studies, and using these arrays in proof-of-principal studies of phenotypes controlled by quantitative trait loci (QTLs) related to diet-induced serum lipoprotein responses in this species. The successful candidate will participate in cDNA library design and construction, and will take a leading role in EST data analysis and database development, annotation of the *M. domestica* genome, and comparative analysis of this genome to those of other vertebrates. The exact nature of these comparative analyses and the level of participation in the design of oligonucleotide microarrays and the expression-profiling studies will be determined largely by the interests of the candidate.

Other research foci in the laboratory include comparative analyses of the structure and functional characteristics of the marsupial MHC and other immune-related gene families, and use of linkage and physical genome data to examine the unusual patterns of meiotic recombination seen in *M. domestica* (strongly reduced female recombination) as a means to detect molecular features that influence the distribution and rates of meiotic chromosome exchange in the genomes of *M. domestica* and other vertebrate species. The successful candidate will be welcome to join in these ongoing projects, or to develop alternative studies in the general area of vertebrate genomic analysis, according to her/his interests. Opportunities also exist for interaction with a large group of vertebrate genomicists and quantitative geneticists in the College of Veterinary Medicine at TAMU, and with collaborators in the Departments of Human Genetics and Computational Biology at the UPG, to develop skills in the analysis of quantitative genetic and gene mapping data.

Position is open until filled. Interested parties should

send current curriculum vitae, a brief statement of research interests, copies of relevant publications, and the names and contact information for at least three references to:

Paul B. Samollow, Professor Department of Veterinary Integrative Biosciences College of Veterinary Medicine and Biomedical Sciences Texas A&M University 4458 TAMU College Station, TX 77843-4458

Phone: 979 845-7095 FAX: 979 845-9972 Email: psamollow@cvm.tamu.edu

psamollow@cvm.tamu.edu

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## UAdelaide Interorganellar Transfer

Postdoctoral Position - Interorganellar Transposition of DNA; University of Adelaide, Australia

A Postdoctoral position is available immediately to conduct research on the interorganellar transposition of DNA using the *Chlamydomonas* and tobacco systems. The movement of DNA between organelles is established as a major driving force in eukaryotic evolution. In yeast, about 75% of all nuclear genes derive from protomitochondria, while 4,500 nuclear genes of *Arabidopsis* are plastid derived. Whereas it appears that DNA transfer per se continues in all higher cells, in many eukaryotes the functional transfer of genes is now rare or has stopped, but it continues at a high rate in higher plants, giving them unique potential in evolutionary genome studies. We have established experimentally that DNA moves frequently from the plastid (chloroplast) genome to the nucleus. The main aims of this project are to determine the mechanism of transfer and to measure the frequency of transposition of DNA from the plastid to the mitochondrion. The position requires experience in standard molecular biology techniques and, preferably, experience with *Chlamydomonas* culture. The position will be held in the laboratories of Professor Jeremy Timmis and Dr. Jack da Silva in the School of Molecular and Biomedical Science. This research is funded by a grant from the Australian Research Council to Professor Timmis and Drs. J. da Silva and M. Ayliffe. For information on the laboratories and School, please see: <http://www.mbs.adelaide.edu.au/people/genetics/-jtimmi01.html> <http://www.mbs.adelaide.edu.au/people/genetics/jdasilva.html> For enquiries and to apply, contact Jeremy Timmis, School of Molecular and Biomedical Science, University of Adelaide; email

jeremy.timmis@adelaide.edu.au.

jack.dasilva@adelaide.edu.au

jack.dasilva@adelaide.edu.au

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## UAntwerp EcolModeller

University of Antwerp - Department of Biology POST-DOC POSITION FOR THEORETICAL BIOLOGIST/MATHEMATICAL MODELER

Position Description and Information Applications for a postdoctoral position at the University of Antwerp are welcomed from persons who are either biologists with experience in mathematical modeling, or mathematicians with a strong interest in population biology. The applicant will join a group of researchers working on rodent-borne diseases and population dynamics. The modeling expertise of the applicant is required for a variety of research projects. Three currently ongoing projects where the modeler will be involved are 1) the impact of land- use and climate change on the distribution of zoonotic diseases in Europe, 2) the disease risk from commensal rodents in Africa, 3) the population dynamics of earwigs in fruit orchards in Belgium.

Essential selection criteria 1.A higher degree (Ph.D. or equivalent) in either the mathematical, biological or applied biological sciences. 2.Evidence of successful experience in mathematical modeling in biology. 3.Evidence of research achievement through publication in refereed journals. 4.A demonstrated ability and desire to communicate and collaborate with scientists working in fields outside of the mathematical sciences.

Desirable selection criteria 1.Experience in one or more of the following subjects; population ecology, entomology, wildlife disease, mathematical epidemiology, remote sensing, geography. 2.A demonstrated ability to attract research funds.

Timing The position is available initially for one year but can be extended. It can be taken up immediately, preferably from April 2006 but timing can be discussed.

An application letter and full CV is expected before 28 February 2006 and should be addressed to secretariat\_evobio@ua.ac.be

More information can be obtained at <http://www.ua.ac.be/evobio> or directly from Prof. dr. Herwig Leirs, [herwig.leirs@ua.ac.be](mailto:herwig.leirs@ua.ac.be), phone: +32 3 2653469

– Prof. dr. Herwig LEIRS Evolutionary Biol-

ogy Group, Universiteit Antwerpen Groenenborgerlaan 171, B-2020 Antwerpen, Belgium phone: +32 (0)3 2653469 fax: +32 (0)3 2653474 <http://www.ua.ac.be/herwig.leirs> [herwig.leirs@ua.ac.be](mailto:herwig.leirs@ua.ac.be)

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## UCalSanDiego EvolGenomics

Postdoctoral position: Evolutionary Genomics

An NIH-funded postdoctoral position is available in the lab of Doris Bachtrog at the University of California, San Diego. Research in the lab focuses on i) the evolutionary significance of sex and recombination, ii) the causes of Y-chromosome degeneration, iii) and the evolution of gene expression and dosage compensation. Interested applicants should have expertise in one of the following areas: molecular genetics/functional genomics, evolutionary genetics/ theoretical population genetics, comparative genomics/bioinformatics. For more detail on current research visit <http://www.biology.ucsd.edu/labs/bachtrog/>.

UC San Diego has a large and highly interactive group in biology, bioinformatics, computer science and bioengineering with many faculty having active research programs in evolutionary genetics, bioinformatics and functional genomics. More information about these departments is available at <http://www-biology.ucsd.edu/>, <http://www-bioinformatics.ucsd.edu/>, <http://www-cse.ucsd.edu/> and <http://www-cse.ucsd.edu/bioeng.ucsd.edu/>. The UCSD campus is located in beautiful La Jolla, just north of downtown San Diego, overlooking the Pacific ocean.

Interested applicants should send the following information (in pdf format) to [dbachtrog@ucsd.edu](mailto:dbachtrog@ucsd.edu): a CV, a brief statement of research interests, and names and contact information for three references. Applications will be reviewed as they are received and the position will remain open until filled. Informal inquiries are also welcome!

Doris Bachtrog Assistant Professor, Division of Biological Sciences University of California, San Diego 9500 Gilman Drive, MC 0116 La Jolla, CA 92093

Doris Bachtrog <[dbachtrog@ucsd.edu](mailto:dbachtrog@ucsd.edu)>



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## UChicago NatSel HumanPops

A postdoctoral position is available in the laboratory of Anna Di Rienzo in the Department of Human Genetics at the University of Chicago. Research projects in the lab focus on empirical and modeling studies of natural selection in human populations. We are particularly interested in evolutionary models for the susceptibility to common diseases, such as diabetes, obesity, asthma and hypertension, and in the history of local adaptations in humans. We combine population resequencing and SNP genotyping data with coalescent-based analyses and population genetics modeling. Most projects are in collaboration with the research groups of Jonathan Pritchard and Molly Przeworski, which are located on the same floor as the Di Rienzo lab, and that of Richard Hudson, located one block away, in the Department of Ecology & Evolution.

For additional information on the Di Rienzo lab and the Department of Human Genetics please visit: <http://genapps.uchicago.edu/labweb/index.html> and <http://www.genes.uchicago.edu>. A strong background in molecular genetics and population genetics is required. Familiarity with Unix systems and programming skills are desirable. Starting dates are flexible. Salaries are commensurate with qualifications and experience.

Please send cv and three letters of reference to Dr. Anna Di Rienzo by email to: [dirienzo@genetics.uchicago.edu](mailto:dirienzo@genetics.uchicago.edu), or by regular mail to: Anna Di Rienzo, Ph. D. Department of Human Genetics University of Chicago CLSC 507F 920 E. 58th Street Chicago, IL 60637

Anna Di Rienzo <[dirienzo@genetics.uchicago.edu](mailto:dirienzo@genetics.uchicago.edu)>

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## UEastAnglia AvianMHC

Postdoctoral Research Associate SEXUAL SELECTION AND THE MHC IN THE FOWL

Salary £20,044 to £25,565 per annum Ref: RA251

A NERC funded postdoctoral position is available from March 2006 for a period of three years (the first 1.5

years based at UEA and the second 1.5 years at Oxford). The goal of the research is to establish the role of the Major Histocompatibility Complex (MHC) in sexual selection in birds, using the red junglefowl, *Gallus gallus*, and its domestic subspecies, *G. g. domesticus*, as model systems. The researcher will help develop a molecular protocol to screen for MHC variation and then use this to; (i) determine the extent to which sexual selection is MHC-mediated under natural conditions, and, (ii) to experimentally identify the mechanisms of pre- and post-insemination sexual selection through which the MHC influences variation in paternity.

Applicants must have, or be about to obtain, a PhD in a relevant discipline such as evolutionary or molecular ecology and have a keen interest in sexual selection and sperm competition. Practical experience in modern molecular techniques, such as PCR, cloning and sequencing, is essential. Field experience/animal handling will also be a benefit.

The project will be undertaken jointly at UEA and Oxford. At UEA, the researcher will be based with Dr D.S Richardson in the School of Biological Sciences (RAE 5-rated), and will be part of the Centre for Ecology, Evolution and Conservation (CEEC). The school and research centre provide excellent research facilities and a stimulating and dynamic research environment. Further information about the school can be found at <http://www.uea.ac.uk/bio/>. At Oxford the researcher will be based with Dr T. Pizzari in the Edward Grey Institute of Ornithology, at the Department of Zoology of the University of Oxford. The Department of Zoology at the University of Oxford has a long-standing reputation for world class research and teaching. The EGI is one of the fastest-growing groups of the Department, and conducts research in behaviour, ecology, evolution and conservation of birds, with a strong emphasis on understanding organisms in their natural environments. Further information about the Department and the EGI can be found at <http://www.zoo.ox.ac.uk/>. Informal enquiries to Dr David S Richardson ([david.richardson@uea.ac.uk](mailto:david.richardson@uea.ac.uk)) or Dr T. Pizzari ([tommaso.pizzari@zoo.ox.ac.uk](mailto:tommaso.pizzari@zoo.ox.ac.uk)). Closing date: 16 March 2006 Further particulars and an application form can be obtained from the University's web page at: <http://www.uea.ac.uk/hr/jobs/> or by e-mail at: [hr@uea.ac.uk](mailto:hr@uea.ac.uk) or by calling the answerphone on 01603 593493 or by mail to the Human Resources Division, University of East Anglia, Norwich NR4 7TJ.

UNIVERSITY OF OXFORD Edward Grey Institute of Ornithology Department of Zoology Department of Animal and Avian Sciences, University of Maryland

UNIVERSITY OF EAST ANGLIA Centre for Ecology,  
Evolution & Conservation School of Biological Sciences

————— Dr. David S. Richardson School of  
Biological Sciences, University of East Anglia, Norwich  
NR4 7TJ England

email david.richardson@uea.ac.uk [http://-](http://www.uea.ac.uk/bio/people/faculty/DSr.htm)  
[www.uea.ac.uk/bio/people/faculty/DSr.htm](http://www.uea.ac.uk/bio/people/faculty/DSr.htm) Tele-  
phone 01603 591496 FAX 01603 592250

“David S. Richardson” <david.richardson@uea.ac.uk>

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## UJena FloralEvoDevo

2 PhD positions or 1 Postdoc position

In our group we have openings for two graduate students or one Postdoc with strong interest in the evolutionary developmental biology of plants. The project focuses on the evolution of the interaction of floral homeotic proteins (MADS-domain proteins) by integrating experimental and bioinformatic approaches.

Floral homeotic proteins of higher eudicotyledonous flowering plants are key determinants of floral organ identity. They exert their function by constituting multimeric complexes that bind to cis-regulatory DNA sites in their target genes. We wonder how this situation originated during evolution by studying evolutionary informative taxa such as gymnosperms and basal flowering plants. Given the enormous importance of floral homeotic proteins and their interaction behaviour for flower development in eudicots, unraveling the evolutionary trajectories that led to the present day interaction network may help to elucidate the origin of the angiosperm flower - still on of the most enigmatic questions in biology.

In the experimental part of the project, interactions of floral homeotic proteins are studied by “wet lab techniques” such as gel retardation assays, the yeast-2/3/4-hybrid system and co-immunoprecipitation assays. Candidates applying for this part of the project should have a Diploma or Master degree in Biology, Biochemistry or related fields. Experience in the techniques mentioned above is of advantage, but not absolutely required. Demonstrable practical experience in standard molecular biology techniques, including molecular cloning is essential, however.

In the bioinformatics part of the project, the question is addressed as to whether protein-protein interactions affect the rates of protein evolution. Candidates apply-

ing for this part of the project should have a Diploma or Master degree in Bioinformatics, Biochemistry, Biology or related fields, and should have demonstrable experience with methods of phylogeny reconstruction (e.g. Neighbor Joining, Maximum Likelihood, Maximum Parsimony) using sequence data, and profound knowledge of Molecular Evolution methods.

Postdocs applying for the position should be prepared to work in both parts of the project. Candidates will be considered on a competitive basis and only applications containing all the required documents will be reviewed. Applicants will be considered from 1st of March 2006 until the positions are filled. Interested candidates should send the following, preferably as PDF files via e-mail:

1. A statement detailing your research experience and scientific interests.
2. An updated Curriculum Vitae (including a complete list of publications).
3. The names and contact information of at least two scientists available for reference.

Please send your application or informal inquiries to Prof. Günter Theißen, Friedrich-Schiller-Universität Jena, Lehrstuhl für Genetik, Philosophenweg 12, D-07743 Jena, Germany; E-mail: guenter.theissen@uni-jena.de; Tel.: +49-3641-949550.

Introductory literature: Kaufmann et al. (2005). *Gene* 347, 183-198. Becker, A., Theißen, G. (2003). *Mol. Phy. Evol.* 29, 464-489. De Bodt et al. (2003). *Trends Plant Sci.* 8, 475-483. Theißen, G., Saedler, H. (2001). *Nature* 409, 469-471.

mariana.mondragon@uni-jena.de

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## UKansas FishEvol

POST-DOCTORAL POSITION - Molecular Ecology of Freshwater Fish

A 2-year NSF postdoctoral position (with possible extension) is available at the University of Kansas to study the molecular ecology of freshwater fish in the laboratory of Dr. Garrick T. Skalski ([www.ku.edu/~eeb/faculty/skalski.html](http://www.ku.edu/~eeb/faculty/skalski.html)) as part of a joint project with Dr. Bruce S. Weir

(<http://www.biostat.washington.edu/people/faculty.php?netid=bsweir>). The broad objective of the project is to examine the evolutionary ecology of fish popula-

tions while evaluating a method for high-throughput allele frequency estimation using micro satellite markers. Specific areas of interest include the analysis of spatial population structure, landscape genetics, the estimation of effective population size, and the identification of heritable traits of ecological significance. The ideal candidate will be highly motivated, open-minded, and enthusiastic about working in the field and laboratory with individuals at all levels of training. Complete details and the online application can be found at position #000666674 via <https://jobs.ku.edu>. Review of applications will begin 1 March 2006. Informal inquiries are encouraged and should be directed to Dr. Garrick T. Skalski ([skalski@ku.edu](mailto:skalski@ku.edu), 785-864-5877). The University of Kansas is an EO/AA employer. Paid for by KU. Lawrence is a fun university town located just west of Kansas City. The community offers museums, performing arts, restaurants and clubs, bookstores, an excellent public school system, and a variety of recreational activities. Within the Division of Biological Sciences are many dynamic and collegial groups studying behavior, ecology and evolution that meet regularly for seminars and discussions ([www.ku.edu/~eeb/faculty](http://www.ku.edu/~eeb/faculty)).

[jdorothy@ku.edu](mailto:jdorothy@ku.edu)

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### UOxford CompEvolBiol

Applications are invited for a one year fixed-term post-doctoral research position starting immediately. The post is in association with the Evolutionary Biology Group and the Ancient Biomolecules Centre, Department of Zoology, at the University of Oxford.

The position is to be entirely computer-based, and will involve the analysis of DNA sequences (both ancient and modern) with the aim to address broad evolutionary issues such as domestication, population genetics, and coalescent processes. Potential candidates should have an interest in phylogenetics and evolutionary biology. The successful candidate will have the freedom to define the exact scope of the project, although it should fit within the current research programme of the group. Experience with computer programming and/or statistical techniques is desirable, and the post could involve the development of new evolutionary models within our existing Bayesian MCMC software.

More information about research taking place in our groups is available from website: <http://>

[/evolve.zoo.ox.ac.uk](http://evolve.zoo.ox.ac.uk) and <http://evolve.zoo.ox.ac.uk>  
[abc.zoo.ox.ac.uk](http://abc.zoo.ox.ac.uk). Further particulars available by Tel: 01865 271190; E-mail: [recruit@zoo.ox.ac.uk](mailto:recruit@zoo.ox.ac.uk). Applications, including curriculum vitae, contact details of three referees and a description of your research achievements and interests, should be sent to the Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS quoting reference number: AT 06008. The closing date for applications is 10 February 2006.

For more information, please contact

Dr. Beth Shapiro Acting Director, Henry Wellcome Ancient Biomolecules Centre Oxford University, Depts. of Zoology and Statistics Oxford, OX1 3PS, UK +44 (0) 1865 281248

[beth.shapiro@zoo.ox.ac.uk](mailto:beth.shapiro@zoo.ox.ac.uk)

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### UParis AntPhylogeny

Post-doctoral Fellowship in phylogenetics of ant species complex.

A position is available to explore phylogenetic relationships and phylogeography in a ant species complex of Ponerinae, in collaboration with Chantal Poteaux and Dominique Fresneau (U. of Paris 13) at the Laboratory of Experimental and Comparative Ethology (LEEC, France). The applicant will have to: 1/ determine genetic variation to reconstruct the phylogeny of Ponerine ants, with particular attention to the tribe Pachycondyla. 2/ elucidate fine-scale relationships within a complex including several close ant species with molecular methods (nuclear and mitochondrial DNA sequences analyses). Candidates should have experience in phylogenetics and/or population genetics. Application should be established according to a form to be obtained from the Foundation Fyssen: <http://www.fondation-fyssen.org/bourseUS.html> <http://www.fondation-fyssen.org/bourseUS.html>. Salary will be of approximately 2000 euros per month. Prospective applicants should first send a curriculum vitae including a brief statement of previous research experience, and names and e-mail addresses of 2 referees by e-mail before March, 15th 2006 to Chantal Poteaux (<mailto:poteaux@leec.univ-paris13.fr>) [poteaux@leec.univ-paris13.fr](mailto:poteaux@leec.univ-paris13.fr)). In a second time, the selected applicant will present his/her application for the collaborating project to obtain the expected grant. For details of the LEECs research,

please see: <<http://www-leec.univ-paris13.fr/>><http://www-leec.univ-paris13.fr/> Best regards, Chantal Poteaux, PhD LEEC Université Paris 13 Avenue J-B Clément F-93430 Villetaneuse

Chantal Poteaux <[Chantal.Poteaux@leec.univ-paris13.fr](mailto:Chantal.Poteaux@leec.univ-paris13.fr)>

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## UParisSud MicrobialGenomics

A 30 months post-doctoral position, funded by ANR, is presently (spring 2006) available to join the group Evolution Moléculaire et Bioinformatique des Génomes (Institut de Génétique et Microbiologie, Université Paris-Sud, Orsay).

Candidates will design a relational database (PostgreSQL) in order to organize the homology data obtained after a comparison of complete microbial genomes. This database will be integrated in Microbiogenomics (<<http://microbiogenomics.u-psud.fr/>><http://microbiogenomics.u-psud.fr/>), a data warehouse under construction that is one of the main objectives of the ANR ongoing project. These data will be further used to better understand the molecular evolution of microbial genes, to trace back protein history and to check the topology of the tree of life using phylogenomics approaches. This work will be made in collaboration with our two partners of the ANR project: the Bioinformatics group at the Laboratoire de Recherche en Informatique (Université Paris Sud) and the group MIG (INRA at Jouy-en-Josas).

See our recent references at <<http://www.igmors.u-psud.fr/LABEDAN/LABEDAN.htm>> <http://www.igmors.u-psud.fr/LABEDAN/LABEDAN.htm>

The candidate must have a solid practical experience of relational databases (PostgreSQL), of languages C++, Perl, and Java. Knowledge of XML schemas and web architecture (HTML, PHP) would be appreciated. Good experience in Microbiology, Genomics, and knowledge of molecular evolution concepts would be an advantage.

Candidates for the post-doctoral position should have completed their Ph.D. during the last five years. Knowledge of the French language is not required but would be appreciated.

The salary will be 1740 per month. A Social Security cover is included in this salary. There will be no funding for travel expenses.

The targeted starting date is May 1, 2006. Any people interested must contact me rapidly and before 26 March 2006. I need a detailed CV and a short introduction letter.

Contact : Bernard Labedan, <<mailto:bernard.labedan@igmors.u-psud.fr>>[bernard.labedan@igmors.u-psud.fr](mailto:bernard.labedan@igmors.u-psud.fr) IGM, CNRS UMR 8621, Université Paris-Sud, Bâtiment 400, 91405 Orsay Cedex, France Tel: +33 1 69 15 35 60 - Fax: +33 1 69 15 72 96

Bernard Labedan, Directeur de Recherche au CNRS Evolution Moléculaire et Bioinformatique des Génomes Institut de Genetique et Microbiologie, CNRS UMR 8621 Université Paris Sud, Batiment 400, piece 101 91405 Orsay Cedex, France Tel : +33 1 69 15 35 60 Fax : +33 1 69 15 72 96 <http://www.igmors.u-psud.fr/LABEDAN/LABEDAN.htm>

[bernard.labedan@igmors.u-psud.fr](mailto:bernard.labedan@igmors.u-psud.fr)

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## USaarland AllelicVariation

Advertisement of a Vacancy at the University of Saarland

The following position is available at the Medical Faculty, Department of Theoretical Medicine and Biosciences, Institute of Human Genetics

Mode of Employment: Scientific Assistant (Postdoc)  
Qualification: University degrees Diploma and Ph.D. (or equivalent) in biology or chemistry  
Post: Department of Human Genetics, Medical Faculty, Homburg/Saar (Germany)  
Start of contract: As soon as possible  
Volume of employment: Full-time (100%)  
Duration of employment: 2 years with optional extension (according to §§57a ff HRG)

Job Specification Requisites: We are seeking a highly motivated postdoctoral researcher to study allelic variation in human endogenous retroviruses. The successful applicant will have well established expertise in the characterization of allelic variation and, preferably, repetitive elements. He/she will join an established research group at the Department of Human Genetics at the University of Saarland (Homburg, Germany). Desired: High motivation and interest in scientific work, team spirit. Duties: To conduct research in the field of human endogenous retroviruses, in particular, examination of allelic variation.

Salary will accord to tariff and other applicable terms of the University of Saarland. Full-time positions are, in principle, divisible (§7 Abs. 1 TzBfG). University of Saarland pursues a higher proportion of women in this field of activity according to the affirmative action plan for women. Women are therefore emphatically invited to apply. Severely handicapped persons will be favored when equally qualified.

Please send complete applications by e-mail or regular mail until March 31 2006 to:

Dr. Jens Mayer FR 2.6, Human Genetics, Medical Faculty Building 60 66421 Homburg Germany (reference number Y90) jens.mayer@uniklinik-saarland.de

Please send copies only as application documents will not be returned. Also, do not send binders or the like.

–

Dr. rer. nat. Jens Mayer Human Genetics, Building 60 Medical Faculty University of Saar 66421 Homburg Germany

phone-office: (49) 06841-1626627 phone-lab: (49) 06841-1626189 fax: (49) 06841-1626186 e-mail: jens.mayer@uniklinik-saarland.de

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## UStellenbosch AbaloneEvol

Post Doctoral position available in the Department of Genetics, University of Stellenbosch (1 Feb 2006)

A Post Doctoral position in molecular genetics is available in the Aquaculture Division, Department of Genetics, Stellenbosch University with the project title "Genetic improvement of the abalone, *Haliotis midae*."

*Haliotis midae*, known locally as 'perlemoen', occurs along the Western, Southern and Eastern shores of South Africa and is the only one of the six species that occurs in South Africa that is commercially exploited. *H. midae* displays a very slow growth rate, taking two to five years to reach market size. This is an obstacle in the profitable farming and global competitiveness of this species. In order to increase the productivity and the profitability of the commercial activity, a research program has been designed that makes use of the modern technology currently applied to other aquaculture species. The research program consists of three main tears: a) establishment of breeding programs with the assistance of genetic markers, b) generation of linkage maps and QTL identification, c) and the application of

gene transfer technology.

The successful candidate will be primarily responsible for developing AFLP markers in the abalone species, *Haliotis midae*. AFLPs have been developed in only one other *Haliotis* species. Together with other genetic markers such as microsatellites and SNPs, these AFLP markers will eventually be used to generate the first genetic linkage map for *Haliotis midae*. Candidates must have a strong background in molecular genetics with applicable knowledge in the development and analysis of AFLP markers. Practical experience with the basic molecular techniques required for AFLP generation such as DNA isolation, primer-labelling, PCR, polyacrylamide gel-electrophoreses and a sound knowledge of AFLP analysis or related software is a prerequisite. Experience with radioactive isotope handling and experience with mapping or linkage analysis software will be a strong recommendation. The position is available for 2 years

Interested researchers are requested to send their CV to Dr. Rouvay Roodt-Wilding at roodt@sun.ac.za

Closing date: 3 March 2006.

Dr. Rouvay Roodt-Wilding Aquaculture Division Department of Genetics JC Smuts Building Room 213 University of Stellenbosch Private Bag X1 Matieland SOUTH AFRICA 7602 Tel: +27 (0) 21 808 5831 Fax: +27 (0) 21 808 5833

"Faith is taking the first step even when you don't see the whole staircase." Martin Luther King, Jr

roodt@sun.ac.za

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## UppsalaU ComparativeGenomics

POSTDOCTORAL FELLOWSHIP AT UPPSALA UNIVERSITY

A postdoctoral fellowship is immediately available to study Comparative Genomics of Diplomonads at the Department of Cell and Molecular Biology (ICM), Uppsala University, Sweden. The position is within the Protist Genome Evolution group, and will be in collaboration with Staffan Svärd's group at ICM, and Björn Andersson's group at the Department of Cell and Molecular Biology at Karolinska Institutet.

Diplomonads is a group of heterotrophic, mostly bacterivorous flagellates found in micro-aerophilic environments, which include human and fish pathogens (i. e.

*Giardia lamblia* and *Spiroplasma karyophilum*), as well as free-living and endocommensal species. We have previously shown that diplomonads have adapted to their environment by gene acquisitions from prokaryotes (e.g. *Curr Biol* 13, 94-104) and identified differences in codon usage and mutational patterns within the group (manuscript in preparation). Our collaborators have interests in diplomonad cell biology (Svärd), and genome analysis of parasites (Andersson).

The project will use a comparative genomics approach to study the cell biology and evolution of diplomonads. Isolates from diverse environments will be cultivated, and expressed sequence tag (EST) libraries will be created and sequenced randomly. Genomic similarities and differences within diplomonads will be identified using a variety of bioinformatic approaches, including phylogenomic analyses. This approach may be complemented with biochemical studies. Particular question that could be addressed include whether there are differences between lineages in the patterns of gene acquisitions from prokaryotes, and if gene exchange with other eukaryotes occurs.

For further information please contact Jan Andersson

Jan O. Andersson, Assistant Professor Department of Cell and Molecular Biology Uppsala University, Uppsala, Sweden Telephone: +46-18-4715046 Fax: +46-18-530396 E-mail: Jan.Andersson@icm.uu.se URL: <http://www.icm.uu.se/micro/people/andersson.html> Jan.Andersson@icm.uu.se Jan.Andersson@icm.uu.se

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## VirginiaTech ComputationalGenomics

A postdoc position is available immediately in my group in the Department of Computer Science at Virginia Tech. Candidates should have a strong background in evolutionary biology, population genetics, molecular evolution, or statistical genetics. Experience in statistics and programming is highly desired. Available projects include evolutionary and computational genomics of the completed animal genomes. The successful candidate is expected to be able to develop independent research topics within this broad scope. The initial contract is for one year, with the possibility of one-year renewal depending on the performance of the candidate. Please send (1). Your C.V., (2). A statement of your research interests, and (3). Detailed contact information of three referees to [lqzhang@cs.vt.edu](mailto:lqzhang@cs.vt.edu). Informal inquiries are welcome. Review of applications will begin immediately and the position will remain open until filled.

Liqing Zhang, Ph.D. Assistant Professor 2160K Torgersen Hall Department of Computer Science Virginia Tech Blacksburg, VA 24061 Office: (540) 231-9413 Fax: (540) 231-6075

[lqzhang@cs.vt.edu](mailto:lqzhang@cs.vt.edu) [lqzhang@cs.vt.edu](mailto:lqzhang@cs.vt.edu)

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## WorkshopsCourses

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### BalboaPanama TaxCaribbeanSponges Jul17-28

A SHORT-COURSE IN: TAXONOMY AND ECOLOGY OF CARIBBEAN SPONGES

Dates: July 17-28, 2006. Location: The Smithsonian Tropical Research Institute, Bocas Research Station, Bocas del Toro, Panama. Registration Fee: \$400 (some fellowships are available).

Instructors: Dr. Cristina Diaz, Smithsonian Institution  
Dr. Robert Thacker, University of Alabama at Birmingham  
With several guest lecturers.

Application: This course is directed towards graduate students and advance Licenciado candidates and will be conducted in English. Please e-mail your CV, 1 letter of recommendation, and a 1-2 page statement explaining your background and reasons for taking the course, to Rachel Collin at CollinR@si.edu before March 4, 2006. Limit 10 students. For more information see <http://www.stri.org/bocas> –

Dra. Rachel Collin Director, Bocas Research Station  
Smithsonian Tropical Research Institute Apartado  
Postal 0843-03092 Balboa, Ancon, Republic of Panama  
collinr@si.edu <http://striweb.si.edu/collinlab/> Phone:  
+507-212-8766

Bocas del Toro Research Station <http://www.stri.org/bocas> Rachel Collin <collinr@si.edu>

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### BalboaPanama TunicateTaxonomy Aug13-27

A SHORT-COURSE IN: TAXONOMY AND BIOLOGY OF TUNICATES

Dates: August 13-27, 2006. Location: The Smithsonian Tropical Research Institute, Bocas Research Station, Bocas del Toro, Panama. Registration Fee: \$400 (some fellowships are available).

Instructors: Dr. Rosana Rocha, Universidade Federal do Paraná, Brasil  
Gretchen Lambert, University of Washington Friday Harbor Laboratories  
Dr. Charles Lambert, University of Washington Friday Harbor Labs

Application: This course is directed towards graduate students and advance undergraduate or Licenciado candidates and will be conducted in English. Please e-mail your CV, 1 letter of recommendation, and a 1-2 page statement explaining your background and reasons for taking the course, to Rachel Collin at CollinR@si.edu before March 4, 2006. Limit 10 students. For more information see <http://www.stri.org/bocas> –

Dra. Rachel Collin Director, Bocas Research Station  
Smithsonian Tropical Research Institute Apartado  
Postal 0843-03092 Balboa, Ancon, Republic of Panama  
collinr@si.edu <http://striweb.si.edu/collinlab/> Phone:  
+507-212-8766

Bocas del Toro Research Station <http://www.stri.org/bocas> Rachel Collin <collinr@si.edu>

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### Barcelona Genomics June19-30

2nd International Postgraduate Course in Genomics

Universitat Autònoma de Barcelona (Barcelona, SPAIN) June 19-30, 2006

Invited Professors:

Laurent Duret Laboratoire de Biométrie et Biologie Evolutive  
Université Claude Bernard Lyon 1 (France)

Dimitri Petrov Department of Biological Sciences  
Stanford University (California, USA)

Content: Size of nuclear and organelle genomes. Types of DNA and organization of the eukaryotic genome. Mapping and sequencing of genomes. Bioinformatics. Databases. Annotation, alignment and comparison of DNA sequences. Transcriptomes and proteomes. Molecular evolution. Neutral theory of molecular evolution. Nucleotide polymorphism. Rates of nucleotide substitution. Detection of natural selection at the molecular level. Codon bias. Functional genomics. Microarrays. Genome organization and gene expression. Transposable elements (TEs). Classification and abundance of TEs in diverse genomes. Impact of TEs on the host genome. Gene duplications and gene families. Orthologous and paralogous genes. Processed pseudogenes and retrogenes. Chromosomal rearrangements. The Human genome. Number, size, structure and distribution of human genes. Homologues of human proteins. Architecture of human proteins. Non-coding RNA genes. Nucleotide variability (SNPs) in humans.

Linkage disequilibrium and haplo type diversity. Evolution of genome size.

Dates: June 19-30, 2006, 9:30 a.m. – 13:30. For registration and information, please contact: Julia Provecho, Departament de Genètica i de Microbiologia, Universitat Autònoma de Barcelona, 08193 Bellaterra (Barcelona), SPAIN. Tel. 34-93-581-2724, FAX 34-93-581-2387, E-mail: d.genetica@uab.es.

Alfredo Ruiz, Departament de Genètica i de Microbiologia, Universitat Autònoma de Barcelona, 08193 Bellaterra (Barcelona), SPAIN. Tel. 34-93-581-2729, FAX 34-93-581-2387, E-mail: Alfredo.Ruiz@uab.es.

Alfredo.Ruiz@uab.es

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## MBL MolecularEvol

Workshop on Molecular Evolution

<http://workshop.molecularevolution.org/> Michael P. Cummings, Director

23 July - 4 August 2006 plus extended topics session 5 August - 11 August 2006

Application Deadline 1 March 2006

The Workshop on Molecular Evolution has been the finest course of its type in the world since it was started in 1988. The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. A distinguishing feature of the Workshop is a well-equipped computer laboratory with Linux workstations and servers for comparative analysis of molecular data. Authors and experts in the use of computer programs and packages such as Clustal W and Clustal X, FASTA, GCG, LAMARC, MrBayes, PAML, PAUP\*, and PHYLIP provide demonstrations and consultations. This two-week program is designed for established investigators, postdoctoral fellows, and advanced graduate students with prior experience in molecular evolution and comparative genomics. Scientists with a strong interest in molecular evolution, systematics, and population genetics are encouraged to apply. Enrollment is limited to 60 students, and 15 students will be admitted to an extended topics session for the purpose of analyzing their research data sets. Many participants find the extended topics session to be especially useful.

Topics to be covered include:

\* Databases and sequence matching; database search-

ing; protein sequence versus protein structure; homology; mathematical, statistical, and theoretical aspects of sequence database searches \* Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis, hypothesis testing \* Character analysis in a phylogenetic context: analysis of quantitative and discrete characters; hypothesis testing \* Maximum likelihood theory and practice in phylogenetics and population genetics: coalescent theory; maximum likelihood estimation of population genetic parameters \* Bayesian methods in phylogenetic analysis \* Molecular evolution integrated at different levels: population biology; biogeography; ecology; systematics and conservation \* Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution \* Comparative genomics: genome content; genome structure; genome evolution \* Transposable elements: types; history; evolutionary dynamics; as a major component of genomes

Partial funding support for the Workshop comes from the National Aeronautics and Space Administration (NASA).

Fee: \$2000 (room and board at no additional charge), plus an additional \$750 for the extended topics session.

Students find that staying for the extended t

Application Form at <http://www.mbl.edu/education/-admissions/applications/> Further information at <http://workshop.molecularevolution.org/> mike@umiacs.umd.edu

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## MountainLakeBioStation courses

Dear Biologist,

The Mountain Lake Biological Station is pleased to announce its summer 2006 program. Our NSF REU-Sites program will be in its 14 year, and we'll offer five exciting field-based courses (2 and 4 week). See details below, and attached. Or visit our web site any time.

We appreciate any help you can lend posting or distributing this material to your colleagues and students. Thanks for your help.

If the attachments don't make it, here are the links:  
[http://mlbs.org/download/MLBS\\_REU\\_Announce.pdf](http://mlbs.org/download/MLBS_REU_Announce.pdf)  
[http://mlbs.org/download/MLBS\\_REU\\_Poster.pdf](http://mlbs.org/download/MLBS_REU_Poster.pdf)

Best wishes and Happy New Year,



Eric Nagy Associate Director, MLBS

P.S. Apologies for any multiple copies of this mailing. Your email address may occur on more than one of the lists we use.

#### MOUNTAIN LAKE BIOLOGICAL STATION

<file:///www.mlbs.org>mlbs.org SUMMER 2006

The Mountain Lake Biological Station (University of Virginia) announces paid research opportunities for undergraduates and university-level credit courses in field biology. We offer students hands-on experience and training in a wide variety of biological field studies. Students are invited to join us for an exciting and unforgettable summer in a beautiful and stimulating teaching and research environment. Scholarships and financial aid for courses are available.

NSF-Funded Research Experience for Undergraduates (REU) Program <<http://www.mlbs.org/-REU.html>>mlbs.org/REU.html We match undergraduate students with visiting scientists for 10 weeks of advanced, independent research on a project of the student's own design. REU positions come with a "take home" stipend of \$3,640. And the program covers all room and board expenses. Minority students are especially encouraged to apply. Deadline for receipt of applications is March 1.

#### Field Courses

<<http://www.mlbs.org/courses.html>>mlbs.org/-courses.html

1) Plant Biodiversity and Conservation May 30 - June 23 (4 weeks). The extraordinary diversity of the Southern Appalachians will serve as a backdrop to explore the world of plants.

2) Biology of Fungi June 26 - July 21 (4 weeks). An introduction to the biology of fungi, with emphasis on field identification and current experimental methods used to study fungal genetics, ecology and evolution.

3) Stream Ecology June 26 - July 21 (4 weeks). This course will focus on integrating principles of stream and watershed ecology as a means of gaining insight into stream dwelling organisms and their environments.

4) Ecology & Conservation of Freshwater Fishes July 24 - August 4 (2 weeks). An investigation of the ecology and conservation of freshwater fishes through a series of discussions, lectures, lab and field exercises.

5) Biodiversity in the Southern Appalachians July 24 - August 4 (2 weeks). This course will teach students how historical processes and current land-use patterns shape the compositions of ecological communities.

Our field station is located on a mountaintop in southwestern Virginia and is home to a lively re-

search, teaching and social community. For details on these programs, full course descriptions, application material, and a list of research areas see our web page <<http://mlbs.org/>>mlbs.org University of Virginia, Mountain Lake Biological Station, PO Box 400327, Charlottesville VA 22904-4327, U.S.A., <mailto: mlbs@virginia.edu> mlbs@virginia.edu, +1-434-982-5486

Eric S. Nagy, Ph.D. Associate Director, Mountain Lake Biological Station Research Assistant Professor, Department of Biology University of Virginia / Mountain Lake Biological Station P.O. Box 400327 / Charlottesville, VA 22904-4327 USA street address: 485 McCormick Road / 238 Gilmer Hall tel: +1-434-982-5486 (+1-540-626-5227 June-August) fax: +1-434-982-5626 (+1-540-626-5229 June-August) cel: +1-434-906-3122 eml: <mailto: enagy@virginia.edu> enagy@virginia.edu personal web page: <<http://faculty.virginia.edu/nagy>>faculty.virginia.edu/-nagy MLBS web page: <<http://www.mlbs.org/>>mlbs.<<http://www.mlbs.org/>>org

enagy@virginia.edu

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### PortalAZ BeeCourse

Of relevance to anyone interested in bees, pollination biology, etc., the BEE COURSE is held each year at the AMNH's Southwest research station in Portal Arizona. Taught by various North American experts with a very advantageous teacher/pupil ratio.

Full details can be found at the URL below.

Best wishes

Laurence Packer

<http://research.amnh.org/invertzoo/beecourse/> laurencepacker@yahoo.com

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### Tuebingen EvolEcolHermaphrodites Aug4-6

HERMAPHRODITE MEETING TUEBINGEN Her-MeeT

We are organising an informal meeting on the evolution-

ary ecology of hermaphrodites in Tuebingen (Germany) from Fri 4 until Sun 6 August 2006.

This is the third meeting of its kind. It is meant as a forum for all levels of Ph.D. students, post-docs or seniors to exchange ideas and to discuss recent findings. The scope can range from genes to behaviour, and includes theory, plants or animals (with some bias towards the latter).

Preliminary programme Thu evening/Fri morning: Arrival Fri afternoon: Start of presentations Fri evening: social evening in the historic city centre Sat: Presentations and extended discussions Sat evening: social evening in the historic city centre Sun: Departure day, with option for further discussions, lab visits, etc. We offer a lot of time for informal interaction (long breaks). Talks will be max 20 min + 10 min discussion (or shorter). Posters possible.

All attendants cover their own costs. Cheap student accommodation is available and we can help you with bookings (if you register in time).

If you are interested, send a brief Email to [nils.anthes@uni-tuebingen.de](mailto:nils.anthes@uni-tuebingen.de) <[mailto:nils.anthes@uni-tuebingen.de](mailto:mailto:nils.anthes@uni-tuebingen.de)> with your intent to participate as soon as possible. Formal registration involves sending us the following details before 31 May 2006:

- Name and contact details
- Preference for oral or poster contribution
- Title of contribution
- Number of nights in Tuebingen
- Preferred accommodation (hotel, guesthouse, youth hostel, camp site, floor space, not required)
- Vegetarian or other special requirements

Looking forward to seeing you in Tuebingen.

Nils Anthes & Nico Michiels

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Nils Anthes Zoological Institute Animal Evolutionary Ecology Eberhard Karls-Universität Tübingen Auf der Morgenstelle 28 72076 Tübingen, Germany Tel: ++49-(0)7071-29 74841 Fax: ++49-(0)7071-29 5634 E-Mail: [Nils.Anthes@uni-tuebingen.de](mailto:Nils.Anthes@uni-tuebingen.de)

<http://www.uni-tuebingen.de/evoeco/>

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**UCSantaBarbara**  
**AnalyticalPaleobiol June27-July24**

PALEOBIOLOGY DATABASE INTENSIVE SUMMER COURSE IN ANALYTICAL PALEOBIOLOGY

The Paleobiology Database (<http://paleodb.org>) is sponsoring an intensive course in analytical paleobiology that will be held at the National Center for Ecological Analysis and Synthesis at the University of California, Santa Barbara. The course will take place between Tuesday, June 27th and Monday, July 24th 2006.

Topics will include community paleoecology, quantitative biostratigraphy, diversity curves, speciation and extinction, morphometrics, and phylogenetics. Both simulation modelling and data analysis methods will be explored. The course will combine lectures and labs, and students will be given hands-on instruction in programming and the use of analytical software, with an emphasis on R. In addition to the course coordinator, each week a new instructor will be present. Participating instructors are expected to include John Alroy, Michael Foote, Nigel Hughes, Mark Patzkowsky, Pete Wagner, and Mark Webster.

There is no fee for registration, and students will be housed for free in apartments on the UCSB campus. Students are urged to apply for travel funds from their home institutions. If such funds are not available, all travel expenses beyond the first \$400 will be reimbursed completely, regardless of the country of origin. Students are responsible for meal expenses. Additional funding for students from outside of the United States, Canada, and Western Europe may be provided. There are no other charges of any kind, and no other major expenses are likely.

Participating students should be in the early stages of their own research in paleontology. They should have a background in basic statistics, and preferably also programming. The course is open to all students, but first or second year graduate students are particularly encouraged to apply, as are international students. Applications from professionals who have completed their studies will be considered, but strong preference will be given to students.

Applications should be submitted in PDF form to John Alroy ([alroy@nceas.ucsb.edu](mailto:alroy@nceas.ucsb.edu)) no later than March 1st. Applications should consist of a one page statement, plus a recommendation letter written by the student's academic advisor and e-mailed separately. No form needs to be filled out. The statement should include a description of current research plans, a list of relevant classes taken and degrees earned, and an account of the student's background in statistics and programming. Applicants are encouraged to explain why the topics addressed by the course are of special interest to them, and which of these subjects are taught at their home institutions.

[alroy@nceas.ucsb.edu](mailto:alroy@nceas.ucsb.edu) [alroy@nceas.ucsb.edu](mailto:alroy@nceas.ucsb.edu)

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## UEdinburgh QuantGenetics

MSc in QUANTITATIVE GENETICS AND GENOME ANALYSIS UNIVERSITY OF EDINBURGH <http://www.qgen.co.uk> This full-time degree programme (12 months M.Sc./ 9 months Diploma) starts each September and provides a solid foundation in population and quantitative genetics together with experience in relevant statistical methodologies. It includes options in evolutionary genetics, human genetics and animal breeding. There is a growing need for individuals with these combined strengths to apply quantitative genetics theory to practical problems in both the biomedical and agricultural industries; and to undertake research on current problems in population genetics, genome analysis, and analysis of complex traits. This Masters course is an excellent platform for doctoral studies.

The course is based at the Institute of Evolutionary Biology <http://www.biology.ed.ac.uk/research/-institutes/evolution/> with substantial input of teaching and research facilities provided by the Roslin Institute, Scottish Agricultural College, the Medical Genet-

ics Section of the Department of Medical Sciences, and the MRC Human Genetics Unit. These are all internationally recognised centres for research in quantitative genomics and research training is an integral part of the course.

**\*\*STUDENTSHIPS AVAILABLE FOR SELECTED APPLICANTS \*\***

The course has a number of scholarships open to UK applicants and other EU nationals. Details are at <http://www.qgen.co.uk>. Studentships will be awarded on a competitive basis.

We welcome applications from able graduates (expected 2.1 or higher) in either

1. Biosciences, Genetics, Agricultural Sciences, Medicine or Veterinary Medicine who have an interest in, and aptitude for quantitative biology, or
2. Mathematics, Statistics or Physical Sciences who wish to apply theory to genetic problems.

Closing date for applications 31 March 2006 but earlier applications welcome.

The application form can be downloaded from the Postgraduate Office web pages at <http://www.postgrad.ed.ac.uk> Informal enquiries and requests for further information to <http://qgen@ed.ac.uk> [n.barton@ed.ac.uk](mailto:n.barton@ed.ac.uk)

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## Instructions

Instructions: To be added to the EvoDir mailing list please send an email message to [Golding@McMaster.CA](mailto: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](mailto:Golding@McMaster.CA). In addition, if it originates from ‘blackballed’ addresses it will be sent to me at [Golding@McMaster.CA](mailto: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](mailto: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 [evoldir@evol.biology.McMaster.CA](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as  $\LaTeX$  files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category

“Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

## Afterward

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.