# EvolDir

January 1, 2010

Month in Review

## Foreword

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

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

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

—— / ——

# Conferences

## Amsterdam MEEGID X Nov3-5

CALL FOR PAPERS Abstract submission deadline: June 4, 2010

INTRODUCTION Infectious Diseases and Epidemiology have never been more important topics than they are today. In these exciting times, we are proud to announce the 10th edition of the highly successful international conference series on the Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID). Together, the MEEGID congress series and its companion journal, Infection, Genetics and Evolution, represent the main forum for cross-fertilization between evolutionary science and biomedical research on infectious diseases. This major scientific event will be held in Amsterdam, the Netherlands, from 3 - 5 November 2010.

PROGRAMME MEEGID is a wide-ranging conference that deals with the molecular evolution of all pathogens: viruses, pathogenic bacteria, fungi, parasites and prions of medical, veterinary or agronomical relevance. Through plenary lectures and symposia, special emphasis will be given to HIV/AIDS, malaria, tuberculosis, ebola and influenza. Attendance at this conference will enable you to:

Access unique, high-quality content and gain a state-of-the-art report on the latest developments in infectious diseases and epidemiology research Learn from experts in the field and meet with international researchers sharing a common interest. Present your latest research Network with an interdisciplinary group - including academics and researchers, as well as health and industry professionals.

SCOPE AND TOPICS The programme will be organised around the following themes:

Molecular epidemiology Evolutionary genetics, genomics, proteomics Mathematical modeling & bioinformatics Molecular diagnostics Population biology Genetics, population biology and morphometrics of vectors Host genetic susceptibility to infectious diseases All pathogens and infectious models will be considered, including those of veterinary or agronomical relevance. Contributions are solicited in all aspects of these themes with emphasis on interdisciplinary studies that support the development of new science hypotheses and innovative management applications.

ONLINE ABSTRACT SUBMISSION NOW OPEN Abstracts for oral and poster presentation should be submitted online using the online submission form at www.meegidconference.com Abstract submission deadline: June 4, 2010.

REGISTRATION INFORMATION Elsevier is committed to making this conference accessible to the widest possible range of delegates from around the world and has made available 100 places at a specially reduced registration fee of just 350 plus tax. These places are reserved for students (50 places) and delegates from low-income countries (50 places). For more information, visit the conference website.

SCIENTIFIC COMMITTEE Chair: Michel Tibayrenc, editor-in-chief Infection, Genetics and Evolution and IRD, France Francisco J. Ayala, University of California, Irvine, USA Jean-Claude Dujardin, Tropical Medicine Institute Prince Leopold, Belgium Roger Frutos, CIRAD, France Paul Keim, Northern Arizona University, USA Tovi Lehmann, NIAID, NIH, USA Thierry de Meeus, CIRDES, Burkina Faso Serge Morand, CNRS, France James Musser, The Methodist Hospital Research Institute, USA Martine Peeters, IRD, France Marie-Anne Shaw, University of Leeds, UK Marc Struelens, Laboratoire de Microbiologie, Belgium Loubna Tazi, Houston School of Public Health, USA Alex Van Belkum, EMCR, The Netherlands

ORGANISERS MEEGID X is sponsored and hosted by Infection, Genetics and Evolution and is the 10th in a series of annual meetings covering the latest developments in the field.

Conference Chairman <mailto:Michel.Tibayrenc@ird.fr> Michel Tibayrenc

Conference Secretariat <mailto:meegidconference@elsevier.com> Kay Russell

Michel.Tibayrenc@ird.fr

## Europe Astrobiology Jun14-18

Conference: AbGradCon 2010

In 2010, AbGradCon, the foremost astrobiology meeting for early-career researchers, will be held in Europe for the first time in its history (June 14-18). Graduate students and early-career postdocs from all over the world will come together to present their research in a comfortable environment, to learn of the latest developments in astrobiology, to network and to forge new collaborations. The meeting will comprise oral and poster presentations, half-dayworkshops and a one-day field trip to geologically instructive sites in the the astrobiologically interesting Siljan impact crater. Attendees are encouraged from the very wide range of subjects pertinent to astrobiology. Financial assistance will be available to invited attendees.

For more information, please visit the official website at http://www.abgradcon2010.org marc.hoeppner@molbio.su.se marc.hoeppner@molbio.su.se

## Ghent AlgalGenomics Apr7-9

*Se**cond circular ESIL2010: A decade of algal genomics (April 7-9, Ghent)*

Dear colleagues and friends,

We are pleased to invite you to the “ESIL2010: A decade of algal genomics” meeting (7-9 April, Ghent, Belgium). The meeting marks the release of the assembled Ectocarpus genome, the first genome of a complex multicellular alga and the publication of the accompanying paper(s). Previous meetings have served as a forum for researchers working on Ectocarpus or by extension brown algae and diatoms to present their ongoing research. For the upcoming meeting we are broadening up the perspective by inviting leading scientists who have gone through the process of assembling and annotating genomes and are now in the phase of using these data to address specific research questions.

The meeting will have plenary lectures from keynote speakers in several research fields related to development, functional and environmental genomics of algae, and will offer young investigators the chance to discuss their research with more experienced senior researchers in a relaxed atmosphere.

Sessions will include presentations providing an overview and update of - organism and cell biology of algal model organisms - environmental genomics - comparative genomics - systematics / phylogenomics

Registration and call for paper. For those wishing attend this meeting, and anyone wishing to present a Contributed Paper or a Poster, please view the Conference webpage at: http://www.phycology.ugent.be/ectocarpus/. The deadline for early registration is March 7. Do notice that registration is only definite after confirmation of payments.

Venue The venue is at the city centre of Ghent, a beautiful medieval town that combines a rich historical patrimonium with a cheerful, flourishing city culture and a creative atmosphere for lively exchanges and debates.

Students Students are invited to apply for grants through the British Phycological Society (BPS, http://www.brphycsoc.org/funding.lasso) as well as the Federation of European Microbiological Societies (FEMS, http://www.fems-microbiology.org/). Decisions are made on the basis of each application.

On behalf of the organizing committee and hope to see you in Ghent,

Olivier De Clerck & Mark Cock

Onderzoeksgroep Algologie, UGent. Krijgslaan 281, S8, 9000 Gent; Belgium NEW TEL. -32-9-2648500 // Fax. -32-9-2648599 http://www.phycology.ugent.be/ Olivier De Clerck Onderzoeksgroep Algologie, UGent. Krijgslaan 281, S8, 9000 Gent; Belgium NEW TEL. -32-9-2648500 // Fax. -32-9-2648599 http://www.phycology.ugent.be/ odclerck@gmail.com

---

## Girona Spain SpongeEvolution Sep20-24 ExtendedDeadline

Dear Evoldir people

Some time ago we announced the opening of the registration for the VIII International Sponge Conference, to be held in Girona (Spain), 20-24 September 2010. Those interested can look at our webpage

http://www.spongeconference2010.org/ We had notice that there are people experiencing problems with the payment of the early registration fee due to the end of the budgetary year in many institutions.

We have therefore decided to extend the deadline for early registration with reduced fees until FEBRUARY 15, 2010, to allow time for the opening of the 2010 budgets everywhere.

Remember that you don't need to pay at the time of Registration, but you have to do so BEFORE the deadline.

Best regards

Xavier Turon - on behalf of the Organizing Committee

PD. As our webmaster is on holydays, do not mind if this new deadline does not appear in the webpage for some days.

–

Xavier Turon Dept. of Aquatic Ecology Center for Advanced Studies of Blanes (CEAB, CSIC) Accés a la Cala S. Francesc 14 17300 Blanes (Girona) Spain

E-mail: xturon@ceab.csic.es Phone: +34 972 336101 Fax: +34 972 337806 http://www.ceab.csic.es/ http://www.ub.edu/beb/english/invertebrates/turon/turon.htm Xavier Turon <xturon@ceab.csic.es>

---

## InstitutPasteur Monod

To commemorate the 100th birthday of Jacques Monod, Nobel Laureat and co-founder of molecular biology, The Institut Pasteur and Molecular Microbiology are organizing a one-day young scientists minisymposium devoted to topics close to Jacques Monods interests. The programme will include several talks (30 minutes) on gene expression and signalling in bacteria. The speakers will be selected on the basis of abstracts submitted by young scientists (PhD students, postdocs and junior faculty) wishing to attend the meeting. The programme will also include two keynote speakers and a poster session (50 places).

To avoid disappointment, register NOW as a speaker, poster-presenter or participant (see registration form in attached document). Registration coffee breaks and a buffet lunch are all free

With best wishes,

The organizing committee

Agnes Ullmann Nienke Buddelmeijer Armelle Lavenir Tony Pugsley

molecularmicrobiology@yahoo.co.uk

---

## IowaStateU MEEC2010 Mar26-28 CallAbstracts

Hi folks,

I am pleased to announce that The Midwest Ecology and Evolution Conference (MEEC) will be held Friday, March 26 to Sunday, March 28 2010, on the campus of Iowa State University, in Ames, Iowa.

MEEC is a conference organized by and geared toward undergraduate and graduate students to present research and make connections. The heart of this event is composed of oral and poster presentations contributed by participating undergraduate and graduate students.

The conference will also include an opening mixer, a banquet Saturday evening, and keynote addresses from three leading researchers in ecology and evolution, including Dr. Jeff Feder from the University of Notre

Dame, Dr. Alan K. Knapp from Colorado State University, and Dr. Ellen Damschen from Washington University.

Abstract Submission

In keeping with MEEC tradition, posters and oral presentations are limited to students undergraduate and graduate. Faculty and post-docs are encouraged to attend in support of the students. The deadline for Abstract Submission is February 15, 2010. Students interested in submitting poster/paper abstracts or in putting together a special session should visit http://www.midwesteec.org/guide.html . For more information, please visit MEEC 2010 online at http://www.midwesteec.org/ Cheers,

Erik

Erik Otárola-Castillo Ecology and Evolutionary Biology Graduate Program 253 Bessey Hall Iowa State University Ames, IA 50011-1050 Phone 631-796-7331 < http://www.public.iastate.edu/ ˜ eotarola/homepage.html > http://www.public.iastate.edu/˜eotarola/homepage.html eotarola@iastate.edu

---

## Leuven DaphniaGenomics Mar26-30

Daphnia Genomics Consortium (DGC) Meeting 2010

When: 26th through 30th of March, 2010 Where: Leuven, Belgium

Pre-registration and abstract submission is now open! http://bio.kuleuven.be/DGCmeeting2010.html Early registration and abstracts submission deadline is January 15, 2010.

Please register early, because space is limited to 120 participants.

Dear colleagues and friends,

We are pleased to invite you to the DGC Meeting 2010.

The Daphnia Genomics Consortium (DGC) is an international network of scientists with a common goal to foster the freshwater crustacean Daphnia as a premier model system for genomics in ecology, evolution and the environmental sciences.

This meeting aims to bring together the members of the consortium at large, to facilitate the exchange of information on recent developments and results obtained from the ongoing investigations into the genome biology of Daphnia. Additionally, we welcome researchers working with Daphnia who are not yet DGC participants and researchers working with other model or non-model organisms in the field of ecological genomics.

The DGC meeting will have a significant impact on the future development of the research groups involved in the consortium. By this time, we will have finalized our initial investigations of the draft D. pulex genome sequence, and we will begin the work of exploring data obtained from the D. magna genome sequencing project. This upcoming meeting continues the tradition of also promoting collaborations between researchers working within related disciplines, including limnology, ecotoxicology, quantitative and population genetics, systematics, molecular biology and evolution, developmental biology, genomics and bioinformatics.

The meeting will have plenary lectures from keynote speakers in several research fields related to Daphnia and other model organisms. The symposia of our meeting will touch on several research topics:

* Ecology and Evolutionary Genomics * Toxicology and Environmental Genomics of Natural and Human Stressors * Genotype by Environment Interactions * Comparative Genomics and Development * Gene Expression and Gene Function

Plan to also learn about the latest open source bioinformatic and high-throughput research tools, including databases, expression and genotyping microarrays, mapping panels for trait locus mapping, molecular genetic protocols and services.

The venue is at the five century-old Katholieke Universiteit Leuven, in Belgium. Leuven is a beautiful medieval town that combines a rich historical patrimonium with a cheerful, flourishing city culture and a creative atmosphere for lively exchanges and debates.

We look forward to welcoming you in Leuven.

The local organization committee (Luc De Meester, Luisa Orsini, Ellen Decaestecker, Kevin Pauwels, Mieke Jansen, Joost Vanoverbeke) and the co-organizers Dries Knapen, Ronny Blust and Wim De Coen (University of Antwerp), Karel De Schamphelaere and Colin Janssen (University of Gent), Michael Pfrender (University of Notre Dame) and John Colbourne (Indiana University).

on behalf of the committee

–

Dr Luisa Orsini Laboratory of Aquatic Ecology and Evolutionary Biology, Katholieke Universiteit Leuven, Ch. Deberiotstraat 32, 3000 Leuven, Belgium

Phone: +32 016323707 Fax: +32 016320771 e-mail luisa.orsini[at]bio.kuleuven.be website:http:/-

/bio.kuleuven.be/de/dea/people.php Luisa Orsini <luisa.orsini@bio.kuleuven.be>

## Roscoff Brittany FungalEvolution Apr17-21

Roscoff Brittany Emerging Fungal Disease&Evolution April17-21

2nd Call << New and Emerging Fungal Diseases of Animals and Plants : evolutionary aspects in the context of global changes>>

The CNRS and Conferences Jaques Monod are hosting a 4-day meeting at the French Marine Biology research station in Roscoff, Brittany on the evolution and dynamics of emerging fungal pathogens. This meeting will focus on the widening impacts that fungi are having on human, plant and animal health by considering the factors that drive their emergence within an evolutionary context. Specifically, the meeting will consider whether environmental change is facilitating fungal range expansions and genotypes, and to what extent this is predictable. The meeting will bring together leading evolutionary biologists, theoreticians and fungal biologists/ecologists in a beautiful setting to consider these questions and to formulate new research strategies.

Plenary speakers:

François Balloux ; Imperial College London, UK Lynne Boddy ; University of Cardiff, UK Bruno Le Cam ; INRA Angers, France Ignazio Carbone ; North Carolina State University, USA Jean Carlier ; CIRAD Montpellier, France Jean Marie Cornuet ; Centre de Biologie et de Gestion des Populations Sybren de Hoog ; CBS Fungal Biodiversity Centre, Netherlands François Delmotte ; INRA Bordeaux, France Marie-Laure Desprez-Loustau ; INRA Bordeaux, France Matthew Fisher ; Imperial College London Sylvain Gandon ; CNRS Centre d'Ecologie Fonctionnelle et Evolutive Montpellier, France Trenton Garner ; Insitute of Zoology, UK Greg Gilbert ; University of California, Santa Cruz Tatiana Giraud ; CNRS - Université d'Orsay, France Michael Hood ; Amherst College, USA Mogens Hovmoller ; Aarhus University, Denmark Levente Kiss ; Plant Protection Institute of the Hungarian Academy of Sciences Linda Kohn ; University of Toronto, Canada Marc Henri Lebrun ; INRA BIOGER, France Celeste Linde ; Australian National University David Lodge ; University of Notre Dame, USA Benoît Marçais ; INRA Nancy, France Bruce McDonald ; ETH Zurich, Switzerland Michael Milgroom ; Cornell University, USA Ingrid Parker ; University of California, Santa Cruz Amy Pedersen ; Sheffield University, UK Anne Pringle ; Harvard University, USA Virginie Ravigné ; CIRAD Montpellier, France Eva Stukenbrock ; University of Århus, Denmark John Taylor ; University of California at Berkeley, USA Frank van den Bosch ; BBSRC, Rothamsted Research, UK

Conference website:

http://www.ese.u-psud.fr/-CJMemergingdiseases2010/ To participate, please contact:

Matthew Fisher <matthew.fisher@imperial.ac.uk>

Tatiana Giraud <tatiana.giraud@u-psud.fr>

matthew.fisher@imperial.ac.uk
matthew.fisher@imperial.ac.uk

## RutgersU DivergenceEstimation Jan8 2

Northeast Symposium on Evolutionary Divergence Time at Rutgers University, NJ Friday, January 8, 2010 Dr. Jessica Thomas and Dr. Jessica Ware jthomas@aesop.rutgers.edu, jware@amnh.org

The following one-day symposium may be of interest to Evoldir subscribers. Registration is free, but space is limited; please pre-register soon so that we will have an idea of numbers (http://www.doodle.com/-z53imdqy23t8w4fg, nsedt.rutgers.edu or email: jware@amnh.org).

Details: Friday, January 8th, 2010, from 8:30 am Rutgers, the State University of New Jersey Rutgers Student Center (College Avenue Campus Centre), 124 College Ave, New Brunswick, NJ, 08901, USA

Hosted at Rutgers University, sponsored by the Office of the Executive Dean of Agriculture & Natural Resources (http://execdeanagriculture.rutgers.edu/), the Department of Ecology, Evolution & Natural Resources (www.rci.rutgers.edu/ ˜ deenr/), the Department of Entomology (http://www.mosquito.rutgers.edu/-index.html), and the Office for the Promotion of Women in Science, Engineering and Math (WiSEM) (http://rufair.rutgers.edu/; Rutgers University is a recipient of an NSF ADVANCE grant).

Organizers: Dr. Jessica Thomas

(jthomas@aesop.rutgers.edu) & Dr. Jessica Ware (jware@amnh.org) Executive Sponsors: Executive Dean Dr. Robert Goodman, and Chair of Department of Ecology and Evolution, Dr. Henry John-Adler

This is a one-day symposium.

Background: Divergence time estimation is an exciting current area of interest, and we are seeing great advances in both methodologies and taxonomic coverage. Research on arthropod divergences is vital due to their extreme biodiversity and both ecological and economic importance. Dating in arthropods can provide insight into fascinating questions such as the timing of the great angiosperm divergence, co-evolution of parasites and hosts, and a variety of other aspects of life on earth, encompassing subject areas across anthropology, vector biology, paleontology, geology and geography.

This workshop on molecular dating in arthropods intends to provide an opportunity to share new methodological advances, explore current results on taxa of interest and provide interface time among fossil and molecular researchers. The set up of this workshop is specifically aimed to promote networking and collaboration, with extended lunch and coffee times provided for discussion.

We have a broad program of speakers, ranging from molecular researchers to paleontologists, with a diverse range of talks from organismal work to methodology.

Speaker line-up: Sean Brady, Frank Burbrink, Seth Bybee, CJ Geraci, David Grimaldi, Akito Kawahara, Karl Kjer, Jessica Light, Corrie Moreau, Sergios-Orestis Kolokotronis, Chris Owen, Alex Pyron, Sara Ruane, Hojun Song, Gavin Svenson, Jessica Thomas, Jessica Ware.

Rutgers University is centrally located in the Northeastern US, ideal for easy accessibility by car, Amtrak, NJ transit or plane (Newark, JFK or LaGuardia). For maps please visit: http://rumaps.rutgers.edu/ Register at: http://www.doodle.com/z53imdqy23t8w4fg or contact the organizers by email. You can also find this meeting on facebook: http://www.facebook.com/-event.php?eid=184322426771&ref=mf and on the official event website, http://nsedt.rutgers.edu !

Jessica Ware <jware@amnh.org>

---

## UAlberta ButterflyEvolution Jun29-Jul2 CallSubmissions

Dear butterfly biologists everywhere!

The 6th International Conference on the Biology of Butterflies will be held at the University of Alberta, Edmonton, Canada from June 29 through July 2, 2010. This meeting has been held at irregular intervals since 1981 and recognizes the role that the study of butterflies has played in our understanding of both evolutionary biology and ecology. The meeting will include Symposia, Contributed Papers, Posters, Banquet and Field Trips.

For those wishing attend this meeting, and anyone wishing to present a Contributed Paper or a Poster, please view the Conference webpage at: http:/-/www.biology.ualberta.ca/biobutterfly2010 Deadline for lower-cost Registration: March 31, 2010 Deadline for Abstract submission: May 17, 2010

Felix Sperling <felix.sperling@ualberta.ca>

---

## UManchester CommunityGenetics Jan7-8 LastCall

Hello

The deadline for registration and abstract submission for the 1st European Community Genetics Conference, to be held in Manchester, Uk January 7th-8th is fast approaching.

We have an exciting two day programme planned, with Marc Johnson coming from North Carolina State University and Tom LIttle from Edinburgh University to give the plenary lectures. We have participant presentations confirmed from delegates from six european countries and a few slots still available for oral or poster presentations.

You can find more information and registration forms at the meeting website or by contacting me directly. www.communitygenetics.eu Best wishes Jenny Dr Jennifer Rowntree Preziosi Lab Faculty of Life Sciences University of Manchester Smith Building Oxford Road Manchester M13 9PT

+44-(0)161-2755108

http://web.me.com/jkrowntree/-Jennifer_K_Rowntree/Jennifer_K_Rowntree.html

1st European Community Genetics meeting 7-8th January 2010 The University of Manchester http://www.communitygenetics.eu/ jennifer.rowntree@manchester.ac.uk

## UMichigan ExperimentalEvol Apr17

The deadline for nominations for the Early Career Scientists Symposium on EXPERIMENTAL EVOLUTION to be held in Ann Arbor, MI, USA on April 17, 2010 is approaching. We are pleased to announce that the keynote lecture will be given by Dr. Richard Lenski (Michigan State U.). All selected speakers' expenses will be covered thanks to a generous donation from Nancy Walls. This symposium provides an opportunity for future leaders in this growing field to meet and exchange ideas.

CALL FOR NOMINATIONS

SIXTH ANNUAL UNIVERSITY OF MICHIGAN EARLY CAREER SCIENTISTS SYMPOSIUM:

EXPERIMENTAL EVOLUTION

The Department of Ecology and Evolutionary Biology at the University of Michigan invites nominations of outstanding scientists early in their careers to take part in a symposium on experimental evolution. This symposium will be held in Ann Arbor, Michigan on Saturday, April 17, 2010. Eight scientists will be selected to present their work. All research involving observation of long-term changes in controlled populations, investigating response of natural populations to experimental manipulation, or performing evolution in silico, will be favorably considered.

Early career scientists are defined as senior graduate students (who will receive their Ph.D. within one year) or postdoctoral researchers. Potential speakers can be nominated by their advisor or a senior colleague.

Nominations must include a brief letter of recommendation addressing the nominee's scientific and communication skills, a copy of the nominee's curriculum vitae, and a brief abstract of the proposed presentation (< 200 words, written by the nominee). Nominations can be sent electronically (in a single file if possible) to kuhnlein@umich.edu with the subject line: "Nominee for ECSS." More information is available at http://-sitemaker.umich.edu/ecss2010 . All nominations must be received by December 15, 2009. Selected participants will be contacted by January 15, 2010.

For more information, contact Gail Kuhnlein (kuhnlein@umich.edu).

2010 ECSS organizing committee: Alex Kondrashov kondrash@umich.edu, Timothy James tyjames@umich.edu, Amanda Izzo mizzo@umich.edu, Zhi Wang zcwang@umich.edu

EEB Web site: http://www.eeb.lsa.umich.edu Timothy Y. James Assistant Professor & Curator of Fungi Department of Ecology and Evolution University of Michigan Ann Arbor, MI 48109 734-615-7753 tyjames@umich.edu

tyjames@umich.edu tyjames@umich.edu

## Uruguay VertebrateEvolution Jul26-31 Deadline

Dear Evolutionary Biologists,

This is a reminder that final deadline for registration and abstract submission to the 9^th International Congress of Vertebrate Morphologists, to be held in Punta del Este (Uruguay) from 26^th to 31^st July 2010, is: *February 10^th , 2010*. After this date, only posters will be accepted. Once you've registered and paid, you'll be able to submit your abstract.

Faithfully,

The Local Committee of the 9^th ICVM .

Visit the website of the 9^th ICVM at: http://icvm-9.edu.uy/ passer@fcien.edu.uy

## UStirling EcoGenetics54th meeting Apr6-8

Conference Announcement: EGG 2010 University of Stirling

The 54th annual meeting of the Ecological Genetics Group will be held at the University of Stirling and hosted by the School of Biological and Environmental Sciences.

The conference will start on Tuesday 6th April 2010 lunchtime and will run through to lunchtime on Thursday 8th April 2010.

In 2010, we will have two guest speakers, Professor Laurent Excoffier (University of Bern) and Professor Richard Abbott (University of St Andrews).

EGG is an informal meeting that brings together scientists working in population genetics and evolutionary ecology, mainly, but by no means exclusively, from the United Kingdom and other European Countries. Talks, discussion topics and posters are welcomed from students giving their first presentation, to senior academics presenting completed work.

Please visit the EGG 2010 website for meeting details :

http://www.sbes.stir.ac.uk/egg/index.html The deadline for submitting titles and abstracts for oral and poster presentations is 8th February 2010.

Details for registration are available from the EGG 2010 website.

Early registration is encouraged as talks and shared accommodation will be allocated on the first-come first-served basis.

Thanks, Cecile

Cecile FE Bacles Ph.D. Lecturer in Ecological Genetics School of Biological and Environmental Sciences University of Stirling Cottrell Building 4B148 Stirling FK9 4LA Tel: +44 (0) 1786 46 ext 6897 Email:c.f.bacles@stir.ac.uk

– The Sunday Times Scottish University of the Year 2009/2010 The University of Stirling is a charity registered in Scotland, number SC 011159.

c.f.bacles@stir.ac.uk

## UUppsala Climate and Evolution Sep1-3

The conference will be “An interdisciplinary conference linking research from veterinary and human medicine, ecology and evolution”. The organizers of this conference are mainly evolutionary biologist and several evolutionary biologist are also going to be the keynote speakers on the conference, (from fields of evolutionary medicine, pathogen evolution, adaptations of organisms to the climate change in the future and from the historical perspective).

Climate Change: Health and Ecology An interdisciplinary conference linking research from veterinary and human medicine, ecology and evolution.

September 1-3, 2010, Uppsala, Sweden

Registration is now open! For more information about the conference and to register, please see http://-/tiny.cc/SVA_Climate2010 or http://www.sva.se/-sv/navigera/tjanster_produkter/Utbildningar-och-kurser/Climate-Change-Health-and-Ecology/ The complexity of the information required to address Climate Change issues is vast, requiring an interdisciplinary approach. Therefore, the National Veterinary Institute, Uppsala, Sweden will hold an interdisciplinary conference to link research and philosophy from evolutionary, ecological and medical fields of expertise with the objective of reviewing current understanding and proposing future action. The keynote speakers will cover the topics of organismal adaptations to the climate change in both terrestrial and aquatic environments and in human society.

Submission of abstracts for poster presentations welcome!

NEW! According to Swedish legislation and routines, VAT will be added for delegates from outside Sweden who register from 1 January 2010. If you register by 31 December 2009 and payment is done within 30 days from registration date, no VAT will be added. VAT will be added for payments made later than 30 days after registration.

Welcome to Uppsala and Sweden in September!

Dr. Mare Lõhmus research scientist

Climate Centre Section for Environment and Biosecurity Department for Chemistry, Environment and Feed Hygiene

NATIONAL VETERINARY INSTITUTE tel. +46 18 67 44 18 mob. +46 733 824579 e-mail. mare.lohmus@sva.se fax. +46 18 30 91 62 address: Ulls väg 2B; 751 89 Uppsala webb. www.sva.se Löhmus Mare <mare.lohmus@sva.se>

# GradStudentPositions

## Brisbane Bioinformatics

PhD Student Position in Transcriptional Profiling

A PhD student position is available in the field of transcriptional profiling in vertebrate and invertebrate species. The project will analyse gene expression levels in conserved genes across evolutionary divergent groups. The study is a collaboration between University and Government with practical outcomes for natural resource management. It is based in the laboratories of Dr Jennifer Seddon in the School of Veterinary Science, University of Queensland (www.uq.edu.au/vetschool) and Dr Jenny Ovenden in the Molecular Fisheries Laboratory in the Department of Primary Industries and Fisheries, Queensland, Australia(www.dpi.qld.gov.au/28_6844.htm).

We are looking for a motivated student with experience in bioinformatics and basic molecular genetics as the project involves database mining, RNA extraction and real time PCR analyses.

There is currently no scholarship attached to this position but scholarships are available to students through the University of Queensland, awarded on the basis of academic excellence. Further information on scholarships and tuition fees are available at http://-www.uq.edu.au/study/scholarships/.

Further information can be obtained by email from Dr Jennifer Seddon (j.seddon1@uq.edu.au) or Dr Jenny Ovenden (Jennifer.Ovenden@deedi.qld.gov.au).

Dr Jennifer Seddon Senior Lecturer in Animal Genetics School of Veterinary Science St Lucia QLD 4072 Australia Tel: +61 (0)7 3365 1278 Fax: +61 (0)7 3365 1255 Email: j.seddon1@uq.edu.au CRICOS No. 00025B

j.seddon1@uq.edu.au j.seddon1@uq.edu.au

## CarletonU InsectPopulationGenetics

Interested in obtaining graduate degree in biology? I am looking for graduate students (PhD or MSc) who want to work with insects. My lab focuses on the general question of how variation is maintained in sexually selected traits. Students in the lab work on sexual selection, acoustic mating signals, aggression, post-conflict displays, female mating behavior, behavioral syndromes, and the interplay between diet and behavior.

I have funds available to support a few students who are interested in starting their MSc or PhD program in 2010 (January or September start dates). Applicants must be Canadian citizens or permanent residents (landed immigrant status). Unfortunately, people from outside Canada need not apply as my funds for international graduate students have already been utilized for this year.

If interested, please contact Sue Bertram at:

Email: Sue_Bertram@carleton.ca

Website: www.carleton.ca/˜sbertram Please include the following in your email:

1. Curriculum Vitae 2. Transcripts (unofficial are fine) 3. A statement describing what questions you are interested in focusing on for your graduate research and why 4. A sample of your writing (e.g., a term paper, a thesis, essay, a publication that you wrote)

Regards, Sue

Susan M. Bertram, PhD Assistant Dean of Science Carleton University

Sue_Bertram@carleton.ca

## CarlvonOssietzkyU FishPopulationgenetics

Position for a Ph.D. student

Population genetics and local adaptation in marine organisms

A Ph.D. position is available in the laboratory of Gabriele Gerlach "Animal Biodiversity and Evolution" at the Carl von Ossietzky University Oldenburg, Germany.

We are seeking a highly motivated person to work on population genetics, selection processes and adaptive evolution. The candidate should be interested in marine organisms, especially coral reef fish and their behavior.

Skills of molecular methods (analysis of DNA, RNA, cDNA, gene expression) are requested as well as interest in evolutionary biology and population genetics.

In the Gerlach lab we examine the dynamics of the genetic structure of marine organisms. We are interested in analyzing dispersal processes and local adaptation.

For more information, contact Gabi.Gerlach@uni-oldenburg.de

Applications should be sent by email stating your reasons for applying and including a CV, copies of degree certificates, summary of the Master thesis and addresses of two potential referees (email and telephone number) who are willing to write letters of recommendation. We would like to fill the position soon; applications are requested by *20.1.2010 by email.*

Prof. Dr. Gabriele Gerlach Animal Biodiversity and Evolutionary Biology IBU, Faculty V Carl von Ossietzky University Oldenburg 26111 Oldenburg Germany

Email: Gabi.Gerlach@uni-oldenburg.de

http://www.biodiv-evo-tiere.uni-oldenburg.de/-index.html Gerlach <gabriele.gerlach@uni-oldenburg.de>

## CityUNewYork phylogeography

A PhD position in integrative and model-based phylogeography is available at the City University of New York (CUNY).

The candidate will develop multi-taxa phylogeographic models that can be specified by a wide range of hypotheses relevant to community assembly, speciation, natural selection, and biogeographic responses to climate changes. By developing and using the tools of approximate Bayesian computation (ABC) to specify complex demographic/evolutionary models, the candidate will enable powerful new techniques for community-level phylogeographic inference.

Although this approach will allow the candidate to address questions in a wide variety of biogeographic contexts, the emphasis will be on developing multi-taxa ABC models that can be built from ecological niche models and can incorporate the subgenomic data emerging from next-generation sequencing technology. The student will work with Mike Hickerson (see http://qcpages.qc.cuny.edu/Biology/-Hickerlab/index.html) and will interact with a strong phylogenetics/phylogeography group spread across several CUNY campuses and the AMNH.

Interested applicants should first send a CV, a statement of research interests, and contact information for three references, to michael.hickerson@qc.cuny.edu . Application materials are found at the CUNY Graduate Center Ecology, Evolutionary Biology, and Behavior subprogram - http://web.gc.cuny.edu/biology/ Students are guaranteed annual stipends, ful tuition waver and benefits for the full 5 years. Applications are due in January. Informal inquiries before the application are encouraged.

Mike Hickerson Assistant Professor Biology Department Queens College, CUNY 65-30 Kissena Boulevard Flushing, NY 11367-1597 Office Phone: 718 997 3447 Lab Phone 718 997 3415 office E114 lab E321

Mike Hickerson <michael.hickerson@qc.cuny.edu>

## ColoradoStateU 2 EvolutionaryMathematicalEcol

Two positions for PhD students.

We seek two graduate students: one with a background in evolutionary biology and one with a background in mathematical biology for an exciting opportunity to work on a collaborative project at the interface of demography and ecological genetics.

The project focuses on the contributions of demography and genetics in the founding and spread of new populations, combining a model biological system (Tribolium flour beetles) and quantitative models. The evolutionary ecologist will conduct the experiments: previous experience in lab experiments using insects or other model organisms would be helpful, and a strong background in evolutionary ecology is vital. This student would join the lab of Ruth Hufbauer at Colorado State University (http://lamar.colostate.edu/-˜ hufbauer/, http://www.ecology.colostate.edu/ , http://www.evolution.colostate.edu/), and will have the opportunity to collaborate closely with the mathematical biologist.

The student in mathematical biology will develop models to quantify the contributions of genetics and demography from experimental data. Previous experience with stochastic processes, and likelihood or Bayesian methods of model estimation would be a plus but all students with a genuine interest in mathematical biology are encouraged to apply. The student would join the active and growing lab of Dr Brett Melbourne at University of Colorado, Boulder (http://www.colorado.edu/eeb/facultysites/-melbourne/ ) where related projects are developing theory in population biology applied to extinction, invasion, climate change, and biodiversity maintenance.

Applications should be submitted as soon as possible to the relevant program given the late date. Please get in touch with either Ruth or Brett for additional details on how to apply. When you write, please send a CV that includes information on coursework and grades.

Ruth A. Hufbauer Associate Professor Colorado State University

2009-2010 sabbatical bourse de la Commission franco-américaine CBGP/INRA France

email: hufbauer@lamar.colostate.edu http://-/lamar.colostate.edu/ ˜ hufbauer/ http://-www.invasionsrcn.org/ hufbauer@lamar.colostate.edu

## ETH Zurich EvolutionaryGenetics

PhD position in Theoretical Evolutionary Genetics / Computational Biology / Molecular Evolution at the Theoretical Biology Group, ETH Zurich, Switzerland

A PhD position is available at the Theoretical Biology Group, ETH Zurich (http:/www.tb.ethz.ch) under the supervision of Dr. Frederic Guillaume and Prof. Sebastian Bonhoeffer to study the genetics of adaptation using both bioinformatics resources and computational modeling approaches. The position is funded for three years by ETH Zurich, starting from now.

The project asks questions related to the evolution of pleiotropy and of the modular structure of the genotype-phenotype map in the context of phenotypic evolution in multivariate traits space. A first step will be to define meaningful ways of measuring pleiotropy or modularity of genes affecting phenotypic characters in order to accurately describe the constraints acting on their evolution and the variation of the modularity of the genotype-phenotype map in model systems. The second step will seek to integrate the type of patterns observed into models of phenotypic evolution in order to understand the evolutionary significance of variation of modularity of the genotype-phenotype map. Specific questions related to the genetics of adaptation will then be asked within this evolutionary model. The candidate will be encouraged to develop her/his own questions within this general framework.

The applicants should have a strong background and interests in evolutionary genetics and molecular evolution. The skills needed are mainly knowledge of bioinformatics tools, computer programming, and an affinity with mathematics and statistics. Knowledge of a programming language will be considered a plus (C/C++ would be ideal). A master degree in biology or related fields is required.

Motivated applicants should send (as PDFs) a CV with a brief summary of past research experiences, a one page statement of research interests, and complete contact information for at least two references to frederic.guillaume@env.ethz.ch. Informal inquiries before application are encouraged.

Dr. Frederic Guillaume Institute for Integrative Biology ETH Zurich, CHN H76.1 Universitaetstr. 16 CH-8092 Zurich Switzerland

t: +41 44 632 5872 f: +41 44 632 1271

frederic.guillaume@env.ethz.ch

## ETH Zurich Plant Evolutionary Genetics

Ph.D. student position in Plant Evolutionary Genetics (3 years)

in the Plant Ecological Genetics group (Institute of Integrative Biology) at ETH Zurich, Zurich, Switzerland, starting on 1 March 2010 or as soon as possible thereafter.

We seek a highly motivated Ph.D. student to work on genome-wide nucleotide diversity of wild tomato species (Solanum section Lycopersicon), with a particular focus on historical demography and evidence for natural selection at the molecular level. Our broader project entails both neutrally-evolving reference loci and candidate genes for putatively adaptive traits. The analysis of previously published sequence data is also possible.

We offer a stimulating scientific environment and first-rate computational and molecular facilities (the newly established Genetic Diversity Center Zurich is located in our building). Our group of scientists and students is international in composition, with all group meetings, seminars etc. being held in English. The main study organisms in other (non-tomato) research projects are species of Silene and Arabidopsis (see http://www.peg.ethz.ch).

Applicants should have a Master degree (or equivalent) in Evolutionary Biology/Population Genetics, Plant Biology, Computational Biology, or Environmental Sciences. A background in molecular population genetics is highly desirable, as is familiarity with coalescent simulations and computer programming. Good quantitative, analytical, and English skills are essential, as is the ability to work independently.

Applicants should submit a single PDF file by e-mail containing the following items:

* A cover letter including a brief summary of previous research experience and professional motivation * Curriculum Vitae * Copies of degree certificates and list of coursework, including grades obtained * Names, addresses and e-mails of two professional references

Application received until 15 January, 2010 are assured of full consideration, but the position remains open until a suitable candidate has been identified. Please send applications to

Dr. Thomas Staedler Plant Ecological Genetics Institute of Integrative Biology (IBZ) ETH Zurich Universitätstrasse 16 CH-8092 Zurich Switzerland

thomas.staedler@env.ethz.ch
thomas.staedler@env.ethz.ch

## Florida MNH CampanulaceaeSystematics

A Ph.D. fellowship is available at the Florida Museum of Natural History and in the Department of Biology, University of Florida, under the supervision of Dr. Nico Cellinese. The successful applicant will work on the systematics, evolution, and biogeography of Mediterranean Campanulaceae. This work will contribute to a large species-level phylogeny and analysis of pattern of endemism in the Aegean area. Active interaction with international collaborators and extensive fieldwork in the Aegean Archipelago and surrounding areas are expected. Candidates must have a strong interest in systematics and evolutionary biology, and prior laboratory experience (e.g., molecular techniques including PCR, cloning, sequencing, etc.) is required. Interested students must apply as soon a possible, at least by uploading their CVs and a letter stating that they will send the rest of the application to Ms. Karen Patterson, Dept. of Biology, in early January. All guidelines can be found at http://gradschool.ufl.edu/students/application-and-admission.html . For any additional information, please contact Dr. Nico Cellinese ncellinese@flmnh.ufl.edu , tel. 352-273-1979.

Nico Cellinese, Ph.D. Assistant Curator, Herbarium & Informatics Adjunct Assistant Professor, Department of Biology

Florida Museum of Natural History University of Florida 354 Dickinson Hall, PO Box 117800 Gainesville, FL 32611-7800, U.S.A. Tel. 352-273-1979 Fax 352-846-1861

Nico Cellinese <ncellinese@flmnh.ufl.edu>

---

## GeorgetownU EvolutionaryBiol

Multiple PhD Positions Available in Ecology, Evolution and Behavior

The Department of Biology at Georgetown University has multiple opportunities for doctoral study in ecology, evolution and behavior (EEB).

The faculty and graduate program in Biology at Georgetown help doctoral candidates develop into insightful researchers and effective teachers and communicators. Funding for graduate study is supported by a combination of assistantships, teaching fellowships and research grant support. Our program and institution welcomes students of all racial, ethnic and religious backgrounds.

Students interested in any of the opportunities listed below are strongly encouraged to contact the relevant faculty member(s) via email. The Department of Biology graduate program is described at http://biology.georgetown.edu/graduate/applicants/. Information about graduate school application procedures and deadlines can be found at http://grad.georgetown.edu/pages/admissions.cfm . Community Ecology and Landscape Genetics: Dr. Gina Wimp is seeking students interested in understanding the mechanisms that lead to the loss of biodiversity and increased risk of extinction in fragmented habitats. Dr. Wimp's work takes place in the intertidal salt marsh where a rise in mean tidal height over the past 60 years has led to a change in the demography of the two dominant grass species, with the more flood-intolerant grass (Spartina patens) contracting in size. She uses manipulative experiments to examine the effects of habitat loss and fragmentation in S. patens on the abundance, diversity and composition of the dependent arthropod community. The Wimp and Hamilton labs have developed microsatellite genetic marker loci to examine the effects of habitat fragmentation on gene flow in two of the dominant herbivore species found in S. patens, both of which are flightless, specialist planthoppers. Interested students should contact Dr. Gina Wimp via email (gmw22@georgetown.edu).

Applicants interested in pursuing graduate research in community ecology will work with Gina Wimp (http://biology.georgetown.edu/ faculty/wimp/research/) and students interested in pursuing research in landscape genetics will work with both Gina Wimp and Matthew Hamilton (http://www9.georgetown.edu/faculty/hamiltm1/). Applicants should have a demonstrated interest in community ecology and/or ecological genetics.

Mechanisms of phenotypic evolution: Dr. Peter Armbruster seeks a highly motivated PhD student to join his laboratory's research on mechanisms of phenotypic evolution in natural populations. The Armbruster lab is currently focusing on the invasive and medically important mosquito Aedes albopictus. This mosquito invaded the US in 1985 and spread rapidly over approximately 15 degrees of latitude. This natural experiment in evolution provides an exciting opportunity to identify the molecular and physiological mechanisms underpinning climatic adaptation during invasion and range expansion. Dr. Armbruster's research is currently supported by grants from both NIH and NSF, and integrates a broad range of approaches, including molecular biology, bioinformatics, physiology, and quantitative genetics. Interested students should contact Dr. Peter Armbruster (paa9@georgetown.edu).

For further information on the Armbruster lab see: http:// www1.georgetown.edu/ departments/ biology/ faculty/ armbruster/

Mathematical Population Biology: Faculty in the Departments of Biology and Mathematics have ongoing collaborations centered on quantitative modeling and analysis of population genetic data. Ongoing projects span a wide spectrum of applications including the development of coalescent models that better suit natural populations in order to infer biological mechanisms acting on genetic polymorphism to the development of novel quantitative models to analyze the evolution of HIV within an infected individual. These projects are highly interdisciplinary, drawing on approaches and techniques from both disciplines.

Dr. Matthew B. Hamilton (Biology) and Dr. Sivan Leviyang (Mathematics) are seeking an outstanding student to pursue a jointly mentored PhD in mathematical biology. The course of study will include classes in biology, mathematics and computer science, with the goal of providing the student with a firm background in population genetics, ecology, statistics, probability, and computation. The specific topic of research is flexible and can favor theory or application depending on the students' interest. The ideal student should possess a bachelor's degree in biology or

— / —

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

## Granada PistachioEvolution

PhD position is available to work on the project: "Development of Molecular Tools for Pistachio Genetic Improvement", supported by Science and Innovation Spanish Ministry and included in the FPI (Formación de Profesorado Universitario) program. Main objective is to construct a first pistachio genetic map based on microsatellite markers and to characterize sequences related to sex determination and other features economically important (fruit quality, production or disease resistance). The candidate would integrate in the Molecular Genetics Group BIO200 at Departamento de Genética, Facultad de Ciencias, Universidad de Granada, Granada (Spain), which has a research line for Molecular and Cytogenetical Analyses on different plant species, focusing on sex-determination and sex-chromosomes origin and evolution.

Call is imminent (January 2010) and deadline for applications will be 15 days after that date. Full details and conditions will be published at http://www.micinn.es . Applicants should have completed a degree in Biology, Biochemistry or similar. Skills in lab DNA-based methods and computing would be desirable. To apply, please send a cover letter and your CV to: Dr. Rafael Navajas-Pérez E-mail: rnavajas (at) ugr.es

For tentative information, previous year announcement (likely to be similar in 2010) can be found at: (http://web.micinn.es/contenido.asp?menu1=3D1&menu2=3D&menu3=3D&dir=3D03_Plan_IDI/00-LIAs/00@LIARRHH/00-Formacion/00-FPI/001Con09)

– Rafael Navajas-Pérez, PhD Associate Professor Departamento de Genética Facultad de Ciencias Universidad de Granada SPAIN Voice: +34 (958) 243080 Fax: +34 (958) 244073 e-mail: rnavajas@ugr.es website: http://www.ugr.es/ ˜ rnavajas r.navajas.perez@gmail.com

## INIA Spain ForestEvolutionaryEcology

Graduate position (PhD) in Forest Evolutionary Ecology at the Forest Genetics and Ecophysiology Lab, Forest Research Centre, INIA, Madrid, Spain.

We are looking for a highly motivated PhD student interested in evolutionary ecology and conservation genetics of forest trees to join our team in fall 2010.

Current research in our lab employs molecular genetic tools and statistical genetics models to investigate multi-scale population genetic processes and patterns that are relevant to tree conservation management. The PhD candidate will participate in a project on the adaptive consequences of gene flow among pine populations, involving field work, molecular and quantitative analysis in the lab, and development and application of related statistical methods.

The position will be covered by a 4-year PhD scholarship from the Spanish Ministry of Science (2010 FPI program), which includes the salary plus funded research visits of 2-6 months per year to other national or foreign labs. The PhD student will benefit from a dynamic, multidisciplinary and international research environment in our group, with opportunities for collaboration with several other Spanish, European and American teams.

The successful candidate should have an excellent academic record and a good background in evolutionary ecology, population genetics and statistical analyses.

High levels of written and spoken English are important. Experience in molecular techniques will be beneficial.

If you are interested, please send me an email including a CV, a statement of research interests, a brief overview of your previous academic and research experiences, and names and email addresses of two references. The review of applications will begin immediately and will remain open until about mid-January 2010 (the exact deadline will be announced by the Ministry of Science soon).

Juan J. Robledo-Arnuncio

CIFOR-INIA

jjrobledo@gmail.com http://sites.google.com/site/-jjrobledo2/ jjrobledo@gmail.com

## KansasStateU PlantPopGenet

PhD student position in population genomics

A PhD position in population genomics is available in the laboratory of Chris Toomajian at Kansas State University. The lab studies the population and evolutionary genomics of plants and plant pathogens. Of particular interest are questions related to the forces responsible for standing genetic variation found in populations and the connection of this variation with natural phenotypic variation. Please see http://sites.google.com/-site/toomajianlab for a description of the lab and its research.

A student is needed to assist in a multi-year project investigating transcriptome variation in Arabidopsis thaliana, in collaboration with Richard Clark of the University of Utah. The student will be encouraged to develop a PhD project related to this project, though other components can be developed in collaboration with the lab PI.

A strong undergraduate (or master's) background in biology is required, as is some prior research experience. Some prior training in statistics, population genetics, and molecular evolution and working knowledge of a computer programming language are highly desirable. Relevant experiences such as the analysis of genome data (DNA sequence, gene expression levels) and training in molecular genetic techniques are also preferred.

Those interested should contact Chris Toomajian (toomajia@ksu.edu) and provide the following as PDF documents: your current CV, with contact information for three references, and a cover letter that includes a statement of your future research interests and a summary of your relevant prior research or educational experiences. If available, provide your GPA and GRE scores. Informal inquiries are also welcome.

The selected student is expected to enroll either in the Interdepartmental Genetics program (http:/-/www.ksre.ksu.edu/genetics/) or the Department of Plant Pathology (http://www.plantpath.k- state.edu). Contact Dr. Toomajian for further information about policies and entrance requirements pertaining to Graduate School admission, or consult www.k-state.edu/-grad/ .Stipend levels for PhD students in either program are above $22,000 after payment of tuition fees for the 2010-2011 academic year. The KSU Department of Plant Pathology is a diverse and nurturing graduate training environment with little teaching assistant duties required for the degree. The lab also participates in K-State's Ecological Genomics Institute, a vibrant community composed of faculty, post-docs, and graduate students from a number of disciplines. Applications are due before the end of January 2010 for fall admission to either graduate program.

Christopher Toomajian Assistant Professor Kansas State University Department of Plant Pathology 4024 Throckmorton Plant Sciences Center Manhattan, KS 66506 office: (785) 532-0879 fax: (785) 532-5692 toomajia@ksu.edu http://sites.google.com/site/-toomajianlab/ toomajia@k-state.edu toomajia@k-state.edu

## LaurentianU MolEvol

Graduate student positions are available in the Merritt Lab at Laurentian University. Research in my lab examines the genotype and phenotype connection, focusing on the molecular evolution of enzymes and metabolic networks. Research projects are interdisciplinary combining molecular genetics, biochemistry, and bioinfomatics, and utilize both naturally occurring and laboratory-engineered genetic variation. A current interest in my lab is identifying complex phenotypes that are modified by variation across a simple metabolic network in the model species Drosophila melanogaster. Other projects are quantifying the connection between transcriptome and proteome. Future projects will investigate the evolution of a neurally-expressed vertebrate gene family and the evolution of metabolic networks in simple microbial communities.

A minimum of one MSc and one PhD position are available to start September 2010. Successful applicants will be expected to develop research projects of their own, while building on current projects in the lab, especially targeting novel phenotypes and functional variation across species and life stages.

Recently, Laurentian University has had one of the fastest growing research programs in Canada. Research at LU includes an active group of evolutionary biologists, geneticists, and biochemists. Student interactions and collaborations across the LU Departments of Chemistry & Biochemistry, Forensic Sciences, and Biology will be encouraged.

Supported for the Merritt lab comes from the National Science and Engineering Research Council, The Canadian Foundation for Innovation and the Canada Research Chairs program.

For more information, contact Dr. Thomas Merritt at tmerritt@laurentian.ca or visit the Merritt Lab web site (http://web.mac.com/tjsmerritt)

Thomas Merritt, PhD Assistant Professor Department of Chemistry and Biochemistry Laurentian University 935 Ramsey Lake Road Sudbury, Ontario P3E 2C6 Canada e-mail: tmerritt@laurentian.ca phone:705-675-1151 ext. 2189

tmerritt@laurentian.ca tmerritt@laurentian.ca

---

## ManchesterU GeneticVariation

Fully funded PhD studentship starting October 2010

FUNDING AVAILABLE FOR ALL EU STUDENTS

The effects of genetic variation in the social environment on behavioural and life history traits

Supervisors: Dr Reinmar Hager and Dr Richard Preziosi

The social environment provided by family or group members has been shown to be highly influential for adult phenotypes and variation in individual fitness, particularly in early development. Recent research has highlighted that the social environment is determined by the genotypes of interacting individuals and can thus respond to selection and evolve, yet, the significance of this is poorly understood. The aim of the project is to investigate how important genetic variation in the social environment is in determining phenotypic variation in both behavioural and life history traits. What is the nature and the genetic basis of social interactions, how do these interactions affect complex traits such as parental behaviour or sexually selected traits and how do they differ across taxa and why? The project will address these unresolved issues using experimental work in model (mice) and non-model organisms (insects e.g. cockroaches and earwigs) combining behavioural, genetical and statistical analyses. There is the opportunity to develop own research projects in conjunction with ongoing research in the tropics and to contribute to teaching on field courses.

Further Information This studentship is open to all nationalities although no funding is available to cover the higher tuition fees for non-EU applicants.

* NB A living expenses stipend is available also for non-UK students as long as they are from the EU. *

Applicants should have an excellent undergraduate record and ideally some research experience. Further information can be obtained by contacting Reinmar Hager reinmar.hager@manchester.ac.uk

How to Apply Applications must be submitted online and accompanied by a number of supporting documents by 5 January 2010: http://www.ls.manchester.ac.uk/-postgraduate/ukoreu/research/apply/ AND send an email to openday.lifesciences@manchester.ac.uk expressing your interest in attending the external admissions day on 7 January 2010 if possible.

Reinmar Hager <reinmar.hager@cantab.net>

---

## MartinLutherU 2 HostParasiteEvolution

Two PhD Positions in Host-Parasite Evolution at the Martin-Luther University Halle/Wittenberg, Germany:

The Molecular Ecology Work Group at the Martin-Luther University Halle/Wittenberg (http://www.mol-ecol.uni-halle.de) is offering two PhD positions in the EU funded project BeeDoc (pending approval by the European Commission). The successful candidates are expected to conduct research in the field of host-parasite evolution with the honeybee Apis mellifera and two of its parasites (Varroa and Nosema) as model system, applying molecular tools. The positions are for three years and available from the 01.03.2010; salary is according to 0.5 TVL 13 (Ost). Job requirements include: - Master in Biology or a related field - Experience in the field of evolution of host-parasite systems - Experience in molecular biological methods (e.g. Real Time PCR, RNAi) - Experience in bee pathology and genetics - Fluent English - Ability to work with living honeybees To apply please sent your CV, motivation letter and names (email) of two references to: Prof. Robin Moritz, Martin-Luther-Universität Halle/Wittenberg, Institut für Biologie, Molekulare Ökologie, Hoher Weg 4, 06099 Halle (Saale) or in electronic form via email: kraus@zoologie.uni-halle.de Application deadline is 30.12.2009

kraus@zoologie.uni-halle.de kraus@zoologie.uni-halle.de

## MaxPlanck ComputationalBiology

Dear colleague,

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

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

The PhD program is open for international students holding a Master (or equivalent) degree in bioinformatics, computer science, physics, mathematics, or biology.

The closing date for applications is February 21, 2010.

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

http://www.imprs-cbsc.mpg.de/download/-poster2010.pdf For further details and the application procedure, please visit

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

the IMPRS-CBSC team

International Max Planck Research School for Computational Biology and Scientific Computing (IMPRS-CBSC)

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

## MichiganStateU ArthropodEvolution

The Department of Entomology at Michigan State University has one graduate research assistantship available at the Ph.D. level starting Fall 2010. Our lab works on ecological, behavioral and evolutionary questions related to arthropod pests of vegetables. The current project focuses on population genetics of Colorado potato beetles. This project is part of an exciting national and international collaboration that will provide the student with an excellent opportunity to build a valuable professional network.

Prior training in statistics, population genetics, and molecular evolution and working knowledge of bioinformatics are highly desirable. Michigan State University offers a diverse and nurturing graduate training environment. Position comes with an annual stipend of $22,000, full tuition waiver, and benefits package including health insurance.

If you are interested in the position, please contact me for more information. To apply, send a letter of interest, unofficial transcripts, GRE scores, CV and contact information for three references to: Dr. Zsofia Szendrei at szendrei@msu.edu. Application deadline is Feb. 1, 2010. Additional information about research in our lab can be found at http://vegetable.ent.msu.edu/, and information about the entomology department can be found at http://www.ent.msu.edu/ Zsofia Szendrei Assistant Professor Department of Entomology Michigan State University 439 Natural Science Bldg. East Lansing, MI 48824 szendrei@msu.edu 517-974-8610 http://-/vegetable.ent.msu.edu/ zsofia.szendrei@gmail.com

## MississippiStateU ComparativePhylogeography

Mississippi_State_Comparative_Phylogeography

I am seeking an independently-minded PhD student starting in Fall, 2010 to help develop a collaborative project on Comparative Phylogeography in the Southeastern United States. The Southeastern United States harbors a high degree of faunal diversity which, in most cases, has not been examined in detail at the genetic level. The focus of the lab is primarily on birds, but students interested in other vertebrate and invertebrate taxa are also encouraged to inquire. Taxa in the study currently include birds, freshwater mussels, crayfish and fish, but we anticipate expanding to other groups. The project will involve field collection with collaborators at the Center for Bottomland Hardwoods Research, Oxford, MS and extensive lab work here at Mississippi State University involving both traditional genetic markers (mitochondrial and nuclear intron) and the development of anonymous nuclear markers. In Fall, 2010, the Department of Biological Sciences will be moving in to the newly renovated Harned Hall which will feature start-of-the-art laboratory space. Mississippi State University has a number of world-class research institutes including the Center for Computational Sciences (http://www.ccs.msstate.edu/) the GeoSystems Research Institute (http://www.gri.msstate.edu/), among many others under the umbrella of the High Performance Computing Collaboratory http://www.hpc.msstate.edu/ (See also http://www.research.msstate.edu/centers/). The Ecology and Evolutionary Biology faculty in the Department of Biological Sciences is a diverse group that values and promotes highly motivated students. Graduate Program information in the Department of Biological Sciences can be found at: http://www.msstate.edu/dept/biosciences/prospectiveStudents.htm. For more information about the research, the department and the University, please contact me directly. Diana C. Outlaw, Ph.D. Assistant Professor Department of Biological Sciences Mississippi State University Mississippi State, MS 39762 662 325-4803 ph doutlaw@biology.msstate.edu http://www.biology.msstate.edu/outlaw/ Diana C. Outlaw, Ph.D.

Assistant Professor Department of Biological Sciences Mississippi State University Lab: Harned 107; Office: Harned 107A http://www.biology.msstate.edu/outlaw/ 662 325-4803 ph doutlaw@biology.msstate.edu

Diana Cummings Outlaw <DOutlaw@biology.msstate.edu>

---

## NewZealand HybridEvolution

PhD position: Untangling complex evolution

Hybridisation is an important evolutionary process that can play a role in adaptive radiations where species rapidly colonise new niches and respond to new environments. Hybrids inherit genetic material from two parent species, making them hard to detect when studying single genes. Fortunately, innovations in DNA sequencing now make it affordable to study many genes simultaneously. However, hybridisation is not easy to distinguish from other biological processes; current methods assume that evolutionary relationships inferred for different genes are error-free; all conflict is attributed to hybridisation. In reality conflict is often caused by estimation errors, the random nature of inheritance within populations, and missing data. This Marsden funded project will create the statistical methods and software necessary for evolutionary biologists to understand how prevalent hybridisation has been in shaping the New Zealand biota.

We are seeking to appoint two PhD students. The sorts of skills we need are very broad - knowledge of mathematics and/or statistics, algorithm development and computer programming, and genetics and evolution. We realise that it may be unrealistic to expect all these skills in any one candidate so we are seeking two people with complementary skill sets.

The positions will be based within the Allan Wilson Centre at Massey University, Palmerston North, New Zealand. (You must also be willing to spend some time working at the University of Tasmania during the PhD programme.) http://www.allanwilsoncentre.ac.nz/ http://www.massey.ac.nz/ The stipend will be $25,000 NZD per annum and all student fees will also be covered.

To apply, or for more information, please contact Barbara Holland and/or Lara Shepherd. b.r.holland@massey.ac.nz l.d.shepherd@massey.ac.nz

Applications should include a cover letter, a CV which includes evidence of your academic record, and contact details for two referees. Applications close 31st January 2010.

brhollan@googlemail.com

---

## NewZealand MothSexualSelection

PhD Scholarship available to investigate sexual conflict in the New Zealand moth genus Izatha

We are seeking a motivated and enthusiastic candidate to fill a fully funded PhD position in the School of Biological Sciences at the University of Auckland, New Zealand. The project will combine experimental and comparative approaches to assess the role of sexual conflict in driving the evolution of complex genitalia in the moth genus: Izatha. This genus is endemic to New Zealand and possesses extraordinarily complex and diverse male genitalia. Most intriguingly, males of some species possess detachable spines (cornuti), which are left embedded in the female reproductive tract after mating. The successful candidate should have research experience, a strong academic record and a keen interest in behavioural ecology, evolutionary biology and/or entomology. They should also be meticulous, with an attention to detail and an ability to work at a fine scale. Experience, or a willingness to learn molecular phylogenetic skills and imaging techniques such as electron microscopy and x-ray tomography, will be an advantage, and applicants will be expected to demonstrate evidence of proficiency in English (for those applicants whose first language is not English). The successful candidate will be under the supervision of Dr Greg Holwell (The University of Auckland), Dr Thomas Buckley (Landcare Research) and Dr Robert Hoare (Landcare Research) and will have access to a range of world-class facilities at both the University of Auckland and Landcare Research. This position is funded through the Marsden Fund of the Royal Society of New Zealand, and the successful applicant is expected to begin in early 2010.

Interested candidates should contact Dr Greg Holwell ( g.holwell@auckland.ac.nz ) to express their interest and provide some details as to their suitability.

Dr Greg Holwell School of Biological Sciences University of Auckland Private Bag 92019 Auckland 1142 New Zealand Phone: +64 (0)9 373-7599 extn 83652 http://www.sbs.auckland.ac.nz/uoa/science/about/departments/sbs/research/ecolevol/dr-greg-holwell/dr-greg-holwell_home.cfm Gregory Holwell <g.holwell@auckland.ac.nz>

---

## NorthernArizonaU EvolutionaryBiol

*Northern Arizona University IGERT Program in Integrative Bioscience: Genes to Environment * Northern Arizona Univ. IGERT PhD positions: Genes to Environment

NAU invites applications for up to 4 PhD student traineeships for students admitted for the 2010/11 academic year. The purpose of this program is to provide students with instruction and research training focused on linkages between molecular genetics and ecosystem phenomena, with emphasis on multi-scale modeling approaches. Applicants will work with a mentor from the Biology or Forestry PhD programs at NAU. This program is funded by the National Science Foundation.

Program graduates will have the skills to address fundamental and applied questions of genetic influences on ecosystem function and response to environmental change. Unique aspects of this program include: 1) multidisciplinary research with a special emphasis on working across scales, 2) inclusion of molecular methodology and applied statistics coursework in all programs of study, 3) seminar courses covering scientific ethics, statistics and modeling, and student research, featuring guest speakers from integrative disciplines, 4)unique internships with community colleges, federal agencies, and Native American high schools to broaden the graduate experience and enhance connections between the research and the broader community. The NAU Integrative Bioscience PhD program will prepare innovative and creative scientists to become leaders in research, science outreach and communication, and environmental problem solving.

Traineeship packages will include $30,000/year stipend support for two years, with continued support as teaching or research assistants at more traditional stipend levels. Applicants must concurrently apply to doctoral programs in the Department of Biological Sciences http://www6.nau.edu/biology/ or the School of Forestry http://www.for.nau.edu/cms/ at Northern Arizona University. Application deadlines for the 2010/11 academic year will be February 1, 2010. Applications will consist of 1) standard applications required for Biology or Forestry graduate programs (including three letters of reference) and 2) a 2 page essay on how this program would address your research, educational, and career goals.

Please go to http://www.mpcer.nau.edu/igert/ or contact us by email or phone for more information: Dr. Catherine Gehring: Catherine.Gehring@nau.edu, (928)523-9158 or Dr. Amy Whipple: Amy.Whipple@nau.edu, (928)523-8727

Amy.Whipple@nau.edu Amy.Whipple@nau.edu

## NorwegianUSciTech PopulationGenetics

A PhD position in population genetics is available at the Department of Biology, Norwegian University of Science and Technology (NTNU) in Trondheim.

The candidate will be working with population genetic questions in landrace crops, in particular barley (Hordeum vulgare). He or she will be studying the contribution of adaptive and non-adaptive processes to the genetic composition of 19th century crops, to understand the roles of introduction and trading routes and selection for desired traits prior to modern plant improvement. The project aims to answer questions regarding agricultural history, how modern plant improvement has affected crop species and the identification of selected alleles. The research project will be carried out in collaboration with the Swedish Museum of cultural history and will involve genetic characterisation of historic seed samples from the Museum's collections.

The position requires a Master of science (MSc/Cand scient) degree or similar within biology. Experience in molecular genetic laboratory techniques as well as a solid understanding of population and evolutionary genetics will be helpful to the successful candidate.

For further information contact Jenny Hagenblad (Jenny.Hagenblad@ebc.uu.se) or Matti Leino (matti.leino@nordiskamuseet.se) or visit: http://innsida.ntnu.no/ nettopp_lesmer.php?kategori=nyheter&dokidK04fd78a25c41.31764142

Jenny Hagenblad, PhD Assistant Professor Uppsala University EBC, Plant Ecology Norbyv 18D SE-752 36 Uppsala Sweden

Tel: (+46)(0)18 471 2863 Email: Jenny.Hagenblad@ebc.uu.se

http://www.anst.uu.se/jenha377/Jenny/
jenny.hagenblad@ebc.uu.se jenny.hagenblad@ebc.uu.se

## OklahomaStateUniv milkweed phylogeny genomics

Mark Fishbein (Oklahoma State University, Department of Botany) seeks a graduate student (PhD or MS) to apply genomic approaches to the phylogeny of American milkweeds (Asclepias, Apocynaceae). The student will participate in an NSF-funded collaborative project with Dr. Aaron Liston and Dr. Richard Cronn at Oregon State University.

Milkweeds have served as a important model system for studies of the evolution of pollination systems and plant defenses against herbivory. Continued phylogenetic study is required to fully resolve species level relationships, to further test and expand upon theories of coevolution of plants, pollinators, and herbivores, and to develop milkweeds as a model system for the comparative study of genomes.

Graduate research in the Fishbein lab may include working with the complete genome of Asclepias syriaca (common milkweed) and chloroplast genomes from ca. 150 species of Asclepias and relatives. Research activities can involve field work in the US, Mexico, and/or South America, next-generation DNA sequencing, and phylogenetic and phylogenomic anlalysis. Opportunities exist for PhD students to develop independent projects making use of the considerable data generated for this research.

Students will be supported by a combination of research and teaching assistantships. Information about the Botany department can be found at http://botany.okstate.edu and the Fishbein lab at http://fishbein.okstate.edu

To be eligible for stipend enhancements for Fall 2010 admission, applications must be submitted by Feb. 1, 2010; however, early inquiries are encouraged. Inquiries should be directed to mark.fishbein@okstate.edu

mark.fishbein@okstate.edu mark.fishbein@okstate.edu

## OxfordU BacterialSocialEvolution

UOXFORD:BACTERIAL SOCIAL EVOLUTION

THERAPY

The Griffin and Brown labs (Department of Zoology, University of Oxford, UK) are seeking an outstanding candidate to put forward for a Christopher Welch scholarship to pursue a PhD on the evolutionary biology of bacterial infections. Project details are below.

Interested candidates should contact Ashleigh Griffin ( ashleigh.griffin@zoo.ox.ac.uk) or Sam Brown (sam.brown@zoo.ox.ac.uk) ASAP, and no later than 15 Jan.

****Developing a novel approach to antimicrobial treatments: social dynamics in bacteria and the Trojan Horse*** * We aim to exploit our understanding of bacterial social dynamics, for clinical applications. Specifically, we propose to genetically engineer competitively dominant strains of bacteria to drive medically beneficial alleles, such as antibiotic sensitivity, into wildtype populations.

Background: This interdisciplinary project (theory, experimental evolution, molecular microbiology) builds on a series of experiments showing that behaviours important for bacterial virulence (e.g, production of extracellular products) are cooperative (Griffin et al. 2004, Nature; Diggle et al. 2007, Nature). A cooperative behaviour is one where the cost of performance is borne by a single individual, while the benefit is shared. We developed the bacteria Pseudomonas aeruginosa as a model system for testing predictions about when populations of cooperative individuals can be invaded by non-cooperative cheats. We found that the presence of cheat strains has consequences for virulence in a mouse model: in mixed cooperator-cheat infections, the mortality rate was reduced by 50%, relative to cooperator-only infection (Rumbaugh et al. 2009, Current Biology). This work has led to filing of a patent.

Outline: The student will develop a method of exploiting the invasive ability of cheat strains to drive medically beneficial alleles, such as antibiotic sensitivity, into wildtype populations (the cheat is therefore the Trojan Horse). We have produced theoretical models to demonstrate that if the cost of expressing a Trojan gene could be offset by the reduction of costs conferred by being a social cheat, then a Trojan cheat could outcompete wildtype populations (Brown et al. 2009 Phil Trans R Soc). We have already shown in vivo that the invasion of a cheat will lead to immediate reductions in virulence but using Trojan cheats we also generate the opportunity for subsequent control using antibiotics, for example. By reshaping the antibiotic resistance profile of the infective population, this strategy offers a novel response to multiply resistant infections.

Collaborators: Ashleigh Griffin, Sam Brown (Dept Zoology, Oxford) and Steve Diggle (Molecular Medical Sciences, Nottingham)

Sam Brown <sam.brown@zoo.ox.ac.uk>

---

## RoyalBelgianInstNatSci AncientGenomes

A two year MSc position (with possible extension for two years) is vacant at the Royal Belgian Institute of Natural Sciences (http://www.naturalsciences.be/).

The successful candidate will be encouraged to initiate a PhD. The major challenge in the project “Genomic Studies on Natural History Collections: A feasibility study” will be the application and development of next generation sequencing approaches for phylogenomic and genomic research on Natural History Collections. This project will be carried out in close collaboration with the Genomic Core Facility of the Katholieke Universiteit Leuven (http://www.kuleuven.be/).

Project summary:

Recently developed high-throughput gene sequencing methods offer exciting opportunities for genomic research on zoological museum specimens, as this technology is not hampered by the degraded state of the obtained DNA. This project adopts next generation DNA sequencing methods and adapts them to be used on a selected specimen/tissue RBINS/RMCA collection. This pilot study uses the Muridae as a test case to illustrate the potential use/limitations of zoological museum specimens for future comparative genomic studies. The implementation of these novel genomic technologies will add a new dimension to the future scientific valorization of NHCs way beyond the scope of this project.

We offer a two year MSc position (2 years, with a possible extension of 2 years):

Successful candidates will have the opportunity to start a PhD and will manage/conduct laboratory assays designed to develop the protocol that allows the amplification and sequencing of multiple genetic markers from museum specimens by NGS technology. Candidates must have an MSc and experience in genomics and/or phylogenetics, proficiency in both written and spoken English, excellent social skills, ability to work independently and high motivation will be assets.

The position will start in February/March 2010 and the project will run for 2 years, with a possible extension of 2 years.

Applications should include a covering letter motivating your interest, full C.V. and names of three referees.

Only complete applications will be considered and should be sent (preferably in one single file) by e-mail to: jeroen.vanhoudt@bio.kuleuven.be.

Erik VERHEYEN

Vertebrate department Royal Belgian Institute of Natural Sciences Vautierstaat 29, 1000 Brussels, Belgium

phone +32 2 627 42 86 - fax +32 2 627 41 41 - cellular +32 0485 08 23 62 E-mail (office): erik.verheyen@naturalsciences.be (home): erik.verheyen@inbox.com

URL: http://www.naturalsciences.be/institute/structure/molelabo/vertebrates Erik Verheyen <Erik.Verheyen@naturalsciences.be>

## TexasStateU EvolutionaryEcol

Texas State University Summer Predoctoral Fellowship Program in Evolutionary Ecology

Texas State University[1]s Graduate College is pleased to announce that we are accepting applications for the 2010 Summer Predoctoral Fellowship Program. An overview is provided below and the complete announcement and application may be viewed at http://www.gradcollege.txstate.edu/Predoc_Fellow.html < http://www.gradcollege.txstate.edu/Predoc_Fellow.html > .

The predoctoral fellowship program brings doctoral candidates from other institutions that have completed their course work and are in the process of writing their dissertations (ABD), to spend June and July on the Texas State campus working with faculty and students in their field. Participants may also be considered as potential candidates for future faculty positions as appropriate. The program is only available to doctoral students who are U.S. citizens and permanent residents.

Interested parties should visit The Department of Biology[1]s website ((http://www.bio.txstate.edu/ < http://www.bio.txstate.edu/ > ) to examine potential faculty advisors. Currently, we offer a strong environment in evolutionary ecology or ecology. Potential faculty includes: Caitlin Gabor (Behavioral ecologist), Noland Martin (Plant population genetics), and Chris Nice (Speciation in insects and phylogeography). Jim Ott (Insect-plant interactions and ecological genetics), Susan Schwinning (Plant ecologist), Joe Veech (Wildlife ecologist).

The graduate student must secure a commitment from a Texas State faculty member to serve as their mentor for the summer program prior to submitting an application. Please start by contacting the faculty member you are interested in working with and then proceeding from there.

Caitlin R. Gabor, Ph. D. Associate Professor Texas State University Department of Biology, Supple Building Room 384 San Marcos, TX 78666-4615 Work: (512) 245-3387; Fax: (512) 245-8713 E-mail: gabor@txstate.edu

http://www.bio.txstate.edu/~gabor/gabor.htm "Gabor, Caitlin" <Gabor@txstate.edu>

## TuftsU EvolutionaryGenetics

Graduate Student Positions In Evolutionary Genetics

I. Speciation Genomics in the European Corn Borer
II. Genetics and Evolution of Copy-Number Polymorphism

PhD positions in evolutionary genetics are available in the laboratory of Erik Dopman in the Department of Biology at Tufts University. Efforts in the lab are directed towards understanding speciation and mutation. Our work on speciation addresses the evolution of phenotypic differences between diverging populations, with an emphasis on so- called "speciation genes" that contribute to reproductive barriers. Our work on mutation investigates large-scale changes in the number of chromosome segments or gene copies, which are commonly known as copy- number polymorphisms (CNPs). Please see http://ase.tufts.edu/biology/labs/dopman/default.asp for a detailed description of the lab and its activities.

We seek creative and motivated graduate students to work on either of the labs two main research projects, but the potential for developing new research directions is high. A trusted colleague once said that successful PhD students have ability to work with others, and a sense of humor, both of which are needed to make science fun and worthwhile. In addition to these attributes, a strong undergraduate background in evolutionary biology is required, as is some prior research experience. Relevant and highly desirable experience includes application of molecular genetic techniques (e.g., PCR, cloning, sequencing, microarrays), or analysis of gene or genome data (e.g., DNA sequence, transcript abundance).

Contemporary biology is built on understanding life at the molecular, cellular, organismal, population and community levels. The Department of Biology at Tufts is dedicated to providing a unified and comprehensive view of biological processes. Evidence for excellence in research at Tufts can be found in Carnegie Foundations ranking Tufts as a /Research Extensive institution V its highest classification for degree-granting colleges and universities. The Department of Biology is located on Tufts main campus in Medford, MA. With two additional Tufts campuses (in Boston, MA, and Grafton, MA), other research universities (e.g., Harvard, MIT), and the vibrant city of Boston all within reach, Medford and Tufts are ideal places to live and work. See http://ase.tufts.edu/biology/ for more information on the Biology Department.

Interested individuals should immediately contact Erik Dopman (erik.dopman@tufts.edu ) and provide in PDF format the following documents: (1) a 1-2 page cover letter that includes a statement of research interests, and summaries of educational background and prior research experience, and (2) a CV that includes GRE scores and the names and contact information of three references. Applications to the graduate program are due on 15 January, with Department review occurring shortly thereafter. See http://ase.tufts.edu/biology/-graduate/index.asp for more information on the graduate program in Biology at Tufts.

Erik Dopman <erik.dopman@tufts.edu>

---

## UBath PlantEvolutionaryGenetics

The Kover Lab (University of Bath- UK) have opportunities for students to pursue a phD in plant evolutionary genetics.

Projects can include: the molecular basis of adaptation using experimental evolution, molecular diversity and conservation, or using MAGIC lines to investigate the genetic basis of complex traits (such as flowering time, seed size, plasticity, etc). One position is available for UK students only, while the second is open for highly qualified international students (with support from the Gatsby foundation).

Interested candidates please contact Paula Kover through email at: p.x.kover@bath.ac.uk.

“Paula X. Kover” <p.x.kover@bath.ac.uk>

---

## UCincinnati EvolutionaryBiol

Fellowship & Stipend Opportunities for Graduate Studies in Biological Sciences at the University of Cincinnati.

The Department’s research and graduate program is diverse, with several laboratories focusing on Ecology, Evolution, Behavior, Neuroethology and Organismal Biology. The Department awards MS and PhD degrees and has many faculty members with integrative research approaches that span a wide range of biological scales. Our graduate program is geared towards preparing graduate students for a broad array of careers in research, health professions, industry, teaching, and stewardship agencies.

For general information on the graduate program please visit http://www.artsci.uc.edu/collegedepts/biology/-grad/application_info.aspx Most of our students are supported financially by research or teaching assistantships and tuition fellowships. In addition the following special fellowships/awards are available: 1) Graduate Research Fellowship for Outstanding Incoming PhD Students. The Department of Biological Sciences at the University of Cincinnati, offers a fellowship for outstanding incoming PhD students. In addition to a one year fellowship ($ 20,162) a $3000 Research Grant will be awarded to successful candidates. All applicants to the PhD program automatically compete for this fellowship. Underrepresented minority students are especially encouraged to apply. The deadline is February 1st. 2) Yates Scholars Program. The goal of this program is to enrich the educational environment for all graduate students by supporting the recruitment and retention of underrepresented ethnic minorities who are U.S. citizens or permanent residents with high potential for academic success. The Graduate School provides $12,000 to each selected Yates awardee. Potentially eligible applicants should consult with their perspective advisors to assure nomination to this program. 3) Choose Ohio first Scholarships. The goal of this scholarship is to increase enrollment of Ohio residents as graduate students in the STEMM disciplines. Scholarships provide partial support for entering MS or PhD students for up to 4 years ($4500/student/year). All Ohio residents that apply to our program automatically compete for this fellowship. 4) Research and Travel Grants. Several research and travel grants are available on a competitive basis to all our graduate students.

Elke Buschbeck Associate Professor Director of Graduate Admissions Biological Sciences University of Cincinnati Cincinnati, OH 45221-0006

Elke Buschbeck <buschbek@ucmail.uc.edu>

## UFlorida SeasonalAdaptation

The Hahn lab at the University of Florida is looking to recruit a new MS or PhD student to join our group in the fall of 2010. We are a small but fun group interested broadly in how genetic and physiological variation underlie organismal performance, and ultimately fitness (http://danhahn.ifas.ufl.edu). Our work is integrative and includes numerous tools and perspectives from next-generation population genetics and functional genomics to more traditional whole organism physiology and performance. Current projects in the lab largely focus on one of three main areas:

1) Mechanisms of life history timing and adaptive diversification. Over the last 200 years native flies that fed on hawthorn fruits shifted onto a newly introduced host, domesticated apples, and divergence in the fruiting times of these two host races has driven temporal isolation and genetic differentiation between the two host races, making the Rhagoletis pomonella system a test-book case of sympatric speciation and adaptive ecological divergence in action. In collaboration with Jeff Feder's group at the University of Notre Dame (http://biology.nd.edu/JeffreyFeder.shtml) we are studying the genetic architecture and physiological mechanisms of diapause (hibernation) timing and overwintering energetics in the host races of the apple maggot.

2) Mechanisms of seasonal and reproductive phenotypic plasticity. The world is always changing and many organisms deal with these changes with plastic phenotypes. We study the underlying mechanisms and consequences of seasonal phenotypic plasticity in insect diapause (overwinter hibernation) and reproductive timing. Diapause is a great escape mechanism that insect use to mitigate the stresses of winter and to time their life histories to exploit favorable periods, but diapause also has costs. Post-diapause insects often suffer lower survival and fecundity than non-diapause individuals of the same species. How do they deal with these costs? For example, many diapause-destined insects increase their fat reserves prior to overwintering, but how do they do it (e.g., what physiological and nutritional mechanisms are involved in increased fattening?) and what are the consequences of increased fat stores (e.g., do big fat animals survive better or reproduce more after winter than skinny ones?). Moths, butterflies, and flies are our current favorite model organisms for this work and John Hatle at the University of North Florida is a key collaborator (http://www.unf.edu/~jhatle/).

3) Stress and sex. Too hot, too cold, too dry...life is stressful, particularly for small ectotherms like insects. We are currently investigating the role of both natural and extreme environmental stress on the physiology and sexual performance of males in the Caribbean fruit fly, a lekking species with substantial male-male competition. The Caribbean fruit fly is a good model for exploring the role of male condition on sexual selection and it is a model for invasive fruit fly species, like the devastating Mediterranean fruit fly, making this project an excellent opportunity for both basic evolutionary ecology and potential applications to the Sterile Insect Technique as an ecologically-friendly control method in an economically important insect pest.

Our lab is located in the Department of Entomology and Nematology at the University of Florida. We are the largest department of our kind in the United States with approximately 60 faculty and well over 100 graduate students. The size of our department combined with the dozens of insect biologists housed next door at the USDA Center for Medical and Veterinary Entomology and colleagues in departments across campus (e.g., Biology, Genetics, and the UF Med School) provide the enormous intellectual and physical resources that make UF an excellent place to study evolutionary ecology and integrative physiology. In addition to the work mentioned above, students may develop their own projects if it fits into our larger conceptual framework.

Interested students should contact Dan Hahn (dahahn@ufl.edu<mailto:dahahn@ufl.edu>) as soon as possible because while applications are due later in the spring, departmental assistantships are typically allocated to the top students in January. Please include a current copy of your CV including course history and grades, GRE scores, and research experience. Dan and members of the lab will be at the Entomology meetings in Indianapolis from December 13-16 and at the Society for Integrative and Comparative Biology meetings in Seattle January 3-7, if you want to come by and meet us.

Daniel A. Hahn Assistant Professor Department of Entomology and Nematology The University of Florida P.O. Box 110620 Gainesville, FL 32611-0620 Ph: 352-273-3968 Fax: 352-392-0190 dahahn@ufl.edu

— / —

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

## UGeorgia EvolutionaryBiol

The Department of Genetics at the University of Georgia invites prospective students to apply to our graduate program. For full consideration, applications are due by January 5, 2010; further details are available at http://www.genetics.uga.edu/graduate_application.html . Our department provides a unique training opportunity, with researchers working across the diversity of life at scales ranging from molecular and genomic processes up to the evolution of populations and species. Students and faculty in our department also have close working relationships with researchers throughout the biological sciences at the University of Georgia, including the Odum School of Ecology; the Warnell School of Forestry and Natural Resources; and many other Departments such as Biochemistry and Plant Biology. The Department also includes faculty in a number of integrative centers and working groups representing fields such as development and global disease.

Students are guaranteed support through teaching or research assistantships, merit fellowships, and our NIH-supported training grant in Genetics. For further information please contact our Director of Graduate Studies at gencoord@uga.edu or see our departmental website (http://www.genetics.uga.edu).

cheers,

John Wares

John Wares <jpwares@uga.edu>

## UGeorgia EvolutionInvasiveSpecies

PHD STUDENT FELLOWSHIPS ECOLOGICAL GENETICS OF INVASIVE SPECIES

UNIVERSITY OF GEORGIA

Graduate Student Fellowships are available starting in Fall 2010 to study the ecological genetics of invasive species, including plant pathogens. Fellowships offer a highly competitive stipend as well as funds for research and travel.

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

Students can work with any senior personnel on the UGA-PIRE program (see list below and at http://www.genetics.uga.edu/pire/people_senior_US.html). Students should contact a prospective major adviser directly and apply through that department. For additional information concerning the application process, interested students should refer to our web site (http://www.genetics.uga.edu/pire) and contact Dr. Rodney Mauricio, UGA-PIRE Program Director, via email (mauricio@uga.edu). General inquiries can be directed at Dr. Mauricio as well.

Current List of Senior Personnel on the UGA PIRE:

Michael Arnold (Department of Genetics, University of Georgia) Jeff Bennetzen (Department of Genetics, University of Georgia) John Burke (Department of Plant Biology, University of Georgia) Jeb Byers (Odum School of Ecology, University of Georgia) Donald Champagne (Department of Entomology, University of Georgia) Shu-Mei Chang (Department of Plant Biology, University of Georgia) John Drake (Odum School of Ecology, University of Georgia) Travis Glenn (School of Public Health, University of Georgia) James

Hamrick (Department of Plant Biology, University of Georgia) Paul Hendrix (Professor of Ecology, University of Georgia) John Maerz (Department of Forestry and Natural Resources, University of Georgia) Rodney Mauricio (Department of Genetics, University of Georgia) Richard Meagher (Department of Genetics, University of Georgia) Andrew Paterson (Departments of Crop and Soil Sciences, Plant Biology, and Genetics, University of Georgia) Harald Scherm (Department of Plant Pathology, University of Georgia) William Vencill (Department of Crop and Soil Sciences, University of Georgia) Ronald Walcott (Department of Plant Pathology, University of Georgia) John Wares (Assistant Professor of Genetics, University of Georgia)

_

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

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

## UGeorgia PlantEvolution

The Department of Plant Biology at the University of Georgia in Athens, GA seeks highly motivated Ph.D. students to join our graduate program in evolutionary biology. Ongoing research in the Department investigates fundamental questions in organismal and molecular evolution using a range of approaches including population and quantitative genetics, molecular systematics, and comparative genomics.

Graduate fellowships, assistantships, research support and travel grants are available for qualified candidates. Applications are due on December 15th. More information can be found on the web at:

http://www.plantbio.uga.edu/graduate.html Plant Biology-affiliated faculty with evolutionary interests include:

Mike Arnold (http://www.genetics.uga.edu/people_bio_arnold_m.html) Jeff Bennetzen (http://www.genetics.uga.edu/jlblab) John Burke (http://www.theburkelab.org/) Shu-Mei Chang (http://www.plantbio.uga.edu/~chang/chang.html) Katrien Devos (http://www.cropsoil.uga.edu/personnel/faculty/devos.html) Lisa Donovan (http://www.plantbio.uga.edu/~donovan/donovan.html) Mark Farmer (http://www.uga.edu/cellbio/farmer.html) Jim Hamrick (http://www.plantbio.uga.edu/~hamrick/hamrick.html) Jim Leebens-Mack (http://www.plantbio.uga.edu/~jleebensmack/ JLMmain.html) Russell Malmberg (http://www.plantbio.uga.edu/~russell/index.html) Rodney Mauricio (http://www.genetics.uga.edu/mauriciolab) Andy Paterson (http://www.plantgenome.uga.edu/) Xiaoyu Zhang (http://www.plantbio.uga.edu/~xiaoyu/) Wendy Zomlefer (http://www.plantbio.uga.edu/~wendyz/wendyz.html)

Jim Leebens-Mack 4505 Miller Plant Scinces Department of Plant Biology University of Georgia Athens, GA 30602-7271

Phone: 706-583-5573 Fax: 706-542-1805 email: jleebensmack@plantbio.uga.edu url: http://www.plantbio.uga.edu/~jleebensmack/JLMmain.html jleebensmack@plantbio.uga.edu jleebensmack@plantbio.uga.edu

## UGuelph 2 AntPhylogenetics

MSc positions in ant phylogenetic diversity and biogeographic linkages across the Mozambique Channel M. Alex Smith, Department of Integrative Biology, Biodiversity Institute, University of Guelph

Positions for MSc students are available in my lab to work on assessing the phylogenetic diversity and biogeographic linkages for ant species across the Mozambique Channel.

This research project will generate hypotheses of biotic diversification and biogeography using ants across the southwest Indian Ocean islands (SWIO) islands, and assess their relationships to the fauna of mainland Africa using mitochondrial and nuclear gene sequence data. This project targets six genera from three ant subfamilies, Cerapachyinae, Myrmicinae and Pseudomyrmecinae, for detailed species-level revisions and phylogenetic analyses. These taxa are groups of considerable ecological and phylogenetic interest.

Some question to be asked include: (1) How many colonization events occurred from Africa to the SWIO islands for each genus? (2) What was the role, if any, of the Comoros islands as stepping stones? (3) Was there any backward movement from Madagascar to the African mainland or to other SWIO islands? (4) What was the timeframe for these dispersal events? (5) Are patterns of ant community change with elevation comparable to an ongoing project in Costa Rica?

The specimens collected from the Seychelles, Tanzania and Mozambique will be permanently archived in the California Academy of Sciences where technicians will ensure that the ant specimens are shipped to Guelph. Here it will be the responsibility of the student filling this position to extract DNA, sequence and manage and analyse the data for these specimens in the BOLD datasystem (www.barcodinglife.org).

An undergraduate background with courses and/or research experience in evolution, genetics, ecology, and basic molecular techniques is preferred. Motivated students with a keen interest in understanding the phylogenetics and biogeography of this interesting group of organisms would be ideal.

This funded position will permit a student to take advantage of opportunities and research interests in the lab, but it is expected that the successful applicant will develop novel research hypotheses and approaches to testing these hypotheses. For more information, contact Dr. Alex Smith at salex@uoguelph.ca or visit the website (www.uoguelph.ca/~salex).

Interested students should submit a resume, unofficial transcript, a statement of research interests and arrange for three letters of reference to be sent by e-mail to: Dr. Alex Smith (salex@uoguelph.ca). Expected start date(s) will be May, 2010 and September, 2010. While all qualified candidates are encouraged to apply, Canadian citizens and permanent residents of Canada will be given priority.

Dr. M. Alex Smith Biodiversity Institute of Ontario Department of Integrative Biology University of Guelph

– M. Alex Smith PhD Assistant Professor Biodiversity Institute of Ontario & Integrative Biology University of Guelph 50 Stone Road East Guelph, Ontario, Canada N1G 2W1 phone - 519-824-4120 ex 52007 fax - 519-824-5703 www.biodiversity.ca www.barcodinglife.org www.uoguelph.ca/~salex/ salex@uoguelph.ca

---

## UGuelph EvolutionaryTheory

Evolutionary Theory/Computational Biology/Theoretical Evolutionary Physiology

There is an MSc or PhD position available in the broad area of evolutionary theory in my lab. Below I summarize current projects that I am working on and a student would be welcome to work on these or pursue their own line of research.

Both projects that I am currently working on seek to understand how multivariate traits evolve. In the first project, gene-genealogical approaches are used to model multivariate trait evolution. In the second project, biophysical principles are used to model a multivariate trait, and the evolution of the multivariate trait and its underlying physiology is subsequently modeled. This second project is currently focused on the multivariate trait associated with calcium signaling in animals.

Most processes in biology are part of a multivariate context. For instance, adaptation involves Hutchinson's idealized concept of the multivariate niche. Likewise, in applied problems such as agriculture, a challenge is to optimize multiple traits to maximize yield or sustainability. In medicine, problems such as the adverse effects of medication are not related to the target of the medication, but side-effects with are of a multivariate nature. The broad theme of research in my lab is to understand how evolution works in a multivariate context. Part of the research is of an abstract nature, while other parts are applied. With respect to applied components, calcium signaling is widely used in animals and is associated with health problems such as cancer and diseases of the heart.

For more information about my lab, my website is http://www.uoguelph.ca/ib/people/faculty/griswold.shtml . A student can start in January or September of 2010.

Contact information: Dr. Cortland Griswold Department of Integrative Biology University of Guelph 50 Stone Rd E Guelph, Ontario N1G 2W1 Canada

519-824-4120 ext. 56240

cgriswol@uoguelph.ca cgriswol@uoguelph.ca

---

## UHeidelberg PlantEvolution ChalconeSynthase

Evolution of the Chalcone synthase gene in cruciferous plants: Orthologues, Paraloques and Pseudogenes - gene duplication, neofunctionalization and silencing.

Project leader: Koch, Marcus A.

Application deadline from/to: 11/24/2009 - 01/31/2010

Start of PhD project (mm/dd/yyyy)*: 03/01/2010

Project description: The Brassicaceae are developing into the most important model group in plant science aside the grass family. This is not only because of the model organisms Arabidopsis thaliana and Brassica napus, but also the enormously increasing knowledge on all aspects of biology and evolution concerning this family The family is characterized by frequently occurring hybridization and poly-ploidization, which, as a consequence, is greatly affecting genome size and structure, but also any mode of speciation. Nonetheless, it is still unclear if the evolution of the Brassicaceae on the various taxonomic/temporal levels and of its evolutionary lineages is mostly or even best explained by multiple radiation events. A fact that can also account for the difficulties to resolve deep phylogenetic relationships within the family. In the overall project we are aiming to use the actually available knowledge and phylogenetic data and a phylogenetic backbone to address these principles questions of crucifer evolution by adding genome size and cytogenetic data across the whole family. In the proposed PhD project the chalcone synthase has been selected as candidate locus to reconstruct such a robust framework phylogeny with a nearly constant molecular clock. This will enable calibration of any evolutionary hypothesis. In order to obtain this evolutionary framework, chs genes have to be characterized in detail (copy number, ortholoques, paraloques, pseudogenes) in a representative set of taxa across the whole Brassicaceae family. Subsequent functional and theoretical analysis will provide additional information on modes of molecular evolution creating chs diversity in the entire family.

References: KOCH M.A., AL.SHEHBAZ, I.A. (2009) Molecluar Systematics and Evolution of “wild” crucifers (Brassicaceae or Cruciferae). In: Biology and Breeding of Crucifers (ed. S. Gupta). Taylor and Francis Group. Pp. 1-22.

LYSAK M.A., KOCH M.A., LEITCH I.J., BEAULIEAU J.M., MEISTER A. (2009) The dynamic ups and downs of genome size evolution in Brassicaceae. Mol. Biol. Evol. 26 (1): 85-98.

KOCH M.A, DOBES C, KIEFER C, SHMICKL R, KLIMES L, LYSAK MA (2007) SuperNetwork identifies multiple events of plastid trnF (GAA) pseudogene evolution in the Brassicaceae. Mol. Biol. Evol. 24: 63-73.

KOCH, M.A, HAUBOLD, B., MITCHELL-OLDS, T. (2001): Molecular systematics of the cruciferae: Evidence from coding plastome matK and nuclear CHS sequences. Amer. J. Bot. 88 (2): 534-544.

KOCH, M.A, WEISSHAAR, B., KROYMANN, J., HAUBOLD, B., MITCHELL-OLDS, T. (2001): Comparative genomics and regulatory evolution: conservation and function of the Chs and Apetala3 promoters. Mol. Biol. Evol. 18 (10): 1882-1891.

Methods that will be used: Cloning of genomic DNA incl. promoter fragment, expression studies and RT-PCR, SNP- analysis (characterization of allelic diversity), flow cytometry and cytogenetics (estimation of DNA content and ploidylevels), additional focus on theoretical analysis in molecular evolution

Profile of candidate‘s qualification: Highly motivated candidates, preferentially with a background in plant systematics and evolution (theory and/or practice) and molecular biology are invited to apply.

Prof. Dr. Marcus A. Koch Heidelberg Institute of Plant Sciences Director Division Biodiversity and Plant Systematics Director Botanical Gardens and Herbarium Heidelberg (HEID) Dean (Studies) Faculty of Biological Sciences University of Heidelberg Im Neuenheimer Feld 345 D-69120 Heidelberg, Germany Tel.: +49 (0)6221 54 4655 Fax +49 (0)6221 54 5508 eMAIL mkoch@hip.uni-heidelberg.de WWW http://www.bot.uni-heidelberg.de/ “Prof. Dr. Marcus A. Koch” <mkoch@hip.uni-heidelberg.de>

## UHelsinki AntEvolution

PhD position: Cannibalism and conflict in Formica ants University of Helsinki, Faculty of Biological and Environmental Sciences, Department of Biosciences http://www.helsinki.fi/science/ants/Heikki.htm http://www.helsinki.fi/science/ants/ The project Cannibalism and conflict in Formica antsâ(abstract below), funded by the University of Helsinki Research Funds, is looking for a PhD student. Requirements are motivation and enthusiasm for research especially in social evolution and behavioural ecology, ability to work efficiently and independently, as well as in a team, and an MSc degree in a suitable field. Experience of behavioural ecology research, especially of microsatellite analyses and experimental design is a bonus. Funding (incl. a salary according to the University of Helsinki salary system, ca. 1800â/ month) is guaranteed until the end of 2012. If necessary, more funding will be applied after this.

The project is based on testing predictions from inclusive fitness theory concerning selfish brood cannibalism in several species of Formica ants. The project builds on experimental work on colonies collected from the field, complemented by microsatellite analyses of the kin structure of colonies. The field and experimental work is carried out at Tvärminne Zoological Station in Southern Finland, a beautiful place to do research (http://luoto.tvarminne.helsinki.fi/-english/index.htm). Depending on the skills and interests of the student and the progression of the project, the project can be extended to include e.g. theoretical models and chemical analyses of recognition through the collaborative network of the group.

The research group of Dr. Heikki Helanterä is part the group studying social evolution in ants at the Department of Biosciences of the University of Helsinki (Prof. Lotta Sundström, Prof. Pekka Pamilo, Dr. Perttu Seppä). The group has a long tradition in studying behavioural, genetic and ecological aspects of social evolution, especially in Formica ants.

Send your application to heikki.helantera@helsinki.fi . Attach a CV, publication record, contact details of two references (e.g. MSc thesis supervisor), and a two page (max) description of your research interests and why you would be a suitable candidate for the project. Screening of the applications will start on the 8th of January, and the position will be filled when a suitable candidate is found. The work can be started in January already, and needs to start in the beginning of April at the latest (thatâs when the field season starts).

More info: heikki.helantera@helsinki.fi

Cannibalism and conflict in Formica ants Principal Investigator: Heikki Helanterä, PhD

The differentiation between queens and workers in social insect colonies, such as those of ants, bees and termites, is fundamental to their huge evolutionary and ecological success and diversity. Despite the apparent unity of their societies, which individuals develop into which caste is a source of intense evolutionary and behavioural conflict between indivuals within the colonies. This is because each individual would increase their fitness by developing into a reproductive queen that produces offspring in the next generation, rather than any of their nestmates. The competition for a breeding position is why larvae behave cannibalistically and eat other brood in the colony. This competition is predicted to be the more intense, the less related the nestmates are to each other, because harming closely related individuals decreases the amount of shared genes transferred to future generations.

We will study determinants of the variation in cannibalism in the ant genus Formica using experimental and genetic data. The research will have two angles. First, we will study what are the evolutionary and ecological determinants of variation, concentrating especially on the queen number of colonies, that determines the relatedness between individuals, but is also a key feature of ant ecology. Second, we will investigate the flexibility and information use that underlies the behavioural decisions made by larvae. Combining these two angles gives us a comprehensive picture of adaptive social behaviour in its ecological and evolutionary setting. Furthermore, the research will increase our understanding of a fundamental feature underlying the success and diversity of social insects.

---

## UHouston EvolutionaryBioinformatics

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

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

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

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

Dan Graur John and Rebecca Moores Professor Department of Biology & Biochemistry University of Houston 369 Science & Research Building 2 4800 Calhoun Road

Houston, TX 77204-5001 USA

dgraur@gmail.com

## UKansas Hydrozoan EvoDevo

Graduate Opportunity at the University of Kansas in Hydrozoan Evo-Devo

I am seeking a PhD student to work on a newly funded project to study of the evolution and development of hydrozoans. My lab focuses on many aspects of cnidarian evolution, including molecular systematics, biogeography and development. Students that are interested in combining phylogenetics with developmental gene expression to study character evolution are encouraged to apply. Student must be highly motivated, have a demonstrated ability to work independently and show a keen interest in hydrozoans, phylogenetics, developmental processes and evolution.

The Ecology and Evolutionary Biology program at the University of Kansas offers five years of guaranteed support through a combination of graduate teaching assistantships, research assistantships, and university fellowships. For more information, please go to: http://www.people.ku.edu/ ˜ pcart/index.html and http://www2.ku.edu/˜eeb/ . For additional information or to apply please contact me at by email; pcart@ku.edu.

Paulyn Cartwright Assistant Professor Department of Ecology and Evolutionary Biology 1200 Sunnyside Ave. Haworth Hall, Rm. #7016 University of Kansas Lawrence, KS 66045

Phone: 785/864-4432 Fax: 785/864-5860

http://www.people.ku.edu/˜pcart/index.html Paulyn Cartwright <pcart@ku.edu>

## UManchester Bioinformatics

Hi,

I've a funded PhD position available for UK or EU students (see below). I'd be very grateful if you could pass this message on to any potential applicants.

Thanks, David

COMPUTATIONAL ANALYSIS OF NEXT GENERATION SEQUENCE DATA Second generation sequencing technologies such as 454 GS-FLX have massively parallelized the determination of nucleotide order within genetic material resulting in the ability to produce extremely large data sets at relatively low cost. However, the sequence reads produced are significantly shorter than Sanger sequencing and error rates can be high and non-uniform. As a consequence we are currently in a situation where experiments are generating data sets of such magnitude and complexity that we do not have appropriate methodologies for efficiently processing them let alone for effective analysis. In this project we will focus on the analysis of variation in next generation population data sets available in public databases or from academic or industrial collaborators. The study of high-depth (or ultra-deep) data sets is of particular importance in the identification of low frequency mutations or variants in the context of viral infections (Archer et al. 2009), bacterial populations and metagenomic projects. The specific aims of the project will be to investigate polymorphism frequencies versus error rates, phylogenetic inference and visualisation of evolutionary history (Archer and Robertson, 2007), co- evolution (Hakes et al., 2007), recombination (Archer et al., 2008; Simon-Loriere et al., 2009) and other appropriate properties of high- depth data sets. This will complement existing projects in the Robertson group, for example, www.bioinf.manchester.ac.uk/-segminator (Archer et al. 2009). Note, the exact remit of the project can also be changed to fit with other on-going projects in the group, see < http:/-/www.bioinf.manchester.ac.uk/robertson/ > for more details.

References

(1) Archer J, and Robertson DL (2007) Understanding the diversification of HIV-1 groups M and O. AIDS. 21:1693-1700. (2) Hakes L, Lovell SC, Oliver SG, and Robertson DL (2007) The relationship between sequence diversity, co-evolution and specificity in protein interactions. PNAS 104:7999-8004. (3) Archer J, Pinney JW, Simon-Loriere Etienne, Arts EJ, Negroni M, and Robertson DL (2008). Identifying the important HIV-1 recombination breakpoints. PLOS Computational Biology, 4:1000178. (4) Simon-Loriere E, Galetto R, Hamoudi M, Archer J, Lefeuvre P, Martin DP, Robertson DL, and Negroni M (2009) Molecular mechanisms of recombination restriction in the envelope gene of the human immunodeficiency virus. PLOS Pathogens, 5:e1000418. (5) Archer J, Braverman MS, Taillon BE, Desany B, James I, Harrigan PR, Lewis M, and Robertson DL (2009) Detection of low- fre-

quency pretherapy chemokine (CXC motif) receptor 4 (CXCR4)-using HIV-1 with ultra-deep pyrosequencing. AIDS, 23:1209-1218.

To apply go to < http://www.ls.manchester.ac.uk/-postgraduate/ukoreu/research/apply/ >. Informal enquires to david.robertson@manchester.ac.uk. We'd like to short-list early January so please apply ASAP if you're interested.

You can find information on Manchester here http://-www.manchester.ac.uk/aboutus/video/ .

David Robertson <david.robertson@manchester.ac.uk>

## UMaryland EvolutionaryBiology

Doctoral Program in Behavior, Ecology, Evolution, & Systematics (BEES) at the University of Maryland, College Park

For many years the University of Maryland, College Park has provided outstanding graduate training in animal behavior, ecology, evolutionary biology, and systematics. In the last decade the BEES program has been the center of this activity. We are delighted to announce the first application cycle for BEES in its new form as a concentration area within the new Biological Sciences umbrella program. This change preserves BEES historical rigor and disciplinary focus, while enabling trainees to create a customized curriculum, develop research projects extending beyond its traditional disciplines, and participate in optional lab rotations. The overall goals of the BEES concentration area remain to conduct cutting-edge research on all aspects of biodiversity, facilitate communication and collaboration among faculty and students, and provide an incomparable environment for training the next generation of ecological and evolutionary biologists.

BEES consists of over 60 distinguished faculty from ten departments in five Colleges at the University of Maryland, as well as adjuncts from nearby research institutions, such as the Smithsonian Institution, United States Department of Agriculture, and the National Institutes of Health. Together these individuals have expertise in behavioral ecology, community ecology, comparative and functional genomics, conservation biology, evolutionary developmental biology, evolutionary ecology, evolutionary genetics, molecular evolution,neuroethology, paleobiology, physiological ecology, population ecology, population genetics, quantitative genetics, and systematics.

To learn more about BEES and to initiate the application process, please see: http://chemlife.umd.edu/bisi or http://bees.umd.edu/

Please note that applications for enrollment in Fall, 2010 must be received by January 6, 2010 to receive full consideration for financial assistance.

Eric S. Haag Associate Professor Director, BEES-BISI Graduate Program Department of Biology University of Maryland College Park, MD 20742

phone: (301) 405-8534

fax: (301) 314-9358

http://www.life.umd.edu/biology/faculty/haag/ "Eric S. Haag" <ehaag@umd.edu>

## UMunich EvolutionaryBiol

*Master's Program in Evolution, Ecology and Systematics in Munich, Germany*

The Ludwig-Maximilians University of Munich (LMU) offers a two-year Master's Program in Evolution, Ecology, and Systematics (EES). Funded by the Volkswagen Foundation, the EES Masters is a multidisciplinary program for German and international students with a strong background in biology or a related subject. All courses are offered in English.

In addition to intensive scientific coursework, the EES Master's program contains many innovative elements such as a mentoring program; courses on writing, giving presentations, and leading discussions; and individual research training. We also apply a feedback and revision system instead of simple grading. Students can also apply for research and travel money and for funds to invite international speakers.

The LMU is located in one of Germany's most vibrant cities just one hour by train from the Alps. Recently awarded the highest excellence status in a nation-wide competition, the LMU is the only German university that offers evolutionary research at a broad scale. The EES Program is a collaboration between the LMU's Department of Biology and Department of Earth- & Environmental Sciences, the Max Planck Institute for Ornithology and the Bavarian Natural History Collections.

Start date: October 4, 2010

Application deadline: January 31, 2010 (international students); June 30, 2010 (EU students). All students are encouraged to apply by the earlier deadline.

Cost: Registration fees are approximately 1100 euros per year. Currently, the university does not provide any stipend funding to Master's students.

For more information and application instructions, please see our website (www.eeslmu.de) or contact the program coordinator, Dr. Elena Berg (berg@bio.lmu.de).

Elena C. Berg, Ph.D.

EES Program Coordinator Biozentrum - Department Biologie II University of Munich (LMU) Großhaderner Str. 2 D-82152 Planegg-Martinsried Germany

Phone: +49 (0)89-2180 74208 Email: berg@biologie.uni-muenchen.de Web: www.eeslmu.de berg@biologie.uni-muenchen.de

## UNevadaReno Woodrat Hybrids

A Ph.D. and M.S. Graduate Research Assistantship are available to study the ecological, behavioral and genetic dynamics of contact zones between two species of woodrats (genus Neotoma) in California. Successful applicants will play a large role in the design and implementation of several projects that integrate data from fieldwork focused on individual survival, reproductive success, and resource use with laboratory behavioral trials and molecular genetic analyses. Candidates will also have an opportunity to participate in a high school outreach program focused on the application of molecular genetics in ecology and evolution. Candidates should be creative and highly motivated with strong writing and communication skills. Candidates must have a B.S. in biology or a closely related discipline, field experience, ability to work under rigorous field conditions and interest in evolutionary ecology, genetics, and science education. Positions are available Fall 2010 or earlier depending on applicant availability. Review of applications will begin December 15 and continue until the positions are filled. Submit (preferably by email) a letter of interest that includes a description of work experience and career goals including both research and education, curriculum vitae, transcripts, GRE scores, and 3 letters of reference to: Marjorie Matocq, Department of Natural Resources and Environmental Science, Mailstop 186, University of Nevada Reno, Reno, Nevada, 89509; 775-784-4621; mmatocq@cabnr.unr.edu

"Matocq, Marjorie" <mmatocq@cabnr.unr.edu>

## UNotreDame MalariaEvolution

Graduate positions: Systems Genetics of Malaria Parasites The Ferdig lab, in the Eck Institute for Global Health at the University of Notre Dame, is seeking graduate students motivated to use the tools of genomics and classical genetics to understand the evolution of drug resistance and virulence in malaria parasites. Solving the challenges of malaria will require knowledge of the multitude of complex molecular interactions within the parasite cell. In the systems genetics framework we can identify how allelic variation drives a cascade of measurable traits, from transcript abundance (eQTL, Gonzeles et al, PLoS Biology, 1 September 2008) to protein and metabolite levels to cellular physiology, that lead to the critical phenotypes like drug resistance and virulence that make malaria such a devastating disease. Whole-genome network views and computational methods promise new avenues for attack against malaria. Our lab combines wet-lab and computational approaches with a strong evolutionary perspective. The Eck Institute (http://www.nd.edu/~eigh/) is a multidisciplinary group of principal investigators, research scientists, post-doctoral fellows, technicians, and students. Many projects rely on the Genomics and Bioinformatics Core Facilities housed in the department and the University is committed to growth in Computational Biology. The Eck researchers focused on tropical disease organisms interface with the strong group in population and evolutionary genetics, and the department boasts an NSF (IGERT) training grant: http://globes.nd.edu/. Contact Michael Ferdig ferdig.1@nd.edu The University of Notre Dame is an Affirmative Action/Equal Opportunity Employer. Women and minority candidates are encouraged to apply.

Mike Ferdig U. Notre Dame 574-631-9973

Michael Ferdig <ferdig.1@nd.edu>

## UOulu Goose domestication

PhD student position at the Department of Biology, University of Oulu, Finland

Domestication history of the European goose

Domestic goose Anser anser domesticus has been one of the earliest and most important examples of bird domestication. In Europe alone there are approximately 50 recognised breeds. However, virtually nothing is known about timing, location and manner of goose domestication, and how it compares to domestication of other species. This will be the first detailed study of these phenomena. We will use molecular markers (mtDNA, microsatellites, genome sequencies) and geometric morphometrics to study modern wild and domestic as well as archaeological specimens. The project brings together multidisciplinary expertise in population and conservation genetics (Minna Ruokonen, University of Oulu), phylogeography (Jeremy Searle, University of York/Cornell University), livestock domestication and archaeology (Keith Dobney, University of Aberdeen). A bioinformatician will join the project in 2011.

The student will be based at the Department of Biology, University of Oulu, where he/she will join the Population Genetics Group (to be formed in 2010) with ca. 30 academic researchers and technical staff. The group belongs to the Population Genetics Graduate School. The studentship will involve substantial periods of research at both Cornell University and the University of Aberdeen.

The position is for four years (2010-2013) and the starting date is early 2010. Starting salary is ca. 2000 eur per month, and can be raised after assessment of personal performance (as evaluated by ECTS and publications) and changes in the job demand level. The position includes some teaching responsibilities (48 hours over the four years).

We invite motivated applicants with background and M.Sc. in a relevant field (e.g. population or conservation genetics, molecular archaeology). The applicants should submit their CV, contact information of two referees and a short statement of their research interests (including a summary of MSc or undergraduate work) as a single .pdf file to minna.ruokonen@oulu.fi. Review of the applicants will begin January 11th , but applicants will be considered until the position is filled.

For additional information contact: minna.ruokonen@oulu.fi keith.dobney@abdn.ac.uk or Jeremy Searle at jbs3@york.ac.uk

More information at: www.flcrp.org http://cc.oulu.fi/~biolwww/PopGenSchool/ http://cc.oulu.fi/~biolwww/english/index.html http://www.abdn.ac.uk/archaeology/staff/staff.php?id=keith.dobney http://bioltfws1.york.ac.uk/biostaff/staffdetail.php?id=jbs Minna Ruokonen Department of Biology POB 3000 FIN-90014 University of Oulu FINLAND minna.ruokonen(at)oulu.fi +358-(0)8-553 1807 (office) +358-(0)8-553 1061 (fax) http://cc.oulu.fi/~mruokone/ http://www.flcrp.org/ Minna Ruokonen <minna.ruokonen@oulu.fi>

## UOulu GooseEvolution

PhD student position at the Department of Biology, University of Oulu, Finland

Domestication history of the European goose

Domestic goose Anser anser domesticus has been one of the earliest and most important examples of bird domestication. In Europe alone there are approximately 50 recognised breeds. However, virtually nothing is known about timing, location and manner of goose domestication, and how it compares to domestication of other species. This will be the first detailed study of these phenomena. We will use molecular markers (mtDNA, microsatellites, genome sequencies) and geometric morphometrics to study modern wild and domestic as well as archaeological specimens. The project brings together multidisciplinary expertise in population and conservation genetics (Minna Ruokonen, University of Oulu), phylogeography (Jeremy Searle, University of York/Cornell University), livestock domestication and archaeology (Keith Dobney, University of Aberdeen). A bioinformatician will join the project in 2011.

The student will be based at the Department of Biology, University of Oulu, where he/she will join the Population Genetics Group (to be formed in 2010) with ca. 30 academic researchers and technical staff. The group belongs to the Population Genetics Graduate School. The studentship will involve substantial periods of research at both Cornell University and the University of Aberdeen.

The position is for four years (2010-2013) and the starting date is early 2010. Starting salary is ca. 2000 eur per month, and can be raised after assessment of personal performance (as evaluated by ECTS and publications) and changes in the job demand level. The position includes some teaching responsibilities (5% from the annual working time).

We invite motivated applicants with background and M.Sc. in a relevant field (population or conservation genetics, molecular archaeology). The applicants should submit their CV, contact information of two referees and a short statement of their research interests (including a summary of MSc or undergraduate work) as a single .pdf file to minna.ruokonen@oulu.fi. Review of the applicants will begin December 15th, but applicants will be considered until the position is filled.

For additional information contact: minna.ruokonen@oulu.fi keith.dobney@abdn.ac.uk or Jeremy Searle at jbs3@york.ac.uk

More information at: www.flcrp.org http://cc.oulu.fi/ ˜ biolwww/PopGenSchool/ http://cc.oulu.fi/ ˜ biolwww/english/index.html http://www.abdn.ac.uk/archaeology/staff/staff.php?id=keith.dobney http://bioltfws1.york.ac.uk/biostaff/staffdetail.php?id=jbs Minna Ruokonen Department of Biology POB 3000 FIN-90014 University of Oulu FINLAND minna.ruokonen(at)oulu.fi +358-(0)8-553 1807 (office) +358-(0)8-553 1061 (fax) http://www.flcrp.org/ Minna Ruokonen <minna.ruokonen@oulu.fi>

## UOxford EvolutionarySocialEcol

DEPARTMENT OF ZOOLOGY, UNIVERSITY OF OXFORD

Graduate Research Assistant Evolutionary Social Ecology

Grade 6 Starting salary Â£25,623 p.a.

A Graduate Research Assistant position is available, for 4 years and 3 months, from 1 April 2010, to work on a project studying social networks in birds from an ecological and evolutionary perspective. The post is funded as part of an ERC Advanced Investigator grant of 2.5M over five years to Prof Ben Sheldon. The post will be based in the Edward Grey Institute, Department of Zoology, University of Oxford. The main duties of the post-holder will be to carry out fieldwork around Oxford to collect data on social behaviour and social relationships in wild birds, and to participate in experiments testing a range of hypotheses about the causes and consequences of social behaviour. This is an exceptional opportunity to participate in a major research project, for which extensive pilot data are already available, and for which funding is guaranteed at a very high level for the duration of the project.

The successful candidate will have a BSc in biology or a related subject, and demonstrate skill and enthusiasm for biological research. Experience of fieldwork under arduous conditions, and of working as part of a multidisciplinary team are desirable, as are fieldwork skills involving birds. There will be an opportunity to register to study for a DPhil (Oxford version of a doctorate) after the first year, subject to mutual agreement.

The post is based in a dynamic and expanding research-active institute, of c. 40 people, fully integrated within the Department of Zoology. Further details about the institute available at: http://www.zoo.ox.ac.uk/egi/ Informal inquiries (with CV) to Prof Ben Sheldon (ben.sheldon@zoo.ox.ac.uk)

Further particulars and application forms can be downloaded from http://www.zoo.ox.ac.uk/jobs or are available from the Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS (tel: 01865 271190); email: recruit@zoo.ox.ac.uk . Applications, together with CV and contact details of three referees and a cover letter explaining how the candidate meets the selection criteria, as outlined in the further particulars, should be sent to the above address quoting reference number AT09042. The closing date for applications is 5 February 2010. Interviews will take place in late February.

Prof. Ben Sheldon Edward Grey Institute Dept of Zoology University of Oxford (00 44) 01865 281069 ben.sheldon@zoo.ox.ac.uk

http://www.zoo.ox.ac.uk/egi/ Ben Sheldon <ben.sheldon@zoo.ox.ac.uk>

## UOxford Phylogeography

DPhil Studentship in Indian Ocean Biomolecular Archaeology

Applications are invited for an ERC-funded DPhil studentship to investigate the translocation of commensal small mammals in the ancient Indian Ocean. The project will work within the framework of phylogeography to infer ancient pathways of colonisation and interaction. Three common commensal animals that are now widely distributed in the Indian Ocean, and likely hold clues to ancient patterns of human seafaring, trade, migration and colonization, may be investigated: the black rat Rattus rattus, the house mouse Mus musculus and the house shrew Suncus murinus. The 3-year studentship is offered as part of the SEALINKS Project, which is taking a unique interdisciplinary approach to maritime prehistory, drawing on archaeology, molecular genetics and historical linguistics methods. The studentship will be of particular appeal to students whose interests bridge the humanities and natural sciences.

The selected student will undertake background research in archaeology, biogeography and molecular genetics, fieldwork in South Asia, Southeast Asia and Africa to collect samples, and laboratory work employing molecular genetics techniques. The project will be based between the University of Oxford (archaeology) and Cornell University (molecular genetics), with the student receiving an Oxford DPhil. Candidates should hold or expect to hold, by the time of the project start date, a very good honours degree (at least a 2.1 or equivalent) or Masters degree in a relevant subject, and a strong background in either the biological sciences or archaeology. They will receive appropriate training, but should also be self-motivated. The student will be jointly supervised by Dr. Nicole Boivin (Oxford) and Prof. Jeremy Searle (Cornell).

The studentship covers the full cost of a home/EU student (tuition, college fees, and living expenses). Funding for fieldwork is also available.

Requests for further information should be directed to Dr. Boivin or Prof. Searle (who will transfer from York to Cornell in October 2010). Start date: October 2010.

For further details about the Sealinks Project see:

http://sealinks.arch.ox.ac.uk/ Applications should be submitted directly to the University of Oxford. Details of how to make formal application to the DPhil Programme at the School of Archaeology can be found at:

http://www.arch.ox.ac.uk/graduate-applying.html Applications are completed on-line at:

http://www.ox.ac.uk/admissions/-postgraduate_courses/apply/index.html Applicants should indicate on their application form and statement that they wish to apply for the ERC Sealinks Studentship in Indian Ocean Biomolecular Archaeology, and also whether or not they would wish their application to be considered more generally if they do not get this studentship and what funding options they would consider.

Applicants should submit a well-documented research proposal discussing the use of commensal species in archaeological research and outlining a possible approach (or approaches) to the study problem (the applicants background will be taken into account in assessing this). In this statement they should address their interest in and experience relevant to the position.

Key words: Biomolecular Archaeology/Archaeology/Molecular Genetics/Phylogeography

Closing date for applications: 22 January, 2010

Nicole Boivin, Senior Research Fellow Research Laboratory for Archaeology and the History of Art University of Oxford Phone: +44 (0)1865 275377

Nicole Boivin <nicole.boivin@rlaha.ox.ac.uk>

## USheffield Fish EvoDevo

Evo-Devo of tooth replacement in fish

Supervisors: Dr Gareth Fraser

Key words: Fish Evo-Devo, Malawi cichlids, sharks, dental diversity, tooth development

Project Description

The complex process of tooth replacement varies across vertebrates. At present we know little of the genetic underpinnings of tooth replacement in any vertebrate. Fish offer exceptional developmental models for tooth regeneration with continuous tooth production. Unlike mammals, fish replace their teeth continually through life with a constant production of new teeth. Among fish groups the system of repeated tooth production differs. Sharks have a unique tooth replacement system where a conveyer-belt of multiple preformed teeth replaces each functional tooth in the dentition. Most teleosts exhibit a different system, where a single replacement tooth forms to replace each functional tooth.

We are interested in the genetic network that acts to regulate tooth replacement and we ask how these networks can evolve to facilitate the diversity of tooth replacement across vertebrates. Our recent work has characterised a gene network associated with regulating an essential dental stem cell niche,from which new replacement teeth are born. This studentship will focus on the developmental basis of tooth replacement in a range of fish models including Malawi cichlids and the catshark, Scyliorhinus canicula, to discover how these complex and conserved gene networks can alter to produce diverse tooth replacement mechanisms across vertebrates.

This is laboratory-based with the successful applicant receiving training in developmental biological techniques, including in situ hybridisation, microscopy and genetic manipulation. Applicants should have, or expect to obtain at least a 2:1 degree in a relevant subject. Informal enquiries can be directed to Dr. Gareth Fraser (email: g.fraser@sheffield.ac.uk).

Starting date: 1 October 2010

How to apply: Complete an on-line application form via University of Sheffield web site at http:/-/www.shef.ac.uk/postgraduate/research/apply/-index.html. Send a full CV, via email to Mrs S Carter, s.a.carter@sheffield.ac.uk, or a hard copy to Mrs S Carter, Department of Animal and Plant Sciences, University of Sheffield, Sheffield S10 2TN.

Closing date for applications: 31 January 2010.

– Gareth J. Fraser, Ph.D Lecturer in Zoology Department of Animal and Plant Sciences Alfred Denny Building University of Sheffield Western Bank Sheffield S10 2TN UK Phone: +44(0)1142224706 Email: g.fraser@sheffield.ac.uk

"Gareth J. Fraser" <G.Fraser@sheffield.ac.uk>

## USherbrooke KangarooMatingStrategy

Ph.D. on reproductive strategies of male kangaroos.

I am looking for a Ph.D. student to work on the determinants of variability in male reproductive success in eastern grey kangaroos in Victoria, Australia. This research is part of a long-term program on kangaroo evolutionary and population ecology in collaboration with Dr. Graeme Coulson of the University of Melbourne. We are monitoring three populations of kangaroos and have marked over 300 individuals. The Ph.D. will involve behavioral observations during three breeding seasons (November to January), capture, marking and measuring of kangaroos, remote measurements of body size using parallel lasers, collection of tissue samples from pouch young and DNA analyses in the laboratory of Dr. Dany Garant in Sherbrooke to identify fathers.

Assets for this position include a M.Sc. degree, publications, a knowledge of French (or a strong willingness to learn it), fieldwork experience, strong quantitative skills and laboratory experience in molecular ecology. Canadian candidates will be preferred, but strong foreign candidates will be seriously considered.

A tax-free scholarship (Can $ 17,000/year for 3.5 years) is available, and financing for travel, fieldwork and lab expenses has been secured. The program can begin in either May or September 2010.

For information on my research, see http://-pages.usherbrooke.ca/mfesta/marco.htm and for details about grad studies in my lab see http:/-/pages.usherbrooke.ca/mfesta/advice.htm Interested candidates should e-mail a CV, a statement of research interests and the e-mails of two referees to Marco Festa-Bianchet: m.festa@USherbrooke.ca –

Marco Festa-Bianchet Département de biologie, Université de Sherbrooke Sherbrooke, Québec J1K 2R1 CANADA Tel +1 (819) 821-8000 ext. 62061 Fax (819) 821-8049 http://pages.usherbrooke.ca/-mfesta/marco.htm m.festa@USherbrooke.ca m.festa@USherbrooke.ca

## USherbrooke Treeswallow

M.Sc. or Ph.D. project on tree swallow

I am looking for a M.Sc. Ph.D. student to explore the effects of agricultural intensification on stress hormone and immunity in tree swallow (Tachycineta bicolor). This research is part of a long-term program on the effect of human-driven changes on wild populations in collaboration with Profs. Marc Bélisle and Dany Garant of the Université de Sherbrooke. Since 2004, we are monitoring 400 next-boxes across a gradient of agricultural intensification. The project will involve behavioural observations during at least two nesting seasons (April to July), capture, marking and measuring of the birds, collection of blood and feather samples for hormone and DNA analyses.

Assets for this position include a M.Sc. degree (for the Ph.D. application), publications, a knowledge of French (or a strong willingness to learn it), fieldwork experience, strong quantitative skills and laboratory experience in endocrinology and molecular ecology. Canadian candidates will be preferred, but strong foreign candidates will be seriously considered.

A tax-free scholarship is available, and financing for travel, fieldwork and lab expenses has been secured. The program can begin in either May or September 2010.

For information on my research, see http://-pages.usherbrooke.ca/fpelletier/ Interested candidates should e-mail a CV, a statement of research interests and the e-mails of two referees before the 1st of March to Fanie Pelletier: fanie.pelletier@usherbrooke.ca

Fanie Pelletier, Ph.D. Professeure Adjointe Université de Sherbrooke Département de biologie Faculté des Sciences Sherbrooke (Québec) CANADA J1K2R1

tel.: 819-821-8000 poste 61092 fax: 819 821-8049

fanie.pelletier@usherbrooke.ca

## UValencia RotiferCoEvolution

Spanish Research Training Fellowship for Population Biology Studies

Institute Cavanilles of Biodiversity and Evolutionary Biology (ICBiBE)

University of Valencia (Spain)

The Spanish Ministry of Science and Innovation (MCI) will open a call for the so-called FPI (Formación de Personal Investigador) Fellowship Program in January 2010. One of these fellowships is associated to the research project ‘Implications of the environmental and demographic fluctuations on the coexistence of cryptic rotifer species‘, leaded by Manuel Serra (http://www.uv.es/ ˜ serram/) at the Evolutionary Ecology Laboratory - ICBiBE (http://www.uv.es/ ˜ biodiver/v/index.htm).

The project focuses on the hypothesis that salinity fluctuations, besides demographic fluctuations caused by the life cycle, allow stable coexistence of zooplankters with high similarity in their resource exploitation and predation vulnerability. Methods and techniques involved in this project are pond sampling, taxonomic identification using molecular markers, laboratory experiments using chemostats, modelling of ecological and evolutionary processes, and advanced statistical analysis. Therefore, a strong background in population ecology and evolution is required to be awarded with the above mentioned fellowship. Skills in statistics, population genetics, molecular biology and computer programming are welcome.

Details will be given in the official call made by MCI. However, based in previous calls, the fellowship is expected to have the following features:

(1) The fellowship will provide support for four years.

(2) The fellow will follow post-graduate studies (master and doctorate for fellows with a BS, or doctorate for fellows with a MSc; http://www.uv.es/postgrau/index.htm) at the University of Valencia.

(3) Eligible students must have a degree, obtained after January 1, 2006, which allow them the access to post-graduate studies at the University of Valencia.

(4) The time window to submit applications will be fifteen days after the call is opened.

(5) The fellow is expected to start his/her work in September 2010.

Students interested in applying for the fellowship should e-mail Manuel Serra (manuel.serra@uv.es; cc: María José Carmona <maria.j.carmona@uv.es>), stating his/her interest, and enclosing his/her CV. Those applicants with a degree obtained outside the European Space for Higher Education should obtain degree recognition at the University of Valencia before application submission to MCI.

Manuel Serra

Institute Cavanilles of Biodiversity and Evolutionary Biology University of Valencia (Spain)

Home page: //www.uv.es/ ˜ serram Manuel Serra <Manuel.Serra@uv.es>

## UWyoming EvolutionaryBioinformatics

Graduate Assistantship for PhD in Statistics related to Evolutionary Bioinformatics

The Department of Statistics at the University of Wyoming is pleased to announce 1 fully funded 12-month Graduate Assistantship for 4 years, starting in August 2010, and funded by the Wyoming Bioinformatics Core supported by INBRE (IDeA Networks of Biomedical Research Excellence). Applicants with strong backgrounds in undergraduate Mathematics and Biology will be considered; computer programming skills, some knowledge of Statistics, protein structure, and genetics are crucial. In addition, written and oral communication skills and the ability to work in an interdisciplinary setting will be considered. The GA will be a PhD student in Statistics, will work with Drs. Huzurbazar in Statistics and Liberles in Molecular Biology and will interact with the evolutionary bioinformatics students and researchers in the Liberles group (see http://-

www.wyomingbioinformatics.org/LiberlesGroup). Interested applicants should first send a CV, a statement of research interests, and contact information for three references, to lata@uwyo.edu. Informal inquiries before the application are encouraged.

Dr. Snehalata Huzurbazar Associate Professor, Department of Statistics, University of Wyoming

Phone: 307-766-4826 Mailing Address: Dept 3332, 1000 E. University Avenue, Laramie, WY 82071

“Snehalata V. Huzurbazar” <Lata@uwyo.edu>

## ValenciaPolytechniqueU ViralEvolution

PhD Fellowship offer.

Principal Investigator: Prof. Santiago F. Elena

Group and Center: Evolutionary Systems Virology Group. Institute for Plant Molecular and Cellular Biology. Spanish National Research Council â Valencia Polytechnique University. Campus UPV CPI 8E, Ingeniero Fausto Elio s/n, 46022 Valencia, Spain:

Institute Website: www.ibmcp.upv.es Group Website: bioxeon.ibmcp.upv.es/EvolSysVir. This site contains valuable information about the groupâs ongoing research, publications and other scientific achievements.

Period: 24 months of fellowship + 24 months of contract.

Abstract of the Project: One of the major threats to human and animal health as well as to agronomy is the emergence of new infectious diseases, most of which are caused by RNA viruses. RNA viruses show a remarkable evolvability owed to their large population size, short generation times and high mutation and recombination rates. Understanding the mechanisms by which a virus becomes an emerging one is thus pivotal for the rational design of antiviral therapies and control strategies. In this project we are interested in learning what are the population genetic mechanisms determining the emergence of new viruses and what changes, both in viral genome and in the plant-virus interaction, take place during the process of emergence and adaptation to the new host. We will take an experimental approach using the Tobacco etch potyvirus as model system complemented with evolutionary genetics analyses and with an in silico Systems Biology modeling approach. First, we will characterize the distribution of mutational effects and epistatic interactions among pairs of random mutations across potential hosts and test predictions of models recently proposed to this end. Second, we will perform a large-scale evolution experiment simulating the process of emergence of an RNA virus in a population of genetically heterogeneous hosts. From this experiment and the corresponding analyses, we will learn: (i) about the constraints imposed by different hosts and the specificity of adaptation, (ii) about the reproducibility of evolution at the phenotypic and molecular level and about the targets of selection in the viral genome, (iii) about the cellular components (genes and networks of interactions) to which viruses adapt and how their manipulation may result in virulence, and (iv) by comparing our transcriptomic data, and an inferred model of host interactome, with those obtained for other viruses infecting the same host, we will try to elucidate whether phylogenetically related viruses target the same components in the host interactome while unrelated viruses target widely different components. Finally, by using the new ultra-deep pyrosequencing technologies, we will obtain an unprecedented description of how virus genetic variability is generated, distributes spatially on different plant tissues and evolves within a single infected host plant.

Requirements: We are seeking for a person genuinely interested in developing a scientific career in an interdisciplinary area where Virology, Evolutionary Genetics and Systems Biology merge. The candidate must be a very motivated person, with skills for working in a dynamic international group, initiative and absolute disponibility. In particular, we are interested in students holding a BSc (or equivalent) degree in Biology, Biochemistry or alike, with graduation after January 1st, 2005. An outstanding academic record is necessary. In addition, previous experience in Evolutionary Genomics, Molecular Biology and Bioinformatics will be positively valorized.

Deadline for submission. The exact days for submission have not yet been published by the Ministry, but it will be likely open by mid January 2005. More information can be obtained at the Ministry of Science and Innovation website (http://web.micinn.es/-contenido.asp?menu1=1&menu2=&menu3=&dir=-03_Plan_IDI/00-LIAs/00@LIARRHH/00-Formacion/-00-FPI/001Con09).

Potential candidates, please contact the PI as soon as possible at the e-mail address below

Prof. Santiago F. Elena, PhD Evolutionary Systems Virology Group Institute de BiologÃ’a Molecular y Celular de Plantas (CSIC-UPV) Campus UPV, CPI 8E, lab. 3.0.4 Ingeniero Fausto Elio s/n, 46022 Valencia, Spain Phone: +34 963 877 895 Fax: +34 963 877 859 E-mail: sfelena@ibmcp.upv.es Web: http://bioxeon.ibmcp.upv.es/EvolSysVir The Santa Fe Institute 1399 Hyde Park Road Santa Fe, NM 87501 USA

"Santiago F. Elena" <sfelena@ibmcp.upv.es>

# Jobs

## ArizonaStateU InsectSystematics

The International Institute for Species Exploration (IISE) and School of Life Sciences, Arizona State University, invite applications and nominations for the position of Associate Director of the IISE, Cybertaxonomist, and Curator of Insects. The successful candidate will join a trans-disciplinary team of faculty, staff, and students dedicated to modernization and advancement of descriptive taxonomy through innovation in cyberinfrastructure, e-monography, and collaborative taxonomy. Position will be filled at Assistant or Associate Professor rank, salary commensurate with experience. Requirements include an earned doctorate in insect taxonomy and demonstrated commitment to comparative morphology, taxonomic revisions, and collection growth and enhancement. Core research efforts are expected to be collaborative: organizing and leading a taxon knowledge community', seeking competitive external funding, leading expeditions, producing online monographs, and working with a team of scholars, scientists and engineers to identify and remove impediments to taxonomy through technology and practices. Candidate will teach a course in area of expertise.

To apply, please submit a letter indicating the level for which you are applying; your curriculum vitae; three publications and/or selected articles; and research and teaching statements. A minimum of three letters of recommendation should be sent electronically; please include the names and e-mail addresses of each letter writer with your application. Your application materials should be sent to Dr. Quentin Wheeler, Chair, Cybertaxonomist Search Committee, School of Life Sciences, Arizona State University, c/o Ms. Anna Fields, PO Box 874501, Tempe, AZ 85287-4501. Electronic applications as pdf files to anna.fields@asu.edu are preferred. The initial closing date of applications is January 4, 2010; applications will be reviewed weekly thereafter until the position is filled. A background check is required for employment. Arizona State University is an equal opportunity/affirmative action employer committed to excellence through diversity. Women and minority candidates are enco uraged to apply. For additional information on this position and the School of Life Sciences, please visit http://sols.asu.edu/jobs .

## Canberra PlantSystematist

Plant Systematist https://recruitment.csiro.au/asp/job_details.asp?RefNo=3D2009/976 The Centre for Plant Biodiversity Research at CSIRO Plant Industry seeks a qualified, skilled and motivated scientist to research molecular and morphological systematics of key groups of the Australian flora. The research will involve establishing the identity, diversity and origins of Australian plant groups - including characterising relationships using morphology and molecular data, developing hypotheses and phylogenies of plant lineages in an evolutionary context. In particular we are seeking a researcher to initiate a research program focusing on the Australian members of the Asteraceae, one of the largest and less understood groups of the Australian flora. Projects will use the collection resources of the Australian National Herbarium (ANH), The Australian National Botanic Gardens (ANBG) and its partner Australian herbaria and overseas agencies.

Possible projects include systematics of major lineages of Australian Asteraceae, including plants of horticultural utility. These studies may include morphological and anatomical studies, investigation of polyploidy, ecotype differentiation, plant-animal interactions, population genetics and the application of Next GenerationDNA sequencing technologies to address these questions. The successful applicant will work with a team and develop a collaborative research program. Experience in Asteraceae systematic is beneficial but highly qualified applicants that are willing begin a new research program in Asteraceae systematics are encouraed to apply.

Location: Canberra, Australia Salary: $83k to $90k Reference: 2009/976 Close date: 31 December 2009 Contact: Should you require more information on this position please contact Dr Joe Miller by email: Joe.Miller@csiro.au<mailto:Joe.Miller@csiro.au>

Application information is available on https://recruitment.csiro.au/asp/job_details.asp?RefNo=-2009/976 Joe.Miller@csiro.au Joe.Miller@csiro.au

## CityUNewYork Bioinformatics

Hunter College of The City University of New York

CUNY Cyberinfrastucture Initiative

Hunter College of The City University of New York invites applications for a tenure-track faculty position in bioinformatics and high performance computing. The anticipated start date is Fall 2010 or earlier.

We seek candidates with expertise in the development, adaptation and implementation of algorithms applied to such data-intensive biological areas as (but not limited to) next-generation sequencing, biomedical ontologies, and systems biology.

A PhD in biology, computer science or a related field is required. Preference will be given to mid-career candidates with strong records of peer-reviewed publications and external funding and substantia\l experience in high performance computing within bioinformatics. Exceptional junior candidates will also be considered.

The successful applicant is expected to conduct an independent research program and establish interdisciplinary research collaborations with cyberinfrastructure colleagues at Hunter and across CUNY as part of the university's initiative in this area. Hunter faculty members conduct research, teach undergraduate and graduate courses and supervise graduate and undergraduate participation in research. The appointment will be made in the Department of Computer Science or the Department of Biological Sciences depending on qualifications.

Hunter's biomedical research community, including the Center for Study of Gene Structure and Function, is supported by extensive funding from NIH and NSF. Hunter College is strategically located in Man\hattan near other major biomedical research centers and universities and attracts an engaging and diverse student body. Further information is available at:

http://www.hunter.cuny.edu/csci (Computer Science) http://biology.hunter.cuny.edu (Biological Sciences) http://www.hunter.cuny.edu/qubi (Bioinformatics)

Applicants should submit a cover letter with a list of three references, a curriculum vitae and statements of research and teaching interests to bioinformatics@hunter.cuny.edu or to the address below. Referees should send their recommendations on letterhead as PDF attachments by email to bioinformatics@hunter.cuny.edu or as hard copy mailed to:

Drs. William Sakas and Weigang Qiu Co-Chairs, Bioinformatics Search Committee c/o The Office of the Provost, East Building 1701 Hunter College of the City University of New York 695 Park Avenue New York, NY 10065

Review of applications will begin on January 15, 2010, and will continue until the position is filled. Inquiries may be emailed to bioinformatics@hunter.cuny.edu.

Hunter College is an Equal Employment Opportunity/Affirmative Action/Immigration Reform and Control Act/Americans with Disabilities Act Employer. Female and minority candidates are encouraged to apply.

Weigang Qiu, Associate Professor Department of Biological Sciences Hunter College, City University of New York 695 Park Ave, New York, NY 10021 Tel. 1-212-772-5296

Weigang@GENECTR.HUNTER.CUNY.EDU
Weigang@GENECTR.HUNTER.CUNY.EDU

## CornellU 2 BioinformaticsProgrammer

Bioinformatics Programmer Positions (2) at Cornell University: Computational Genomics and Analysis of Next-Generation Sequencing

Two scientific programmer positions are available immediately in the laboratories of Andrew Clark and Alon Keinan at Cornell University, to join a group of investigators using computational approaches to tackle current problems in the analysis of whole-genome data.

The positions involve developing and applying computational methods as part of multiple research projects at the interface of human population genomics, human complex disease risk prediction, and the analysis of large-scale sequencing data. Responsibilities include programming, database construction and management, and research-related tasks. The successful candidate will take part in mining emerging genome-wide data sets, such as those being developed by the 1000 Genomes Project (http://1000genomes.org).

The ideal candidate will have a strong quantitative background involving graduate-level research in computer science, mathematics, physics, or a related field, substantial programming experience involving large data sets, and an interest in working in genetics. Previous experience in biology is preferable, but not required.

The Clark and Keinan labs are part of the broader population genomics community at Cornell focused around the recently launched Cornell Center for Comparative and Population Genomics (http://vivo.cornell.edu/all/individual/vivo/-CornellCenterforComparativeandPopulationGenomics). Competitive salaries commensurate with experience and skills will be offered, as well as generous benefits. One of the positions can be part time.

Interested applicants should send a PDF with CV and contact information for three references to ak735@cornell.edu, indicating “position 303” in the subject line. Informal inquiries are welcome.

Alon Keinan, Assistant Professor Department of Biological Statistics & Computational Biology 102A Weill Hall | Cornell University | Ithaca, NY 14853 ak735@cornell.edu | 607-254-1328 phone | 607-255-4698 fax http://keinanlab.cb.bscb.cornell.edu/ Andrew Clark, Professor Department of Molecular Biology and Genetics 227 Biotech | Cornell University | Ithaca, NY 14853 http://mbg.cornell.edu/cals/mbg/research/-clark-lab ak735@cornell.edu ak735@cornell.edu

## CSIRO Australia CottonBollwormPhylogenomics

Postdoctoral Fellowship or Research Scientist: Phylogenomics - A Comparative Study of the Cotton Bollworm Genome

The position Salary: $73K - $90K (AUD) plus superannuation Ref. No: 2009/1056 Closing date: 29 January, 2010

Applications are invited for a three-year Postdoctoral Fellowship or Research Scientist position in phylogenomics. The position will be based at CSIRO Entomology, which is part of the Black Mountain Laboratories in Canberra, Australia. The appointee will join the newly established Bioinformatics and Phylogenomics Laboratory, led by Dr Lars Jermiin, and will be involved in comparing the Helicoverpa genome and proteome to those of other insects, with the aim to improve our understanding of how these genomes and their encoded products (e.g., enzymes, metabolic pathways, etc.) might have evolved.

You will be annotating and comparing genomic and proteomic data from a range of insects with the aim to develop a better understanding of how the Helicoverpa genome and proteome have evolved in relation to these of other species. A key component of your work will be to relate your discoveries to species-specific life-history traits from the insects compared (e.g., insecticide resistance, diet, etc.). In examining these data, there is an opportunity to use CSIROs excellent high- performance IT resources. You will be expected to be strongly self-motivated and able to work collaboratively as well as independently on a variety of projects; hence, being able to multitask is highly desirable.

To be considered for this position, you will need to be an early to mid-career scientist with:

* PhD and/or postdoctoral experience in Comparative Genomics and/or relevant related areas (due to the interdisciplinary nature of this project, applicants with a PhD and postdoctoral experience in, e.g., bioinformatics and/or molecular evolution will also be well regarded) * Practical experience in relevant areas of Statistics, Computational Science and scripting languages (e.g., Python, Perl, etc) * Evidence of an ability to develop and pursue novel research approaches * Excellent communication, personal, and inter-personal skills * Familiarity with programs for genome annotation, phylogenetics analysis, whole-genome comparisons, and protein structure and function prediction * A documented record of publishing papers in international, peer- reviewed journals

For further details regarding the position and on how to apply, please go to https://recruitment.csiro.au/asp/Job_Details.asp?RefNo=2009%2F1056 Dr Lars Jermiin OCE Science Leader CSIRO Entomology GPO Box 1700 Canberra ACT 2601 Australia

+61-2-6246-4043 (pho) +61 - (mob) +61-2-6246-4094 (fax) lars.jermiin@csiro.au (email) http://csiro.au/people/Lars.Jermiin.html (web)

Lars Jermiin <Lars.Jermiin@csiro.au>

---

## Field assist Great tits Switzerland

I am seeking enthusiastic candidates interested in assisting a field study on Great tits in Bern, Switzerland. The study aims to study the influence of avian predators, through maternal effects, on life-history traits of Great tits, and possible additional effects on the ectoparasites of the tits. The great tits are a good system to examine the effects of predators and ectoparasites on life-history of birds since they readily accept nest boxes making them easy to manipulate and follow from egg laying to offspring fledging. I will require 3 field assistants that will help with all the aspects of the work, including ringing the birds, simulating predators, conducting behavioral observations and recordings, and more. The study will take place in a forest near Bern, starting roughly at mid-March 2010, and running until around the end of May 2010. Applicants with a BSc/Msc in Biology/Ecology and with bird handling experience would have an advantage. However, motivation will play a key role: the work is hard and demanding, may take place in changing weather and requires long hours at times. Motivated applicants could develop their own individual research on a topic related to the program and their own interests, and if particularly motivated could be involved in the publications. Accommodation and transportation within Europe will be provided. Some financial assistance will also be available to cover living expenses. Candidates must hold a valid European driving license. For further details please contact Michael Coslovsky at m.coslovsky@students.unibe.ch <mailto:m.coslovsky@students.unibe.ch> or at + 41 31 631 3019.

mcoslov@gmail.com

---

## FordhamU EvolutionaryEcology

This is a clarification of our ad posted on Nov 18. Specifically, we seek someone who studies invertebrates, microbes, or freshwater fish (i.e., our previous ad listed freshwater fish first, thus potentially giving the impression that “freshwater” applies to all taxa).

ECOLOGY FACULTY POSITION

The Department of Biological Sciences of Fordham University invites applicants for a tenure track faculty position at the ASSISTANT or ASSOCIATE PROFESSOR level for Fall 2010. We seek a population, community or evolutionary ecologist who studies invertebrates, microbes, or freshwater fish. The successful applicant will have access to Fordham’s biological field station - the Louis Calder Center, and our new Center for

Conservation, Evolution and Urban Ecology (CCEUE), as well as the opportunity to work with scientists at the Wildlife Conservation Society, American Museum of Natural History, the New York Botanical Garden, and other scientific institutions in the region. The successful candidate is expected to make use of local and regional resources to develop or continue a rigorous, externally- funded research program, and is expected to teach courses and mentor individual research projects at both the undergraduate and graduate level. Postdoctoral experience is expected.

Applicants should email one PDF file containing a cover letter, curriculum vitae, contact information for three references, and a research statement to thornhill@fordham.edu. The cover letter should be addressed to Dr. William Thornhill, Chair, Department of Biological Sciences, Fordham University, 441 E. Fordham Road, Larkin Hall 160, Bronx, NY 10458. Candidates will be reviewed when their applications are received and we will continue to accept applications until the position is filled. Fordham University is an independent, Catholic university in the Jesuit tradition that welcomes applications from men and women of all backgrounds. Fordham is an EOE.

Gordon Plague

plague@fordham.edu plague@fordham.edu

## France evolution

Dear all

This is to inform you about an attractive job offer in France the yearly announcement of researcher positions financed by the French Funding Organization Centre National de la Recherche Scientifique (CNRS). These are *life-time 100 % research* positions offered in an international competition to excellent candidates. The web page is http://www.sg.cnrs.fr/-drhchercheurs/concoursch/default-en.htm. Posts are available, for instance in section 20 Continental Surfaces and Interfaces (which to some degree includes ecosystem, landscape or palaeo ecology), section 29 Biodiversity, evolution and biological adaptations: from macromolecules to communities, and in interdisciplinary committees 43 and 44. The deadline, regrettably, is January, 5.

THE TYPES OF POSTS (see also

http://www.sg.cnrs.fr/drhchercheurs/concoursch/-pdf/guide-en.pdf, http://www.sg.cnrs.fr/-drhchercheurs/concoursch/pdf/metier-en.pdf including

salaries): There are 2nd and 1st degree chargs de recherche and 2nd and 1st degree directeurs de recherche, i.e. Associate Scientists after dissertation and after some years of postdoctoral experience, and Senior Scientists after about 8 or more years of experience, respectively. Please note that the announced posts of directeurs de recherche, may in reality be less numerous than announced. In the past these posts were usually de facto only for promotion of people that already have a position of a charg drecherche within CNRS. This year this seems to improve.

According to my experience already the Chargs de Recherche are actually free to do what they want within an overall, very large disciplinary category (there are some 40 categories defined for all sciences together).

The competition for such positions is tough, in particular in the section 29 Biodiversity, evolution and biological adaptations: from macromolecules to communities. Even though strange things are happening, multiple first or senior authored publications per year each with an impact factor of 4 or more seem to be useful, and Nature, Science, PNAS are highly appreciated.

Further criteria (in French) are given at http://www.cnrs.fr/comitenational/sections/critere/-section29.htm THE PROFILES If you go to http://gestionoffres.dsi.cnrs.fr/fo/offres/default-en.php you will find a number of posts offered, e.g. in the in the sections 20, 29, 45. Note that by further clicking on the numbers given to the jobs (e.g. N29/02) you will find that the Chargé positions (Associate Scientists) are often focused to more restricted fields of research. This is where often science politics comes into play. But sometimes the profiles only indicate a preference in case two equally strong candidates show up. Very strong candidates that have little to do with a published profile may in cases be preferred over weak candidates that perfectly match a profile, in particular in competitive sections.

THE RECRUITMENT PROCEDURE. Deadline for applications is, regrettably, January 5. A visit to the lab after having submitted the application seems to be very much expected in all cases. Generally, French institutions *do not* reimburse candidates the travel costs to visit labs or to come to interviews etc. Yes, this is a shame. We likely have some funds here at Rennes to pay for expenses.

Each application must contain a scientific project this project needs to be compatible with the host lab you apply to.

After having applied *all* eligible candidates will be invited to a short presentation and an interview in Paris in spring 2009. The tentative dates are given on http://www.sg.cnrs.fr/drhchercheurs/concoursch/pdf/Calendrier_2010.pdf.

Candidates should be available for the dates indicated. Travel costs will *not* be reimbursed by the CNRS, but at the level of host Units funds may be available. Presentations and interviews can be in English, French is possibly a plus. These interviews are a major effort for both, the candidates, the local labs and the national recruitment committees. For people from abroad it is thus strongly advised to apply only if they are convinced of their CVs.

I PERSONALLY COULD OFFER help in putting together an application for qualified candidates with a project willing to choose University of Rennes 1 and to work here (at least partly) on the interface between ecology and phylogeny (preferably involving plants but also other taxa). My personal web page (somewhat outdated) is given below, my team Ecology of

— / —

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

---

## IndianaStateU ChairBiology

Professor and Chair of Biology Indiana State University Terre Haute, Indiana, USA

Indiana State University invites applications for the position of Chair of the Department of Biology to begin in the fall of 2010. The department delivers programs leading to a B.S., B.A., M.S., and Ph.D. in Biology, and provides highly enrolled courses for non-majors. The Chair leads the department's efforts to maintain the highest quality of undergraduate and graduate education, enhance extramural funding for research, and advance the university's mission of experiential learning and community engagement. The Chair should also maintain an exemplary record of scholarly achievement. The successful candidate will have a Ph.D. in any area of biology and experience commensurate with the rank of Full Professor in a Ph.D.-granting department. Candidates who are currently at the rank of Associate Professor and who possess a strong record of research, teaching, and service are also encouraged to apply. The ideal candidate would also present evidence of administrative experience and effective leadership at an academic institution. Applicants should submit materials online at https://jobs.indstate.edu , including a curriculum vitae and statements of research interests, teaching experience, and administrative experience and philosophy. Applicants should have three letters of recommendation sent electronically to biologychairsearch@mama.indstate.edu. Review of applications will begin on January 4, 2010 and will continue until the position is filled. For more information, visit the department's web page at http://www.indstate.edu/biology . Indiana State University is an equal opportunity/affirmative action employer committed to excellence through diversity. The University actively encourages the applications of women, minorities, and persons with disabilities.

Dr. Elaina M. Tuttle Associate Professor Department of Biology Indiana State University Science 287E, 403-25 North 6th Street Terre Haute, IN 47809, USA

office phone: 812-237-2838 fax: 812-237-3378 email: elaina.tuttle@indstate.edu http://www.whitethroatedsparrow.org http://biology.indstate.edu "Nothing in biology makes sense except in the light of evolution." Theodosius Dobzhansky

Elaina.Tuttle@indstate.edu

---

## London RoyalSocietyJournals

We are currently recruiting an editorial coordinator to work on our journals. The job information is available at http://royalsociety.org/Editorial-Co-ordinator/ and further information about Royal Society Publishing and our journals (which include Biology Letters, Proceedings B and Philosophical Transactions B) is available at http://royalsocietypublishing.org It is an entry level publishing job, suitable for recent graduates or those with Masters/PhDs also. A first degree in a science subject is preferred and the deadline is 21 December, as we're looking to fill the position as soon as possible.

The job is based in London, UK and you must be eligible to work in this country to apply.

Thank you.

Fiona Pring Publishing Editor, Biology Letters

The Royal Society 6-9 Carlton House Terrace London, SW1Y 5AG tel +44 (0) 207 451 2654 web http://rsbl.royalsocietypublishing.org< http://rsbl.royalsocietypublishing.org/ >

*** Special features and opinion pieces, celebrating Darwin 200, available here< http://rsbl.royalsocietypublishing.org/site/misc/darwin_200.xhtml > ***

*** To keep up with all the latest Biology Letters content sign up for alerts here< http://rsbl.royalsocietypublishing.org/cgi/alerts > ***

*** Become a fan of Royal Society Publishing on Facebook here< http://www.facebook.com/RoyalSocietyPublishing.FanPage > and follow us on Twitter here< http://twitter.com/rsocpublishing >***

*** To celebrate our 350th anniversary in 2010, Royal Society Publishing will be launching several commemorative initiatives< http://royalsocietypublishing.org/seefurther > ***

Royal Society - Registered Charity No. 207043 twenty ten and beyond | 350 years of excellence in science

"Pring, Fiona" <fiona.pring@royalsociety.org>

---

## LouisianaStateU 3 ComputationalBiology

ASSISTANT PROFESSOR

(Computational Biologist/Two positions)

Department of Biological Sciences

and

ASSISTANT/ASSOCIATE/FULL PROFESSOR

(Computational Biologist)

Department of Biological Sciences & Center for Computation & Technology (CCT)

Louisiana State University invites applications for three faculty positions in Computational Biology, broadly defined. Required Qualifications: (All positions) Ph.D. or equivalent degree; successful track record of productive research; (Asst Prof) A.B.D. candidates considered, with Ph.D. by May 2010. Additional Qualifications Desired: (All positions) A computational biologist who investigates fundamental biochemical, cellular, developmental or evolutionary questions; areas of interest should include, but are not limited to: biomolecular dynamics and structure-based drug design, proteomics, bioinformatics, systems biology and interaction networks, metabolomics, evolutionary genomics, and metagenomics analyses. Responsibilities: (All positions) establishes a vigorous, extramurally funded research program; contributes to undergraduate and graduate teaching; contributes to the development of a center of excellence in Computational Biology at LSU.

The open rank professor will work closely with faculty in Biological Sciences and other departments at LSU, as well as the CCT faculty to foster the development of a center of excellence in Computational Biology at LSU. The CCT (http://www.cct.lsu.edu/home) offers an innovative and interdisciplinary research environment for advancing computational sciences, including a highly competitive computing environment with access to 100 TFlops of computing resources in conjunction with the Louisiana Optical Network Initiative (LONI). The LONI Institute (http://institute.loni.org/) is a bold new inter- university collaboration aiming to fill a dozen new faculty positions in related areas. LSU is part of the national TeraGrid. For additional information visit our departmental website: http://www.biology.lsu.edu . We encourage applications from women and minorities. Rank and salary will be commensurate with qualifications and/or experience. An offer of employment is contingent on a satisfactory pre-employment background check. Application deadline is January 29, 2010 or until candidates are selected. Apply online at: www.lsusystemcareers.lsu.edu. Asst. Prof. #034191 and Asst/Assoc/Full Prof. #034190.

LSU SYSTEM IS AN EQUAL OPPORTUNITY/EQUAL ACCESS EMPLOYER

Quicklink to Asst. Professor ad: https://lsusystemcareers.lsu.edu/applicants/Central?quickFind=51561 Quicklink to Asst/Assoc/Full Prof.: https://lsusystemcareers.lsu.edu/applicants/Central?quickFind=51562 Dr. Christopher Austin Associate Professor, Department of Biological Sciences Head Curator of Amphibians & Reptiles, Museum of Natural Science Systematics, Ecology & Evolutionary Pacific Islands Genetics Group 119 Foster Hall Louisiana State University Baton Rouge, LA 70803-3216

e-mail: ccaustin@lsu.edu tel: 225-578-2841 fax: 225-578-3075 http://www.museum.lsu.edu/Austin/lab.html AND Bryan C. Carstens Assistant Professor Department of Biological Sciences Louisiana State University

mail 202 Life Sciences Building Louisiana State University Baton Rouge, LA 70803 USA e-mail carstens@lsu.edu bryan.c.carstens@gmail.com

web http://www.lsu.edu/faculty/carstens/ office A114 Life Sciences Annex (225) 578-0960

lab A153 Life Sciences Annex (225) 578-4918

Christopher Austin <ccaustin@lsu.edu>

## MurdochU ConservationBiol

* 4 year Fixed Term appointment at Murdoch University, Perth, Australia * $82,802 to $100,036 including employer superannuation contributions and an opportunity to salary package

The School of Biological Sciences & Biotechnology welcomes your application to join a highly research active and strong teaching School at Murdoch University for a four year contract position of Lecturer (Level B, fulltime) in molecular biology and biochemistry. The successful applicant will be expected to have experience in molecular biology techniques, undergraduate teaching and research supervision.

The appointee will contribute to unit development and coordination, lecturing and laboratory teaching in units in the Molecular Biology, Forensic Biology & Toxicology and Conservation and Wildlife Biology programs.

The appointee will be expected to undertake research in projects aligned closely with the Ancient DNA and Wildlife Identification laboratories, contribute to the supervision of research students and apply for external research funds.

For further information please contact Associate Professor Carolyn Jones, on C.Jones@murdoch.edu.au or alternatively on +61 8 9360 2159.

Application procedures and a position description with detailed selection criteria are available from the University's web site at http://jobs.murdoch.edu.au/ . All applicants should address the selection criteria within their application.

Closing date: Monday, 28 December 2009

further details can be found at: https://wwwforms.murdoch.edu.au/pls/news/NEWSQIT$NITEM.QueryView?P_UNIQUE_KEY1=4980 Dr Michael Bunce Ancient DNA Lab School of Biological Sciences and Biotechnology Murdoch University South Street Western Australia 6150 Australia Em: M.Bunce@murdoch.edu.au Ph: +61 (08) 93607649 Mobile: 0406 998025 Fax: +61 (08) 9360 6303 website:http://wwwstaff.murdoch.edu.au/ ~ mbunce/ Mike Bunce <m.bunce@murdoch.edu.au>

## NewZealand TerrestrialVertCurator

The position of Curator of Terrestrial Vertebrates at Te Papa has just been advertised on our website. Here's the link which gives you all the details:-

http://www.tepapa.govt.nz/AboutUs/JobsAtTePapa/Pages/CuratorofTerrestria lVertebrates.aspx

Please pass this information on to anyone who might be interested.

Curator of Terrestrial Vertebrates The Museum of New Zealand Te Papa Tongarewa is seeking to appoint a Curator of Terrestrial Vertebrates within its Natural Environment team. The appointee will work closely with the Curator of Fossil Vertebrates and a Collection Manager. The position will have primary responsibility for Te Papa's collection of 28,000 birds and 10,000 other terrestrial vertebrates.

The successful candidate will be expected to:-

* Develop and curate all groups represented in Te Papa's collection of terrestrial vertebrates.

* Conduct biosystematic research on priority groups of New Zealand terrestrial vertebrates, preferably using both morphological and molecular techniques.

* Work proactively with the Curator of Fossil Vertebrates to develop strong research partnerships, secure external research funding, and build relationships with stakeholders in other organisations and institutions.

* Contribute to the development of Natural Environment exhibitions, visitor experience products, and outreach activities, especially in relation to terrestrial vertebrates.

* Actively develop web-based products that contribute to Te Papa's website, Collections Online and other online initiatives.

The successful applicant will have a PhD or equivalent competency, a track record of published research in terrestrial vertebrates, experience of curating or working with collections, and a commitment to outreach activities and exhibition development in a team-based museum environment.

This is a full time permanent appointment.

Applications close at 10am on Monday 1 February 2010.

For further details contact recruitment@tepapa.govt.nz and quote reference TP1020.

LeonP@tepapa.govt.nz LeonP@tepapa.govt.nz

## NorthDakotaStateU EvolutionaryBiolEducation

Faculty position in Biology Education: Open Rank

The Department of Biological Sciences at North Dakota State University invites applications for a 9-month tenure-track faculty position in biology education to begin August, 2010. The position is 40% teaching, 50% research and 10% service. Teaching duties include 1 course per semester and advisement of undergraduate/graduate students. We seek applicants whose primary research interests focus on biology education at the higher education level. Requirements include: An earned PhD by the time of appointment in biology (or biology-related field) or in science education (with a minimum of a MS degree or equivalent in biology or a biology-related field); a demonstrated research focus in education within the biological sciences; graduate-level coursework in science education; demonstrated ability to teach biology courses at both the upper-level undergraduate and graduate levels as evidenced by classroom teaching experience; strong oral, written, and interpersonal communication skills, including demonstrated ability to work/collaborate with others. An advanced appointment requires a substantial record of scholarship, demonstrated success in obtaining and leading funded research projects, and a pattern leading to national leadership in science education. Review of applicants will begin 4 January 2010 and remain open until the position is filled. For a complete detailed position announcement and electronic application, please link to the following site for submission of materials. https://www.ndsu.edu/jobs, posting number 0900255 NDSU is an equal opportunity institution. Women and minorities are encouraged to apply

craig.stockwell@ndsu.edu

## StanfordU Tech MicroAnalysis

Temporary technician, Stanford Univ. Microsatellite analysis: DNA extraction and PCR to prepare for subsequent identification. 3-5 months beginning ASAP. Please contact Deborah Gordon, dmgordon@stanford.edu with 'lab tech' in the subject

Deborah M Gordon Professor

Dept of Biology Stanford University Stanford CA 94305-5020

tel: 650 725 6364 email: dmgordon@stanford.edu website: http://www.stanford.edu/~dmgordon Deborah M Gordon <dmgordon@stanford.edu>

## UAntwerp EvolutionaryEcol

TENURE POSITION IN ECOLOGY: UNIVERSITY OF ANTWERP

The University of Antwerp has a tenure position in Ecology and Environment, with closing date 21 december 2009. The position is open to researchers in a number of broad fields, including Ecology & Environment. The position is highly competitive, aiming at researchers with a strong publication record and experience in obtaining grants, and a PhD obtained after 1 Oct 2003. The general idea is that candidates should be at the level corresponding to ERC starting grant applications. Candidates have to submit a research plan that should fit in the general theme of Ecology & Environment, and that also fits within the activities of one of the research groups in the Faculty (for example the Evolutionary Ecology group). Although the application does not have to be supported by a particular staff member, it is nevertheless advisable to discuss the research plan with an eligible group to maximize the chances. The Evolutionary Ecology Group (Herwig Leirs, Erik Matthysen, Stefan Van Dongen) is particularly interested in a combination of population biology and modelling, but all options are open. The application requires a cv and research plan. More information :

http://www.ua.ac.be/main.aspx?c=-3D*VACATURES&n=3D26394&ct=3Dc025734&e=-3D214138 Prof Erik Matthysen, Evolutionary Ecology Group, University of Antwerp

Erik.matthysen@ua.ac.be

## UArizona InsectSystematics

Assistant Professor of Insect Systematics and Curator of the Insect Collection, Department of Entomology, The University of Arizona (http://ag.arizona.edu/-ento/) Academic year appointment, Tenure-eligible. Salary will be commensurate with qualifications Minimum qualifications: A Ph.D. in Entomology or related discipline, a cutting edge command of contemporary and traditional systematic methods and demonstrated excellence in research and publication. Preference will be given to candidates with postdoctoral experience and demonstrated skills in management and development of biological collections. Nature and Purpose of the Position: The incumbent will conduct research in the area of insect systematics, oversee curation of the insect collection, participate fully in graduate and undergraduate education, and provide service to the Department, University and scientific community. Research (60%). The candidate will establish and maintain a vigorous, externally funded research program in insect systematics, with relevance to insect diversity, evolution and ecology. This position is open to specialists of any insect taxon. The incumbent will be expected to use molecular, morphological, and modern phylogenetics approaches, including historical biogeography in their research.

Curation (20%). The incumbent will maintain and expand the University of Arizona Insect Collection and enhance the collection's usefulness to serve scientists and the general public. Teaching (20%). The candidate will teach a graduate course in insect systematics and phylogeny and an undergraduate course. The incumbent will be expected to mentor graduate students in the interdisciplinary program in Entomology and Insect Science. Service (not assigned an explicit percentage). The successful candidate is expected to maintain professional competence at all times, contribute expertise to relevant professional activities both nationally and internationally, and serve on committees at the departmental, college and/or university level. To apply: Applications will be reviewed beginning February 10, 2010. Please send Curriculum Vitae, a letter describing experience and directions for research, curation and teaching; 3 reprints; and the names and addresses of 3 references to: Dr. Yves Carrière, Professor, 410 Forbes Bldg, Department of Entomology, The University of Arizona, Tucson, AZ 85721-0036, ycarrier@ag.arizona.edu The University of Arizona is an EEO/AA Employer - M/W/D/V.

Yves Carrière, Professor Department of Entomology Forbes Building, Room 410 College of Agriculture and Life Sciences The University of Arizona, Tucson, AZ 85721-0036

Yves Carriere <ycarrier@Ag.arizona.edu>

## UCaliforniaBerkeley MuseumWebDataCoordinator

People can apply to this position via the UC Berkeley job website (Job ID number 10296) at:http://-jobs.berkeley.edu/ VertNet is a new multi-institution, collaborative project that will combine the online accessibility of four distributed data networks for vertebrates: ORNIS (http://ornisnet.org), HerpNET (http:// herpnet.org), MaNIS (http:// manisnet.org/) and FishNet (www.fishnet2.net/). Together, these taxon-based web portals now serve georeferenced data on vertebrates from approximately 90 museums, 48 of which are participating in multiple portals. The majority of these institutions are in the United States, but their collections are global in scope. These data portals make museum specimen data available freely to the public and researchers, and serve information such as museum catalog number, locality information, georeferenced coordinates, and other specimen related data. The goal of these portals is to facilitate studies in conservation, ecology, and evolution. We are seeking a person to fill the position of VertNet Project Coordinator. This person will oversee integration of ORNIS, HerpNET, MaNIS, and FishNet, research in biodiversity information, and will pursue integration with other biodiversity information sites such as Encyclopedia of Life (EOL) and AmphibiaWeb, and will promote research and outreach in the field of biodiversity informatics. They must have a background in biodiversity informatics and be aware of various research (GIS, evolutionary biology, systematics) that takes advantage of these data.

40% Conduct semi-independent research in the field of biodiversity informatics, including applications of global biological collections data for conservation and evolutionary biology. Analyze these data for technological improvements to data portals, and, working closely with lead programmers, ensure implementation compatibility with existing and developing infrastructures. These investigations include surveying the status of bioinformatic resources at global natural history collections.

20% Develop grant proposals (with steering committee) to various funding agencies for the VertNET project and develop other biodiversity data portal research materials in pursuit of funding opportunities.

15% Liaise with and provide support to the VertNet steering committee and database programmers at various institutions by facilitating communications, updates and other written, oral and e-mail contacts.

15% Coordinate and ensure communication across participating institutions, and recruit new institutions to participate in the data portal. Train participants in georeferencing, mapping using GIS (Geographic Information Systems), and other research applications in evolutionary biology of these data via workshops.

10% Assist with design and test development of VertNet data portal technologies and website, such as development of phylogenetic tree applications and more user-friendly mapping and data querying abilities.

Required Qualifications: Bachelors degree or Masters degree in biology, information sciences, bioinformatics, geography, environmental sciences or other relevant discipline required. Fundamental computer skills in Microsoft Office, Google Earth, and the Internet required. Must have experience with relational databases (e.g., Microsoft Access). Ability to understand and follow technical instructions required. Excellent organizational skills and attention to detail required. Excellent communication (written and oral) and interpersonal skills are necessary. Demonstrated expertise of biodiversity informatics and its applications in evolutionary and conservation biology. Ability to quickly learn new programs required.

Preferred Qualifications: Familiarity and experience working with natural history museums and biodiversity databases (i.e., HerpNET, ORNIS, MaNIS, FishNET, and/or GBIF) and their data managers strongly recommended. Familiarity with MaNIS/HerpNET/ORNIS georeferencing methods and GIS and mapping experience strongly recommended. Familiarity with state and federal agencies, especially granting agencies, useful. Experience with website design and html scripting desirable but not required.

Salary Range: Annual salary: $37,920 to $39,456

This position is funded through August 31, 2010, with extension subject to renewed funding.

– Carol L. Spencer Staff Curator of Herpetology & Researcher Museum of Vertebrate Zoology 3101 Valley Life Sciences Building University of California, Berkeley, CA, USA 94720-3160 atrox10@gmail.com atrox@berkeley.edu TEL: 510-643-5778 /FAX: 510-643-8238

http://www.herpnet.org http://mvz.berkeley.edu/ Carol Spencer <atrox@berkeley.edu>

## UCaliforniaRiverside Tech StreamEvolutionaryEcol

Field technician position in tropical stream evolutionary ecology

Research technicians needed for a multi-disciplinary, multi- investigator study in Trinidad led by David Reznick (UCRiverside) and funded by the Frontiers for Integrative Biological Research program of NSF. Our research integrates study the interactions between ecological and evolutionary processes in montane streams. Primary duty is assisting in monthly censuses of guppy populations . The censuses include long hours of laboratory time. Qualifications: Research is in semi-remote areas of Trinidad sometimes under bad weather conditions. Applicants must be able to live and work well with others. Research requires carrying heavy packs over slippery and steep terrain. Applicants must be in good physical condition and be able to meet the demands of field research. Ability to drive a standard transmission vehicle is desirable. Applicants with first-aid/first responder training, skills in automobile maintenance, and construction skills are highly desirable. Please address these skills when applying.

Research technicians will be required to spend a minimum of 3-months in Trinidad, with possibility of extension for a year. Starting dates are flexible . Successful applicants will earn a stipend of $500/month and have their travel expenses, accommodation and insurance covered.

Send cover letter, CV and the names and phone numbers of two professional references to Andrés López-Sepulcre (andresls@ucr.edu) and David Reznick (gupy@ucr.edu).

– Thank you very much! Sincerely, Andrés

Andres Lopez-Sepulcre Department of Biology University of California, Riverside tel. +1 951 403 3199 andresls@ucr.edu

Andres Lopez-Sepulcre <andresls@ucr.edu>

## UCaliforniaSanDiego AssistMuseumScientist

Please circulate the following jog postiing: Assistant Museum Scientist position at the Pelagic Invertebrates Collection, Scripps Institution of Oceanography, University of California, San Diego.

https://jobs.ucsd.edu/bulletin/job.aspx?cat=-new&sortby=post&jobnum_in=50431 Not that the job will remain open until filled (i.e., the application period will not close on 8 Dec. as stated online).

Sincerely,

Mark D. Ohman Professor, and Curator of Pelagic Invertebrates Scripps Institution of Oceanography University of California, San Diego La Jolla, CA 92093-0218

Mark Ohman <mohman@ucsd.edu>

## UCincinnati ResearchTech PlantEvol

RESEARCH TECHNICIAN POSITION: PLANT EVOLUTIONARY GENETICS/GENOMICS, UNIVERSITY OF CINCINNATI

A full-time technician is available early 2010 in the laboratory of Regina Baucom in the Dept of Biological Sciences at the University of Cincinnati. General research in the laboratory centers on projects concerning adaptation to environmental stresses in morning glory species and other weedy plants, as well as metagenomics and plant comparative genomics. Duties will include working at the University's main campus in Cincinnati, OH and a nearby field research site. A one year commitment is desired, and preference will be given to a candidate who can commit to a second year.

The technician will be responsible for basic lab and greenhouse set-up and maintenance, the maintenance of large field and greenhouse experiments, and performing molecular genetics studies. While programming experience is desired (either perl or C), proficiency in a programming language is not required, although comfort with performing basic blasts at the command line and a willingness to learn further informatics techniques is necessary. Basic molecular techniques such as DNA isolation, PCR and cloning are also desired.

Ideally, the candidate should have a BA or BS in biology, genetics, horticulture or plant sciences, previous experience performing independent research, the ability to work well in a group environment, and the willingness to supervise undergraduates. The position is ideal for a highly motivated person interested in gaining field and laboratory skills prior to starting graduate school or other work in the life sciences.

While I cannot accept official applications until this position is created at the University level, if this would be a position in which you might be interested, please email a CV, a cover letter of qualifications and interests, and the names and contact information of three references to regina.baucom@uc.edu. Please feel free to contact me with any questions at the above email. Review of applications will begin January 1, 2010 and continue until a suitable candidate is found.

– Regina S. Baucom Dept of Biological Sciences University of Cincinnati Cincinnati, OH 45221 (706) 542-9729

gina.baucom@gmail.com

## UExeter BehaviorEvolution

Lecturer in Animal Behaviour or Behavioural Ecology

Centre for Research in Animal Behaviour, University of Exeter, UK

This new full time post is available from 1 September 2010 on a permanent basis.

The Centre for Research in Animal Behaviour (CRAB) at the University of Exeter is building an enthusiastic, integrative, interactive, and broad group in Animal Behaviour with the goal of making it an international centre of excellence. We seek future colleagues who would like to understand the why and how of natural behaviour; the neural mechanisms which control it, its function and adaptive value, and its origin, maintenance, and changes over evolutionary time.

We seek highly interactive individuals who can integrate their research programme with existing research in both the animal behaviour research group and other research groups in the school of Psychology. We have a preference for those interested in cognitive, ecological or behavioural aspects of animal signalling, mate choice, habitat choice, foraging and prey choice, orientation and navigation, behaviour phylogenetics or behaviour genetics, in the context of behaviour in the natural environment.

The successful applicant will show evidence of an original and independent research programme, an established record of high quality research publications, and preferably a record of successful applications for research funding and management of the resulting projects. You will have some experience of teaching and supervision of student projects at least at undergraduate level. You will have the opportunity to develop specialist teaching at the postgraduate and undergraduate levels in your area of research expertise.

Before submitting an application you may wish to discuss the post further by contacting Professor Stephen Lea, Head of School, email S.E.G.Lea@exeter.ac.uk.

The starting salary will be from £31,513 up to £35,469 on Grade F, depending on qualifications and experience.

Application packs are available from http://-www.admin.ex.ac.uk/personnel/jobs/L04N1527.pdf e-mail hradmin@exeter.ac.uk; quoting reference number L04N1527.

The closing date for completed applications is 12 noon 4 January 2010.

We expect to hold interviews in Exeter on 19 February 2010.

The University of Exeter is an equal opportunity employer and promotes diversity in its workforce and, whilst all applicants will be judged on merit alone, is particularly keen to consider applications from groups currently underrepresented in the workforce.

Please contact: hradmin@exeter.ac.uk

For further information please see: http://-admin.exeter.ac.uk/personnel/jobs.php?action=-job&areaid=4&jid=4324 “Croft, Darren” <D.P.Croft@exeter.ac.uk>

## UHawaii Hilo Bioinformatics

People interested in bioinformatics and modeling are encouraged to apply

Assistant Professor of Computer Science Institution: University of Hawai‘i at Hilo Location: Hilo, HI

Posted: 11/05/2009 Application Due: Open Until Filled Type: Full Time

Position Number 83782; UH Hilo (Hilo) College of Arts & Sciences, Department of Computer Science and Engineering; general funds; full-time; tenure-track; nine-month appointment; to begin August 16, 2010.

DUTIES: Teach a variety of introductory and advanced undergraduate courses in computer science; perform scholarly research and professional service in computer science; participate in on-going course and curriculum development activities; advise students; carry out departmental, professional, and university service activities.

MINIMUM QUALIFICATIONS: Ph.D. (by June 30, 2010) in Computer Science or closely related discipline from an accredited college or university; evidence of ability to teach a variety of computer science / engineering courses effectively at the undergraduate level; evidence of commitment to ongoing scholarship in computer science; ability to communicate clearly in written and spoken English.

DESIRABLE QUALIFICATIONS: Research areas of interest include, but are not limited to data modeling and visualization, Bio/Medical Informatics, and high-performance computing. Ability and willingness to teach core engineering courses and work toward ABET accreditation is also desired.

SALARY: Salary commensurate with qualifications and experience.

TO APPLY: Submit letter of application, vita, transcripts (copies are acceptable, however, official transcripts will be required at the time of hire), and statements of research and teaching interests electronically to Dr. H. Keith Edwards, CS Search Committee Chair, applycs@hawaii.edu Additionally, have three current letters of recommendation emailed directly by your references to the above address.

INQUIRIES: Dr. H. Keith Edwards, applycs@hawaii.edu

CLOSING DATE: Review of applications will begin January 15, 2010, and continue until position is filled.

Application Information

Contact: Dr. H. Keith Edwards Department of Computer Science and Engineering University of Hawai'i at Hilo Email Address: applycs@hawaii.edu

Dr.Donald K. Price Professor, Biology Department Director, Tropical Conservation Biology & Environmental Science (TCBES) Graduate Program

University of Hawaii at Hilo 200 W. Kawili St, Hilo, HI 96720

donaldp@hawaii.edu tel: 808-974-7365 Fax: 808-974-7693

http://www2.hawaii.edu/ ˜ donaldp/ http://www2.hawaii.edu/ ˜ tcbes/ http://www.hawaii.edu/uhhbiology/ http://www.epscor.hawaii.edu/

"The test of a first-rate intelligence is the ability to hold two opposed ideas in mind at the same time and still retain the ability to function." - F. Scott Fitzgerald

Donald Price <donaldp@hawaii.edu>

---

## UNebraska Lincoln ChairBioSciences

Director, School of Biological Sciences, University of Nebraska-Lincoln.

We are seeking an extraordinary individual to serve as Director of the School of Biological Sciences at the University of Nebraska-Lincoln (UNL), an AAU and Land Grant University with a total enrollment of over 24,000 students. The School of Biological Sciences (SBS) is part of the College of Arts and Sciences, and plays a central role in undergraduate and graduate education and research at UNL. SBS has 640 undergraduate majors and high enrollments in our service and pre- professional courses. The forty-six SBS faculty pursue research across the full spectrum of areas in biology; the school$B!G(Bs strategic plan (see http://biosci.unl.edu/DOWNLOADS/SBS_STRAT_PLAN_2009.pdf) is based upon a commitment to understanding biological systems at multiple organizational levels, from genes, cells, and physiology through organisms to populations, communities, and ecosystems. SBS faculty currently mentor 93 MS and PhD students, and have $33 million in competitive extramural research support, primarily from NIH and NSF.

UNL is committed, as an institution, to achieving very high levels of academic excellence, as detailed in its $B!H(B2020 Report$B!I(B (see http://www.unl.edu/svcaa/documents/2020report.pdf) , and to the continued growth and development of its Life Sciences programs. The successful candidate for Director will be a dynamic individual with outstanding scientific credentials, a commitment to quality education and the desire, ability and vision to lead the School. Candidates for this position must have a PhD degree, an outstanding record of extramural research funding, and demonstrated commitment to excellence; candidates must qualify for the rank of Professor with tenure. Candidates with research interests in any recognized biological discipline will be considered. The successful candidate will receive a competitive salary and start-up package.

Additional information about the department can be found at http://www.biosci.unl.edu . For consideration, applicants must complete the online Faculty/ Administrative form and submit application materials at http://employment.unl.edu , requisition #090659. Application materials should include a cover letter, a curriculum vitae with a full list of publications, a summary of past, current, and pending research support, the names of three references, and a brief statement of research, educational, service, and administrative interests. Inquiries regarding the position or the application process should be directed to: BioSciDirectorSearch@unl.edu, or SBS Search Committee Chair, College of Arts and Sciences, University of Nebraska-Lincoln, 1223 Oldfather Hall, Lincoln, NE 68588-0312 (Fax: 402-472-1123).

Review of applications will begin January 15, 2010 and continue until the position is filled. The University of Nebraska has an active National Science Foundation ADVANCE gender equity program, and is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers.

Etsuko Moriyama <emoriyama2@unlnotes.unl.edu>

---

## USGS SanDiego ConservationGenetics

The U.S. Geological Survey, Western Ecological Research Center, San Diego Field Station is searching for a geneticist (GS09). This is a full-time, term position initially set for 13 months, however may be extended up to 4 years. The geneticist will work with a team of scientists as a member of the Center's Conservation Genetics Laboratory located in San Diego, CA. The selected candidate will collect genetic data for rare amphibian, reptile and bird populations. Duties will include screening microsatellite loci, optimization of multiplex PCR, and analyzing genotypic and DNA sequence data. He/She will also be responsible for conducting statistical analyses of population genetic structure and play a significant role in report and manuscript preparation. Successful applicants will have completed at least 2 years of progressively higher-level graduate education in genetics, or be able to demonstrate a pattern of training that places major emphasis on population genetics. Previous experience with microsatellite and SNP development, data collection and landscape genetic analysis techniques is highly desirable. Preferred start date is February 2010.

Annual Salary: 50,547.00 - 65,712.00 USD

Full details and application instructions are posted at www.usajobs.gov. [http://jobview.usajobs.gov/-GetJob.aspx?JobID=85025316&JobTitle=-Geneticist%2c+GS-0440-09+%28CA-DEU-TERM%29&q=usgs&vw=b&re=0&FedEmp=-N&FedPub=Y&jbf565=&caller=default.aspx&pg=-1&cnme=San+Diego&rad=20&rad_units=-miles&AVSDM=2009-12-09+00%3a03%3a00]

Applications (resume and application questions) for this vacancy must be received on-line via USAJOBS before midnight Eastern Time (Washington, D.C. time) on the closing date of the announcement, December 30th, 2009. U.S. citizenship is required. Questions about the application process should be directed to Candace Azevedo (916-278-9399, wrjobs@usgs.gov).

Dr. Amy Vandergast Geneticist USGS, Western Ecological Research Center San Diego Field Station San Diego, CA 92101

avandergast@usgs.gov

–

Amy Vandergast <avandergast@usgs.gov>

## UToronto Mississauga TheoreticalEvolutionaryBiol

Assistant Professor - Theoretical Evolutionary Biologist - Job # 0900795

The University of Toronto Mississauga (UTM), Department of Biology, invites applications for a tenure track faculty position at the level of Assistant Professor effective July 1, 2010.

We are searching for a Theoretical Biologist who is asking cutting edge questions in evolutionary biology. The successful candidate may pursue purely theoretical paths of inquiry, or employ laboratory or field-based experiments in their research.

Of great interest is the scope and novelty of the proposed research. We are particularly interested in cross-disciplinary approaches designed to produce a more broadly integrated conceptual framework. Excellent opportunities exist for collaboration within the Department of Biology, other departments at UTM with strong research ties to biology, and with biology faculty at other campuses of the University of Toronto. UTM offers a broad spectrum of programs in which theoretical biology is relevant and a valuable addition to our teaching mandate. The successful applicant will have a Ph.D., an outstanding academic record, and will demonstrate potential for excellence in research and teaching. Salary will be commensurate with qualifications and experience. The appointee will be located in the Department of Biology, University of Toronto Mississauga, and will also be a member of the graduate Department of Ecology and Evolutionary Biology or Cell and Systems Biology. The graduate departments are University-wide, including UTM, the downtown (St. George) and Scarborough campuses.

The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from visible minority group members, women, Aboriginal persons, persons with disabilities, members of sexual minority groups, and others who may contribute to the further diversification of ideas.

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

We strongly encourage you to submit your application online http://www.jobs.utoronto.ca/faculty.htm . If you are unable to apply online, please submit your application and other materials to the following address:

Professor Robert Reisz, Chair Department of Biology University of Toronto Mississauga Mississauga, Ontario, Canada L5L 1C6

Email: robert.reisz@utoronto.ca.

Closing date for submissions is January 8th 2010.

Stefanovic Sasa <sasa.stefanovic@utoronto.ca>

## UWisconsin Milwaukee Biomathematics

Assistant or Associate Professor, Biomathematics, University of Wisconsin-Milwaukee

The Department of Biological Sciences, University of Wisconsin-Milwaukee invites applicants for a faculty position in biomathematics at the assistant (tenure-track) or associate professor level. We are seeking outstanding candidates with a Ph.D. in biology or a related area and with postdoctoral research experience. Applicants whose work has an aquatic focus, and with expertise in bioinformatics, genomics, computational genetics, ecological modeling, evolutionary biology, systems biology, or biological aspects of climate modeling, are preferred. The successful candidate will be expected to develop a vigorous, externally-funded research program, take an active role in directing undergraduate and graduate education, and contribute to teaching in biomathematics and core biology courses. This position is part of an interdisciplinary research initiative in Aquatic Biomathematics, involving Biological and Mathematical Sciences and the UWM Great Lakes WATER Institute. Potential applicants are encouraged to visit our websites: www.biology.uwm.edu, www.math.uwm.edu, and www.glwi.uwm.edu. To apply, please go to www.jobs.uwm.edu/applicants/-Central?quickFindQ144 . A completed application should include: cover letter, curriculum vita, statement of research goals, statement of teaching interests, and 3 representative publications. Applicants should arrange to have 3 letters of professional reference sent as pdf attachments to the departmental chair (sandgren@uwm.edu) or mailed to Biomathematics Search at the following address: Department of Biological Sciences, University of Wisconsin-Milwaukee, P.O. Box 413, Milwaukee, WI 53201. Screening of candidates will begin January 18, 2010 and continue until the position is filled. Appointment begins August 2010. UWM is an Equal Opportunity/Affirmative Action Employer.

Emily K. Latch Assistant Professor Dept. of Biological Sciences University of Wisconsin - Milwaukee 3209 N. Maryland Ave. Milwaukee, WI 53211

Email: latch@uwm.edu Tel: 414-229-4245

Emily K Latch <latch@uwm.edu>

## UZurich ResAssist EvolutionaryEcol

Research Assistant position available in the Institute for Evolutionary Biology and Environmental Sciences at the University of Zurich

The research group in Evolutionary Biology and Biodiversity led by Professor Tony Wilson in the recently established Institute for Evolutionary Biology and Environmental Sciences at the University of Zurich (http://www.zm.uzh.ch/agwilson/) is seeking a research assistant for a one-year project investigating the reproductive ecology of nearshore fishes, starting in February 2010.

Our group concentrates on the role of sexual selection in the speciation process. Integrating molecular phylogenetic, population genetic and functional genomic approaches, our work spans a broad temporal scale in an effort to derive testable hypotheses on the evolution of taxonomic diversity. Over the past several years, our research has concentrated on syngnathid fishes (seahorses and pipefish), a group of particular interest due to specialized morphological adaptations for male parental care and female-dominated competition for access to mates. This work involves ongoing collaborations with researchers in America, Europe and Australia.

The research assistant will be involved in a project studying the influence of fecundity selection on body size variation in populations of Syngnathus pipefish. Recent research has documented a positive association between ambient water temperature, body size and fecundity in nearshore pipefish species (Wilson 2009). The researcher will investigate this hypothesis in European pipefishes (Rispoli & Wilson 2008), combining the analysis of historical collections with field and common garden experiments investigating the role of ambient water temperature on growth rates and development times of captive-reared populations. This project is ideally suited for a recent Masters graduate interested in questions of evolutionary ecology in aquatic systems.

Interested candidates should submit a Curriculum vitae and statement of research interests, along with a list of references, by email or post to Tony Wilson (tony.wilson@zm.uzh.ch) before January 15, 2010. Any questions on the position can also be directed to Prof. Wilson.

Tony Wilson Assistant Professor, Evolution and Biodiversity Zoological Museum University of Zurich Room Y44J55 Winterthurerstrasse 190 CH 8057 Zurich Switzerland Tel: 41 44 635 4790 Fax: 41 44 635 4780 tony.wilson@zm.uzh.ch http://www.zm.uzh.ch/agwilson tony.wilson@zm.uzh.ch

## Vienna AdminManager PopGeneticsProgram

Administrative manager for the Vienna PhD Program in Population Genetics

We are searching for a communicative, independent person, who has very strong management skills and enjoys working in an international environment. The position is based at the Institute of Population Genetics at the Vetmeduni Vienna (http://i122server.vu-wien.ac.at/pop) and embedded in the evolutionary research community in Vienna (http://www.evolvienna.at).

Requirements:

- fluent in German and English

- PhD in one of the following disciplines: Life sciences, statistics, informatics; previous experience with population genetics is a bonus

Duties:

- Management of research grants and active participation on securing further funding for the PhD program

- Planning and coordination of training activities, workshops and meetings

- International networking with other institutions operating similar training program

- PR activities

- Administrative support of the PhD students (visa, housing, health related issues)

- Support of the PhD students in basic statistics, programming, IT

- Some limited teaching

The successful applicant will receive a postdoctoral salary including health benefits, contribution to pension funds etc. according to the FWF rules (http://www.fwf.ac.at/de/projects/personalkostensaetze.html). The position is initially for one year, but can be extended up to 12 years.

The position is available from the 15.1.2010 and the search continues until the position has been filled.

Applications should be sent to Christian Schlötterer (christian.schloetterer@vetmeduni.ac.at).

Christian Schlötterer Institut für Populationsgenetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://i122server.vu-wien.ac.at/pop schlotc@gmail.com

## WoodsHole PopulationGenetics

Dear Colleagues,

Attached and pasted below is a job announcement for a tenure track position in the Biology Department at the Woods Hole Oceanographic Institution. We are especially interested in candidates with interests in Population Genetics and Climate Change. I would greatly appreciate you sharing this announcement with potential candidates. Thank you.

Sincerely, Judith E. McDowell Chair, Biology Department Woods Hole Oceanographic Institution

The Biology Department at the Woods Hole Oceanographic Institution (WHOI) invites applications for a full-time tenure-track position. We seek exceptional candidates from the biological, mathematical and physical sciences to complement our existing interdisciplinary strengths in oceanography and marine ecology. Both theoretical and empirical approaches are welcome.

Candidates in all areas are welcome to apply; research topics of particular interest include:

Climate Change: Scientists who conduct research on the effects of climate change (including ocean acidification) on populations, communities, and ecosystems, especially in the context of large-scale or global climate processes and models.

Population Genetics: Scientists who use population genetics to address questions about the structure, dynamics, conservation, or biogeography of marine populations.

We expect to hire at the Assistant Scientist level, but we will consider an appointment at a higher level for an exceptionally qualified candidate. Successful candidates will be expected to develop an internationally recognized and externally funded research program. They also have the opportunity to advise graduate students and teach courses in the MIT/WHOI Joint Program in Oceanography. While members of the Institutions Scientific Staff are expected to provide for their salaries from grants and contracts, the Institution provides salary support when no other funding is available. Candidates hired at the Assistant Scientist and Associate Scientist without Tenure levels will receive an initial appointment for four years with salary guaranteed.

WHOI is the largest private, non-profit oceanographic institution in the world, with staff and students numbering about 1,000. Its mission is to advance our understanding of the ocean and its interaction with the Earth system, and to communicate this understanding for the benefit of society. The Institution is located in the community of Woods Hole, Massachusetts, a world-renowned center for marine, biomedical, and environmental science.

Applications may be sent by email to the chair of the Biology Department, Dr. Judith McDowell in care of Ms. Ann Sweck (asweck@whoi.edu); the candidate should include a 2-3 page research statement, a CV with the names and addresses of four references, and copies of up to three relevant publications. The application review process will begin on Jan. 15, 2010. To apply online, please visit http://jobs.whoi.edu . Female and minority applicants are particularly encouraged. WHOI is sensitive to the issues of dual career scientists and will work with applicants to address them.

WHOI is an Affirmative Action/Equal Opportunity Employer, M/F/D/V/EOE; it is also a member of the New England Higher Education Recruitment Consortium (NEHERC).

Judy McDowell <jmcdowell@whoi.edu>

# Other

## Alternatives for GenBank Submission

Dear Colleagues,

Has anyone found a less cumbersome interface than Sequin for preparing large batches (>200 individuals) of sequence data to GenBank. I've spent days tearing my hair out in the past trying to make Sequin work, and am dreading doing it again.

Along those lines, I would be interested in hearing about the experience of other submitters in dealing with GenBank submissions and subsequent processing of your annotations.

Regards,

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

email: csmith@willamette.edu csmith@uidaho.edu chris_smith@post.harvard.edu

http://www.willamette.edu/˜csmith/ChrisSmith.htm
Chris Smith <csmith@willamette.edu>

## AnimalGenetics paper

Dear Colleagues,

I am looking for the following paper which is cited in so many places but I couldn't find it in the mentioned Vol and Issue, may I request you to helpme if any send a copy of it to me:

Paper tiltle: A novel polymorphism in the bovine insulin-like growth factor binding protein-3 (IGFBP3) gene.

Maciulla JH Zhang HM DeNise SK Animal Genetics, 1997 Vol. 28,No.5,1997

Regards

Nasrollah Pirany Assistant Professor University of Tabriz Faculty of Agriculture Dept. of Animal Science 29th Bahman Bolvard, East Azarbaiejan, Tabriz, Iran. Phone (Office):+98-411-3392060- Mobile:+98-9144177930 Fax: +98-411-3356004-3345332 Alternative Email: n_pirani@tabrizu.ac.ir

Nasrollah Pirany <npirany@gmail.com>

## Apple tree samples

Dear EVOLDIR members,

I am currently starting my PhD supervised by Tatiana Giraud at the University of Paris 11. I am working on the population genetic structure of /Malus sylvestris/ (wild apple tree of Europe, known as the European Crabapple) in France to open perspectives of bioconservation in a long term. I am planning to extend my study to the European scale. I already have in hands samples of /M. sylvestris/ from several countries but I would like to increase the number of locations represented in my dataset.

More precisely, I would need wild individuals from natural forests in Europe, with a minimum of 5-10 individuals per location.

I would really appreciate if someone could help me in this task, by providing sample, or giving me geographical locations where I could get some.

Thanks a lot for your help,

Best regards,

Amandine CORNILLE

PhD student Ecology Systematic and Evolution lab Bat 360 â First floor University of Science, Paris XI 91405 Orsay

amandine.cornille@u-psud.fr

–

Tatiana

Tatiana Giraud

Departement Genetique et Ecologie Evolutives Laboratoire Ecologie, SystÃ©matique et Evolution UMR 8079 CNRS-UPS-AgroParisTech BÃtiment 360 UniversitÃ© de Paris-Sud 91405 Orsay cedex France

phone: +33 1 69 15 56 69 + 33 6 34 64 45 14 fax: +33 1 69 15 46 97

English: http://www.ese.u-psud.fr/pages_perso/-spip.php?article21 Francais: http://www.ese.u-psud.fr/pages_perso/spip.php?article41
http://www.ese.u-psud.fr/ Tatiana Giraud <tatiana.giraud@u-psud.fr>

## Arthropod Genomics Consortium

Participants at the annual symposium sponsored by the Arthropod Genomics Center at Kansas State University formed the Arthropod Genomics Consortium to increase collaboration and information exchange among the community of scientists performing genomic studies on arthropods. We are developing a wiki, at http://arthropodgenomes.org < http://arthropodgenomes.org/ > , to help the community self-assemble. Our goal is to provide a central location for information about arthropod genomics projects, bioinformatics tools, and people interested in arthropod genomics. We think this is a great way to "identify the community"; information from the wiki can be used to support white papers and grant proposals. It will also serve as a central location for links to arthropod genomics resources, news releases and meeting announcements.

We have constructed the initial wiki pages, which include templates for entering your information. Please take a moment to visit the wiki, http://arthropodgenomes.org < http://arthropodgenomes.org/ > , register and enter information about yourself and the organism or problems you study. Even if you don't work directly on a genome project, we would like to know how you would benefit from genome level knowledge. If you do work on a genome project, please list the genomic resources that currently exist for your organism(s) and what resources are needed or planned. Please encourage your colleagues to participate.

To organize such a large area, we have set up four main working groups based on research interest: 1) plant pests and beneficials, 2) vectors of disease, 3) Evo/Devo, and 4) EcoGen/PopGen. Your interests or research organism may fall into multiple categories. If so, you can list more than one.

Thank you for your participation.

Sue Brown, Director K-State Arthropod Genomics Center for the Arthropod Genomics Consortium

by

Doris R. Merrill, dmerrill@k-state.edu Program Coordinator Arthropod Genomics Center, www.k-state.edu/agc Kansas State University, Division of Biology, 318 Ackert Manhattan, KS 66506-4901 Phone: (785) 532-3482, Fax: (785) 532-6653

Plan to attend the 4th Annual Arthropod Genomics Symposium June 10 to 13, 2010, in Kansas City! Details are available at www.ksu.edu/agc Doris Merrill <dmerrill@ksu.edu>

## Astrobiology SummerProgram 2010

Please announce to your undergraduates:

Penn State's Astrobiology Summer Program - 2010 (An NSF-REU Site)

Each summer the program supports 10 students from universities and colleges across the U.S., between their freshman and senior years, to conduct research with astrobiologists (including evolutionary biologists) for 10 weeks at Penn State (6 June to 14 August, 2010). Activities also include a behind-the-scenes field trip to NASA-Goddard Space Flight Center, NASA Headquarters, the Smithsonian Air and Space Museum, as well as weekly seminars, discussion groups and a research symposium. The program covers the cost of travel (up to $500), room, and meals and provides a $4,000 stipend. For further information see http://evo.bio.psu.edu/asp/. Review of applications begins February 19th.

sbh1@psu.edu sbh1@psu.edu

## Behaviour videos

I am guest-curating a section of an upcoming exhibition of works from the Grinnell College's collections for our art gallery which is loosely centered around the emotional context of depictions of animals. As part of this, I'd like to have a looping presentation of animal behavior on video, ranging from art film, to "nature shows", to unedited footage of behavior used by for quantitative analyses. The idea is for viewers to consider how our response to animals is affected by movement itself and the context of the presentation (e.g., editing cuts, music, commentary etc.)

If you are willing to donate clips of your research video for this effort, I'd be happy to use them. I'm interested in both video of animals in natural settings (better if they are animals that are not familiar to the lay person) and video which isolates organisms in artificial environments (e.g., fish in tanks, spiders in arenas, etc.).

Give the size of digital video files, I'd appreciate it if you would contact me first to describe what you have, and we can then figure a way for me either to download it or have it sent to an email account that can accept large files.

Many thanks,

Jackie

Jonathan (Jackie) Brown Professor of Biology Biology Department Grinnell College Grinnell, IA 50112 USA

Web: www.grinnell.edu/individuals/brownj Email: brownj@grinnell.edu

phone: 641-269-3096

brownj@grinnell.edu brownj@grinnell.edu

## Bird RingOuzel samples

Hello,

I actually write my masters thesis at the University of Marburg. I am interested in obtaining genetic material (feathers or tissue) from ring ouzels (/Turdus torquatus/), specially from the breeding grounds in Europe, for genetic works. If you have any specimen you can share, please sent me an email at Bachtm[at]students.uni-marburg.de

Thanks for your time Michael

Michael Bacht (MSc student)

Philipps Universität Marburg Fachbereich Biologie AG "Allgemeine Ökologie und Tierökologie" Prof. Dr. Roland Brandl Karl-von-Frisch Str. 8 35043 Marburg - GERMANY -

Tel.: ++49 6421 28 26665 Fax: ++49 6421 28 23387

www.tieroeko.de Michael Bacht <Bachtm@students.uni-marburg.de>

## Database diArk

Dear colleague!

Recently, we have launched a major upgrade of diArk (www.diark.org), a resource for eukaryotic genome research. DiArk has been developed for researches working in any field related to eukaryotic genomics. It provides the most comprehensive and complete compilation of eukaryotic genome and EST sequencing projects worldwide. We do not only provide extensive search options, but also many meta-data like assembly coverage, genome data release dates, and BLAST search services. These data are very important, because the different databases (Broad, DOE-JGI, Sanger, NCBI, etc.) often provide access to different versions of the genomes (via their BLAST or ftp pages). We also provide downloads of genome data (contigs, supercontigs, mitochondrions, chromosomes, and many other types) of species submitted to NCBI.

Compared to the release of the first version in 2007, there are the following substantial changes:

Content: December 2009 (July 2007 in brackets) Species: 680 (516) Projects: 1421 (984) genomic DNA projects: 479 (299) Publications: 350 (269) genome files: 1500 files analysed, 240 GB of fasta files for download

These numbers do not include the many new releases and updates of already sequenced genomes!

Functionality: New search module: Genomes, allows searching for genome file release dates, coverage, GC-content, specific genome types (mitochondrial, chromosomal, chloroplast, apicoplast, etc.), and more. New result modules: Genome-file: all genome files (including files from all sequencing centers) were analysed, providing information about type, version, assembly-date, completeness, coverage, GC-content, size (GBp), contig numbers, illegal characters, accession numbers, comments. Many minor improvements.

Thus: > 160 eucaryotes have been sequenced and assembled in the last 2 years, 80 analyses of eucaryotic genomes have been published. It is obvious that sequencing is much faster than analysing. diArk has become the most important database for eukaryotic genomes.

We would be happy if diArk would be useful for your research.

With best wishes,

your diArk-Team (Bjoern Hammesfahr and Martin Kollmar)

– Dr. Martin Kollmar

Max-Planck-Institute for Biophysical Chemistry Group

Systems Biology of Motor Proteins Department NMR-based Structural Biology Am Fassberg 11 37077 Goettingen, Deutschland

www.motorprotein.de (Homepage) www.cymobase.org (Database of Cytoskeletal and Motor Proteins) www.diark.org (diArk - a resource for eukaryotic genome research) www.webscipio.org (Scipio - eukaryotic gene identification)

Mkollgr MBPC <mkollgr@gwdg.de>

## Decommissioning Drosophila species stocks 2

The UCSD Drosophila Species Stock Center will be decommissioning the majority of its D. mauritiana insert stocks. We will retain the following subset of the stocks, with an insert on each Muller element:

14021â0241.98 14021â0241.90 14021â0241.88 14021â0241.109 14021â0241.61 14021â0241.132

The stocks to be decommissioned are listed on the site:

https://stockcenter.ucsd.edu/info/welcome.php Investigators wishing to order stocks to be decommissioned should do so by January 10, 2010.

Thank you,

UCSD Drosophila Species Stock Center

Therese Ann Markow, Professor Amylin Chair in Life Sciences Section of Ecology Behavior and Evolution Division of Biological Sciences Muir Biology Building 2215 9500 Gilman Drive University of California at San Diego La Jolla, CA 92093-0116

Email: tmarkow at ucsd.edu Phone: (858) 246 0095 Laboratory: (858) 246 0402 FAX:(858) 534-7108

http://biology.ucsd.edu/labs/markow/ http://stockcenter.ucsd.edu Therese Markow <tmarkow@ucsd.edu>

## Diversity Project

Dear Colleagues,

For the sixth consecutive year, we will be running The Diversity Project, an NSF funded research opportunity designed to increase participation of under-represented undergraduate students in the marine sciences. In collaboration between UCLA and Old Dominion University, students will integrate hands-on field research in the Coral Triangle with cutting edge genetic research. The project will explore the origins marine biodiversity in the Coral Triangle in an effort to improve conservation of this remarkable ecosystems. Students are fully funded for both living and travel expenses. This year our destination is Bali, Indonesia. Visit http://www.eeb.ucla.edu/Faculty/Barber/Intro.htm for more information and on-line application.

This research opportunity has been a remarkable personal and professional experience for the students who have participated. Please encourage any students whom you believe would benefit from such an experience to apply. Applications are due January 15, 2010. For further information, please contact Dr. Paul Barber (paulbarber@ucla.edu). We look forward to hearing from you.

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

## Intelligent Design Book

Stephen Wheeler has sent the email listed below to AMAZON in response to the text by S.C.Meyer “Signature in the Cell: DNA and the Evidence for Intelligent Design”.

You can add your voice to his.

To do this you have to be a registered Amazon user, and have an account.

Go to: www.amazon.com Sign In (top of page) Click: help (small blue text link near top right) In the right-hand column (far right of screen), under Self Service, click the button: Contact Us Click the tab: E-mail (up and left of center) Leave the filed Order # blank Write in the free text field and click: send e-mail

—–

Dear Amazon,

I strongly object to Amazon’s product description for the book: “Signature in the Cell: DNA and the Evidence for Intelligent Design”.

Author: Stephen C. Meyer

Amazons description states:

“One hundred fifty years ago, Charles Darwin revolutionized biology, but did he refute intelligent design (ID)? In Signature in the Cell, Stephen Meyer argues that he did not.”

This is a lie. Based on his discovery of incalculable numbers of examples of the process of transmutation of species, Charles Darwin’s great scientific work, On The Origin Of Species, presented his thesis that the (then current) belief that species were unchanging parts of a designed hierarchy was discredited.

On The Origin Of Species presents the founding facts on which many new areas of scientific enquiry are based. Daily, scientists today make discoveries that underpin new understanding and success in human endeavours as varied as history, medicine, agriculture and biology. These scientific discoveries and technologies would simply not be possible without Darwins discovery of the facts of evolution by natural selection.

Amazons description also states:

confusion surrounds the theory of intelligent design. Frequently misrepresented by the media, politicians, and local school boards, intelligent design can be defended on purely scientific grounds in accordance with the same rigorous methods that apply to every proposed origin-of-life theory.

This is also a lie. Judge John E. Jones, was very succinct and clear in his Conclusion to the case that he heard [Tammy Kitzmiller, et al. v. Dover Area School District, et al.]. He wrote:

“ ... we have addressed the seminal question of whether ID is science. We have concluded that it is not, and moreover that ID cannot uncouple itself from its creationist, and thus religious, antecedents ... ”

This view is also the most widely held view in the scientific community. The following link will refer you on to the majority scientific views:

http://en.wikipedia.org/wiki/Intelligent_design#cite_note-unscientific-12 Whatever Signature in the Cell is, it is not the work of science its author claims. Amazon’s classification, presentation and description of this book are based on falsehoods.

I have no objection to Mr. Meyer, or his book. He is perfectly entitled to disseminate his personal religious, philosophical and political opinions, and it must continue to be listed on Amazon.

However, your customers deserve better. The listing of Signature in the Cell should reflect its religious and political nature.

May I suggest a description along the following lines?

150 years ago Charles Darwin revolutionized science through his discovery of evolution by natural selection.

In Signature in the Cell Stephen Meyer makes a comprehensive case for his philosophical hypothesis that the theory of intelligent design can be based upon recent discoveries in DNA, and cellular biology V and that this supports his fundamental objections to the adequacy of all purely naturalistic or materialistic descriptions of the natural, physical, world in which we live.

Meyer embarks on an investigation of DNA and evolution from the foundation of his own beliefs. He concludes that current evolutionary theories are lacking, and he reflects on the evidence that he presents and the arguments that, ultimately, led him to support intelligent design (ID).

Clearly defining his meaning of what ID is and is not, Meyer attempts to demonstrate that the minority argument for intelligent design theory is not based on ignorance or “giving up on science,” but instead upon our growing scientific knowledge of the information stored in the cell.

A leading proponent of intelligent design (a presentation of the mature theories of creationism and the teleological arguments for Theism), Meyer presents a compelling case that will generate heated debate, and command attention, from deists and theists around the world.

The Author, Stephen C. Meyer, Ph.D., is Director of the Center for Science and Culture at the Discovery Institute in Seattle. The Discovery Institute actively pursues religious, cultural, and legal missions.

Please make the necessary changes.

— / —

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

---

## IntelligentDesignBook 2

Hello all, Regarding submission of comments to Amazon, I was able to submit comments without an account with Amazon. There is a tab below the fields for account name and password that allows one to skip the log in. Submitting the message does still require a name and email address.

Cheers, Laurie

Dr. Laurie Dries, Ph.D. Endangered Species Biologist Watershed Protection Dept. City of Austin Austin, TX 512-974-6340 laurie.dries@ci.austin.tx.us ldries@mac.com

Laurie Dries <ldries@mac.com>

## LondonEvolutionNetwork AGM ChristmasSocial Dec3

Dear all,

The LERN year will be coming to a close at the end of the year 2009 and we would like to invite all members and potential new members to join us for our Annual General Meeting which will be followed by a Christmas Social.

LERN AGM & Christmas Social

December 3rd 2009, at 18:30

Anthropology Postgraduate Common Room

(Anthropology Department - 14 Taviton Street)

The event is free all are welcome!

Wine and mince pies will be served!

This will be a good opportunity to meet fellow LERN members and learn a bit more about LERN's activities.

We are currently looking for new LERN committee members as well as new LERN representatives for 2010, so if you think you would like to be involved in organizing LERN activities either as part of the committee or as a rep, or if you are simply curious about LERN in general and would like to meet other members join us on December 3rd.

Alternatively, if you know that you would like to be part of the next committee, you can email us at info@londonevolution.net to obtain more information on what this entails.

Opportunities to fill the following positions for 2010:

Treasurer (currently, Shakti Lamba)

Events Coordinator (currently, Gillian Pepper)

Secretary (currently, Anna Barros)

Webmaster (currently, Anna Barros)

Chair (currently, Michael DeBarra and Sandra Virgo)

Visit website http://londonevolution.net/ for information on how the event and how to get there.

We hope to see you there!

The LERN Committee

–

LERN: the London Evolutionary Research Network. E-mail info@londonevolution.net or visit http://-londonevolution.net for events and further information. New members and suggestions for speakers are always welcome!

If you do not want to receive any more emails from LERN, http://londonevolution.net/-mailinglist/?p=3Dunsubscribe&uid=-3D8d9cce993952a0074a870e7af9e6d4c0 To update your preferences and to unsubscribe visit http://londonevolution.net/-mailinglist/?p=3Dpreferences&uid=-3D8d9cce993952a0074a870e7af9e6d4c0 – Powered by PHPlist, www.phplist.com –

Gillian Pepper MSc Student - Evolutionary Psychology Brunel University

Department of Psychology School of Social Sciences Brunel University Uxbridge UB8 3PH UK Mobile: 07951 295 751 Email: ht08ggp1@brunel.ac.uk Personal web page: http://www.scienceandsociety.info Science Policy UK Network: http://network.nature.com/-groups/ukpolicy/forum/topics London Evolution Research Network: http://londonevolution.net/- Research and Media Network: http://-researchandmedia.ning.com/profile/GillianPepper ht08ggp1@brunel.ac.uk ht08ggp1@brunel.ac.uk

## London SystematicsAssocLecture and AGM 9thDec

The Systematics Association Annual General Meeting and President's lecture

Gradualism: Darwin's biggest mistake?

Prof. Richard Bateman - Royal Botanic Gardens, Kew and University of Birmingham

The Linnean Society, Burlington House, Piccadilly, London Wednesday 9th December 2009, 6 pm (following AGM at 5pm)

The meeting is open to visitors. Wine will be served after the lecture to members and guests. Please advertise this lecture as widely as you can. The associations' AGM will be held before the lecture at 5pm.

Abstract: Although Darwin's many achievements have been justly lauded worldwide during 2009, his repeated assertions that all evolutionary change is imperceptibly gradual have escaped serious criticism from modern commentators. The evidence that gradual change results in speciation is circumstantial in even the best documented cases, and usually relies on inadequate assessments of fitness. In contrast, saltational mechanisms requiring that radical and instantaneous phenotypic change leads directly to de facto speciation are still widely ridiculed in most biological constituencies, despite accumulating evidence of their viability. This lecture aims to redress the balance between gradual and non-gradual evolutionary change.

James Cotton School of Biological and Chemical Sciences Queen Mary, University of London +44 (0)207 882 3645 j.a.cotton@qmul.ac.uk http://webspace.qmul.ac.uk/jacotton/index.html http://www.sbcs.qmul.ac.uk/staff/jamescotton.html j.a.cotton@qmul.ac.uk

## London SystematicsAssocLecture and AGM 9thDec 2

Dear EvoDir,

The title of Richard Bateman's upcoming lecture is "Gradualism: Darwin's big mistake?".

I may be jumping the gun, the question mark hints at a lecture debunking this myth (though the abstract suggests something else), but I can't help but express some frustration over the habit of evolutionary biologists of enhancing their research programs (or presidential lectures) by claiming to address mistakes or solve difficulties in the Origin of Species.

Darwin had no problem with rapid evolution.

Page 148: ".... a new and improved variety might be quickly formed on any one spot, ...."

Page 310: "I may here recall a remark formerly made, namely that it might require a long succession of ages to adapt an organism to some new and peculiar line of life, for instance to fly through the air; but when this had been effected, and a few species had thus acquired a great advantage over other organisms, a comparatively short time would be necessary to produce many divergent forms, which would be able to spread rapidly and widely throughout the world."

Page 318: "There is some reason to believe that organisms, considered high in the scale of nature, change more quickly than those that are low: ...."

And then there's the first chapter, Variation under domestication. It sets up the whole argument and it is a discussion about variation between different sheep herds and about dog breeds. Darwin remarks (page 93) that "King Charles's spaniel has been unconsciously modified to a large extent since the time of that monarch".

Let's give the man a little rope. The common view in 1859, according to Darwin, was the immutability of species. That gradualism was emphasized shouldn't be surprising in this context.

John Taylor Department of Biology University of Victoria Canada

John Taylor <taylorjs@uvic.ca>

## MaxPlanck Leipzig 2 VolunteerFieldAssist RhesusMonkeys

Two field assistants for rhesus monkey research on Cayo Santiago, Puerto Rico.

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

The successful applicants will be expected to work on Cayo Santiago for 5-6 days a week, and are also required to undertake data entry and/ or processing in the later afternoon and early evenings. The volunteer assisting in the first project will collect behavioral data using focal observations. For this project it is necessary to learn up to 400 animals, living in different groups.

The second volunteer will help carrying out playback experiments as well as record rhesus macaque vocalizations. For this project it is necessary to learn to identify about 150 animals. Appropriate training will be provided, after which a good quantum of independence is expected.

We prefer applicants that stay for the entire period of 6 month. However, in the case of two very good applications for the second projects, a split into two times three months might be possible. Please apply only for one of the two projects (specify in your application!). If you apply for the second one, please mention the period of time you are interested to volunteer.

Applicants should have a Bachelor in Biology, Ecology, Animal Behavior, Physical Anthropology, Primatology, or a related field. Previous field experiences (preferably in the tropics) and knowledge of Spanish is helpful, but not necessary. In general, applicants must be in good physical and mental condition; feel comfortable being far away from family and friends; be emotionally mature, energetic, and very patient; have an excellent eye for detail; dont be afraid of approaching monkeys (!); willing to work in a small team setting and follow instructions; be able to maintain a positive and humorous attitude towards challenging and tiring work.

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

At the moment there is NO financial support available. It is aimed that accommodation costs are shared by the two candidates (450 UD-$/ month for two people). However, if for whatever reason, this is not possible, one candidate needs to be able to pay the entire rent. After very good performance and upon approval of pending grant application, we might be able to partially offset some of the living costs.

Term of Appointment: 10th March until 30th August 2010

Application Deadline: 10th of January 2010

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

Contact Information: Dana Pfefferle danapfefferle(at)googlemail.com

Dana Pfefferle <danapfefferle@googlemail.com>

## Microsatellite genotyping software answers

'Dear all, below a selection of the responses I got regarding the question of available open source/free microsatellite genotyping software. Thanks for all the great suggestions, this helps a lot.

Peter

>ABI just came out with a free software for scoring alleles (based on profiles from an ABI machine, of course). It's called Peak Scanner. Does some of the same things that you can do in Genotyper or Genescan - but better because it's free. I've been using Peak Scanner lately, it's very user friendly - quite simple really, in practice and scope, which may or may not be a limitation for some people. It seems to work great for me. Hope this helps.

>Strand from the University of Davis which is very stable software and quite user-friendly once you learn how it works. You can find it here:

http://www.vgl.ucdavis.edu/informatics/strand.php There is a good user manual and FAQ. It can handle files from ABI sequencers both capillary and slap gels.

There is no automatic binning procedure (allele size are just rounded) but you can export the exact allele size (in pb) and then binn your alleles using various available methods, for instance:

FlexiBin (excel macro) : http://www.zoo.cam.ac.uk/-zoostaff/amos/ Amos et al. 2006 Mol Ecol Notes

MsatAllele (R package) : which specifically refered to STRand http://www.ccmar.ualg.pt/maree/-software.php?soft=msatalle Alberto 2009 Journal of Heredity

Allelogram : may also be usefull. Morin et al., 2009 Mol Ecol Ressources 9 (6)

>We have recently developed a PERL pipeline for dealing with microsatellite data called P2EMA. It is meant to easy the painful task of dealing with microsat data. P2EMA is a Perl/Tk graphical user interface (GUI) that facilitates several tasks when scoring microsatellites. It does so by implementing new subroutines in R and PERL and taking advantage of features provided by previously developed software such as PeakScanner, CREATE and AlleloBin. P2EMA allows running PeakScanner easily from the commandline, analysing

markers from several multiplex groups simultaneously, manual bin definition through a new R script (Binator), direct bin definition through AlleloBin and file conversion through CREATE.

Please, do not hesitate to send us any comments on your experience with P2EMA and recommendations as how it could be improved. You can get the P2EMA pipeline and post your comments at the P2EMA project webpage:

http://sourceforge.net/projects/p2ema/ An application note has been submitted to Bioinformatics:

F Palero, F González-Candelas and M Pascual (submitted) P2EMA (Perl Pipeline for Easy Microsatellite Analysis) - a user-friendly package. Bioinformatics.'

Peter Hoebe Crop & Soil Systems Scottish Agricultural College King's Buildings Edinburgh EH9 3JG

+44 (0)131 535 4370

Peter Hoebe <Peter.Hoebe@sac.ac.uk>

## Microsatellite software answers

Hi all, thanks so much for all the answers!!! I asked for a software that could identify individuals with the same microsatellite profile among several loci. There's some of the sugestions that I received:

Excel adds: GenAlEx GENECAP (Wilberg, M.J. & Dreher, B.P., GENECAP: a program for analysis of multilocus genotype data for non-invasive sampling and capture-recapture population estimation. Molecular Ecology Notes 4, 783-785 (2004).)

Others: GenoDive http://www.bentleydrummer.nl/software/software/GenoDive.html Geneclone, but this one not allows non-available data Cervus http://www.fieldgenetics.com/pages/home.jsp - just click on "Identity checker" GenClone 2.0 http://www.ccmar.ualg.pt/maree/software.php?soft=genclon Microsatellite toolkit http://animalgenomics.ucd.ie/sdepark/ms-toolkit/ R (AutocoR) New Hybrids MSA http://i122server.vu-wien.ac.at/MSA/MSA_download.html Dropout http://www.fs.fed.us/rm/wildlife/genetics/software Network

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

sibelletorres@gmail.com

## Migrate-n SNPs

Dear EvolDir members,

I'm running MIGRATE-n on my SNP dataset using the old SNP data format to force the model into the nucleotide (N) option. So, may data looks like this:

N 15 22 Mig. with Snp (15 populations and 22 loci) 2 1 1 2 1 3 1 1 2 1 1 1 1 1 1 2 2 1 1 5 5 1 28 Alesund # SNP16 locus with two linked snps Zm751 GA Zm753 GA ... # SNP20 locus with a single snp Zm751 C Zm753 T ... ...

As you can see I have some SNPs that are linked and some that are not for 15 locations. All SNP loci are biallelic, but an individual can be heterozygous (e.g. ind. in SNP20 can either be C, T, or Y). To estimate the migration rate between the locations I use the "Nucleotide-polymorphisms" datatype model made for SNPs. If I start the program it runs OK, however there is problem. The "Nucleotide-polymorphisms" model uses the same options as the "Sequence" datatype model. So, you must specify a transition/transversion ratio (ttratio) for the SNP loci. I don't see how that is possible with biallelic loci, and if I run the program in default it comes up with really weird numbers for the ttratio. For instance, for SNP20 the base frequencies are (A C G T): 0.0000 0.8495 0.0000 0.1505 and the ttratio becomes 782516622752057151979520 0.0000 !!!!! With the linked SNPs this problem is less severe because you have, in general, more then two bases (MIGRATE-n handles the linked SNPs as a sequence).

Has anybody working with MIGRATE-n and SNP datasets encountered similar problems and what would be the effect from this on the estimates of migration? Any suggestions and tips will be greatly appreciated.

Thanks

Steven Ferber Ph.D student Department of Marine Benthic Ecology and Evolution Center for Ecological and Evolutionary Studies University of Groningen Biological Center Postbus 14 9751 NN Haren The Netherlands

Telephone : +31 (050) 363 2126 FAX : +31 (050) 363 2261 E-mail: S.Ferber@rug.nl

p227249@rug.nl p227249@rug.nl

## Pheidole microsatellite primers

Dear all,

I am a graduate student working on caste determination in Pheidole ants. One of the dissertation projects I am interested in pursuing examines potential patriline-biased effects on the production of different worker castes in P. spadonia, P. rhea, and P.obtusospinosa. We have currently found one microsatellite primer (Ppal-77) that is suitable for such a study but am having trouble finding additional primers that will help strengthen conclusions drawn from my study. We have also tried Ppal-03, Ppal-33, and Pmeg-11 but these markers did not yield any alleles or showed alleles that are not variable in the three Pheidole species above.

Ppal-77, Ppal-33, and Ppal-03 were used in:

Fournier et al. (2002) Investigation of the population genetic structure and mating system in the ant Pheidole pallidula. Molecular Ecology. 11: 1805-1814.

Pmeg-11 was used in:

Fournier et al. (2008) Isolation and characterization of microsatellite loci from the invasive ant Pheidole megacephala. Molecular Ecology Resources. 8: 919-922.

Is anyone familiar with the other primers listed in the two papers above? If so, which ones may be worth testing in my three species of interest? Or, are you aware of any other cross-species microsatellite primers used on closely related species that may work? Please contact me at mhuang@ag.arizona.edu if you have any advice. Any help you can provide will be greatly appreciated.

Sincerely,

Ming Huang PhD Candidate University of Arizona Dept. of Entomology

mhuang@cals.arizona.edu mhuang@cals.arizona.edu

## Query for Drierite

Dear EvolDir members,

I am a Ph.D. student working on Drosophila melanogaster. I would like to do a desiccation assay on the Drosophila populations maintained in my lab. I have several queries in this regard and require your guidance.

1) I would be using Drierite as a desiccant in these assays. There are several varieties of drierites commercially available with particles of 4-mesh, 6-mesh and 8-mesh size. Now which particle size should I use for the assay. I would be doing the assay in glass vials of dimension 30cm length x 9cm diameter, with 10 flies in each vial.

2) While doing this assay, can inclusion of desiccant in the vials ensure complete dryness? Or do we have to keep the vials in a desiccating chamber as well with provisions of Oxygen supply.

I would be very grateful if you could kindly provide me these information and help me in this matter.

Thanking You,

Sreoshi

Sreoshi Chatterjee Ph.D. scholar, Evolution and Behaviour Ecology Lab, School of Life Sciences, Jawaharlal Nehru University, New Delhi - 110067

sreoshi chatterjee <sreoshichatterjee@gmail.com>

## Smithsonian Internship TreeFrogs

Smithsonian Tropical Research Institute: Internship in Ecology, Evolution & Behavior of Tropical Treefrogs.

Three-month NSF-funded internships for American (citizen or permanent resident) and Latin American students in the Warkentin/Vonesh lab in Gamboa, Panama during the summer of 2010. Participate in cutting-edge ecological research in a biologically rich rainforest environment as part of a diverse and dynamic international community of scientists. Application deadline: January 15, 2010.

For more information on the project or how to apply, visit the Warkentin Lab website: http://people.bu.edu/kwarken/ kwarken@bu.edu kwarken@bu.edu

## Software FamilySim

Hi,

The program “Kinship” had a very useful simulation tool that allowed users to generate simulated individuals of known relatedness based on the user’s allele frequencies. These data could then be used to: (1) assess how much resolution to expect from a given data set (in terms of detecting relatedness patterns); and (2) generate distributions of expected values that could be used for hypothesis testing.

I am not aware of another program that has this functionality, so I have written one. The program is called “Family-Sim” and can run on Windows or LINUX operating systems. It takes a user’s allele frequency file and generates a user-defined number of pairs of individuals of known relatedness (parent-offspring, full-sibs, half-sibs, and unrelated). The output is a genotype file of these individuals that can be run through any relatedness program. I imagine (or at least hope!) that this will be useful to a large number of people, particularly given that these simulations can be analyzed by any relatedness program, rather than being limited to Kinship.

There is not, and will not likely be, a paper describing this program, but it can be downloaded at the following site: http://web.me.com/tfrasier/Frasier_Lab/Software.html Sincerely, Tim Frasier

Timothy R. Frasier Department of Biology Saint Mary’s University 923 Robie Street Halifax, NS B3H 3C3 Canada E-mail: timothy.frasier@smu.ca Tel: (902) 491-6382

Timothy Frasier <timothy.frasier@SMU.CA>

## Software for AFLP data scoring

Dear Evoldir members,

We are analyzing AFLP data from high numbers of individuals.

We would like to know if there is any open source software for automated data scoring and individual genotyping?

We are particularly interested in the resulting data matrix of fragments presence/absence in the samples.

If you know of any user friendly freeware, we would really appreciate your recommendations!

Thanks

Alessia Cariani

Alessia Cariani, PhD

Molecular Genetics for Environmental & Fishery Resources Laboratory -GenMAP- Interdept. Center for Research in Environmental Sciences -CIRSA- via Sant’Alberto, 163 - 48100 Ravenna Ph. +39 0544/937311 - Fax +39 0544/937411

“alessia.cariani” <alessia.cariani@unibo.it>

## Software for AFLP data scoring answers

Dear Evoldir members,

please find copied below all the answers we receive about open source software for automated AFLP data scoring and individual genotyping

Thanks

Alessia Cariani

FROM Roland Schultheiss [Roland.Schultheiss@bio.uni-giessen.de]

Hi Alessia,

we’re having the same issue at the moment in our lab. Hence, I would highly appreciate if you could share the answers you receive with the list. Until now, one of the best solutions we have found is the R package “rawGeno” (< http://www2.unine.ch/webdav/site/ebolab/shared/Programs/Biology08Poster.pdf > http://www2.unine.ch/webdav/site/ebolab/shared/Programs/Biology08Poster.pdf). However, our experience with the package is still limited... By the way: have you considered “Genemarker” from softgenetics (< http://www.softgenetics.com/GeneMarker.html > http://www.softgenetics.com/GeneMarker.html)?

Best regards, Roland

FROM Ben Holt [b.holt@uea.ac.uk]

This is the business:

< http://www.shef.ac.uk/molecol/software˜/aflpscore.html > http://www.shef.ac.uk/molecol/software˜/aflpscore.html

FROM Yael Kisel [y.kisel06@imperial.ac.uk]

Hi Alessia,

I’ve just been investigating AFLP scoring software myself - I’m doing AFLPs on a bunch of orchid species and don't have time left in my PhD for scoring it all by hand! Or the patience =)

Here is my short list of (free) programs to try -

RawGeno - an R package - very quick and easy to use, takes files generated by PeakScanner, which is a free ABI program for looking at .fsa files . .. but I still don't totally understand how it does the scoring, I plan to check on that more.

AFLPScore - another R-based program, which uses files generated by GeneMapper (not free, but maybe you could make the right files in PeakScanner) - I haven't tried this yet, but it also calculates error rates . ..

tinyFLP - a standalone small program that is very fast . ..

and there is an R package called AFLPdat for managing AFLP data in R, which sounds really useful but I also haven't tried yet (I really have just started on analysis).

I'll be really interested to hear what responses you get!

best and good luck,

Yael

FROM Wolfgang Arthofer [Wolfgang.Arthofer@uibk.ac.at]

Hi Alessia,

in June 2009 I published a free package for automated binning of AFLP data; see ref

Arthofer W. (2009) tinyFLP and tinyCAT: software for automatic peak selection and scoring of AFLP data tables. Molecular Ecology Resources,

doi: 10.1111/j.1755-0998.2009.02751.x.

The software works with exported PeakScanner tables, so its mandatory that your AFLPs were run on an ABI platform. It has no fancy interface, but creates relieable 0/1 matrices and infiles for MrBayes and Genalex very fast. Actually, I am working on an additional program to find optimal scoring parameters for a given dataset, this program will be availabe sometimes in early 2010.

If you want to test the program you can download it at < http://sourceforge.net/projects/tinyflp/ > http://sourceforge.net/projects/tinyflp/ (use the 'View all files'

button that will appear!); I would appreciate any feedback if the software was helpful.

regards,

Wolfgang

FROM Licia Colli [licia.colli@unicatt.it]

Try Genographer! It can read ABI data and return 0/1 matrix.

FROM Jérôme Vrancken [jerome.vrancken@uclouvain.be]

Hi;

To my knowledge, this is the only one that is free, user-friendly and that works.

Genographer: < http://hordeum.oscs.montana.edu/genographer/ > http://hordeum.oscs.montana.edu/genographer/

FROM "Kai N. Stölting" [kai.stoelting@access.uzh.ch]

In general, there are several relevant other papers on BMC genomics on the optimization of AFLP experiments. Have a look.

Eukaryotic transcriptomics in silico: Optimizing cDNA-AFLP efficiency

*Kai N Stolting* email < <mailto:kai.stoelting@access.uzh.ch> mailto:kai.stoelting@access.uzh.ch>, *Gerrit

Gort* email < mailto:gerrit.gort@wur.nl>, *Christian Wust* email < <mailto:christian.wuest@math.uzh.ch> mailto:christian.wuest@math.uzh.ch> and *Anthony B Wilson* email <

— / —

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

## Software IMa2 IsolationWithMigration

The IMa2 program is available. This is a program for isolation-with-migration analyses for data from multiple populations. The program was written by Jody Hey, Sang Chul Choi, and Rasmus Nielsen.

Windows executable, linux/unix/mac archive, source code, and documentation for IMa2 can be obtained from the Heylab website

http://genfaculty.rutgers.edu/hey/software#IMa2
IMa2 is for samples for anywhere from 1 to 10 populations. The user must specify the phylogenetic tree.

The program does pretty much everything that the earlier IMa program does, plus several new things. This means that even people using IMa for two populations will want to consider using the new program.

Another program, IMfig, is a companion program to IMa2 for generating nice figures of the Isolation-with-Migration model that is estimated from their data. This program is also available from my website

There are two papers that describe these programs and they are now in press:

Hey, J. in press. Isolation with Migration Models for more than Two Populations. Molecular Biology and Evolution in press.

Hey, J. in press. The Divergence of Chimpanzee Species and Subspecies as Revealed in Multi-population Isolation-with-Migration Analyses. Molecular Biology and Evolution in press.

If you or your institution subscribes to MBE you can get them from MBE advance access http://mbe.oxfordjournals.org/papbyrecent.dtl Jody Hey Professor, Department of Genetics Rutgers University Nelson Biological Labs (rm B326) 604 Allison Rd. Piscataway, NJ 08854-8082

732-445-5272 fax 732-445-5870 hey@biology.rutgers.edu http://genfaculty.rutgers.edu/hey/home "Hey, Jody" <Hey@Biology.Rutgers.Edu>

## Software P2EMA MicrosatAnalysis

"Dear Evoldir members,

We have noticed some recent posting asking for an open source microsatellite genotyping software. We have recently developed a PERL pipeline for dealing with microsatellite data called P2EMA, and would like to make it open for anyone to try it and tell us how could it be improved.

P2EMA is a Perl/Tk graphical user interface (GUI) that facilitates several tasks when scoring microsatellites. It does so by implementing new subroutines in R and PERL and taking advantage of features provided by previously developed software such as PeakScanner, CREATE and AlleloBin. P2EMA allows running PeakScanner easily from the commandline, analysing markers from several multiplex groups simultaneously, manual bin definition through a new R script (Binator), direct bin definition through AlleloBin and file conversion through CREATE.

Please, do not hesitate to send us any comments on your experience with P2EMA and recommendations as how it could be improved. You can get the P2EMA pipeline and post your comments at the P2EMA project webpage:

http://sourceforge.net/projects/p2ema/ An application note has been submitted to Bioinformatics:

F Palero, F González-Candelas and M Pascual (submitted) P2EMA (Perl Pipeline for Easy Microsatellite Analysis) – a user-friendly package. Bioinformatics.

Thanks!

Ferran"

–

FERRAN PALERO Evolutionary Genetics (Floor 1) Institute of Science and Technology Austria (IST Austria) Am Campus 1 A – 3400 Klosterneuburg Austria e-mail: fpalero@ist.ac.at phone: +43 (0)2243 9000 3004

"Mathematics knows no races or geographic boundaries; for mathematics, the cultural world is one country" - David Hilbert -

"...at this rate a man might as well go into a gravel-pit and count the pebbles and describe the colours. How odd it is that anyone should not see that all observation must be for or against some view if it is to be of any service!" - Charles Darwin -

Ferran <fpalero@gmail.com>

## SouthAfrica VolunteerFieldAssist MouseEvolution

Volunteers needed as field assistants for the project:

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

>From May 2010 onwards

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

Project: We study the evolutionary and ecological reasons of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

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

Work of field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers are also expected to help with maintenance of the research station (water pump, solar power, etc.)

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

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1000 (around 90 Euro) must be paid for accommodation at the research station. For students with their own undergraduate project, a fee of Rand 1250 (approx. 110 Euro) per month applies. Students must buy their own food etc in Springbok (costs of about R 2000 or 170 Euro/month). Including extras, you should expect costs of about 300 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

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

When and how long: At the moment we are looking for volunteers to start in May 2010 and especially for the period June to November 2010. Volunteers are expected to stay at least 2 months, but longer periods of up to 6months are preferred.

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

More information under www.stripedmouse.com Contact via e-mail: carsten.schradin@zool.uzh.ch

Dr. Carsten Schradin

Research Assistant, Zoological Institute, Department of Animal Behavior,

University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland.

Tel: +41 - (0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences,

University of the Witwatersrand, South Africa.

WORKING AS A FIELD ASSISTANT IN GOEGAP NATURE RESERVE

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

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

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

After arriving in Goegap, right the next morning my scientific adventure in South Africa began: Setting and checking traps, nest observations and radio-tracking were our daily routine. While I got bitten by the mice quite often in the beginning and my right middle finger was scarred all over, I improved quickly shaking the mice out of the traps, weighing them and checking the number of the ear tag. Other duties like cleaning the cages of the mice in the captive colony, washing the dirt from probably several months out of the traps, painting the new Wendy House and putting in a floor and curtains quickly added to our daily field work activities.

— / —

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

## UCollegeLondon MedawarLecture Nov25

Dear all,

In conjunction with the CEE (Centre for Ecology and Evolution -http://www.ucl.ac.uk/~ucbtcee/-), the London Evolutionary Research Network (http://londonevolution.net) is hosting the annual Medawar Lecture.

This year we are pleased to announce a lecture by Sir Patrick Bateson, Emeritus Professor of Ethology at the University of Cambridge:

Evolutionary Theory Evolving

Location: JZ Young Lecture Theatre, Anatomy Department, UCL

Time & Date: 18.30, Wednesday 25th November 2009

For information on this event, including directions to UCL, please visit the LERN website (http://londonevolution.net/?p=131).

The event is free and everyone is welcome!

The LERN Committee

–

LERN: the London Evolutionary Research Network. E-mail info@londonevolution.net or visit http://londonevolution.net for events and further information. New members and suggestions for speakers are always welcome!

Gillian Pepper MSc Student - Evolutionary Psychology Brunel University

Department of Psychology School of Social Sciences Brunel University Uxbridge UB8 3PH UK Mobile: 07951 295 751 Email: ht08ggp1@brunel.ac.uk Personal web page: http://www.scienceandsociety.info Science Policy UK Network: http://network.nature.com/groups/ukpolicy/forum/topics London Evolution Research Network: http://londonevolution.net/ Research and Media Network: http://researchandmedia.ning.com/profile/GillianPepper Gillian Pepper <ht08ggp1@brunel.ac.uk>

# PostDocs

## AarhusU FishPopulationsGenetics

Postdoc in Fish Populations Genetics and Genomics

A three-year postdoctoral position will be available at the Department of Biological Sciences, Aarhus University, Denmark, starting 1 March 2010 or as soon as possible.

The appointed postdoc will assist Michael M. Hansen (Head of Department) in his research, teaching and student supervision activities. A major part of the research concerns a project on speciation and footprints of selection in Atlantic Anguillid eels (European and American eel). The project involves, among others, a SNP based genome scan and is partly based on unique samples of eel larvae collected in the Sargasso Sea. This is a collaborative project with Thomas Damm Als and Dorte Bekkevold, Technical University of Denmark, Silkeborg, and with Louis Bernatchez (Université Laval, Quebec, Canada) and Gregory Maes (Catholic University of Leuven, Belgium). Furthermore, a Ph.D. student will be recruited to the project.

The postdoc will also be involved in other collaborative projects: one with Øystein Skaala and Kevin Glover (Institute of Marine Research, Norway) concerning QTL mapping of Atlantic salmon in a natural setting, and another project concerning population genetic studies of brown trout, particularly implementation of SNP markers and landscape genetics (with Dorte Bekkevold, Technical University of Denmark, Silkeborg).

Internally at the department there are also excellent relevant collaboration partners, particularly the research groups of Volker Loeschcke, Cino Pertoldi and Trine Bilde.

The position furthermore involves participation in teaching a 3rd-4th year course in Conservation Genetics.

Applicants should have a Ph.D. in evolutionary biology and/or population genetics and must document cutting-edge skills in statistical analysis of molecular markers/population genetic data and excellence in writing scientific papers. Applicants who can document skills in bioinformatics will receive particularly serious consideration. Finally, applicants should be ambitious, show strong capabilities for team-work, and should also be able to take initiatives and responsibility.

Applications should include a CV, publication list, a 1-2 pages description of research experience and research interests, and the names and contact details of three persons, who would be willing to send a letter of recommendation.

The Department of Biological Sciences offers an ambitious, scientifically very strong but also socially pleasant working environment. For more information about the Department of Biological Sciences, see www.biology.au.dk For more information about Michael M. Hansen's research, see www.michaelmhansen.dk For further details on the position, please contact Michael M. Hansen (mmh@biology.au.dk)

Applications MUST be submitted online before 1 February 2010. See http://science.au.dk/en/positions-and-fellowships/academic-positions/ "\"Michael Møller Hansen\"" <mmh@biology.au.dk>

---

## Bangalore ModelOrganism PopulationGenetics

POSTDOC: POPULATION GENETICS OF WILD POPULATIONS OF MODEL ORGANISMS

A postdoc position is available in the lab of Dr. Uma Ramakrishnan at the Department of Ecology and Evolution at the National Centre for Biological Sciences, TIFR, Bangalore, India.

We are interested in the processes governing the response of species to environmental history, climatic perturbation and human history in the context of species ecologies, to gain a better understanding of their evolution. In practical terms, our research focuses on revealing the processes that drive patterns of mammalian genetic variation (in the present and the past). We use field-collected samples, assemble molecular genetic data and analyze these data with phylogenetic, phylochronologic, phylogeographic and population genetic inferences. Much of our research over the last few years has focused on the Indian subcontinent because of (1) its geographic setting, representing the intersection of three major biogeographic realms (Palearctic, Africotropical, Indomalayan); (2) its geologically dramatic history, driven by plate tectonics, volcanism and climatic change; (3) its ecologically diverse habitat types from the highest mountains on earth to very dry deserts and tropical forests, including biodiversity hotspots; (4) the presence of Homonins in India for perhaps one million years, and modern humans in relatively high (and ever increasing) densities for about 70,000 years impacting the Indian biota; and finally the fact that (5) virtually nothing is known about patterns of genetic variation in native Indian species, and even less is known about the impact of climate on species in this region in particular.

Given current advances in genomic methods and technology, we would like to extend our research to investigate evolutionary and population level processes in model organisms (and close relatives) that live in the wild, such as Mus musculus (house mouse), Rattus rattus (brown rat), Macaca mulata (rhesus macaque) and Macaca radiata (bonnet macaque). We will start by investigating population demographic history and structure and move to signatures or selection and comparative studies between species. For further information, please contact Uma Ramakrishnan with a CV at uramakri@ncbs.res.in.

Uma Ramakrishnan <uramakri@ncbs.res.in>

## CSIRO Australia MolecularPhylogenetics

Postdoctoral Fellowship: Molecular Phylogeny - Inference of Ancestral DNA and Protein

The position Salary: $73K-$80K (AUD) plus superannuation Ref. No: 2009/1010 (This is a previously advertised position, previous applicants need not reapply) Deadline: 29 January, 2010

Applications are invited for a three-year Postdoctoral Fellowship in molecular phylogenetics. The position will be based at CSIRO Entomology, which is part of the Black Mountain Laboratories in Canberra, Australia. Joining the newly established Bioinformatics and Phylogenomics Laboratory led by Dr Lars Jermiin, the appointee will develop, test and use phylogenetic methods to infer ancestral nucleotide and/or amino acid sequences under general conditions.

You will be responsible for the development, implementation, and testing of software to estimate ancestral nucleotide and/or amino acid sequences. In writing this software, there is an opportunity to develop it for use on CSIRO's excellent high-performance IT resources. Having developed this software, you will apply it to infer ancestral nucleotide and/or amino acid sequences of genes and/or gene products with useful and/or interesting properties. You will be expected to be strongly self-motivated and able to work collaboratively as well as independently on a variety of projects; hence, being able to multitask is highly desirable.

To be considered for this position, you will need:

* PhD in Phylogenetics or related bioinformatics area (e.g. Statistics, Molecular Evolution, and Computational Science) * Experience in relevant areas of Computational Science and software development (e.g., C, C++, and Java) * Evidence of ability to develop and pursue novel research approaches * Evidence of developing skills in communicating with diverse audiences * Familiarity with phylogenetic programs, and how to write such programs

For further details regarding the position and on how to apply, please go to https://recruitment.csiro.au/asp/-Job_Details.asp?RefNo=3D2009%2F1010 — Dr Lars Jermiin OCE Science Leader CSIRO Entomology GPO Box 1700 Canberra ACT 2601 Australia

+61-2-6246-4043 (pho) +61 - (mob) +61-2-6246-4094 (fax) lars.jermiin@csiro.au (email) http://csiro.au/-people/Lars.Jermiin.html (web)

Lars.Jermiin@csiro.au Lars.Jermiin@csiro.au

## CSIRO Canberra Phylogeographer

PostDoctoral Fellow - Spatial Biodiversity Analyst-Phylogeographer

https://recruitment.csiro.au/asp/-job_details.asp?RefNo=2009/974 The Centre for Plant Biodiversity Research at CSIRO Plant Industry requires a qualified, skilled and motivated scientist to research spatial biological information from the Australian National Herbarium together with phylogenetic data and environmental attributes (such as climate, terrain, soils) to map spatial patterns of biodiversity in environmental space. The appointee will develop and test hypotheses relating to contemporary distribution of particular plant groups in relation to phylogenetic relationships as well as developing predictive approaches to conservation planning at regional and national scales.

The successful applicant will work in a team to develop and maintain standards for the capture, management, visualization, analysis and delivery of the spatial content in the organization's databases, as well as to validate and maintain the spatial data quality. The successful applicant will further develop this team by leading collaborations among CSIRO Plant Industry, the Biodiversity Theme (BRABA) and non-CSIRO scientists throughout Australia and internationally.

Location: Canberra, Australia Salary: $73k to $80k Reference: 2009/974 Term - 3 years (36 months) Close date: 31 December 2009 Contact: Should you require more information on this position please contact Dr Joe Miller by email: Joe.Miller@csiro.au Application information is available on https://recruitment.csiro.au/asp/job_details.asp?RefNo=2009/974 Joe.Miller@csiro.au

## Gainesville ComputationalBiol

I have an opening in my laboratory for a geneticist/computational biologist.

POSITION: Computational Biologist/Research Geneticist

LOCATION: Gainesville, FL

DESCRIPTION OF DUTIES: The position is located in the Center for Medical, Agricultural, and Veterinary Entomology, Imported Fire Ant and Household Insects Research Unit at Gainesville, Florida. The researcher will interact closely with a dynamic group of researchers (including collaborators from University of Lausanne and elsewhere) with expertise in population and evolutionary genetics, functional genomics, and bioinformatics. The incumbent will be a member of a team investigating the population and evolutionary genomics of fire ants through large-scale analysis of whole-genome sequence data. The project will involve comparative genomic studies in fire ants as well as across Hymenoptera, design and use of SNP markers for genetic mapping and population genomic studies, characterization and study of genomic sequence for features of interest (e.g., repetitive elements, regulatory regions), and numerous molecular evolutionary studies (e.g., evolution of gene families, origin and fate of gene duplications). The incumbent will be responsible for providing bioinformatics support to the research group by participating in several of the above studies and will interact closely with other collaborators with bioinformatics experience. The incumbent will have the opportunity to pursue additional molecular evolutionary genomic studies of fire ants, including one or more laboratory experiments, under the supervision of the lead scientist and will be responsible for data analyses and writing scientific manuscripts for publication.

QUALIFICATION REQUIREMENTS: Recent Ph.D. in Genetics, Bioinformatics/Computational Biology or closely related discipline appropriate to the position. The applicant must have an interest in population and evolutionary genetics and ideally should be familiarized with bioinformatics approaches relating to population and evolutionary genetics as well as experience analyzing next generation sequencing data. Applicants with a strong computational background should have demonstrated experience (e.g., refereed publications, Ph.D. thesis) in at least one programming language (Python/Perl/Ruby, C/C++), as well as experience in analysis of genomic (or transcriptomics) data and whole-genome level study. Applicants with mainly an experimental background should have demonstrated experience in standard molecular genetic techniques (PCR, fluorescent-based genotyping and next generation DNA sequencing, gene expression, bioinformatics) as well as experience in basic programming (in any language) and large-scale data analysis (e.g. high-throughput genotyping, comparative genomics).

The full advertisement and description can be found at: jobview.usajobs.gov/ GetJob.aspx?JobID989339& JobTitle=RESEARCH+GENETICIST +%2f+ COMPUTATIONAL+BIOLOGIST++ (Postdoctoral+Research+ Associate)& sort=rv&vw=d&brd876&ss=0& FedEmp=N&FedPub=Y & q=ra-10-036-L& AVSDM 09-12-07+10%3a0 4%3a00

For additional information or queries, please contact DeWayne Shoemaker by email at: dewayne.shoemaker@ars.usda.gov

DeWayne Shoemaker <dewayne.shoemaker@ARS.USDA.GOV>

## INRA Bordeaux ForestEvolutionaryGenetics

Proposal for a 18 months post-doc position: <<≪ Genetic relatedness and viability of oak seedlings in a natural forest >>≫ - UMR BIOGECO (INRA, Universite Bordeaux I)

A 18 months post-doc position is available in our lab (BIOGECO - INRA, University Bordeaux I), starting january 2010, granted by INRA and the Aquitaine Region. The project aims at studying the link between survival, growth, parasite infection and relatedness among pedunculate oak (Quercus robur) seedlings, in a natural forest. We have a dataset of about 1000 seedlings measured during 5 years and genotyped with 10 microsatellite markers. We are looking for a candidate with a strong background in population and quantitative genetics, and with knowledge in evolutionary ecology, to carry out data analyses and to explore relationships between seedling survival and genetic diversity.

Monthly net salary, 1800 Please contact: sophie.gerber at pierroton.inra.fr cyril.dutech at pierroton.inra.fr

Offre de post-doc de 18 mois : <<≪ Apparentement genetique et viabilite de jeunes semis de chene en foeÃt naturell>> - UMR BIOGECO (INRA, Universite Bordeaux I)

Dans le cadre d'un projet INRA-Region Aquitaine, un post-doc de 18 mois est propose au sein de l'UMR BIOGECO (INRA, Universite Bordeaux I), et de buterait en janvier 2010. Le projet's interesse au lien entre survie, croissance, infection parasitaire et le degre d'apparentement d'une cohorte de semis de chenes eÃ©doncelÃ©s (Quercus robur) en eorÃt naturelle. Nous disposons d'un jeu de donne©es reposant sur un millier de jeunes plants suivis depuis plus de 5 ans et ge©notyee©slaide une dizaine de marqueurs microsatellites. Nous recherchons un candidat ayant de solides bases en ge©eÃ©tique des populations etege©nÃ©tique quantitative, et des connaissances en e©cologieeÃ©volutive afin deerÃ©alisel analyse des donne©es et de©tablir les relations entre survie et diversieÃe ge©eÃ©tique des semis.

Salaire mensuel net 1800 Veuillez contacter : sophie.gerber_at_pierroton.inra.fr cyril.dutech_at_pierroton.inra.fr

Sophie Gerber <sophie.gerber@pierroton.inra.fr>

## MartinLutherU HostParasiteEvolution

PostDoc position in Host-Parasite Evolution at the Martin-Luther University Halle/Wittenberg, Germany

The Molecular Ecology Work Group at the Martin-Luther University Halle/Wittenberg (http://www.molecol.uni-halle.de) is offering a PostDoc position in the BMBF funded project FUGAPIS (pending approval). The research network FUGAPIS aims to understand the evolution and dynamics of the host parasite systems of the honeybee Apis mellifera and two of its major parasites, Varroa and American foulbrood. By applying molecular tools like genome mapping in semi natural populations, which evolved resistance towards the parasite, we aim to identify genes which are involved in the evolution of disease resistance in the honeybee. The position is for one year (full time) and is available from the 01.03.2010; salary is up to TVL 14 (Ost) depending on qualification. Job requirements include: - PhD in Biology or a related field - PostDoctoral experience is a plus - Expertise in Evolutionary Biology in general and Host-Parasite Evolution - Experience in molecular biological methods (e.g. Genotyping, QTL Mapping) - Experience in bee pathology and genetics - Fluent English - Ability to work with living honeybees The position includes the administration and coordination of the research network FUGAPIS (http://www.fugapis.uni-halle.de) To apply please sent your CV, motivation letter and names (email) of two references to: Prof. Robin Moritz, Martin-Luther-Universität Halle/Wittenberg, Institut für Biologie, Molekulare Ökologie, Hoher Weg 4, 06099 Halle (Saale) or in electronic form via email: kraus@zoologie.uni-halle.de Application deadline is 30.12.2009

kraus@zoologie.uni-halle.de kraus@zoologie.uni-halle.de

## MPI PloenGermany EvolBiol EvolGenetics

Advanced postdoc in evolutionary genetics of house mice

Max-Planck Institute for Evolutionary Biology, Ploen - Germany Group of Diethard Tautz

We are seeking a person with a strong interest in molecular evolution and experience in one or more of these fields: genomics, population genetics, mouse genetics, epigenetics, and transgenics. The successful candidate will join the wild mouse research group and could also become involved in supervising the genomics unit of the institute (depending on previous experience: including data generation, analysis, and facility operations). There is also the option to contribute to teaching master-level courses in evolutionary genetics within the framework of an international graduate school.

We are using natural populations of the house mouse to study the genetic basis of adaptations. We are employing high level genomic approaches with in-house facilities for microarrays, high throughput genotyping, and next generation sequencing to detect and functionally characterize genes involved in recent adaptations. We have a unique collection of house mouse populations and are currently building up resources for functional analysis at population level scales.

Owing to its history as a limnological institute, we are located in a small town in the middle of a lake district. Our directly neighboring larger towns are Kiel and Lübeck, and we have strong ties to the University of Kiel. Plön is approx. 70km away from Hamburg and its international airport.

Further information on the institute can be found at: http://www.evolbio.mpg.de/english/index.html The initial contract is for two years but is renewable to allow the building of an independent research group with the option of also applying for additional outside funding. It is particularly suitable for researchers after their first postdoc, but more advanced researchers may also apply. Payment will be according to the German public service pay scale TVoeD E13, which includes all social benefits (e.g. medical, dental, retirement).

Applications should be sent to tautz@evolbio.mpg.de and include a complete CV, publication list, short letter of research interests and contact information for three references.

Prof. Dr. Diethard Tautz Max-Planck-Institut fuer Evolutionsbiologie Abteilung Evolutionsgenetik August-Thienemannstrasse 2 24306 Ploen (Germany) Tel.: 04522 763 390 Fax: 04522 763 281

tautz@evolbio.mpg.de

## Netherlands 4 BioDiversity

Netherlands Centre for Biodiversity Naturalis

Early 2010 the Netherlands Centre for Biodiversity Naturalis (NCB Naturalis) will be established in Leiden, The Netherlands. The founding partners are the National Herbarium of the Netherlands (Leiden University branch and Wageningen University branch), the Zoological Museum of Amsterdam (University of Amsterdam) and the National Museum of Natural History Naturalis. The NCB Naturalis will house a natural history museum with over 200 staff members managing a natural history collection containing more than 37 million objects, and a modern research department. Research at the NCB Naturalis will involve systematic/taxonomic studies on the origin and evolution of biodiversity, exploiting the ideas and methods of conservation biology, evolutionary biology, paleontology and mineralogy. A major investment in new scientific infrastructure, including molecular and morphological laboratories, and bioinformatics facilities will be established between 2010 and 2014. These new facilities will greatly improve existing laboratory and analytical facilities and support our new, high profile research.

The NCB Naturalis mission is to be an open archive of Life's Diversity dedicated to reconstruct and understand the Tree of Life, to educate people about our natural world, and to raise awareness for the sustainable use of Earth's living resources.

Starting May 1st 2010, the NCB Naturalis has positions available for:

Four Research Fellows (fulltime)

We seek to attract Research Fellows to support our high profile research themes, namely "Morphology and evolutionary developmental genetics", "Phylogenetics and horizontal genomics", "Biogeography" and "Global Change Biology". You are an energetic and enthusiast scientist with a proven track record and a clear view on how your research program will contribute to the future success of NCB Naturalis. You are eager to join our new institute, to cooperate with the existing staff of the NCB Naturalis, to study the NCB Naturalis collections, and to use the new scientific infrastructure. Developing active interactions between the NCB Naturalis and our partners in biodiversity research as well as acquisition of externally funded projects are essential. You are expected to teach at the undergraduate and graduate levels and to represent the NCB Naturalis in societal and scientific communities. To give your research program a head-start each research fellow will have the opportunity to supervise a PhD candidate (to be appointed).

Requirements

You have a PhD degree in systematics, evolutionary biology, geology, or other relevant discipline and at least two years, and preferably not more than six years, of experience at the postdoctoral level. You have excellent teaching and communications skills in English, both written and verbal.

Furthermore, you have an excellent scientific track record (given the point in your career) and are involved in innovative and multidisciplinary research projects in biodiversity research, operating in an international scientific network. You are able to engage in collaborative networks with students and university partners as well as existing NCB Naturalis research staff.

Depending on the research theme, desired qualifications may include:

* Ample experience with modern molecular techniques, advanced microscopy techniques, GIS applications and/or web-based taxonomy.

* Experience with research popularisation.

* Interest in the applications of systematic research in conservation, environmental management and species identification services.

We offer

A fulltime contract (36 hours per week) for five years. A competitive salary up to a maximum of circa EUR 59,000 gross per year depending on experience and qualifications, including holiday allowance (8%). All our employees are incorporated into a pension fund.

Procedure

You are invited to submit your application including your curriculum vitae, a clearly focused research program of maximum four pages (containing a five year working plan, a proposed budget, and the topic of the PhD candidate's research), a complete list of publications, up to five keywords describing the research area ,a statement of teaching interests and the names and e-mail addresses of at least three persons that can be contacted for reference (and who have agreed to be contacted) before February 1st by e-mail to;

sollicitaties@naturalis.nl, or by mail; Naturalis, HR department, PO box 9517, 2300 RA Leiden, The Netherlands.

For more information on the current research and facilities, see the websites of the founding partners of the NCB Naturalis, on www.naturalis.nl < http://www.naturalis.nl/ > - www.nhn.leidenuniv.nl < http://www.nhn.leidenuniv.nl/ > - www.science.uva.nl/zma -

— / —

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

---

## NewZealand AlpineStickInsectGenomics

Postdoctoral Fellow: Evolution of Cold Tolerance in New Zealand Alpine Stick Insects

We are seeking a post-doctoral researcher on a New Zealand Marsden Fund project "Evolution of Cold Tolerance in New Zealand Alpine Stick Insects". This project is led by Thomas Buckley at Landcare Research, Auckland, New Zealand. Also involved in this project are Brent Sinclair (University of Western Ontario), and Melody Clark (British Antarctic Survey).

This project seeks to identify genes involved in cold tolerance in alpine stick insects and compare patterns of sequence evolution and expression of such candidate genes to other genomic markers. This project will involve Next-Generation DNA sequencing of stick insect transcriptomes, quantitative PCR, and DNA sequencing of candidate genes and other sequence markers. The successful applicant will have a PhD with proven skills and experience in PCR, DNA sequencing, qPCR and associated population genetic and phylogenetic analysis. The candidate will also have experience with the bioinformatic analysis of transcriptome or genomic scale data sets. There is also the option of participating in field work and physiological studies. The successful applicant will be expected to present results at local and international conferences and to lead publication of results. There will also be opportunities to interact with other researchers within Landcare Research and the Allan Wilson Centre for Molecular Ecology and Evolution.

This position will be based at Landcare Research, Tamaki, Auckland, New Zealand and is fixed term for three years. Funding is available from early 2010. Interested candidates will find further information on the following websites:

http://www.landcareresearch.co.nz/research/biosystematics/invertebrates/phasmatodea http://www.landcareresearch.co.nz/research/staff_page.asp?staff_num=3D1110 http://www.allanwilsoncentre.ac.nz/ For a job description and information on how to apply please visit our website, www.landcareresearch.co.nz/jobs. All applications must be received online.

For specific details, please contact Thomas Buckley (buckleyt@landcareresearch.co.nz). Applications will close on 1st February 2010.

Thomas Buckley Landcare Research Tel: (+64 9) 574 4116 | Fax: (+64 9) 574 4101 | Email: buckleyt@landcareresearch.co.nz Post: Private Bag 92170, Auckland, New Zealand | Web: http://www.landcareresearch.co.nz/research/staff_page.asp?staff_num=1110 BuckleyT@landcareresearch.co.nz

## Portugal Celegans experimental evolution

ERC POSTDOCTORAL POSITION ON C. ELEGANS EXPERIMENTAL EVOLUTION FIRST CALL 15 DECEMBER 2009

A postdoctoral position is available in the laboratory of Henrique TeotÃ³nio at the Instituto Gulbenkian de CiÃncia (IGC), Oeiras Portugal (www.igc.gulbenkian.pt).

PROJECT: The research will be focused on the genetic basis of adaptation to novel environments, in particular on the evolution of phenotype distributions in heterogeneous environments using populations of C. elegans manipulated in their mating system and standing levels of genetic variation. We aim to describe adaptation in life-history, behavioral and gene expression phenotypes, and correlate them with genome-wide patterns of DNA sequence variation during long-term experimental evolution. The specifics of the postdoctoral project will be defined according to the applicant's interests and experience, and collaborations with labs in the USA and Europe are envisaged.

REQUIREMENTS: PhD in evolutionary genetics and interest in the topics of adaptation from standing genetic variation, evolution of phenotypic plasticity, and mating system evolution. The ideal candidate will have a strong background in quantitative genetics (analysis of selection gradients, estimation of breeding values, QTL mapping) and the population genetics of DNA sequence data (comparative analysis of heterozygosity and linkage disequilibria). Although not essential, experience with culturing model organisms in the lab is preferred, as well as experience with basic molecular biology techniques. The candidates are expected to have the computational skills to conduct multivariate statistical analysis and data management. Candidates with a PhD in theoretical evolutionary genetics are invited to apply.

FUNDING and STARTING DATE: The postdoctoral position is funded by the European Research Council (ERC), for a monthly salary of about 2000, plus social benefits. The successful applicant can start as soon as March 2010. Yearly evaluations of performance will determine the renewal of the contract for up to a maximum of five years.

APPLICATIONS: Applications should be composed of a CV including professional experience, list of relevant publications, and list of technical competencies. CVs are to be accompanied by a letter of motivation and the contact information of two referees. Applications should be sent by email to _teotonio@igc.gulbenkian.pt_. The call for the position will remain open until a suitable candidate is found.

Henrique Teotonio <teotonio@igc.gulbenkian.pt>

## UAlgarve PlantPhylogenomics

Postdoc: Plastid origins and plant phylogenomics - CCMAR, University of the Algarve, Portugal

POSTDOCTORAL POSITION

(2nd call for applicants.)

Applications are invited for a postdoctoral researcher position at the Centro de Ciencias do Mar (CCMAR), University of the Algarve (CCMAR - http://www.ccmar.ualg.pt/) in the research group of Cymon J. Cox (Plant systematics and bioinformatics). The successful applicant will participate in the project titled "The origin and early diversification of plants: a phylogenomic approach employing novel composition-heterogeneous methods" funded by the Portuguese Foundation for Science and Technology (FCT). The project will be conducted in collaboration with T.M. Embley (Newcastle University, UK) and P.G. Foster (Natural History Museum, London, UK).

Background Plant chloroplasts are derived from an ancient endosymbiotic capture of a cyanobacterium by a heterotrophic eukaryotic ancestor, an event which led to the diversification of three primary plant lineages, namely, the glaucocystophytes, red algae, and green plants, and the eventual emergence of terrestrial ecosystems. The endosymbiosis marked a crucial episode in cell and Earth history, yet our understanding of the phylogenetic context surrounding this momentous event remains obscure in part due to the technical limitations of current phylogenetic methodology in relation to the reconstruction of deep evolutionary divergences.

The project will be conducted entirely "in silico" and implement novel non-stationary composition models in a phylogenomic context. The successful candidate will have a strong background in phylogenetic analyses, Unix/Linux computing, and bioinformatics (biopython/bioperl, cluster management, relational databasing, etc). An extensive publication record will also be advantageous. The position is available for 3 years (after an initial 1 year probation) from January 2010 and is open to all nationalities. The researcher will receive a salary of 1495 euros/month.

Applications should be submitted before 15th January 2010 to Cymon J. Cox (cymon@ualg.pt). Applicants should send a covering letter detailing their research interests, a current C.V., and the email addresses for 3 professional referees. Informal inquires are welcome to the same address.

CCMAR is located on the Gambelas campus, 4km from Faro, the capital city of the Algarve and close to Faro International Airport (FAO). (http://www.ualg.pt/-index.php?option=com_google_maps&Itemid=-2311&lang=en)

FCT announcement (in Portuguese): http://-www.eracareers.pt/opportunities/index.aspx?task=-global&jobId=15465 –

cymon.cox@googlemail.com

## UCaliforniaBerkeley PlantDefenses

POSTDOC IN PLANT DEFENSE CHEMICAL ECOLOGY AND EVOLUTION

A Postdoctoral position is available in the laboratory of Dr. Paul Fine at the Department of Integrative Biology at the University of California, Berkeley to participate in an ongoing project comparing tropical tree chemical defense investment in six Amazonian tree lineages (genera) across divergent habitat types in Peru and French Guiana and to develop new research lines involving the ecology, evolution and functional genomics of defense chemistry in Protium (Burseraceae). See website for descriptions of past and present research projects in the lab (http://ib.berkeley.edu/labs/fine/-Site/ research.html).

Candidates should have a strong background in one or more of the following fields: chemical ecology, chemical characterization of terpenes (or other plant defenses), molecular evolution, population genetics, genomics and bioinformatics. Applicants should have experience with one or more of the following tools: GC/MS, R, a variety of phylogenetic and population genetics programs. Fluency in Spanish is a plus, as well as some knowledge of French.

The Postdoctoral fellow will be based in Berkeley but the position will involve travel to Salt Lake City, UT, Kourou and Cayenne, French Guiana and Iquitos, Peru.

Funding is available for two years, subject to review after one year, with an annual salary range between $37,400 - $41,496 commensurate with experience; generous benefits are included. The start date will be between Feb-Apr 2010.

Applicants should submit a CV, a brief statement of research interests, copies of relevant publications and/or manuscripts, and contact information for three references by email to paulfine@berkeley.edu before 5 January 2010.

The University of California, Berkeley is an equal opportunity employer committed to excellence through diversity. Applicants should ask referees to review the UC Berkeley Statement of Confidentially found at: http://apo.chance.berkeley.edu/evalltr.html Paul V.A. Fine Assistant Professor Department of Integrative Biology University of California, Berkeley, CA 94720-3140 paulfine@berkeley.edu

paulfine@berkeley.edu paulfine@berkeley.edu

## UCaliforniaBerkeley PlantDevelEvolution

EFFECTIVE: 11 December 2009

POSTDOC IN PLANT DEVELOPMENTAL EVOLUTION

A Postdoctoral position is available in the lab of Dr. Chelsea Specht at the University of California, Berkeley in the area of evolution of plant development. My lab's research combines plant phylogenetics with molecular evolution, developmental genetics and bioinformatics to study plant evolution in a number of lineages, particularly monocots ( http://pmb.berkeley.edu/ ˜ specht). The postdoctoral project will focus broadly on determining the genetic networks involved in the evolution of floral form within the monocot order Zingiberales, incorporating preliminary data on floral development and MADS box gene function and collaborating with several ongoing graduate research projects. We are part of the department of Plant and Microbial Biology, and the postdoc will have opportunities for idea exchange and collaboration with the labs of Sarah Hake (Plant Gene Expression Center,USDA), Michael Freeling, Kimmen Sjolander, Renee Sung, and Lew Feldman to study various aspects of plant genetics, genomics, development and evolution. Candidates should have a strong background in plant developmental genetics and/or bioinformatics and molecular evolution as well as familiarity with basic techniques for analyzing gene expression and phylogenetic structure. The position is available immediately and the preferred start date is no later than April 1st. Funding is available for two years, subject to review after one year, with an annual salary of $37,000 plus benefits. Informal inquiries about the research and requirements are encouraged. To apply, send a CV, description of your research interests and PhD research, and contact information for three references to cdspecht@berkeley.edu.

–

Chelsea D. Specht, PhD Assistant Professor Plant and Microbial Biology University of California, Berkeley 111 Koshland Hall, MC 3102 Berkeley, CA 94720

cdspecht@berkeley.edu http://pmb.berkeley.edu/~specht cds@berkeley.edu cds@berkeley.edu

## UCaliforniaDavis PopulationBiol

EFFECTIVE: December 7, 2009

DEADLINE: January 20, 2010

POSTDOCTORAL FELLOW IN POPULATION BIOLOGY–The Center for Population Biology at UC Davis invites applications for a Postdoctoral Fellowship in Population Biology, broadly defined to include ecology, phylogenetics, comparative biology, population genetics, and evolution. We particularly encourage applications from candidates that have recently completed, or will soon complete, their PhD. The position is for TWO YEARS, subject to review after one year, and can begin as early as 1 July 2010. It has an annual salary of $38,000 plus benefits, and $6,000 per annum in research support. The Fellow will be a fully participating member in the Center for Population Biology and will be expected to have an independent research program that bridges the interests of two or more CPB research groups. We strongly encourage candidates to contact appropriate faculty sponsors before applying. We also ask that each Fellow teach a multi-day workshop, discussion or lecture series that is of broad interest to the community of population biologists at UC Davis; faculty sponsors or the Director of CPB, Jay Stachowicz, can provide additional input on this aspect of the fellowship. For samples of past workshop abstracts and more information about UC Davis programs in population biology, see http://cpb.ucdavis.edu/jobs.htm.

ONLINE APPLICATION: Interested candidates should submit a cover letter, CV, a short (1-2 page) description of research accomplishments, a short (1-2 page) description of proposed research including potential faculty mentors, a brief description of their proposed workshop/minicourse, and copies of two publications at http://www2.eve.ucdavis.edu/jobs/ all as PDFs. We require 3 letters of recommendation. The referees you list in the online application will receive an automatic notification from our system instructing them how to directly upload letters to our website. Refer to the on-line instructions for further information. For full consideration, applications should be received by January 20. 2010. The University of California is an affirmative action/equal opportunity employer with a strong institutional commitment to the development of a climate that supports equality of opportunity and respect for differences. E-mail questions to gradcoordinator@ucdavis.edu.

DEADLINE: January 20, 2010

Stephanie Macey-Gallow Center for Population Biology

Stephanie Macey-Gallow <smaceygallow@ucdavis.edu>

## UCaliforniaLosAngeles Phylogenetics

A postdoctoral fellow position is available (immediate or mid-2010 start-date) in Dr. Marc Suchard's research group across the Departments of Biomathematics, Biostatistics and Human Genetics, University of California, Los Angeles. We develop novel techniques in Bayesian statistics and applied probability to address questions in phylogenetic reconstruction and evolutionary medicine. Possible projects include:

* simultaneous inference of alignment and phylogeny,

* phylogeography of viral epidemics (HIV and Influenza) and

* many-core (GPU) algorithm development for computational statistics.

A few representative publications:

Many-core algorithms for statistical phylogenetics, Suchard MA, Rambaut A, BIOINFORMATICS (2009) 25: 1370-1376

Bayesian phylogeography finds its roots, Lemey P, Rambaut A, Drummond AJ, Suchard MA PLOS COMPUTATIONAL BIOLOGY (2009) 5, e1000520

StepBrothers: inferring partially shared ancestries among recombinant viral sequences, Bloomquist EW, Dorman KS, Suchard MA BIOSTATISTICS (2009) 10: 106-120

Alignment uncertainty and genomic analysis, Wong KM, Suchard MA, Huelsenbeck JP, SCIENCE (2008) 319: 473-476

Inferring spatial phylogenetic variation along nucleotide sequences: a multiple change-point model, Suchard MA, Weiss RE, Sinsheimer JS JOURNAL OF THE AMERICAN STATISTICAL ASSOCIATION ( 2003) 98:427-437

I am looking for a candidate with a recent PhD who has training in statistics, applied mathematics or computational biology. Experience in biomedical data or molecular sequence analysis is desirable. The position is funded through research grants from both NSF and NIH.

For consideration, please email a CV, bibliography, brief description of your experience and names of two potential references to: msuchard@ucla.edu

Marc A. Suchard, M.D., Ph.D. Associate Professor Departments of Biomathematics and Human Genetics David Geffen School of Medicine at UCLA, and Department of Biostatistics UCLA School of Public Health 695 Charles E. Young Dr., South 6558 Gonda Los Angeles, CA 90025 310-825-7442 office

msuchard@gmail.com

## UCaliforniaSanDiego SpeciationGenetics

One postdoctoral position (one year with a second depending upon satisfactory performance) will be available starting February 1, 2010 (start date is flexible) working in the area of speciation genetics and reproductive biology of Drosophila. Applicants with experience in molecular biology, sequence analysis, proteomics, expression analysis, knockout techniques and computational techniques will receive the most serious consideration. A Ph.D. in evolutionary biology, or related field, with several years of field and lab research experience, and strong quantitative skills. Expertise is required in at least two of the following areas: molecular biology, sequence analysis, proteomics, expression analysis, knockout techniques and computational techniques. Evidence of research productivity as indicated by scholarly publications is required. Evidence of strong communication and teamwork skills is highly desired. Please email brief letter of interest, CV, and the names and contact details of three referees by January 1, 2010 to Dr. Therese Markow tmarkow@ucsd.edu , subject line: $B!H(BPostdoctoral Position Markow Lab$B!I(B. Review of applications will begin immediately, and continue until the position is filled.

For more information or to apply, please contact: Therese Markow tmarkow@ucsd.edu Telephone: (858) 246-0095 Fax: () - Website: http://www.biology.ucsd.edu/faculty/markow.html Therese Markow <tmarkow@ucsd.edu>

## UColgne ExperimentalProteinEvolution

Postdoc position in experimental evolution

We seek a postdoc for a collaborative project between the University of Cologne (Prof. Joachim Krug) and Wageningen University (Dr. Arjan de Visser) on epistasis, recombination and the predictability of adaptive evolution. The project is part of the Collaborative Research Center 680 “Molecular basis of evolutionary innovations” funded by Deutsche Forschungsgemeinschaft (DFG) (http://www.sfb680.uni-koeln.de < http://www.sfb680.uni-koeln.de/ > ) and coordinated at the University of Cologne. Using evolution experiments and the reconstruction of mutational pathways combined with population genetic theory (see de Visser et al. 2009 Am. Nat. 174: S15-S30), we seek to develop and test predictions about the molecular basis of adaptive pathways. As experimental system we will use TEM-1 beta-lactamase, which causes bacterial resistance to certain classes of antibiotics. We want to use this system to study the distribution of beneficial mutations, characterize fitness landscapes involving these mutations, study the effect of recombination on the rate and level of adaptation, and study factors that enhance the repeatability of evolutionary pathways in replicate populations.

Profile: We seek someone with a PhD in molecular evolutionary biology, microbial genetics or enzyme engineering. Experience with basic microbiological and molecular lab techniques are an absolute requirement; experience with evolutionary theory and quantitative models are an advantage. The postdoc will be appointed at the University of Cologne, and experimental work will be carried out primarily at the Laboratory of Genetics at Wageningen University. The initial appointment is for one year with the possibility for extension to up to four years. Salary will be paid according to level E13 of the German public service salary scale (TV-L).

Applications: Submit enquiries and applications (including CV, letter of motivation and names and contact information of two references) before December 14 to Prof. Joachim Krug or Dr. Arjan de Visser. The University of Cologne is one of the leading German institutions in Molecular and Evolutionary Genetics. Wageningen University is a small but leading university in the field of the life sciences. The laboratory of Genetics is housed at the newly built campus, and its research was ranked 4.5 (scale 0-5) in a recent evaluation. The University of Cologne is an equal opportunity employer in compliance with the German disability laws. Women and handicapped persons are therefore strongly encouraged to apply.

Dr. J. Arjan G.M. de Visser Laboratory of Genetics Wageningen University, Radix building Droevendaalsesteeg 1 6708 PB Wageningen The Netherlands P: (+)31 317 483144 M: arjan.devisser@wur.nl <mailto:arjan.devisser@wur.nl> W: www.gen.wur.nl/UK/Staff/Scientific+Staff/Arjan+de+Visser

Prof. Dr. Joachim Krug Institute for Theoretical Physics Zülpicher Strasse 77 50937 Köln Germany P: (+)49 221 470 2818 M: krug@thp.uni-koeln.de <mailto:krug@thp.uni-koeln.de> W: www.thp.uni-koeln.de/krug/ "Visser, Arjan de" <Arjan.deVisser@wur.nl>

---

## UGraz Cichlid QuantitativeGenetics

The Department of Zoology at the Karl-Franzens-University Graz offers the position of a Post-doctoral scientist (40 hours per week; for an employment of 2 years, starting as soon as possible). The person should join the group of Christian Sturmbauer for research on African cichlid fish populations, financed by research grant No. P20994-B03 of the Austrian Science Fund "Natural selection - driving force of adaptive radiation", to carry out quantitative genetic analyses on African cichlid fish populations, and pond-bred offspring (see also HYPERLINK "http://www.kfunigraz.ac.at/zoowww/"). Candidates should have a Ph.D. in Zoology, Genetics or Evolutionary Biology, as well as experience in quantitative genetics targeting natural populations and breeding experiments. They should be familiar with the use of ASReml and similar tools. Adequate number of scientific publications and conference contributions corresponding to the applicants experience and team spirit are expected. Please apply per e-mail to Prof. Christian Sturmbauer, HYPERLINK "mailto:christian.sturmbauer@uni-graz.at" christian.sturmbauer@uni-graz.at with the following documents: CV, letter of research interests, list of publications, contact coordinates of two persons for reference.

Univ. Prof. Dr. Christian Sturmbauer Department of Zoology University of Graz Universitaetsplatz 2 A-8010 Graz Austria

selma.mautner@uni-graz.at selma.mautner@uni-graz.at

---

## UIdaho TreeOfLife 2

Hello everyone,

I posted an advert for a postdoc a couple of months ago. The position remains unfilled, and the job description (and, importantly, timeline!) have now changed. I'd love to have someone come work with me on this project starting whenever it works for your schedule, including starting Fall 2010.

Postdoc: Measuring the tree of life

A postdoctoral position is available in the laboratory of Dr. Luke Harmon for a project, "Measuring the Tree of Life." The project uses data from the NSF Tree of Life project to test macroevolutionary hypotheses about speciation, extinction, and trait evolution. The postdoctoral scientist will develop and implement comparative statistical methods for measuring the tempo and mode of evolution using phylogenetic and trait data. The ideal candidate will have either a strong computational and/or statistical background or a strong desire to learn, and experience developing or using statistical comparative methods. Applicants with a strong background in phylogenetics will also be considered. The successful candidate will contribute to existing collaborative projects across multiple institutions and will also be expected to develop new independent research directions.

Responsibilities:

Research: 65% (Essential responsibility) - Developing and testing new statistical comparative methods - Generating and analyzing simulated data sets - Compiling and analyzing empirical data sets from tree of life and other related projects

Presentation of Research Results: 20% (Essential responsibility) - Assuming primary responsibility for preparing and publishing scientific papers for peer-reviewed journals, and for presenting findings at scientific conferences

Other Support: 15% (Essential responsibility) - Assisting principal investigator in preparation of federal grant applications - Participating in weekly research group meetings, and attending weekly departmental seminars - Providing technical advice and assistance to others in the research group - Supervising undergraduate and/or graduate student assistants on the project

Qualifications:

1. Ph.D. degree in biological sciences, computer science, statistics or related discipline (must be conferred before starting the position) 2. Demonstrated experience and proficiency with statistical comparative methods or phylogenetics 3. Demonstrated ability to write and publish scientific papers as first author in peer-reviewed journals 4. Demonstrated ability to present data at scientific meetings 5. Willingness to work independently and in a team environment

To apply: https://www.sites.uidaho.edu/AppTrack/Agency/Applicant/ViewAnnouncement.asp?announcement_no=12508031000 Any questions email lukeh@uidaho.edu or call 208-885-0346

Lab web site: http://www.webpages.uidaho.edu/~lukeh/ Luke Harmon Assistant Professor Biological Sciences University of Idaho 208-885-0346

lukeh@uidaho.edu lukeh@uidaho.edu

## UKentucky Genealogy

We invite applications for an NIH-supported postdoctoral position within a research group at the University of Kentucky that studies the underlying genealogical history of speciation and phylogeny. The research focus of this position is on developing theory for analyzing the correlated genealogical divergence among genes evolving within the same species tree history, and co-phylogeny as applied to phylogenomics and host-parasite coevolution.

More details regarding these projects can be found at http://polytopes.net/research/statement.php . Research will be performed under the supervision of Dr. Ruriko Yoshida in the UK Department of Statistics. Prior interdisciplinary experience in statistics/mathematics/computer science/phylogenetics/phylogenomics is preferred, but outstanding candidates looking to broaden their field of interest will also be considered. The anticipated starting date for this position is July 1, 2010. The initial appointment will be for one year, with renewal up to an additional two years pending satisfactory progress and mutual agreement.

Requirements for the position include: (1) PhD in statistics, mathematics, phylogenetics, or other related field; (2) Demonstrated research excellence in your area of expertise; (3) Strong oral and written communication skills.

To apply, send a cover letter, Curriculum Vitae, and a description of current and planned research to ruriko.yoshida@uky.edu. Also arrange to have at least three letters of reference sent directly to ruriko.yoshida@uky.edu. The search will begin immediately and will remain open until the position is filled.

More information about our research group in statistical phylogenetics and evolution can be found here at http://cophylogeny.net More information about the Yoshida Lab can be found at http://polytopes.net Ruriko Yoshida <ruriko@polytopes.net>

## UMontreal PopulationMedicalGenomics

Postdoctoral Positions in Population and Medical Genomics in Montreal

A number of postdoctoral positions are available in a population and medical genomics laboratory at the University of Montreal with Philip Awadalla (

www.philip-awadallalab.org). Researchers will be involved in the analysis, development of methods and collection of next-generation sequencing data. The successful candidate will be nearing the completion/having a PhD or equivalent postdoctoral training in population/evolutionary/statistical genetics. Postdoctoral research scientists can work on projects of their choosing related to the labs current projects.

Possible projects include: 1) Analysis of genome-wide data (whole genome, exome, RNA-seq and CHiP-seq data) with an emphasis on human medical or longitudinal cohorts. Emphasis on analysis and development of methods to identify genetic and environmental control points associated with complex disorders including immunodeficiencies, child-hood cancer, sickle cell anemia and congenital heart defects. 2) Inferring fitness consequences of mutations and demography from genome-wide collections of empirical population and comparative data from humans and pathogens - including malaria. 3) Next-generation approaches to genomic epidemiology studies of biobanks. Our lab is directing the longitudinal collection of genomic material for the CARTaGENE biobank, investigating the development of chronic disorders among over 20,000 French-Canadian participants.

Our lab also works in close collaboration with a number of research laboratories throughout Montreal and internationally, including projects on neurological disorders in the Centre of Excellence in Neuorology at U. of Montreal, and malaria at the National Institute of Allergies and Infectious Disease (NIH). Projects are funded by Genome Canada, Genome Quebec, Canadian Institute of Health Research, Human Frontiers in Science, NIH and other resources. Interested individuals with should please write to Philip Awadalla (philip.awadalla@umontreal.ca).

Sincerely, Philip Awadalla

awadallp@gmail.com

---

## UOttawa SexualSelection

Funding is available for a 2-year postdoctoral fellowship in the laboratory of Howard Rundle at the University of Ottawa, Ontario, Canada.

Using various species of Drosophila, research in the laboratory investigates how natural and sexual selection interact during adaptation, and how both processes contribute to phenotypic divergence and speciation. In particular, we use experimental evolution and quantitative genetics to investigate the evolution of mate preferences within populations, their divergence among populations, and the population genetic consequences of the sexual selection they generate. For more information, consult the lab website at: http://www.science.uottawa.ca/~hrund050 Candidates with a background and interest in quantitative genetics are especially encouraged to apply.

Fellowships are open to Canadian and international candidates. The position is for two years and start date is flexible, although preferably fairly soon. The salary is CDN $40,000 per annum (potentially tax free).

Applications should include a cover letter, a curriculum vitae, a short (~1 page) description of research interests, and the names and contact information (including e-mail) of three referees. All application materials should be submitted via email (preferably in pdf format) to Howard Rundle (hrundle@uottawa.ca), to whom queries may also be addressed. Evaluation of applications will begin immediately and continue until the position is filled.

Located at the confluence of English and French Canada, Ottawa is a rich and vibrant national capital of approximately 1 million inhabitants (http://www.ottawatourism.ca). The city offers a wide range of cultural activities in the visual and performing arts, as well as easy access to green spaces and wilderness. The University of Ottawa is located next to the historic Rideau Canal, steps from Parliament and within easy access to a wide range of research facilities of interest to evolutionary biologists including the Canadian Museum of Nature, the National Wildlife Research Center, Health Canada, and Environment Canada. Carleton University is only a few km away and research ties between the two Biology Departments are strong.

The Department of Biology has an active group of evolutionary biologists with diverse interests (http://www.evolution.uottawa.ca).

Howard Rundle Department of Biology, 30 Marie-Curie Priv. University of Ottawa, Ottawa, ON, K1S 0T1,CANADA Ph: +1 613-562-5800 x2835; Fax: +1 613-562-5486 Skype: howardddrundle http://www.science.uottawa.ca/ ~ hrund050 http://www.evolution.uottawa.ca hrundle@uottawa.ca hrundle@uottawa.ca

## UOxford AvianMalariaEvolution

DEPARTMENT OF ZOOLOGY, UNIVERSITY OF OXFORD

Postdoctoral Research Associate â Ecology and Epidemiology of Avian Malaria

Grade 7: Salary Â£28,839 p.a.

A NERC-funded postdoctoral position is available, for fourteen months, from 1 March 2010, to study the ecology and epidemiology of malaria in birds. The post will be based in the Edward Grey Institute, Department of Zoology, University of Oxford. The work builds on extensive, multi-year, longitudinal and cross-sectional datasets of malaria prevalence and parasitemia in tits Parus; much of the raw data are therefore available. The main aims of the research are to understand the joint roles of host dispersal, environmental variation, and individual differences in contributing to spatial variation in parasitemia and prevalence.

The successful candidate will have a PhD in ecology, evolutionary biology or a related subject, and with proven skills in the use of multivariate statistics (skills in spatial analysis, mark-recapture and multilevel modelling or statistical epidemiology an advantage) and in writing and publishing papers. There will be an opportunity to participate in fieldwork, and supervision of project students, if desired, but previous fieldwork experience and knowledge of avian biology are not vital.

The post is based in a dynamic and expanding research-active institute, of c. 40 people, fully integrated within the Department of Zoology. Further details about the institute available at: http://www.zoo.ox.ac.uk/egi/- Informal inquiries (with CV) to Prof Ben Sheldon (ben.sheldon@zoo.ox.ac.uk)

Start date 1 March 2010 or as soon as possible thereafter.

Further particulars and application forms can be downloaded from http://www.zoo.ox.ac.uk/jobs or are available from the Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS (tel: 01865 271190); email: recruit@zoo.ox.ac.uk . Applications, together with CV and contact details of three referees, a copy of two publications (these can also be sent electronically) and a cover letter explaining how the candidate meets the selection criteria should be sent to the above address quoting reference number AT09040. The closing date for applications is 22 January 2010. Interviews will take place in mid February.

Prof. Ben Sheldon Edward Grey Institute Dept of Zoology University of Oxford (00 44) 01865 281069 ben.sheldon@zoo.ox.ac.uk

http://www.zoo.ox.ac.uk/egi/ Ben Sheldon <ben.sheldon@zoo.ox.ac.uk>

---

## UOxford EvolutionarySocialEcol

DEPARTMENT OF ZOOLOGY, UNIVERSITY OF OXFORD

Senior Postdoctoral Research Associate Evolutionary Social Ecology

Grade 7: Salary: Â£28,839 - Â£32,458 p.a.

A senior postdoctoral position is available, for five years, from 1 April 2010, to study social networks in birds from an ecological and evolutionary perspective. The post is funded as part of an ERC Advanced Investigator grant of 2.5M over five years to Prof Ben Sheldon. The post will be based in the Edward Grey Institute, Department of Zoology, University of Oxford. The main duties of the post-holder will be to study the causes and consequences of variation in social behaviour at the individual level; to study variation in the properties of social networks at a range of scales, and to design and carry-out experiments to test hypotheses derived in the course of this work. In addition, the post holder will be expected to play an important role in discussing and helping to plan the work of other postdocs, research assistants, and graduate students working on this project. This is an exceptional opportunity to participate in the development of a major research project, for which extensive pilot data are already available, and funding is guaranteed at a very high level.

The successful candidate will have a PhD in behavioural ecology, ecology, evolutionary biology or a related subject, and proven skills in the use of multivariate statistics (skills in spatial analysis, mark-recapture and multi-level modelling or network analysis an advantage) and in writing and publishing papers in leading journals in the field. In addition, experience of supervision in a research context, and working as part of a multidisciplinary team are desirable. There will be an opportunity to carry out fieldwork if desired, but previous fieldwork experience and knowledge of avian biology are not vital.

The post is based in a dynamic and expanding research-active institute, of c. 40 people, fully integrated within the Department of Zoology. Further details about the institute available at: http://www.zoo.ox.ac.uk/egi/- Informal inquiries (with CV) to Prof Ben Sheldon (ben.sheldon@zoo.ox.ac.uk)

Start date 1 April 2010.

Further particulars and application forms can be downloaded from http://www.zoo.ox.ac.uk/jobs or are available from the Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS (tel: 01865 271190); email: recruit@zoo.ox.ac.uk . Applications, together with CV and contact details of three referees, an electronic copy of three publications and a cover letter explaining how the candidate meets the selection criteria, as outlined in the further particulars, should be sent to the above address quoting reference number AT09041. The closing date for applications is 5 February 2010. Interviews will take place in late February.

Prof. Ben Sheldon Edward Grey Institute Dept of Zoology University of Oxford (00 44) 01865 281069 ben.sheldon@zoo.ox.ac.uk

http://www.zoo.ox.ac.uk/egi/ Ben Sheldon <ben.sheldon@zoo.ox.ac.uk>

## UTennessee VertebrateGenomics

University of Tennessee: Postdoc in Vertebrate Ecological Genomics

A Postdoctoral position is available in the lab of C. Darrin Hulsey at the University of Tennessee, Knoxville. The specific project is somewhat flexible, but will involve using high-throughput sequencing technology to study the mechanistic basis of morphological adaptation in cichlid fishes. Current research in the lab combines phylogenetics, population genetics, and genomic approaches with biomechanics to study evolutionary and functional adaptation in fish locomotion and feeding. A major focus of the lab is the application of genomic information and molecular tools available in model systems like zebrafish and Tilapia to study closely related North American cyprinids and cichlid fishes in the East African Rift Lakes and Central America.

The Hulsey lab is part of the Ecology and Evolutionary Biology Department at UT-Knoxville that is a highly interactive and integrative group of faculty and students (http://eeb.bio.utk.edu). Our lab group has weekly lab meetings with the labs of Jim Fordyce (http://web.utk.edu/~jfordyce) and Ben Fitzpatrick (http://web.utk.edu/~bfitzpa1) who are also in the Ecology and Evolutionary Biology program. UT-Knoxville is a vibrant campus located in the foothills of the Smoky Mountains and has recently become the home to the National Institute for Mathematical and Biological Synthesis (http://www.nimbios.org).

Applicants for the position should preferably have a background in computational and evolutionary genomics analyses, population genetics, or evolutionary biomechanics. Programming and bioinformatics skills and ability to speak Spanish would be highly desirable. Funds are available to support this position for one year and perhaps more depending on additional funding. The position is immediately available and the search will continue until the position is filled. To apply, please submit by email a CV, a brief description of research interests (no more than one page), and the names and contact information for two references to Darrin Hulsey (chulsey@utk.edu).

For further information about the lab, please visit our website and the departmental website:

http://www.bio.utk.edu/hulseylab/ http://eeb.bio.utk.edu/hulsey.asp C. Darrin Hulsey University of Tennessee Department of Ecology and Evolutionary Biology Knoxville, TN 37996 phone: (865) 874-2189 chulsey@utk.edu

Darrin Hulsey <chulsey@utk.edu>

## UUtah ViralEvolutionaryGenetics

Postdoctoral position in viral evolutionary genetics at the University of Utah

The Departments of Mathematics and Biology at the University of Utah are seeking a post-doc to work on the Ecology and Evolution of Rhinoviruses, the primary cause of common colds. This two year position will focus on analyzing the evolutionary genetics of both archived and newly collected rhinovirus samples, using mathematical models to link population dynamics, viral biodiversity, immunology and evolution. Experience with genetic data analysis is preferred, but not required.

Funding is in place, and the position could begin any time in the before September 2010, salary competitive based on qualifications and experience. Send a curriculum vitae, a statement of research interests, and contact information for three references to adler@math.utah.edu Please address any further questions to Fred Adler at this address.

http://www.biology.utah.edu/adler/ http://www.jsmf.org/grants/d.php?id=2007010 Fred Adler <adler@math.utah.edu>

## UWashington StatisticalGenetics

Two-year postdoctoral position in Statistical Genetics THIS POSITION MUST BE FILLED SOON Department of Statistics, University of Washington, Seattle, WA.

A 100% postdoctoral Research Associate position is available, on funding which started Sept 30, 2009. This position is under the supervision of Dr. Elizabeth Thompson (www.stat.washington.edu/˜thompson), and is funded by NIGMS through ARRA. Salary and benefits will be in accordance with NIH and University of Washington salary scales and policies. Note: Positions on ARRA funding are NOT restricted to US citizens/residents.

Subject to satisfactory performance and availability of funding, this is a two-year position to work on a specific project funded under ARRA. This exciting project involves development of statistical and computational methods to infer coancestry of genome segments among individuals selected from populations. Studies include feasibility and performance analyses, using real haplotypic data imposed on simulated population pedigrees.

Requirements: Ph. D. in Computational Biology or Genomics, Population Genetics, Statistics, Biostatistics, or a related field.

Demonstrated programming skills, including use of the Standard C language and UNIX/Linux operating systems.

Some knowledge/experience in complex stochastic systems (HMMs or MCMC) and/or statistical population genetics.

Enquiries BY PLAIN TEXT E-MAIL ONLY PLEASE, should be sent to Professor Elizabeth Thompson, (eathomp@u.washington.edu). Please do NOT send email attachments as WORD documents, HTML etc. If you wish to provide supporting information, please send a reference to a web page or PDF attachments only. If applying, please provide email addresses of 3 referees.

The University of Washington is building a culturally diverse faculty and strongly encourages applications from women and minority candidates. AA/EOE.

eathomp@u.washington.edu eathomp@u.washington.edu

## UWesternSydney Insect-PlantInteractions

Postdoctoral Research Fellow Insect-Plant Interactions University of Western Sydney (UWS), Hawkesbury Campus

A postdoctoral position is available at the Centre for Plants and the Environment, UWS, to explore insect-plant interactions in eucalypt forests under climate change. The goal of the project is to characterize the ecological, physiological and genetic responses of insect communities and populations that feed on eucalypts under the impact of increased carbon dioxide concentrations, temperature, drought and different nutrient availability as predicted under climate change models. The project will establish a connection between plant biochemistry and insect physiology, and unravel mechanisms of genetic and symbiotic adaptation of insect herbivores. The work will be carried out in conjunction with the Hawkesbury Forest Experiment (HFE), a large collaborative and international field experiment established at UWS. The Centre has atmospherically controlled glass houses, state of the art entomological and molecular biology facilities, including gas exchange analysis-, characterisation science- and DNA profiling equipment, and will be extended with a FACE site and a next-generation sequencing facility. The project is based on the Hawkesbury campus of UWS, located in Richmond, 60 km from central Sydney, in close vicinity to the spectacular Blue Mountains and Wollemi National Parks.

We are looking for a highly motivated PhD with a demonstrated ability to conduct outstanding research on the community ecology, eco-physiology and/or ecological genetics of Australian insects on eucalypts. The successful candidate must have experience in ecophysiology and/or molecular ecology, have an understanding of entomology and plant-secondary chemistry, and demonstrated the capacity of publishing scientific articles. The preferred starting date is early 2010.

Closing date for applications is 15th of January 2010. More information about the position and the application process can be obtained from the UWS e-recruit link https://uws.nga.net.au/cp/ with the reference number 1427/09 which will appear in the system within a few days.

Further information about the position can also be obtained by contacting Dr. Markus Riegler (m.riegler@uws.edu.au) or Prof. David Ellsworth (d.ellsworth@uws.edu.au)

Dr Markus Riegler Centre for Plants and the Environment School of Natural Sciences University of Western Sydney Locked Bag 1797 Penrith South DC NSW 1797 Australia email: m.riegler@uws.edu.au office: +61-(0)2-4570 1229 fax: +61-(0)2-4570 1314

www.uws.edu.au/cpemarkusriegler "be part of symbiosis research"

M.Riegler@uws.edu.au M.Riegler@uws.edu.au

## UZurich ExperimentalEvolution

WAGNER Andreas, Prof. aw@bioc.uzh.ch six digit code: 000010

*Postdoctoral position in experimental evolution*

A two-year postdoctoral fellowship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. The Wagner lab studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Aside from computational projects, the lab has ongoing projects in the laboratory evolution of yeast, as well as in the laboratory evolution of proteins and ribozymes. A sample of the laboratory's research can be found at http://www.bioc.uzh.ch/wagner/.* *Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and fundamental organizational principles of life. **

We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently on a project that he or she will develop. A successful candidate will have substantial research experience with molecular biological techniques, acquired in research projects with an evolutionary orientation. State of the art experimental technology is available through the Functional Genomics Center Zurich, which provides platforms for ultra-high throughput sequencing, transcriptomics, proteomics, and metabolomics. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further.

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch: CV including publication list, a statement of research interests not exceeding three pages, including a sketch of an experimental evolution project, as well as three academic references. Please include the word EXPEVOL in the subject line. The application deadline is January 11, 2010. The position is available immediately.

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

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

Tel. 0041 (0)44 635 61 42 (secretariat Prof. Wagner) Fax 0041 (0)44 635 61 44 (secretariat Prof. Wagner)

Christiane Gujan <gujan@bioc.uzh.ch>

## Vienna FishBehaviorEvolution

Postdoc job

Konrad Lorenz Institute for Ethology [http://www.oeaw.ac.at/klivv] Vienna, Austria

We are seeking a postdoctoral scientist to join a fish behavior project in progress. The position is for one year with the possibility of prolongation. Our project, âMechanisms of breeding aggregations in fishesâ is funded by the Austrian Science Fund (FWF project P20401-B17). The candidate will conduct a series of experiments designed to elucidate the mechanisms of breeding aggregations of our model species, a monogamous, colonial cichlid fish (Neolamprologus caudopunctatus) and will collaborate in writing papers of existing data. The ideal candidate is a behavioral experimental-ist with strong skills in statistics and simulation modelling, especially in spatial analyses.

Applications will be reviewed as received and the candidate may begin as soon as February 2010. Please send a cover letter, CV and two references to:

Dr. Richard H. Wagner, Senior Scientist Konrad Lorenz Institute for Ethology Austrian Academy of Sciences Savoyenstrasse 1a A-1160 Vienna Austria

e-mail: r.wagner@klivv.oeaw.ac.at

phone: +43 1 515 81 27 31 fax: +43 1 515 81 28 00 secretary : +43 1 515 81 27 00

Project summary:

Breeding aggregations are ubiquitous in the animal kingdom, yet experiments are lacking to explain the mechanisms that cause animals to cluster their breeding territories. Interest in animal aggregations is currently undergoing a renaissance with a growing awareness that multiple types of aggregations such as colonies, fish shoals and foraging flocks of birds may be formed by common mechanisms. The emerging concept of public information has the potential to serve as a common thread unifying various types of aggregations. This proposal follows up on an existing FWF project and aims to perform novel experiments that address two hypotheses explaining breeding aggregations: (1) the classic, unresolved hypothesis that high density breeding provides safety from predators and (2) the newer hidden lek hypothesis that sexual selection contributes to breeding aggregations. We examine the taxonomic generality of mechanisms of aggregation by testing hypotheses on fish that have been primarily developed from birds. We combine tightly controlled behavioral experiments in aquariums with complementary field experiments in Lake Tanganyika, including DNA analyses of parentage and other genetic parameters. We have chosen two fish species whose breeding territories are potentially aggregated by different components of mate choice, one of which is also a model species for testing predation avoidance. In our current project we have shown experimentally in three-spined sticklebacks-Gasterosteus aculeatus that females prefer males with territories near a more attractive male, supporting the hidden lek hypothesis. We will build on this result by determining whether males increase their mating success by aggregating their breeding territories around more attractive males. Our principal study species is Neolamprologus caudopunctatus, a monogamous cichlid that breeds in dense colonies in which we propose experiments testing two potential mechanisms of colony formation: 1. Breeders choose to settle near neighbors to increase their chances of pairing with a better mate in the future, and 2. Breeders extract public information from predator warnings that neighbors signal to their offspring. The study of these two contrasting model systems will permit us to evaluate the generality of mechanisms that form various kinds of breeding aggregations.

Dr. Franziska Schädelin Konrad Lorenz Institute for Ethology Savoyenstr. 1a 1160 V ienna Austria

Tel: +43 1515 81 2749 email: F.Schaedelin@klivv.oeaw.ac.at

Franziska Schaedelin <F.Schaedelin@klivv.oeaw.ac.at>

---

## Vienna Next Generation Sequencing Data Analysis

A 2-year postdoctoral position is available to work on Next Generation Sequencing Data Analysis

We are seeking for a highly motivated researcher, who is interested to join a team of postdocs and PhD students collaborating on the analysis of NGS and microarray data. This team of scientists is an integral part of the in house sequencing facility. The successful candidate will have strong bioinformatic skills, a solid background in biology, and a good communication aptitude. We particularly encourage scientists to apply, who have also interest to pursue their own research project(s).

The post is based at the Institute of Population Genetics at the Vetmeduni Vienna. The institute host a dynamic group of researchers covering a diverse range of topics, such as functional Drosophila genetics, population genetics and bioinformatics (http://i122server.vu-wien.ac.at/pop). The Vienna research area is one of the centers of population genetics and evolutionary biology in Europe (http://www.evolvienna.at), with a particular strength in quantitative biology.

The position is immediately available and the search continues until the position is filled.

Applications should be sent to C. Schlötterer (christian.schloetterer@vetmeduni.ac.at), including the names and emails of two academic references and a brief description of the research interests.

Christian Schlötterer Institut für Populationsgenetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-

4390 http://i122server.vu-wien.ac.at/pop schlotc@gmail.com

## WageningenU ExperimentalEvolution

Postdoc position in experimental evolution

We seek a postdoc for a collaborative project between Wageningen University (Dr. Arjan de Visser) and the University of Cologne (Prof. Joachim Krug) on epistasis, recombination and the predictability of adaptive evolution. The project is part of the Collaborative Research Center 680 "Molecular basis of evolutionary innovations" funded by Deutsche Forschungsgemeinschaft (DFG) (http://www.sfb680.uni-koeln.de < http://www.sfb680.uni-koeln.de/ > ) and coordinated at the University of Cologne. Using evolution experiments and the reconstruction of mutational pathways combined with population genetic theory (see de Visser et al. 2009 Am. Nat. 174: S15-S30), we seek to develop and test predictions about the molecular basis of adaptive pathways. As experimental system we will use TEM-1 beta-lactamase, which causes bacterial resistance to certain classes of antibiotics.

Profile: We seek someone with a PhD in molecular evolutionary biology, microbial genetics or enzyme engineering. Experience with basic microbiological and molecular lab techniques is an absolute requirement; interest in evolutionary theory is expected. The postdoc will be appointed at the University of Cologne, and experimental work will be carried out primarily at the Laboratory of Genetics at Wageningen University. Salary will be paid according to level E13 of the German public service salary scale (TV-L).

Applications: Submit enquiries and applications (including CV, letter of motivation and names and contact information of two references) before January 10, 2010 to Dr. Arjan de Visser or Prof. Joachim Krug. The University of Cologne is an equal opportunity employer in compliance with the German disability laws. Women and handicapped persons are therefore strongly encouraged to apply.

Dr. J. Arjan G.M. de Visser Laboratory of Genetics Wageningen University, Radix building Droevendaalsesteeg 1 6708 PB Wageningen The Netherlands P: (+)31 317 483144 M: arjan.devisser@wur.nl W: www.gen.wur.nl/UK/Staff/Scientific+Staff/-Arjan+de+Visser

Prof. Dr. Joachim Krug Institute for Theoretical Physics Zülpicher Strasse 77 50937 Köln Germany P: (+)49 221 470 2818 M: krug@thp.uni-koeln.de W: www.thp.uni-koeln.de/krug/

Arjan.deVisser@wur.nl Arjan.deVisser@wur.nl

# WorkshopsCourses

## Bodega California AppliedPhylogenetics

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

March 6-13, 2010

Sponsored by the

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

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

In March, 2010, for the eleventh year, we will teach a workshop for graduate students interested in applying phylogenetic methods to diverse topics in biology. The one-week course will be an intensive exploration of problems to which modern phylogenetic approaches are being applied. We cover a range of topics in ecology, phylogenomics, functional morphology, macroevolution, speciation, and character evolution. The course starts with recent advances in phylogenetic methodology, and then focuses on methods and tools that can be brought to bear on these "applied" issues in the context of a given phylogeny.

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

Specific Topics to be Covered

* Estimating, evaluating and interpreting phylogenetic trees * Recent advances in tree estimation: Bayesian inference; stochastic optimization strategies; divide-and-conquer methods; gene- tree species tree inference * Estimation of divergence times from sequence data: relaxed clocks, calibration issues * Analysis of character evolution-theory: maximum likelihood and Bayesian approaches; ancestral-state estimation; character correlation; rates of trait evolution * Analysis of character evolution-form and function of complex character systems * Inference of diversification rates: detecting rate shifts, testing key innovation hypotheses * Phylogenetic perspectives on biodiversity and conservation biology * Phyloinformatics: mining sequence databases for phylogenetic analysis * Ecological Phylogenetics: community composition and historical assembly Instructors for the main workshop.

* Peter Wainwright * Brian Moore * Michael Sanderson * Bruce Rannala * Jonathan Eisen * Sharon Strauss * John Huelsenbeck * Rich Glor * Justen Whittall * Thomas Near * Jean Burns * Greg Pauly * Samantha Price * Phil Spinks * Robert Thomson

plus guest lecturers!!

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

Admission and Fees. Students will be admitted based on academic qualifications and appropriateness of research interests. The course fee is $550. This includes room and board at BML for duration of the course (arriving March 6, leaving March 13) and transportation from Davis to BML.

Application Deadline. Applications are due by January 8, 2010. Please send a completed application form (available at http://bodegaphylo.wikispot.org/-Front_Page) and one letter of recommendation from your major advisor. Applications should be sent via email as PDFs to pqspinks@ucdavis.edu. Sorry, but due to the limited size of the class, postdocs and faculty are discouraged from applying. Students will be notified via e-mail by 22 January of acceptance.

Send all application materials to

Dr. Phillip Q. Spinks Department of Evolution and Ecology 2320 Storer Hall University of California Davis Davis, CA 95616

pqspinks@ucdavis.edu pqspinks@ucdavis.edu

## Intl Master EvolutionaryBiol

Erasmus Mundus Joint Master in Evolutionary Biology (MEME)

MEME is a new two-year research oriented master programme for talented and motivated students who are interested in understanding evolution in all its facets. The MEME programme will address the driving forces of evolution at all levels of organismal organisation (from cells and individuals to populations and ecosystems), and it will allow students to study all kinds of organisms (microorganisms, plants, animals) in all kinds of habitats (marine as well as terrestrial) with a diversity of approaches (field, lab, theory). The focus of the programme is not only on how evolution shaped life on our planet in the past, but also on how understanding the principles underlying evolution can provide new insights and help to cope with present-day challenges in a variety of fields, including ecology, epidemiology, physiology, immunology, genetics/genomics, bioinformatics, economics and the social sciences.

Only few universities in the world would be able to offer a programme of such broad scope without compromising scientific quality. For this reason, four European universities: - University of Groningen (Netherlands) - University of Montpellier II (France) - Ludwig Maximilians University of Munich (Germany) - Uppsala University (Sweden) have joined forces with Harvard University (USA). Together, this consortium is able to put together an attractive multidisciplinary programme that meets highest standards. All students have to study at at least two partner universities, and they will receive either a joint MSc degree from the whole consortium or double degrees from two partner universities.

Being financed by the European Community, MEME has to satisfy the high quality standards imposed the prestigious Erasmus Mundus Programme. Full scholarships are available for MEME students and will be awarded in a selective procedure.

Starting date: September 2010

Application deadline: January 3, 2010 (non-European students); April 15, 2010 (European students)

More information and how to apply: www.evobio.eu Questions about the application procedure: Piet van den Berg (pieter.van.den.berg@rug.nl)

Questions about the contents of the programme: Franjo Weissing (f.j.weissing@rug.nl)

Franz J. Weissing Professor of Theoretical Biology Director Groningen Graduate School of Science Faculty of Mathematics and Natural Sciences Nijenborgh 9 9747 AG Groningen tel. +31 50 363 8669 (or: 2131) E-mail: f.j.weissing@rug.nl URL1: www.rug.nl/gradschoolscience URL2: www.rug.nl/biol/theobio f.j.weissing@rug.nl f.j.weissing@rug.nl

---

## Iraklio ComputMolEvol May3-12

Computational Molecular Evolution

3-12 May 2010 Iraklio (Heraklion), Crete http://cwp.embo.org/pc10-25/ Deadline for applications: 31 January 2010

Course summary This EMBO Practical Course aims to provide researchers with the theoretical knowledge and practical skills required to carry out molecular evolutionary analysis on their own data and on data drawn from sequence databases. The course will combine basic assumptions and ideas fundamental to the field with discussion of cutting-edge methodologies, and is therefore relevant to researchers with a range of different experience levels.

This course is essentially the same as that which ran successfully as a Wellcome Trust Advanced Course at the European Bioinformatics Institute, Hinxton, UK, in Spring 2009.

Programme * interpretation of molecular phylogenetic trees and sequence alignments * genomics resources and sequence alignments * phylogeny reconstruction models * hypothesis testing in phylogenetics * coalescent model and inference from population data

Course organisers * Nick Goldman (European Bioinformatics Institute, Hinxton, UK) * Ziheng Yang (University College London) * Aidan Budd (European Molecular Biology Laboratory, Heidelberg) * Alexandros Stamatakis (Technical University of Munich) * Giorgos Kotoulas (Institute of Marine Biology and Genetics, Hellenic Center for Marine Research, Heraklion)

Guest instructors * Michail Averof (Institute of Molecular Biology and Biotechnology, Foundation for Research and Technology, Heraklion) * Martin Embley (University of Newcastle) * Olivier Gascuel (LIRMM, Montpellier) * Javier Herrero (European Bioinformatics Institute, Hinxton, UK) * John Huelsenbeck (University of California, Berkeley) * Carolin Kosiol (Veterinary Medical University, Vienna) * Aoife McLysaght (Trinity College Dublin) * Rasmus Nielsen (University of California, Berkeley) * Bill Pearson (University of Virginia) * Antonis Rokas (Vanderbilt University) * Mikkel Schierup (Aahrus University, Denmark) * Jeff Thorne (North Carolina State University) * Ken Wolfe (Trinity College Dublin)

For full details, see http://cwp.embo.org/pc10-25/ or http://tinyurl.com/cme2010 Nick Goldman tel: +44-(0)1223-492530 EMBL - European Bioinformatics Institute fax: +44-(0)1223-494468 Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK

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

---

## JagiellonianU EvolBiol Feb11-14 2

I post the announcement one more time without polish characters which may be unreadable!

50th Workshop of Evolutionary Biology

Committee of Evolutionary and Theoretical Biology of the Polish Academy of Sciences and the Jagiellonian University

11 -14 February 2010

Field station of the Jagiellonian University, Ochotnica Gorna, Poland

We are pleased to announce that 50th Workshop of Evolutionary Biology and Related Topics will be held in the field station of Jagiellonian University in Ochotnica Gorna (Poland). The station is placed in a beautiful mountain region in southern Poland (120 km from Krakow). The aim of the workshop is to present and discuss planned/ongoing research projects from different fields of evolutionary biology. The workshop is intended for PhD students and Postdocs who will give 12-minutes talks on their research. Some invited professors will give half an hour talks. Titles include: Evolutionary transcriptomics±, Experimental Evolution±, Evolutionary ecology of immune function±.

Invited Professors:

Mariusz Cichon (Jagiellonian University)

Pawe©© Koteja (Jagiellonian University)

Jacek Radwan (Jagiellonian University)

Piotr Tryjanowski (Poznan University of Life Sciences)

Organising Committee:

Krystyna Nadachowska (chief)

Magdalena Zagalska-Neubauer

Magdalena Jarzebowska

The participation is free of charge. However, the participants have to cover their travel costs to Krakow (organizers will provide transport to the field station), accommodation (approximately 3 euro/night) and food (approximately 4 euro/dinner, participants will take care of other meals themselves).

Please sent the abstract (maximum 100 words) till 5th of January 2010 to Krystyna Nadachowska: krystyna.nadachowska@uj.edu.pl. Admission is limited to 15 participants. The list of participants will be announced on 15thJanuary 2010.

For more details please contact Krystyna Nadachowska: krystyna.nadachowska@uj.edu.pl.

– Krystyna Nadachowska, PhD student Institute of Environmental Sciences Molecular and Behavioral Ecology Group Jagiellonian University Gronostajowa 7 30-387 Krakow, Poland tel: +48 12 664 51 49 http://www.eko.uj.edu.pl/molecol/staff/KN.html nadaszek@gmail.com

---

## JagiellonianU EvolBiol Feb11-14 3

This is a reminder that final deadline for registration and submitting the abstract for 50th Workshop of Evolutionary Biology in Poland is 5th of January 2010! Please find all information below.

50th Workshop of Evolutionary Biology

Committee of Evolutionary and Theoretical Biology of the Polish Academy of Sciences and the Jagiellonian University

12 -14 February 2010

Field station of the Jagiellonian University, Ochotnica Gorna, Poland

We are pleased to announce that 50th Workshop of Evolutionary Biology and Related Topics will be held in the field station of Jagiellonian University in Ochotnica Gorna (Poland). The station is placed in a beautiful mountain region in southern Poland (120 km from Krakow). The aim of the workshop is to present and discuss planned/ongoing research projects from different fields of evolutionary biology. The workshop is intended for PhD students and Postdocs who will give 12-minutes talks on their research. Some invited professors will give half an hour talks. Titles include: Evolutionary transcriptomics, Experimental Evolution, Evolutionary ecology of immune function.

Invited Professors:

Mariusz Cichon (Jagiellonian University) Pawel Koteja

(Jagiellonian University) Jacek Radwan (Jagiellonian University) Piotr Tryjanowski (Poznan University of Life Sciences)

Organising Committee:

Krystyna Nadachowska (chief) Magdalena Zagalska-Neubauer Magdalena Jarzebowska

The participation is free of charge. However, the participants have to cover their travel costs to Krakow (organizers will provide transport to the field station), accommodation (approximately 3 euro/night) and food (approximately 4 euro/dinner, participants will take care of other meals themselves).

Please sent the abstract (maximum 100 words) till 5th of January 2010 to Krystyna Nadachowska: krystyna.nadachowska@uj.edu.pl. Admission is limited to 15 participants. The list of participants will be announced on 15thJanuary 2010.

For more details please contact Krystyna Nadachowska: krystyna.nadachowska@uj.edu.pl.

Krystyna Nadachowska, PhD student Institute of Environmental Sciences Molecular and Behavioral Ecology Group Jagiellonian University Gronostajowa 7 30-387 Krakow, Poland tel: +48 12 664 51 49 http://www.eko.uj.edu.pl/molecol/staff/KN.html Krystyna Nadachowska <krystyna.nadachowska@uj.edu.pl>

---

## Montreal PopulationGenomics Jun1-4

Montreal Spring School of Population Genomics and Genetic Epidemiology

1st - 4th June 2010

Extended program

See www.MontrealSpringSchool.ca For details

Instructional Program

Day 1 - June 1st Introductory Concepts in Human Populations and Medical Genomics Instructors: Philip Awadalla and Lluis Quintana-Murci Time: 8:00 - 17:00 Place: Room 1

Lecture will cover major modern concepts in population genetics. Models that describe genealogical histories underlying sampled chromosomes in natural populations are central to the analysis of such data. The lecture covers the derivation and properties of the basic model and its extension to include factors such as recombination, geographical structure.

o Mutation and recombination

o Recombination at pedigree level - concept of linkage disequilibrium (LD)

o Measures of LD and its decay

o Coalescence and population genealogies - demography

Population mutation parameter, population recombination rate

The lab introduces methods of analysis using the statistical software package R.

Data resources

o 1000 genomes project

Demography of human populations. Inferences from uniparental and autosomal markers.

o This lecture will introduce the different models to explain human evolution. It will give an overview of the most recent genetic data explaining the human origins and migration patterns. It will concentrate on phylogeographic studies, mostly concerning uniparentally-inherited genomes.

o A rapid overview of the HapMap contribution to the better understanding of the demographic history of human population will be given.

o A new Human Genome Diversity Project (HGDP) resource

Day 2 - June 2nd Introductory Concepts in Genetic Epidemiology Instructors: Marie-Hélène Roy-Gagnon, Alexandre Bureau, Alexandre Alcaïs and Hélène Vézina Time: 8:00 - 17:00 Place: Room 1

We will first briefly introduce concepts and designs to study familial aggregation followed by basic principles of linkage and association analysis for qualitative traits. Topics covered will include designs and analytical methods used to study genetic linkage. Both parametric and non-parametric linkage analysis will be covered. Presentation of the concepts will be followed by a computer lab application using real data and currently available software such as MLB and MERLIN.

The second part of the lecture will cover designs and analytic methods for genetic association studies. Methods to investigate direct (candidate locus) and indirect (linkage disequilibrium mapping) associations with human disease will be introduced. Both family-based and population based designs will be presented.

Presentation of the concepts will be followed by a computer lab application using real data and currently available software such as FBAT.

Finally, a brief introduction to web resources will be presented, including databases useful in genetic epidemiology studies, an introduction to the BALSAC genealogical resource and presentation of existing tools for their analysis.

Day 3 -June 3rd (Concurrent Sessions - lectures and computer labs - followed by invited lecture)

Advanced Concepts in Population Genomics Instructors: Lluis Quintana-Murci and Luis B. Barreiro Time: 8:00 - 16:15 Place: Room 1

Simulation approaches (e.g. ABC, best-fitting) how we can infer demography from genetic data.

Methods in population genetics and hands-on lab

o Quality control of the data (e.g. test for HW equilibrium)

o Haplotype reconstruction using Phase o Methods to detect selection from molecular data

o Description of interspecies neutrality tests (e.g. dn/ds)

o Sequence-based neutrality tests

o Population differentiation methods (i.e. Fst approaches)

o LD-based methods

Advanced Concepts in Genetic Epidemiology and Statistical Genetics Instructors: Marie-Hélène Roy-Gagnon, Alexandre Bureau and Alexandre Alcaïs Time: 8:00 - 16:15 Place: Room 2

Data quality control (pedigree and genotyping error checks)

Introduction to quantitative genetics theory and linkage and association analysis for quantitative traits I

Introduction to quantitative genetics theory and linkage and association analysis for quantitative traits II

Haplotype analysis

Invited Lecture Speaker: to be determined Time: 16:15 - 17:00 Place: Room 1

Day 4 -June 4th (Concurrent Sessions - lectures and computer labs)

Advanced Concepts in Population Genomics Instructors: Lluís Quintana-Murci, Luis B. Barreiro, Philip Awadalla, Nicolas Lartillot Time: 8:00 - 17:00 Place: Room 1

Analysis of signatures of selection in genomic data - applications

o Analysis of real data on which students will perform all different types of neutrality tests

o Practical examples of natural selection in humans, and its utility in

— / —

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

---

## Portal NewMexico Phylogeography

Course Advertisement: Model-based Phylogeography course at the AMNH Southwestern Research Station near Portal, New Mexico. This course will cover several advanced topics in model-based approaches to the analysis of phylogeographic data, including those based on Monte Carlo simulations and parametric bootstrapping, approximate Bayesian computation, various power analyses, species delimitation, and hypothesis testing. Participants will be asked to bring their own data to the course, and the design and implementation of analyses for individual data sets will be emphasized. To facilitate these analyses, students will learn some basics of UNIX and R.

Course requirements: participants must bring a laptop computer running either Mac OSX or Linux operating systems. We suggest that participants install R and PERL prior to arrival, as well as several other open source programs (ms, seq-gen, msBayes, popABC, DIYABC, STEM, Mesquite, ). Participants will have access to wireless internet at the SWRS, and will be encouraged to conduct analyses remotely on servers at their universities. Prospective students should send a brief letter and a CV by January 20, 2009 to swrs.statistical.phylogeography<at>gmail.com . In the letter, please indicate how model-based phylogeography would enhance your research program and describe the data that you would like to analyze. We prioritize participants with data from empirical systems that can be analyzed during the workshop.

Instructors: Bryan Carstens, Assistant Professor, Louisiana State University http://www.lsu.edu/faculty/carstens/ Mike Hickerson, Assistant Professor, Queens College, City University of New York http://qcpages.qc.cuny.edu/Biology/Hickerlab/index.html Naoki Takebayashi, Associate Professor, University of

Alaska Fairbanks http://www.faculty.uaf.edu/ffnt/ Course Dates: Participants will arrive at the SWRS on Sunday, April 4th. There will be a brief reception Sunday evening, and the first classroom session will begin on Monday, April 5th. The workshop will end at noon on Friday, April 9th.

Course Fees: (including room & board at the SWRS) will be $950

–

Bryan C. Carstens Assistant Professor Department of Biological Sciences Louisiana State University

mail 202 Life Sciences Building Louisiana State University Baton Rouge, LA 70803 USA

e-mail carstens@lsu.edu bryan.c.carstens@gmail.com

web http://www.lsu.edu/faculty/carstens/ http://sites.google.com/site/carstenslabsite/ curriculum vitae http://www.lsu.edu/faculty/carstens/pdfs/Carstens-CV.pdf

office A114 Life Sciences Annex (225) 578-0960

lab A153 Life Sciences Annex (225) 578-4918

“Bryan C. Carstens” <bryan.c.carstens@gmail.com>

---

## Portugal PopulationGenetics Dec

The last course of the 2009 edition og GTPB is

MMPG09A Molecular Markers and Population Genetics (2nd course)

this is the second time we run the course this year. In the first time we had more than 50 applicants but, as usual, we could not take more than 20 participants at a time.

We run the course again now to give a second chance to those that wanted to come in June and to get new participants.

Please send your application as requested in the course website

http://gtpb.igc.gulbenkian.pt/bicourses/MMPG09/ until December 10th, the latest.

Thanks you for your interest in the GTPB bioinformatics training courses

P. Fernandes – Pedro Fernandes GTPB Coordinator Centro Português de Bioinformática Instituto Gulbenkian de Ciência Apartado 14 2781 OEIRAS PORTUGAL

Pedro Fernandes <pfern@igc.gulbenkian.pt>

---

## UBirmingham ModellingMicrobes Jun20-25

The Third Course on Individual-based Modelling of Microbial Interactions & Processes Using iDynoMiCS PhD Course June 20-25 2010 The University of Birmingham, UK

We are once again delighted to offer a hands-on course in modelling of microbial systems. In one stimulating week, this workshop will get you into individual-based modelling of microbial interactions with our newly developed software tool iDynoMiCS (individual-based Dynamics of Microbial Communities Simulator). In particular, you will get an in depth understanding of mathematical modelling of biofilms and other spatially structured microbial systems.

The course is intended for all students and researchers who have started to, or are considering to use, individual-based modelling for microbial systems. By the end of the course, participants will be able to independently use iDynoMiCS and apply it to their own work. The course will consist of a mix of core and guest lectures, tutorials, and a mini-project.

After running this course twice at the Danish Technical University in Lyngby, Copenhagen, with great success, the course will be held at the University of Birmingham in the UK in 2010.

Candidates from the fields of environmental science, microbiology, ecology, computer science, applied mathematics, engineering, and physics are encouraged to apply. Send (i) a brief statement of research interest and level of experience in modelling/programming, (ii) a brief CV, and (iii) a letter of support from your main advisor. The limited number of places will be allocated on a first come first served basis.

Course Credits: 5 ECTS Application Deadline: April 1, 2010 Course Fee: £200 for PhD students, £400 for postdocs

Course Instructors: Jan-Ulrich Kreft, University of Birmingham, United Kingdom Brian Merkey, DTU, Denmark Cristian Picioreanu, TU Delft, Netherlands Barth F. Smets, DTU, Demark

For informal expression of interest, registration, and further information, please email Susanne Schmidt: s.schmidt@bham.ac.uk

cgkanchi@gmail.com

---

## UUppsala Genomics Jan20-22

Dear all,

I would like to advertise an upcoming course entitled “Genomics for Ecologists - fundamentals and practicalities” to be held at the Evolutionary Biology Centre, Uppsala University, Sweden on January 20-22, 2010. The course is aimed at PhD students and postdocs with a background in ecology who are considering or planning to conduct ecological research using genomic techniques. The course is open for all, although places are guaranteed for members of EBC’s “Genomes and phenotypes” graduate school. 25 places remaining.

For more details and the full program of exciting talks see: http://www.ebc.uu.se/gradschool/-genomics_for_ecologists.pdf If you have any questions or to register, simply email me: ted.morrow@ebc.uu.se

Deadline for registration is January 10, 2010

/Ted

–

Edward H. Morrow Department of Animal Ecology Evolutionary Biology Centre Uppsala University Norbyvägen 18-D SE-752 36 Uppsala SWEDEN Email: ted.morrow@ebc.uu.se Tel: +46 18 471 2676 Fax +46 18 471 6484 Webpage: http://www.iee.uu.se/-zooekol/default.php?type=personalpage&id=-119&lang=en Ted Morrow <ted.morrow@ebc.uu.se>

---

## UVirginia EvolutionaryBiology

Dear Colleagues and Friends,

Mountain Lake Biological Station (University of Virginia) is pleased to announce its summer program of field-based undergraduate and graduate-level credit courses and workshops offered by nationally recruited faculty, and its NSF REU undergraduate research internship program, now in its 18th year. Work at MLBS focuses on field-based ecology, evolution, physiology, and behavior. Learn more about the programs or complete an on-line application.

Courses web page: http://mlbs.org/courses.html REU web page: http://mlbs.org/REU.html Please forward this information to colleagues or students you think might be interested. Thanks for your help!

Best wishes, happy and safe holidays.

Anne Marie De Marco Rehm Program Specialist Mt. Lake Biological Station P.O. Box 400327 Charlottesville, VA 22904

Phone: (434) 982-5486 Fax: (434) 982-5626 amrehm@virginia.edu www.mlbs.org amd8c@virginia.edu

---

# Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

# Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.