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# E v o l D i r

January 1, 2009

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

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## 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](mailto:Golding@McMaster.CA).

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

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



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## Conferences

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### Adelaide MathEvolutionaryBiol Apr20-24

Adelaide Conference on Mathematical Evolutionary Biology (April 20-24, 2009) and associated Grad student Phylogenetics Workshop (April 13-17, 2009) Adelaide, South Australia

The second annual Adelaide Conference on Mathematical Evolutionary Biology (ACMEB) will be held on Port Elliot beachfront, South Australia from April 20-24, 2009. This meeting follows the successful inaugural meeting held in Blanche Cave, Naracoorte in 2008 (<http://www.adelaide.edu.au/acad/-events/biomaths/Biomaths08.html>). The ACMEB series aims to bridge the current gap between biologists and mathematicians in Australia, and overseas, by providing a relaxed, informal setting for the discussion of new results and formation of trans-disciplinary collaborations. The emphasis is on the development and application of advanced new analytical methods, and current problems in evolutionary biology. The conference is designed to allow maximum student and academic interaction, and the analysis of datasets during the meeting itself. Topics covered at the previous meeting include: Mathematical methods and Algorithms; Phylogenetics and Networks; Macroevolution; Evolutionary rates and dates; Genome analysis; Bioinformatics; Human evolution; Disease. (A full list of abstracts from

2008 is available ([http://www.adelaide.edu.au/acad/-events/biomaths/biomaths08\\_abstrats.pdf](http://www.adelaide.edu.au/acad/-events/biomaths/biomaths08_abstrats.pdf)).

In a change to the 2008 conference format, there will also be an associated Phylogenetics Workshop for post-graduate students, run by the Australian Centre for Ancient DNA at the University of Adelaide from April 13-17 (Easter week). Workshop attendees are also encouraged to attend and present at the conference at Port Elliot. The workshop will feature hands-on training from 4 international experts, in leading software packages for the analysis of genetic data:

Prof. Mark Pagel, University of Reading; Dr. Alexi Drummond, University of Auckland (BEAST); Prof. Peter Lockhart, Massey University; and Christian Anderson (Serial SimCoal).

The conference features a day devoted to data analysis/recreation with scheduled activities around the Port Elliot area including wine tours, beach activities, and checking out local attractions. Important prizes at the ACMEB include the highly coveted Napkin Award (for the best mathematical solution to a biological problem solved at the conference). Entries must be submitted on the original napkin to allow artistic merit to be considered. Check out the winners of the 2008 award ([http://www.adelaide.edu.au/acad/events/biomaths/-biomaths\\_images/NapkinAward08%20copy.pdf](http://www.adelaide.edu.au/acad/events/biomaths/-biomaths_images/NapkinAward08%20copy.pdf)) (Profs. Allen Rodrigo - Auckland, and Nigel Bean - Adelaide).

The cost, program and further details of the above two events will be posted on our website shortly. Spaces are

strictly limited (20 for the workshop, 50 for the conference), so early registration is strongly advised.

Please follow this link (<http://www.adelaide.edu.au/acad/events/registration/>) to register for these events now.

–

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## AMNH Biodiversity and Health April 2009

EXPLORING THE DYNAMIC RELATIONSHIP BETWEEN HEALTH AND THE ENVIRONMENT The Center for Biodiversity and Conservation Milstein Science Symposium American Museum of Natural History New York City, New York, USA April 2 and 3, 2009 <http://cbc.amnh.org/health> Health and the environment are deeply intertwined for populations, species, and ecosystems, as well as for human lives and livelihoods. Human endeavors in agriculture, energy and food production, transportation, and infrastructure development can have far-reaching and significant impact on the health of humans and the environment. Understanding these relationships is increasingly critical in the context of our changing world and the accelerating loss of biodiversity.

This two-day conference will present a diversity of viewpoints and experiences, spanning the natural, medical, and social sciences, as well as policy planning. Presenters will discuss knowledge/data gaps and the limitations of current approaches, and examine innovative methods that move beyond speculation to a grounded understanding of impacts and realistic solutions. Particular emphasis will be placed on consideration of multiple and interacting stressors and decision making for maximizing benefits to both health and the environment.

CALL FOR POSTERS A limited number of posters will be accepted for presentation during the Symposium. Posters that address any aspect of the relation-

ship between health and the environment will be considered. Topics may include, but are not limited to:

- Links between the health of plants, wildlife, domestic animals, and/ or humans
- Anthropogenic drivers of disease emergence
- Environmental change and disease ecology
- Environmental change and pathogen evolution
- Pathogen discovery in natural reservoirs
- Ecology of host-pathogen interactions
- Climate change and health
- Health-related ecosystem functions and services
- Environmental sustainability and health
- Health and biodiversity conservation
- Capacity building in environment and health

Poster Abstract Submission Deadline: January 30  
Members of a Poster Selection Committee will determine which abstracts are to be accepted based on their relevance and general level of interest.

Special Student Pricing and Early-Registration Discounts

Details available at: <http://cbc.amnh.org/health> Or send an email to: [cbcsymposium@amnh.org](mailto:cbcsymposium@amnh.org)

“Exploring the Dynamic Relationship Between Health and the Environment” is proudly sponsored by the Paul and Irma Milstein Family and by a grant from the Defense Advanced Research Projects Agency of the United States Department of Defense (DARPA).

Please Note: The American Museum is unable to provide financial support to poster presenters for travel or accommodation.

Sergios-Orestis Kolokotronis, PhD Sackler Institute for Comparative Genomics American Museum of Natural History Central Park West at 79th Street New York, NY 10024 -USA- tel +1 212 313 7654 [koloko@amnh.org](mailto:koloko@amnh.org) <http://softlinks.amnh.org> <http://koloko.net> [koloko@amnh.org](mailto:koloko@amnh.org)

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## Austria ImmunityParasiteCoEvolution May 4-9

ESF-FWF-LFUI Conference on 'The impact of the environment on innate immunity: the threat of diseases' 4-9 May 2009, Obergurgl (Tyrol), Austria Programme and applications: <http://www.esf.org/-conferences/09223> Scope: Innate immunity recently came into the focus of evolutionary biologists as an evolutionarily ancient, yet astonishingly effective first-line

defence against many parasites and pathogens that is shared by both vertebrates and invertebrates. This conference will focus on the question how environmental factors influence the co-evolution between innate defence mechanisms and parasite counter-defences.

Grants for young researchers

Closing date for applications: 8 February 2009

Ivanka Angelova Communications Officer - ESF Conferences European Science Foundation - Communications Unit 1 quai Lezay-Marnésia, BP 90015 67080 Strasbourg Cedex, France Phone: +33 (0)388 76 21 48 Fax: +33 (0)388 76 71 80 [iangelova@esf.org](mailto:iangelova@esf.org) <http://www.esf.org> Ivanka ANGELOVA <[iangelova@esf.org](mailto:iangelova@esf.org)>

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## BrownU EnvGenomics Jun8-11

AMERICAN GENETIC ASSOCIATION ANNUAL SYMPOSIUM 2009

THE GENETICS AND GENOMICS OF ENVIRONMENTAL CHANGE 8-11 JUNE 2009 BROWN UNIVERSITY, PROVIDENCE RI

**OVERVIEW OF THE SYMPOSIUM** Environmental change has been a constant challenge for all organisms in the history of life on earth. In the thousands of years since the last glacial maximum, organisms have been forced to adapt to a changing climate. The striking environmental variation we observe from the poles to the equator, from season to season, and from day to night have been met by both physiological and evolutionary adaptations that enable organisms to survive and reproduce. In recent years there has been growing interest and concern over how humans are imposing environmental change on the planet, and how organisms are responding to that change. Environmental change means very different things to different biologists, yet few would deny that the genetic and genomic mechanisms of adaptation to this change are central problems in biology.

The goals of the AGA Symposium for 2009 are to examine environmental change from the perspective of genetics and genomics. Leading researchers in evolutionary, population, and quantitative genetics will discuss how these fields integrate with ecological and geological perspectives on climate change. The symposium will run over three days, with morning and afternoon sessions featuring invited speakers, and an evening poster session that is open to all attendees. Sessions

will be reserved for graduate students and postdoctoral researchers to present their work, as selected from the list of poster abstracts.

The conference will be held at Brown University in Providence Rhode Island. A clambake at the Blithewold mansion on the shores of Narragansett Bay will be held on the second evening and provides an opportunity for meeting attendees to converse in a relaxed and pastoral setting.

Some funds will be available to graduate students and postdocs on a competitive basis to defray the cost of attending the meeting.

### INVITED SPEAKERS

Bill Bradshaw, University of Oregon John Colbourne, University of Indiana George Gilchrist, College of William and Mary Elizabeth Hadly, Stanford University Ary Hoffmann, University of Melbourne/CEASAR Trudy Mackay, North Carolina State University Margie Oleksiak, University of Miami Outi Savolainen, University of Oulu Paul Schmidt, University of Pennsylvania Annie Schmitt, Brown University Jay Storz, University of Nevada Andrew Whitehead, Louisiana State University

### PROGRAM

Monday June 8, 2009 Arrival, Registration 12 noon - 6 pm Opening Reception 630 - 800 pm

Tuesday June 9, 2009 Morning: Clinal variation and environmental gradients Afternoon: Experimental evolution and environmental stress Dinner: on your own in Providence Poster session: 8 PM - 11 PM

Wed June 10, 2009 Morning: Environmental genomics of natural and human stressors Afternoon: Paleontological genetics of climate change Dinner: Clambake at Blithewold Mansion, Narragansett Bay

Thursday June 11, 2009 Morning: Genotype by environment interactions Afternoon: Predicting evolutionary responses to climate change Mid afternoon: Departure

– David Rand Professor of Biology Department of Ecology and Evolutionary Biology Box G-W, 80 Waterman Street Brown University Providence, RI 02912 Voice: (401) 863-2890 (Office - Walter Hall 202) (401) 863-1063 (Lab - BioMed Center 516-518) Fax: (401) 863-2166 email: [David\\_Rand@brown.edu](mailto:David_Rand@brown.edu) web page: <http://www.brown.edu/Departments/EEB/rand/index.htm> [David\\_Rand@brown.edu](mailto:David_Rand@brown.edu) [David\\_Rand@brown.edu](mailto:David_Rand@brown.edu)

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## Gainesville SEEC 2009 Mar27-29

The 2009 Southeastern Ecology and Evolution Conference will feature presentations from undergrad, grad, and postdoc students in the fields mentioned in the title. Seeing as how you manage a directory full of people conducting research in these areas, could you please forward the following message to all the email addresses you have? Thank you.

If you're an undergrad, grad, or postdoc conducting research related to ecology and/or evolution, you're invited to present at the aptly titled Southeastern Ecology and Evolution Conference (SEEC).

The SEEC is a professional, regional conference organized by students, for students. Students from UF and other southeastern schools will share their research in talks and poster sessions at this exciting (science! awards for best talks/posters!) conference as well as enjoy keynote talks by UF faculty, social events, and optional field trips.

This upcoming conference will be the 6th one and the first to be hosted by UF. It will take place from March 27, 2009 to March 29 with the joint hosting of the 32nd Herpetology Conference at the Paramount Plaza Hotel located at 2900 SW 13th Street, Gainesville, FL 32608.

Now that you know what the SEEC is, feel free to submit your abstracts to [seec2009@gmail.com](mailto:seec2009@gmail.com). \*Keep your submissions to no more than 250 words; the tentative deadline is January 6, 2009. Any abstracts even loosely related to ecology/evolution suffice.\* We will then read and categorize them into subjects such as biodiversity, animal behavior, conservation, functional morphology, population ecology, etc. and respond once we've approved what we've read. Be sure to include contact info in your email and your preference of an oral or poster presentation.

Registration should open sometime in the latter half of December, along with a website with more information such as costs and procedures. We'll keep in touch with you once you've submitted an abstract.

SEEC 2009 <[seec2009@gmail.com](mailto:seec2009@gmail.com)>

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## HumboldtU Innovations in phylogenetics Mar4-7

The international conference "Celebrating Darwin: From The Origin of Species to Deep Metazoan Phylogeny" brings together mathematicians, theorists, molecular systematists, and morphologists interested in a critical review of known pitfalls and in the presentation of new analytical tools, new types of characters, and a synopsis of molecular and morphological characters. It is intended to get a critical and constructive view of the state of the art. If you want to go beyond the routine analyses that in the past produced so many conflicting hypotheses, and if you are not a believer but a critical researcher, this is the opportunity to exchange new ideas for alternative ways to analyze deep phylogenies.

On behalf of the organising committee we would like to invite you to this conference, which will take place from 4th - 7th March 2009 at the Humboldt-University and the Museum of Natural History in Berlin, Germany. The meeting will consist of sessions with several invited speakers and open sessions with short presentations. In addition, there will be the possibility to show posters. The meeting focuses on three major themes:

- 1) Innovations in analyses of molecular and morphological data
- 2) Molecular phylogeny: new markers and phylogenomic analyses
- 3) The indispensability of morphology

The conference is organised by the Priority Program "Deep Metazoan Phylogeny" of the German Science Foundation (DFG). The project brings together molecular, morphological and bioinformatic expertise with the goal to establish a robust (hopefully) backbone tree of metazoans. Details on the priority program "Deep Metazoan Phylogeny" can be found at: <http://www.deep-phylogeny.org/>. For more information and to register please visit our website:

<http://www.dmp2009.org/> Please block this period or time in your appointment calendar.

Prof. Dr. J. Wolfgang Waegle Zoologisches Forschungsmuseum Alexander Koenig und Lehrstuhl für Spezielle Zoologie Rheinische Friedrich-Wilhelms-Universität Bonn

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## KansasCity Genomics Jun11-14

Frontiers in Arthropod Genomics

3rd ANNUAL ARTHROPOD GENOMICS SYMPOSIUM

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

KEYNOTE SPEAKER: Fotis C. Kafatos, Imperial College London, “Evolutionary, functional and population genomics of mosquitoes: The perspective of a malariologist.”

OPENING SPEAKER: William M. Gelbart, Harvard University, “Opportunities & Challenges for Arthropod Genomics and Informatics in the NextGen World.”

FEATURED SPEAKERS:

- \* Volker Brendel, Iowa State University
- \* Susan J. Brown, Kansas State University
- \* Jay D. Evans, USDA-ARS Bee Research Lab, Maryland
- \* Marian R. Goldsmith, University of Rhode Island
- \* David G. Heckel, Max Planck-Institute for Chemical Ecology, Jena, Germany
- \* Kristin Michel, Kansas State University
- \* Terence Murphy, National Center for Biotechnology Information/NIH
- \* Marcelo Ortigao, Kansas State University
- \* Yoonseong Park, Kansas State University
- \* José Ribeiro, Laboratory of Malaria and Vector Research, NIH/NIAID
- \* Denis Tagu, French Nat'l Inst. for Agricultural Research, Rennes, France
- \* Doreen Ware, Cold Spring Harbor Laboratory
- \* Stephen K. Wikel, University of Texas Medical Branch, Galveston

POSTER SESSIONS: There will be two poster sessions. A few platform presentations will be chosen from sub-

mitted poster abstracts.

SYMPOSIUM PROGRAM: The symposium sessions will begin Thursday evening, June 11, and continue on Friday and Saturday, with optional events on Saturday evening and Sunday morning. Speakers will present new insights from genomic approaches in arthropods and describe the development of tools for genomic analysis. Workshops will be held Thursday prior to the Symposium and Friday evening. Activities will conclude by noon on Sunday, June 14.

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

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

INFORMATION: Online registration will open soon after 1/1/09! Information regarding poster submission and hotel reservations will also be posted. Visit our website, [www.k-state.edu/agc](http://www.k-state.edu/agc), for updates as details are finalized. Add your name to the Symposium mailing list, by sending your contact information to [dmerrill@k-state.edu](mailto:dmerrill@k-state.edu).

SPONSOR: K-State Arthropod Genomics Center, Kansas State University

Susan J. Brown, Professor

Director, Center for Genomic Studies on

Arthropods Affecting Human, Animal and Plant Health

and

Robin E. Denell, Distinguished Professor and  
Chair, AGC Symposium Organizing Committee

by

Doris Merrill, Program Coordinator

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## London e-Biosphere Jun1-5 extended deadlines

Dear Colleagues,

The e-Biosphere 09 International Conference on Biodiversity Informatics (see [www.e-biosphere09.org](http://www.e-biosphere09.org) <blocked::<http://www.e-biosphere09.org/>> ) will take place in London on 1-5 June 2009. The Conference will be devoted to:

\* Highlighting the accomplishments and capabilities of Biodiversity Informatics; \* Sharing information and demonstrations of databases and software; and \* Gathering input from researchers and users on the directions that Biodiversity Informatics should take in the next 5-10 years.

Input from the Conference will go directly into a two-day planning meeting of major Biodiversity Informatics initiatives. This input will inform their R&D roadmap and help them develop priorities for implementation and funding.

To enable the communities of researchers and users in Biodiversity Informatics to prepare properly for the Conference, the organizers announce:

1. Creation of an Online Conference Forum (OCF). The OCF will be a web-based environment in which research and user communities can interact, hold e-discussions, exchange documents, and communicate in various ways. It will become operational early in January 2009 and we will send an announcement when it is ready for use. The Forum will begin with the following pre-constructed communities, but OCF participants will be able to merge and split communities and to form new communities.

\* Developing world \* Conservation and land use \* Agriculture, forestry, fisheries, and economic development \* Public Health \* Ecology and ecosystems, environmental sustainability, climate change \* Taxonomic groups \* Uses in public, K-12 and higher education \* Basic biodiversity science research \* Training in biodiversity informatics \* Citizen science \* A future road map for Biodiversity Informatics

One session at the Conference will be devoted to parallel discussion sessions of the ten most active online communities. These discussion sessions will enable participants to finalize their vision of where Biodiversity

Informatics needs to develop. These discussion groups will be encouraged to submit group-authored Position Papers to the Conference Proceedings volume.

2. Extension of Conference deadlines. The Conference organizers hope that the OCF will stimulate lots of ideas and interactions that will show up at the Conference as innovative poster abstracts, demonstrations of databases and software, discussion groups, and side-events. To let this process of communication have the greatest possible impact, Conference deadlines have been revised to the latest possible dates:

\* 15 January 2009: Launch of the Online Conference Forum (OCF) \* 1 March 2009: Deadline for submission of poster abstracts <blocked::<http://www.e-biosphere09.org/webforms/abstract>> and applications for travel bursaries <blocked::<http://www.e-biosphere09.org/webforms/travel>> \* 1 April 2009: Deadline for applications for exhibit space and database/software demonstrations <blocked::<http://www.e-biosphere09.org/assets/files/-Exhibitors07Jul08.pdf>> \* 15 April 2009: Deadline for proposals for discussion group topics and side-events. \* 1 May 2009: Conference registration deadline \* 1 May 2009: Release of abstract volume \* 1 May 2009: Release of Third Conference Announcement with final agenda \* 1-5 June 2009: e-Biosphere 09 Conference

Please send inquiries to [inquiries.e-biosphere09@si.edu](mailto:inquiries.e-biosphere09@si.edu) <blocked::mailto:[inquiries.e-biosphere09@si.edu](mailto:inquiries.e-biosphere09@si.edu)> .

Best regards and happy holidays -

David

David E. Schindel, Executive Secretary

Consortium for the Barcode of Life

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 schindeld@si.edu

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### London EvolutionOfSocieties Jan19-20

The Evolution of Society

Discussion Meeting Monday 19 to Tuesday 20 January  
 2009 Location: The Royal Society, London

By Professor Tim Clutton-Brock FRS, Professor R A  
 Foley, Professor F L W Ratnieks and Professor S West

The meeting will synthesise our understanding of the  
 evolution of social behaviour, association and coopera-  
 tion in micro-organisms, invertebrates, vertebrates and  
 man, providing a unified conceptual overview of the  
 mechanisms involved in the evolution of societies, the  
 causes of variation in their structure, the contrasts and  
 similarities between the processes operating in animals  
 and man and the principal questions still unresolved.

The programme is now available here <http://royalsociety.org/downloadaddoc.asp?id=5977> The meet-  
 ing is open for everyone to attend, please register  
 through the meetings website [http://royalsociety.org/-  
 event.asp?id=7431](http://royalsociety.org/-event.asp?id=7431) –

Dieter Lukas Large Animal Research Group Depart-  
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### Marseilles 13thEvolutionaryBiology Sep22-25

Dear All,

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

- Evolutionary biology concepts and modelisations for  
 biological annotation; - Biodiversity and Systematics; -

Comparative genomics and post-genomics (at all tax-  
 onomic levels); - Functional phylogeny; - Environment  
 and biological evolution; - Origin of Life and exobi-  
 ology; - Non-adaptative versus adaptative evolution; -  
 The « minor » phyla: their usefulness in evolutionary  
 biology knowledge.

For more information, do not hesitate to go on: [http://  
 /sites.univ-provence.fr/evol-cgr](http://sites.univ-provence.fr/evol-cgr) Best wishes,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

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### Munich PhDEvolutionaryBiology Mar5-8

DZG (Deutsche Zoologische Gesellschaft / German Zo-  
 ological Society) Phd Meeting 2009

Thursday March 5th - Sunday March 8th, Munich, Ger-  
 many - Botanical Gardens

The annual evolutionary biology PhD meeting of the  
 DZG is an unique opportunity for graduate students  
 (Diplom, Master, PhD) in evolutionary biology to  
 present their work and to get to know each other in  
 an informal environment. Phd, diplom and master stu-  
 dents, as well as young post docs interested in evolu-  
 tionary biology are encouraged to join. The meeting  
 is organized by the evolution group of the Germany  
 Zoological Society (DZG), but botanists, mycologists,  
 theoreticians, phylogeneticists, evolutionary ecologists  
 are all welcome. The meeting is an ideal opportunity  
 to give a talk about your thesis, find out what other  
 researchers are doing and gain insights into where you  
 would like to do a PhD or post doc.

Invited Speakers: Olaf Bininda-Emonds - Carl Von  
 Ossietzky University of Oldenburg, Germany Penelope  
 Haddrill - University of Edinburgh, UK Thomas  
 Schmitt - Albert-Ludwigs-Universität Freiburg,  
 Switzerland

Registration: The registration deadline is February 1st  
 and the number of participants is limited to 100. Par-  
 ticipants may register to give a 10 minute talk or to do  
 a poster presentation. Every participant whose submis-  
 sion is not chosen for the presentation will be given the  
 chance to present his/her work as a poster. The meet-  
 ing will cost around 20 Euros, to cover coffee breaks,  
 one dinner, and a social event on Saturday night.

For registration and more information please see



our website: [http://www.eeslmu.de/eeswiki/DZG\\_PhD\\_Meeting\\_2009](http://www.eeslmu.de/eeswiki/DZG_PhD_Meeting_2009) DZG Meeting 2009 Organizing Committee: Sonja Grath - Evolutionary and Functional Genomics - LMU Munich Stefan Laurent - Evolutionary Biology - LMU Munich Jennifer Lohr - Evolutionary Ecology - LMU Munich

EES LMU Program website: <http://www.eeslmu.de/> Jennifer Lohr DZG Conference committee 2009

Jennifer Lohr <j\_lohr@hotmail.com>

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

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

## StMalo France Biodiversity May17-20

Dear colleagues,

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

The recent years have seen significant advances in understanding the consequences of reticulate evolution and genome duplication that appear a major feature of eukaryotic lineages. The meeting aims at promoting knowledge exchanges and discussions on the latest developments concerning these major drivers of genome shaping and speciation. A wide range of topics will be covered such as the consequences of polyploidy on biodiversity, hybrid and polyploid speciation, meiosis and fertility in polyploid species, genome evolution and structure, transposable elements and DNA methylation, epigenetics and gene regulation, heterosis, phenotypic variation ... Registration is now open at <http://www.icphb2009.univ-rennes1.fr/> , oral and / or poster contributions are welcome.

Saint-Malo is a beautiful and well-known medieval city on the NW coast of France (Brittany region). It is visited by thousands of tourists every year due to its historical centre, attractive coasts and magnificent landscapes. We are looking forward to seeing you in Saint-Malo, France in May 2009!

Scientific Committee: Ainouche M. (France), Alix K. (France), Chalhoub B. (France), Chen J. (USA), Chèvre A-M. (France), Colot V. (France), Comai L. (USA), Doyle J. (USA), D'Hont A. (France), Grandbastien M-A. (France), Jahier J. (France), Jenzcewski E. (France), Kovarick A. (CZ), Leitch A. (UK), Mittelsten Scheid O. (Austria), Pires C. (USA), Quixin S. (China) Rieseberg L. (Canada), Soltis P. (USA),

## Trondheim

### PopGeneticsConservation May23-26

Conservation Genetics: Integrating Population Genetics and Conservation Biology

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

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

Key speakers include John Avise, University of California at Irvine, Fred Allendorf, University of Montana, and Michael Soulé, Colorado.

The conference will be held at Rica Nidelven Hotel, Trondheim (Norway). A web site for the conference is being constructed at [www.nina.no](http://www.nina.no) < <http://www.nina.no> > . Registration opens in the end of December, along with information on accommodation, programme and invitation for abstracts of presentations and posters.

Best wishes,

Kjetil Hindar, Øystein Flagstad and Laila Saksgård, NINA

Hans Stenøien, Gunilla Rosenqvist and Henrik Jensen, NTNU  
jaapderoode@hotmail.com

“Hindar, Kjetil” <Kjetil.Hindar@nina.no>

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## Turin ESEB Aug24-29

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### Turin ESEB 2009 parasite evolution Aug24-29

We are inviting abstract submissions for oral and poster presentations in the symposium “Integrating ecology with parasite evolution” to be held on August 28 2009 at the European Society for Evolutionary Biology (ESEB) meeting in Turin, Italy (August 24-29 2009).

Abstracts should be submitted online at <http://www.eseb2009.it/uk/> by February 15 2009.

**DESCRIPTION OF SYMPOSIUM:** The enormous abundance of parasites and their effects on wild populations, agriculture and human health have given rise to a rapidly growing field centered on using evolutionary principles to understand infectious disease. This field does not only significantly contribute to our general understanding of evolutionary theory, but also has the potential to provide new ways of tackling disease. The last few decades have seen much progress in understanding general evolutionary processes in parasite biology, and have also revealed the important role of genetic interactions between hosts and parasites. However, much less attention has been paid to the effect of the ecological conditions under which hosts and parasites interact. This is a serious problem, because empirical studies are increasingly showing that in-host and external environmental factors (e.g. temperature, host diet and the presence of competitors) can shape parasite virulence, life-histories, within-host dynamics and transmission.

The aim of this symposium is to bring together theoreticians and empiricists to explore how ecology influences the evolution of parasites. This will not only advance understanding of the basic processes by which parasites evolve, but also provide a basis to predict the consequences of human interventions on infectious disease.

#### INVITED SPEAKERS:

Mike Boots, University of Sheffield, UK  
Anna-Liisa Laine, University of Helsinki, Finland

**ORGANIZERS:** Sarah Reece, University of Edinburgh, UK (Sarah.Reece@ed.ac.uk)  
Jacobus de Roode, Emory University, USA (jacobus.deroode@emory.edu)

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jderood@emory.edu jderood@emory.edu

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## UBristol MathModelsinEvolution Sep10-11

Dear colleague,

Mathematical Models in Ecology and Evolution 2009 will be held at the University of Bristol on September 10th-11th 2009. Following the great success of the inaugural meeting in 2007 at Sussex, the 2009 meeting will have a Darwinian flavour, in honour of the bicentenary of Darwin's birth, and 150 years since the publication of *The Origin of Species*. While not a mathematician himself, Darwin's ideas find natural expression in the form of mathematical models, allowing further development and refinement of the theory. MMEE 2009 will showcase the latest developments of formal models in evolution and ecology, and will include keynote addresses on the mathematical modelling of Darwin's key theories and insights from:

- Professor Rob Boyd, Department of Anthropology, University of California Los Angeles - Professor Alan Grafen, Department of Zoology, University of Oxford - Professor Hanna Kokko, Department of Biological and Environmental Science, University of Helsinki - Professor Franjo Weissing, Department of Biology, University of Groningen

Abstracts of no longer than 250 words should be sent to James.Marshall@bristol.ac.uk by June 12th 2009. The organisers welcome abstracts for talks and posters (please indicate your preference if you have one). Registration details and accommodation information will be announced in the New Year, and posted on the conference website: [www.cs.bris.ac.uk/mmee2009](http://www.cs.bris.ac.uk/mmee2009) As space at the conference venue is strictly limited, and we expect a high level of interest, participants will be asked to register early to avoid disappointment.

We look forward to receiving your abstract, and to seeing you in Bristol in 2009. Best wishes, James Marshall  
John McNamara Alasdair Houston

James A. R. Marshall Department of Computer Science University of Bristol [www.cs.bris.ac.uk/~marshall](http://www.cs.bris.ac.uk/~marshall)  
James.Marshall@bristol.ac.uk

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## UIowa SMBE Jun3-7 Call for Contributed Symposia

The 17th annual meeting of the Society for Molecular Biology and Evolution SMBE 2009 will be held in Iowa City June 3-7, 2009, on the campus of The University of Iowa. Visit our website (<http://smbe2009.org>) for the most current information.

The SMBE 2009 Organizing Committee invites you to develop and submit proposals for consideration as contributed Symposia.

Symposium proposals need to include:

Proposed symposium title, along with proposers' address(es) and e-mail(s)

A brief description of the topic and rationale for its inclusion in SMBE 2009 (maximum of 300 words)

The names and contact information of up to five potential participants

Total length of proposals should not exceed two pages

Proposals will be selected by the SMBE 2009 Scientific Program Committee. Decisions will be based on their innovation and relevance to SMBE 2009.

SMBE 2009 will include ~22 symposia of which ~11 will be chosen from contributed proposals. Each Symposium will have two (or possibly three) invited speakers (each with an allocated time of 30 minutes, including questions). Additional contributed talks (each with an allocated time of 15 min, including questions) will be selected from submitted abstracts. Selected contributed symposia will be provided with partial financial support to defray meeting costs for 2-3 invited speakers (TBA).

Symposia being developed by the Organizing Committee currently include:

Types of molecular evolution: Wilson, Maxson & Sarich reprise (McAllister & Maxson) Historical roots of molecular evolution (Graur & Logsdon) Vanishing genomes (Bhattacharya) Early animal genomes (Lavrov) Primate functional and comparative genomics (Ting, Sterner & Xing) Mutation accumulation in eukaryotic genomes (Neiman) Population genomics (Cameron) Molecular evolution of biological complexity: From genetics to systems biology (Gu)

Proposals intersecting, complementing or expanding these topics are welcome and will be fully considered.

Proposals for contributed Symposia (in Word or PDF format) should be sent by e-mail to: [smb2009@uiowa.edu](mailto:smb2009@uiowa.edu) indicating in the subject: SMBE 2009 Symposium Proposal

Deadline: January 12, 2009

Proposers will be notified of the SMBE 2009 Scientific Program Committee's decision on or before January 30, 2009

SMBE <[info@smbe.org](mailto:info@smbe.org)>

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

email <[john-logsdon@uiowa.edu](mailto:john-logsdon@uiowa.edu)> web <<http://cgc.biology.uiowa.edu>> <<http://-euplotes.biology.uiowa.edu>>

[john-logsdon@uiowa.edu](mailto:john-logsdon@uiowa.edu) [john-logsdon@uiowa.edu](mailto:john-logsdon@uiowa.edu)

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## AboAkademiU EiderDuckEvolution

PhD position (4 years) - ARONIA Research Institute at Ebo Akademi University & Novia University of Applied Sciences, Finland

INDIVIDUAL VARIABILITY, COOPERATIVENESS AND CONSEQUENCES OF PARTNER CHOICE  
Project leader Markus Å-st

Like humans, animals too have personalities, some of them being bold and brave, while others are shy and softy. These differences have traditionally been explained away as noise surrounding adaptive population-average behaviour. Recent theory has aimed at adaptively explaining this variability. However, little is known about whether personality affects the tendency to cooperate with others, and whether the mixture of personality types in socially breeding groups has fitness consequences. These open questions can best be addressed by an integrative approach, since genetics and individual state influence endocrine mechanisms that govern behaviour.

This four-year project funded by Academy of Finland aims to 1) demonstrate the existence of personalities, 2) relate personality and physiological stress response to parental care strategy and parental quality and state and 3) explore the distribution of personalities in cooperative groups and its fitness consequences. The model species is the eider duck (*Somateria mollissima*), where females show a variety of parental care strategies, ranging from solo care to joint care with other females.

Fecal steroid analyses are ideal for studying hormone-behaviour relationships. It has previously been shown that stress responses relate to personalities and dominance. We will quantify individual quality, dominance, boldness, activity, exploratory behaviour and physiological social stress response, as judged by fecal glucocorticoid metabolites (GCMs) before and after choosing parental care strategy. This defines individuals on the 'boldness-shyness' personality axis.

Field work will take place at Tvärminne Zoological Station, SW Finland, in a long-term, individually-marked study population. The biochemical analyses (immunoassay) will be conducted abroad. The doctoral student will be based at Ekenäs, Finland, joining the interdisciplinary ARONIA Coastal Zone Research Team established in 2008. The new Ekenäs campus creates an inspirational setting for supervision and training, and the candidate will be enrolled at Ebo Akademi University.

### HOW TO APPLY

We are looking for a self-motivated person with a Master's Degree, able to work both independently and in a team. The position is open from early 2009 (with some flexibility) until the end of 2012. The thesis work will be supervised by Dr. Markus Å-st together with a post-doc. The position is open to anyone with an interest in behavioural ecology, evolutionary biology or physiological ecology. Previous experience of field and lab work, good knowledge of statistics and proficient writing skills in English are desirable qualifications. The salary will be paid according to the guidelines of Ebo Akademi University.

Applications (in English) should include a -Statement

of research interests and motivation for applying for this position, not exceeding 2 pages -CV -Publication list (if available) -Contact information of two academic references

Send your application electronically to Markus Åst, markus.ost@novia.fi. For further information, please e-mail or call Markus Åst (tel. +358-19-224 8414).

Application deadline: 31 December 2008.

Markus.Ost@novia.fi Markus.Ost@novia.fi

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## AboAkademiU EiderDuckEvolution

### 2

Subject: Graduate Position: social behavior in eider ducks

PhD position (4 years) - ARONIA Research Institute at Abo Akademi University & Novia University of Applied Sciences

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Markus Åst <Markus.Ost@novia.fi>

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## EmoryU PopulationBiology

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

<http://www.biomed.emory.edu/PROGRAM.SITES/>-

PBEE/ We would like to announce the available of pre-doctoral training fellowships at Emory University in the graduate program in Population Biology, Ecology, and Evolution (PBEE). The PBEE graduate program provides the multidisciplinary training required for a successful research and teaching career. The program allows the student to learn currently accepted scientific facts and theories; learn to plan, conduct and critically evaluate experiments; make an original contribution to scientific knowledge; become skilled in oral and written communication; and become self-sufficient in continuing education beyond graduate school. The program also prepares the student to teach Population Biology, Ecology, and Evolution and related disciplines in professional and graduate school.

The Emory University graduate program in Population Biology, Ecology, and Evolution (PBEE) is part of the Graduate Division of Biological and Biomedical Sciences. Faculty include members of the departments of Biology, Human Genetics, Anthropology, Environmental Studies and Psychology, as well as faculty in the Rollins School of Public Health and Medical School. The graduate faculty also includes investigators at the US Centers for Disease Control and Prevention, and the Yerkes Primate Center. Founded in 1994, the PBEE program now includes 27 faculty and 21 graduate students. Areas of emphasis and expertise include: The ecology and evolution of infectious diseases and molecular evolution and functional genomics. Our students receive a support package that includes a tuition scholarship, health insurance, and stipend.

The application deadline is January 3. For more information and application materials contact the Graduate Division of Biological and Biomedical Sciences and Emory University (800.727.6028, 404.727.2545 or [gdbbs@emory.edu](mailto:gdbbs@emory.edu), [www.biomed.emory.edu](http://www.biomed.emory.edu))

For more information or to answer questions about the PBEE program, please see the following website: [http:// www.biomed.emory.edu/PROGRAM\\_SITES/-PBEE/](http://www.biomed.emory.edu/PROGRAM_SITES/-PBEE/) Or directly contact:

Dr. Yun Tao Assistant Professor Department of Biology Emory University [ytao3@emory.edu](mailto:ytao3@emory.edu) 404-727-0815

Yun Tao <[ytao3@emory.edu](mailto:ytao3@emory.edu)>

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## Frick Switzerland Biodiversity

Place: Frick, Switzerland Supervisors: Dr. Oliver

Balmer and a professor to be determined

The Research Institute of Organic Agriculture (Forschungsinstitut für biologischen Landbau FiBL) in Frick, Switzerland is the world's leading research, information and documentation centre for organic agriculture. The close links between different fields of research and the rapid transfer of knowledge from research to advisory work and agricultural practice are FiBL's strengths.

The division of Entomology is looking for a highly motivated

PhD student

and master students in parasitoid ecology / biological control / functional biodiversity.

You will join another PhD student and two staff scientists in a fully funded project investigating how and which companion plants are best employed in cabbage fields to improve natural control of lepidopteran cabbage pests by parasitoids in Switzerland. The aim of this approach is to achieve pest control by natural means to reduce pesticide use and increase biodiversity in crop fields.

We are looking for candidates with a strong background in (insect) population biology, parasitoid ecology, plant-herbivore-parasitoid interactions, behavioural ecology, biological control or similar fields and with a keen interest to combine intense field and greenhouse / laboratory work. The ideal PhD candidate has a proven record of scientific achievement and will develop his/her own ideas within the framework of the project. The working language is English, German is an asset for field work. A driver's license is a must. The project will be set up as a collaboration with an external professor (to be chosen depending on the exact project) who will be the official supervisor. The position is open until filled.

Applications should be submitted by email as a single attachment to [oliver.balmer@fibl.org](mailto:oliver.balmer@fibl.org). Please include a brief statement why you are interested and what your career goals are, a description of your experience, your curriculum vitae with publication list, and names and email addresses of two academic references.

Web: [www.fibl.org/en/career/vacancies.html](http://www.fibl.org/en/career/vacancies.html)  
[www.fibl.org/en/switzerland/forschung/entomologie/-functional-biodiversity.html](http://www.fibl.org/en/switzerland/forschung/entomologie/-functional-biodiversity.html) (link may change soon)

Contact:

Dr. Oliver Balmer Forschungsinstitut für biologischen Landbau (FiBL) Ackerstrasse, CH-5070 Frick, Switzerland, Tel. ++41 (0)62 865 72 75 or ++41 (0)61 / 267 03 76 <http://www.fibl.org/en/team/balmer-oliver-en.html> Oliver Balmer <[oliver.balmer@unibas.ch](mailto:oliver.balmer@unibas.ch)>

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## ImperialCollege EvolutionaryEpidemiologyMalaria

Two PhD positions are available for students interested in the evolutionary epidemiology of malaria. Students should be enthusiastic, have a good background in evolutionary ecology and be interested in epidemiology and host-parasite interactions. The positions are part of a research project (funded by The Leverhulme Trust) that investigates ideas about how to block the evolution of resistance in strategies of malaria control. Empirical and theoretical studies are possible on the evolutionary interactions between 2 parasites (a microsporidian and malaria) and their mosquito host.

Starting dates are February 1, 2009 or later. The appointments are for 3 years, with a salary of about 15000£ per year.

Additional information is available from Jacob Koella (jkoella@imperial.ac.uk), Imperial College London, Division of Biology at Silwood Park Campus

Jacob Koella <jkoella@gmail.com>

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## LMU Munich PlantEvolutionaryGenet

PhD position: Plant evolutionary genetics, LMU-Munich

I am looking for a Ph.D. candidate (3 yrs) interested in the evolution of plant-bacterial symbioses. This position is funded by the German Science Foundation (DFG) to study the molecular evolution of plant recognition of nitrogen fixing bacteria. This project will involve functional studies on plants (inoculations with bacteria and trans-gene expression) and classical population genetics.

The student would be employed according to the German civil servant scale and would be enrolled in our graduate program in Evolution, Ecology, and Systematics (<http://www.eeslmu.de>).

Applicants should have a Master's degree or equivalent in biology or a related field. Previous laboratory ex-

perience and coursework in evolutionary biology and genetics are desirable.

The University of Munich has strong, interactive groups in evolutionary biology and genetics, including theoreticians and experimentalists working on both plant and animal systems (<http://www.evol.bio.lmu.de> and <http://www.genetik.bio.lmu.de>). Our group is very international and the everyday working language is English. The city of Munich offers excellent infrastructure and beautiful surroundings, with the Alps in close proximity.

The closing date for applications is January 30, 2009, or when the position is filled. Applicants should send a single PDF file containing a statement of interest and previous research experience, curriculum vitae, and contact information for at least two referees to: Dr. Laura Rose (rose@bio.lmu.de).

rose@zi.biologie.uni-muenchen.de rose@zi.biologie.uni-muenchen.de

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## LouisianaStateU EvolutionaryGenomics

I am seeking a highly motivated graduate student interested in ecological and evolutionary genomics research. We have two major ongoing projects in my lab.

1. Comparative Evolutionary Genomics of Physiological Plasticity: Some species can change their phenotype to compensate for broad changes in environmental conditions, whereas other species have narrow tolerance ranges. Gene regulatory mechanisms are likely to underpin this physiological plasticity. We seek to define the transcriptomic basis of a universally important compensatory response (acclimation to osmotic stress) for several taxa of fish that vary in their ability to tolerate stress based both on laboratory studies and on habitat distributions in nature. Evolutionary comparative analyses of variation in transcriptomic responses are being used test for gene regulatory differences that account for species differences in physiological plasticity.

2. Genomic Basis of Rapid Convergent Pollution Tolerance. Multiple populations of the killifish *Fundulus heteroclitus* have independently evolved to tolerate extraordinarily high concentrations of PCB contaminants. This system provides an excellent template to explore fundamental evolutionary questions including "what is



the genomic and physiological basis of rapid adaptation?" and "is the genomic basis of adaptation the same in parallel-evolved populations?". We are taking three top-down approaches to addressing these questions. First, we are using QTL mapping of hybrid crosses between multiple tolerant and sensitive populations to determine how many loci involved, and whether the same loci are implicated in different tolerant populations. Second, we are genotyping many wild individuals from multiple populations using thousands of markers for association studies to determine outlier loci: a "population genomics" approach. Third, we are using transcriptome profiling of PCB-challenged fish to determine what the individuals from tolerant populations are doing differently at the functional level to enable tolerance, compared to individuals from sensitive populations.

Appropriate tangents to these projects are possible and encouraged for Ph.D. studies.

For more information about my lab, visit: <http://www.biology.lsu.edu/webfac/awwhitehead/-frontpage%20template.htm> To learn more about graduate studies in the Department of Biological Sciences at LSU, visit: <http://www.biology.lsu.edu/> For more information about our research, or to apply, email a CV (including GPA and GRE scores), letter of interest, and contact information for 3 references to Dr. Andrew Whitehead ([andreww@lsu.edu](mailto:andreww@lsu.edu)).

The review of applications will begin immediately and will remain open until the position is filled. Applicants must also apply to LSU Graduate School (deadline Jan 1, 2009) and meet requirements for admission.

Andrew Whitehead, Asst. Professor

Dept. of Biological Sciences, LSU

office: 225-578-8210, lab: 225-578-2688, fax: 225-578-2597

NEW lab webpage: <http://www.biology.lsu.edu/webfac/awwhitehead/frontpage%20template.htm>

[andreww@lsu.edu](mailto:andreww@lsu.edu) [andreww@lsu.edu](mailto:andreww@lsu.edu)

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## Madrid BirdEvolution

### PHD STUDENTSHIP IN BIRD EVOLUTIONARY ECOLOGY (MADRID, SPAIN)

We are looking for a motivated PhD student for a four-year PhD studentship on the role of yolk hormones in

the regulation of bird life history trade-offs, starting in spring 2009.

The study will be carried out in a spotless starling (*Sturnus unicolor*) colony near Madrid, and will look at the adaptive function of maternal hormones that are passed to the offspring in the yolk. Field work is intense (March-July) and will require long field season involving capture of adults, manipulation of hormone levels, follow-up of reproduction in nest boxes.

The successful candidate will have a solid background in evolutionary ecology and statistics. Previous experience in relevant field work will also be important, as well as some knowledge of Spanish (not essential). Although a Bachelor's degree in Biology or Psychology is the required minimum, ideal candidates will be in possession of Master course or DEA in Animal Behaviour or Evolutionary Ecology.

If interested please send CV to Diego Gil ([dgil@mncn.csic.es](mailto:dgil@mncn.csic.es)) as well as a motivation letter explaining your interests in science and your motivation to spent the next four years of your life in Madrid.

Diego Gil Departamento de Ecología Evolutiva Museo Nacional de Ciencias Naturales (CSIC) José Gutiérrez Abascal, 2 28006 Madrid, Spain

email: [dgil@mncn.csic.es](mailto:dgil@mncn.csic.es)

<http://www.mncn.csic.es/investigador.php?cat=-2&pgq> Diego Gil <[dgil@mncn.csic.es](mailto:dgil@mncn.csic.es)>

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## Madrid SexualSelectionSpeciation

### PHD STUDENTSHIP IN SEXUAL SELECTION AND EVOLUTION.

We offer a four-year PhD studentship to study the role of sexual selection in speciation in rodents.

The study will integrate different levels: behavioral ecology, reproductive physiology, and molecular biology. The aim is to understand whether sperm competition promotes rapid changes in reproductive traits which lead to population divergence and speciation.

The study includes both field work and intensive laboratory work to analyse semen quality and sperm traits, to carry out heterospecific in vitro fertilization experiments, and to analyse reproductive proteins.

We are looking for candidates with a solid evolution-

ary background. Previous experience in reproductive physiology and/or molecular biology would be highly desirable. A BSc degree in Biology is the required minimum. Ideally candidates should have a MSc degree or a DEA in the case of Spanish candidates.

If interested please send CV to Montse Gomendio (montseg@mncn.csic.es) as well as cover letter explaining your scientific background, your interests, and your willingness to spend a few years in Spain.

For information about previous and ongoing projects and publications: [www.gebir.csic.es](http://www.gebir.csic.es) Montse Gomendio Reproductive Ecology and Biology Group Museo Nacional de Ciencias Naturales (CSIC) Jose Gutierrez Abascal, 2 28006 Madrid Spain

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Montse Gomendio Research Professor Reproductive Ecology and Biology Group Museo Nacional de Ciencias Naturales (CSIC) c/Jose Gutierrez Abascal 2 28006-Madrid (Spain) Tel. +34-91-411-1328, ext. 1222 Fax +34-91-564-5078 email: montseg@mncn.csic.es

<http://www.gebir.csic.es/> Montserrat Gomendio <montsegk@telefonica.net>

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## MaxPlanckInst 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 computer science, physics, mathematics, or biology.

The closing date for applications is February 27, 2009.

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/-poster2009.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](http://www.imprs-cbsc.mpg.de) hannes luz <luz@molgen.mpg.de>

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## NArizonaU GenesToEnvironment

Northern Arizona University IGERT Program in Integrative Bioscience: Genes to Environment

NAU invites applications for up to six PhD student traineeships for students admitted for the 2009/10 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 IGERT 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 doc-

toral 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 2009/10 academic year will be February 1, 2009. 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](mailto:Catherine.Gehring@nau.edu), (928)523-9158 or Dr. Amy Whipple: [Amy.Whipple@nau.edu](mailto:Amy.Whipple@nau.edu), (928)523-8727

[Amy.Whipple@nau.edu](mailto:Amy.Whipple@nau.edu) [Amy.Whipple@nau.edu](mailto:Amy.Whipple@nau.edu)

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## OxfordU AvianSignalEvolution

A three-year studentship is available in the Department of Zoology, Oxford University, starting October 2009.

Project: A global analysis of birdsong to investigate the role of signal evolution in speciation

Supervisors: Dr Joseph Tobias & Dr Nathalie Seddon

Deadline for application: 16th Feb 2009

Eligibility: UK or EU students only

Animal signals play a central role in mediating mate choice and reproductive isolation. Understanding the evolutionary processes shaping these signals, and driving their divergence, is therefore a key step towards resolving a long-standing puzzle in biology: how species multiply and co-exist.

This PhD will use comparative methods to test evolutionary hypotheses. These include the ecological adaptation hypothesis (EAH), which holds that signals and associated preferences diverge, and reproductive isolation arises, via adaptation to the transmission properties and/or noise regimes of different habitats. Others include the cultural evolution hypothesis (CEH), whereby signal divergence is a by-product of learning, and the species recognition hypothesis (SRH), which predicts that species in sympatry will be more divergent than those in allopatry. Further hypotheses deal with trade-offs or synergisms between different signalling modalities. These ideas have been examined theoretically, but empirical studies have thus far been limited

by small sample sizes or the inability to control for evolutionary age.

Passerine birds offer an ideal opportunity to overcome these limitations. Capitalising on recent growth in digital birdsong archives, sound analysis software and phylogenetics, this project involves quantifying song and plumage traits of 1000+ passerine species and mapping them onto avian phylogenies. This will allow signal divergence and elaboration to be calculated, and related to factors such as evolutionary age, ecology, biogeography, signal multimodality, degree of song learning, and rates of species accumulation (i.e. cladogenesis). The student will receive training in the use comparative methods and meta-analyses to conduct broad-scale empirical tests of evolutionary hypotheses.

The results will shed light on some outstanding questions in evolutionary biology, including the dynamics of multimodal signaling networks, and the relative roles of deterministic processes (selection) and stochastic processes (drift) in signal evolution and speciation.

For more information about research group, visit: [www.zoo.ox.ac.uk/egi/research/tropecol.htm](http://www.zoo.ox.ac.uk/egi/research/tropecol.htm)

For informal enquiries, email: [joseph.tobias@zoo.ox.ac.uk](mailto:joseph.tobias@zoo.ox.ac.uk) or [nathalie.seddon@zoo.ox.ac.uk](mailto:nathalie.seddon@zoo.ox.ac.uk)

To apply: submit two copies of University application form ([www.admin.ox.ac.uk/gsp/](http://www.admin.ox.ac.uk/gsp/)) and include two academic references. Send to the Graduate Administrator, Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS or apply online. Please quote reference DTG11.

[nathalie.seddon@zoo.ox.ac.uk](mailto:nathalie.seddon@zoo.ox.ac.uk)  
[nathalie.seddon@zoo.ox.ac.uk](mailto:nathalie.seddon@zoo.ox.ac.uk)

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## TexasAM MosquitoEvolution

A PhD position is available (starting summer 2009) in the Department of Entomology at Texas A&M to investigate the genetic basis of host preference in Africa's major malaria vector *Anopheles gambiae*. *An. gambiae* is highly adapted to blood feeding on human hosts, and its preference for humans is largely due to its attraction to human sweat. This aspect of *gambiae*'s biology is of vital importance in its ability to transmit malaria. The PhD candidate will investigate the genetic basis of host preference in *Anopheles gambiae* using QTL mapping and evolutionary genetic approaches. The ultimate goal

of the project is to identify genes involved in the adaptation of *Anopheles gambiae* to human hosts.

The PhD candidate should have an interest in evolutionary biology. Some background in genetics and the use of molecular techniques is preferred. The candidate will be expected to conduct experiments in the department of Entomology at Wageningen University in The Netherlands from Aug 2009-Jan 2010.

Some competitive funds are available for prospective candidates to visit the Texas A&M campus Feb 12-14. To be considered for these travel funds an application needs to be received by Dec 21st.

For more information and for a list of documents required for an application, please contact:

Michel Slotman

maslotman@ag.tamu.edu

phone: 979 845 7556

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### UBritishColumbia EvolGeneExpression

A Graduate Assistantship (M.Sc. or Ph.D.) is available in the lab of Dr. Keith Adams at the University of British Columbia (UBC) in molecular evolution and the evolution of gene expression starting in September 2009. My lab's research combines evolutionary biology with molecular genetics to study how gene expression, regulation, structures, and sequences evolve. See my web page at <http://www.botany.ubc.ca/people/-adams.htm> for a description of the research. I am looking for a highly motivated graduate student to help develop and work on a project about the evolution of duplicate gene expression and/or alternative splicing in plants. Candidates should have a strong undergraduate background in biology, with course work in molecular genetics and evolutionary biology. Prior research experience is desirable. For more information and inquiries about the research area contact Keith Adams at keitha@interchange.ubc.ca

Keith Adams Assistant Professor Botany Department and Centre for Plant Research University of British Columbia Vancouver, Canada

keitha@interchange.ubc.ca keitha@interchange.ubc.ca

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### UCincinnati ExperimentalEvolution

A Graduate Assistant position is available starting Fall 2009 in the department of Biological Sciences at the University of Cincinnati. We are seeking an outstanding candidate who is interested in contributing to a project in experimental evolution, using *E. coli*. We use a system to introduce targeted mutations to the *E. coli* chromosome, and then measure the fitness consequences of those mutations. Skill in either microbiology or molecular biology is preferable, but the primary requirement is an interest in fundamental evolutionary questions. If you are interested, we would be happy to provide additional details regarding the project.

In the Department of Biological Sciences, the current Graduate Assistant stipend is \$20,162 for Ph.D. students. All graduate assistantships include a waiver for tuition and the general fee, and coverage of approximately 75% of health insurance costs. For our next incoming graduate class, we are offering one competitive Research Associate position. Otherwise support initially will be as a teaching assistant. An early (Summer 2009) start is also a possibility. If you are interested in an early start, please indicate so in your correspondence. The application deadline is Feb. 1st.

For further information on the department and the application process, please see:

<http://www.artsci.uc.edu/biology>

and:

[http://www.artsci.uc.edu/collegedpts/biology/grad/-application\\_info.aspx](http://www.artsci.uc.edu/collegedpts/biology/grad/-application_info.aspx) Ron DeBry Department of Biological Sciences University of Cincinnati Cincinnati, OH 45221-0006

(513) 556-9743 ron.debry@uc.edu

“Ronald W. DeBry” <ron.debry@uc.edu>

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### UIceland EvolGenomics

Ph.D. Scholarship at the University of Iceland. Molecular evolution of DNA repair pathways in invertebrates.

The project centers on characterizing the evolution of

DNA repair systems in insects. The main objective is to document the evolution of DNA repair genes in invertebrates and flies by a combination of bioinformatic and phylogenetic methods. A masters student and a technician focused on molecular and experimental components of this project, will work along with the Ph.D. candidate.

The candidate should either have a solid background in biology (or related fields) or experience in programming (for instance computer science). The candidate will develop skills in computational biology, in processing high-throughput molecular genetic data, frame and tackle research questions about the evolution of genes and genomes.

The scholarship from the University of Iceland doctorate fund provides support for 3 years, 3,000 K Icelandic kronas (approx 20,700 at the current exchange rate). For acceptance into the PhD program in the Faculty of Science at the University of Iceland the applicant must hold an Masters degree (3 year PhD program) or a Bachelor degree (4 year PhD program including courses) in a relevant field with a grade-point average of 7 out of 10 or equivalent.

The Institute of Biology is an excellent research environment with half a dozen PI's and over 3 graduate students and post docs studying evolutionary and molecular biology. Our group has mainly focused on questions relating to regulatory evolution, patterns of conservation, the insertion/deletion mutation spectrum and the emergence of new enhancers, with other projects including investigations of wing shape, population structure and the role of transcription factor variation in disease.

Those interested please contact Arnar Palsson (apalsson@hi.is) for further background and details. Kindly submit via email a CV along with names and contact information for 3 referees. The application deadline is December 31-st 2008 and the candidate would ideally initiate the study early to mid year 2009.

– Arnar Palsson (Ph.D, M.Sc) Department of Biology University of Iceland Sturlugata 7, 101 Reykjavik, Iceland Tel: +(354) 525 4265 Fax: +(354) 525 4069 E-mail: apalsson@hi.is [www.hi.is/~apalsson](http://www.hi.is/~apalsson) apalsson@hi.is

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## ULondon GeographicProfiling

Applications are invited for a PhD studentship in the

School of Biological and Chemical Sciences, Queen Mary, University of London with Dr Steven Le Comber, on a project entitled Geographic profiling and the origin of invasive species

Invasive species are significant drivers of environmental change and may soon surpass habitat loss as the main cause of environmental degradation. The most effective way to deal with invasive species is to attempt to eradicate or at least contain them before they spread. Here, we propose the use of a technique from criminology that has the potential to dramatically improve the efficiency with which invasive species can be located during the early stages of an invasion, when control efforts are more likely to be effective.

Geographic profiling (GP) is a statistical technique that was originally developed as a tool in criminology. It uses the location of related crime sites to make inferences about the most likely area in which the offender might live, and has been extremely successful in this field. Its recent application to biological data was pioneered by Dr SC Le Comber at QMUL, in collaboration with the techniques inventor, Prof DK Rossmo (Texas State). Here, we aim to extend our earlier work to the study of the spread of invasive species, by demonstrating the ability of GP to identify the source of invasions.

Our objectives are: To show how GP may be used during the early stages of invasion, when control efforts are likely to be most effective, to accurately determine the source of the invasion. To simulate the spread of invasive species using both spatially explicit population simulation models (SEPM) and non-spatial models, and to quantify the improvement relative to other types of search when data derived from different models are analysed. To determine whether GP can be used during later stages of invasions, when sites that have previously been colonised by invasive species act as multiple sources for colonisation.

References Le Comber et al 2006 *J Theor Biol* 240:233-240. Raine et al in press *J Roy Soc Lond Interface*. Rossmo 2000 *Geographic profiling*. CRC.

Applications are invited from candidates with, or expecting to obtain, at least an upper-second class honours degree in an area relevant to the project.

Send your CV, the names and contact details of two academic referees, a covering letter and a note of where you saw the studentship advertised, to Dr SC Le Comber, School of Biological and Chemical Sciences, Queen Mary, University of London, London E1 4NS.

Funding Notes This studentship will be funded by a Natural Environment Research Council Doctoral Training Grant and is available to candidates meeting BB-

SRC eligibility criteria. The funding will cover tuition fees and the student will receive an annual stipend commencing at £15290 (which includes £2000 London Allowance).

The School of Biological and Chemical Sciences is one of the largest departments at Queen Mary, University of London's Mile End campus, with over 70 members of academic staff and 1300 undergraduate and postgraduate students. The School is committed to excellence in research and teaching, and offers an exciting and stimulating environment for staff and students.

Dr. Steven Le Comber [s.c.lecomber@qmul.ac.uk](mailto:s.c.lecomber@qmul.ac.uk) Lecturer

Room 5.03c, GE Fogg Building School of Biological and Chemical Sciences Queen Mary, University of London Mile End Road London E1 4NS

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home page: [http://www.sbcs.qmul.ac.uk/people/steven\\_le\\_comber.shtml](http://www.sbcs.qmul.ac.uk/people/steven_le_comber.shtml) Directions to QM: <http://www.sbcs.qmul.ac.uk/contact.shtml> Steve Le Comber <[s.c.lecomber@qmul.ac.uk](mailto:s.c.lecomber@qmul.ac.uk)>

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## UMunich PlantEvolution

Ph.D. position in plant evolutionary biology

I am looking for a Ph.D. candidate (3 yrs) interested in the evolution of plant reproductive traits, sexual systems, or biogeography. Current research topics in our group can be found at <http://www.umsl.edu/~renners/> and <http://www.botanik.biologie.uni-muenchen.de/botsyst/home.html>. The student would be employed according to German BAT BL IIa/2 and would be part of Munich University's graduate program in Evolution, Ecology, and Systematics: <http://www.eeslmu.de/>. Experience with experimental work and statistical analyses, and the application of molecular methods to evolutionary problems are a plus. German language skills are not needed. Munich has a large and active research community in evolutionary biology and phylogenetics, and the city offers excellent infrastructure and beautiful surroundings, with the mountains in close proximity.

The closing date for applications is January 30, 2009 or when the position is filled. Send your application, together with a full CV, copies of recent-most educational

certificates, and the names of two referees to professor Susanne Renner ([renner@umsl.edu](mailto:renner@umsl.edu)).

Susanne Renner <[renner@lrz.uni-muenchen.de](mailto:renner@lrz.uni-muenchen.de)>

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## UNorthernColorado PlantPopulationGenetics

Graduate positions (MS or PhD) in Plant Population Genetics in the lab of Dr. Mitchell McGlaughlin, School of Biological Sciences, University of Northern Colorado.

I am seeking MS or PhD students interested in the population genetics, conservation, speciation, and phylogeography of plant species. Research in my lab is focused on using population genetics to understand plant speciation and to inform the conservation of rare and endangered taxa. We employ a wide range of genetic data types, including low copy nuclear sequence, chloroplast sequence, and nuclear microsatellite data. Current research projects include, phylogeography of the California Channel Islands, speciation in the Hawaiian silversword alliance, ancestral polymorphism in *Lotus*, and conservation genetic research with native Colorado taxa. Doctoral students are encouraged to develop projects within the scope of research in my lab and masters students can develop their own projects or work on research already initiated in the lab. Funding is available to support graduate students through teaching and research assistantships, scholarships, and grants.

For more information please visit my lab website: <http://www.unco.edu/mcgloughlinlab/> or the department website: <http://www.unco.edu/nhs/biology/index.htm> The University of Northern Colorado is a public institution with about 11,000 undergraduate and 1,500 graduate students, located in Greeley, Colorado. Greeley is situated 50 miles northeast of Denver and 20 miles east of the Rockies, with easy access to Rocky Mountain National Park and other outdoor activities.

Interested applicants should send a letter of interest and CV to Dr. Mitchell McGlaughlin ([Mitchell.mcgloughlin@unco.edu](mailto:Mitchell.mcgloughlin@unco.edu)). To apply, students will need to submit a complete application to the UNC School of Biology (<http://www.unco.edu/nhs/biology/students/gradapp-instructions.html>) and Graduate School (<http://www.unco.edu/grad/index.html>). There is no fixed application deadline, but applications are reviewed when they are received.

– Mitchell McGlaughlin, Ph.D. Assistant Professor 501 20th Street, Ross Hall 1560 University of Northern Colorado Greeley, CO 80639 970-351-2139 Mitchell.McGlaughlin@unco.edu <http://www.unco.edu/mcgloughlinlab>  
Mitchell.McGlaughlin@unco.edu  
Mitchell.McGlaughlin@unco.edu

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## UNotreDame GenomicsBioinformatics

The University of Notre Dame Graduate Program in Biological Sciences invites Graduate Student applications in the area of genomics and bioinformatics.

We are pleased to announce the The Eck Institute for Global Health at Notre Dame (<http://www.nd.edu/~cghid>) is offering graduate student fellowships in Genomics and Bioinformatics. We are conducting several faculty searches to compliment our existing strong program in vector/parasite biology. The graduate program offers exciting opportunities to use whole-genome, integrative approaches to study fundamental processes in parasitology, vector biology, ecology and evolutionary biology. Visit our departmental website (<http://www.nd.edu/~biology/index.shtml>) to learn about the opportunities and application procedures. If you will miss this deadline, we encourage you to contact a potential faculty advisor or send inquiries to Michael Ferdig (ferdig.1@nd.edu). We are committed to the recruitment and education of underrepresented minorities.

Thanks, Kim

– Kim Bogold, Center Coordinator Eck Institute for Global Health University of Notre Dame Department of Biological Sciences Notre Dame, Indiana 46556 Phone: 574-631-2171 Fax: 574-631-3996 <http://globalhealth.nd.edu> Kim Bogold <merz.4@nd.edu>

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## UNottingham SnailEvolution

Funding is available for a PhD studentship, to be awarded on a competitive basis within the School of Biology, University of Nottingham, to investigate the evolution and/or development of sinistral snails

Sinistral (anticlockwise-coiling) snails make up much less than 10% of all snail species. Why are sinistral snails so rare and how do they evolve? Are sinistrals a perfect mirror image of dextrals, or are there fitness consequences of being sinistral? How is the left-right asymmetry of the shell inherited, and at the molecular level, what is the hypothetical F-molecule that ultimately determines asymmetry?

We are establishing the pond snail *Lymnaea stagnalis* as a comparative model organism for the understanding of left-right asymmetry. With BBSRC funding, and in collaboration with Prof Mark Blaxter (Edinburgh, Solexa/454 sequencing, bioinformatics), we have just begun a project to characterise the *Lymnaea* 'chirality' locus, with the ultimate aim to understand the evolution and development of asymmetry at the molecular level. As the lab is also investigating molluscan asymmetry from behavioural, evolutionary and population genetic perspectives, there is a wide scope for PhD project in any of these areas.

Applicants should have, or expect to receive, a good degree in a relevant subject, and an interest and enthusiasm for evolution. Students will experience a variety of 'core' methods, depending upon interests and aptitude (e.g. molecular lab techniques, in situ hybridization, micromanipulation, field work, ultrahigh-throughput DNA sequencing).

In the first instance, prospective students should send a CV and an indication of general area of interest to [angus.davison@nottingham.ac.uk](mailto:angus.davison@nottingham.ac.uk).

Recent publications from the lab may be viewed at [www.molluscs.org](http://www.molluscs.org). Further reading:

Davison, A et al (2008) Mating behaviour in *Lymnaea stagnalis* pond snails is a maternally inherited, lateralised trait. *Biology Letters*, in press. See also *Nature* 20 November 2008, p285

Schilthuizen, et al (2008) Sexual selection maintains whole-body chiral dimorphism in snails. *Journal of Evolutionary Biology* 20: 1941-1949.

Davison A et al (2005) Speciation and gene flow between snails of opposite chirality. *PLoS Biology* 3: e282.

Shibazaki Y, Shimizu M, Kuroda R (2004) Body handedness is directed by genetically determined cytoskeletal dynamics in the early embryo. *Current Biology* 14, 1462-1467.

Schilthuizen M, Davison A (2005) The convoluted evolution of snail chirality. *Naturwissenschaften* 92, 504-515.

Asami T, Cowie RH, Ohbayashi K (1998) Evolution of

mirror images by sexually asymmetric mating behavior in hermaphroditic snails. *American Naturalist* 152, 225-236.

– Dr. Angus Davison

Institute of Genetics The University of Nottingham  
Queen's Medical Centre Nottingham NG7 2UH an-  
gus.davison@nott.ac.uk [www.molluscs.org](http://www.molluscs.org) tel 0115 823  
0322 (int. 30322) fax 0115 823 0338

Angus.Davison@nottingham.ac.uk  
angus.davison@nottingham.ac.uk

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bioinformatics infrastructures. The PhD student will be supported by collaborative students and professors within bioinformatics, genomics, taxonomy and field-oriented evolutionary and ecological research.

Applicants may be requested to come for an interview.

For more information about the position and the application process, go to: <http://www.admin.uio.no/opa/ledige-stillinger/2008/vit/-doctoralresearchfellowBiology-2008-20755.html> For further information, please contact Prof. Dag Klaveness, dag.klaveness@bio.uio.no

havard.kauserud@bio.uio.no  
havard.kauserud@bio.uio.no

## UOslo MicrobialEvolution

Position as Doctoral Research Fellow (PhD-stipendiat) in biology (ChC) available at the Department of Biology, University of Oslo, Norway.

A 4-year PhD position in microbial diversity/evolution is available and will be part of a strategic University program in Microbial evolution (MERG) at the Faculty of Mathematics and Natural sciences. The position includes 25% compulsory work.

Applications and inquiries are invited from qualified, motivated and enthusiastic students wishing to pursue a Ph.D.-degree in microbial diversity and environmental microbiology, with particular emphasis on freshwater environments. Major goals for the research is to reveal the prokaryote and eukaryote diversity within selected freshwater environments using molecular methods, including 454 sequencing. The project has a particular focus upon the difference in diversity between selected oligotrophic lakes and changes in the diversity through depths and time.

The applicant should hold a Cand Scient/MSc or equivalent in biology and have a good knowledge of standard molecular techniques (preferably experience with environmental PCR), bioinformatics and microbiology. Knowledge of taxonomy/systematics within the fields of mycology, protistology and prokaryote microbiology is advantageous. The applicant must have serious research interests in ecology / evolutionary biology and excellent written and oral communication skills. Experience with any or all of the following topics is an advantage: comparative genomics, freshwater biology, microscopy, FISH and statistics.

The MERG research group has access to well-equipped pro- and eucaryote culturing facilities, a Roche 454FLX Genome sequencer, and extensive microscopy and

## UOtago EvolutionaryBiol

A PhD studentship in evolutionary ecology and conservation at University of Otago, New Zealand.

This project uniquely integrates different disciplines - evolutionary biology, conservation biology, behavioural ecology, genetics and endocrinology - to tackle a multitude of questions. The main aim of this project is to test the premises of "Trojan sex chromosome theory" using life bearing Poeciliid fish. Trojan sex chromosome theory utilises hormonal reversal of sex and skewing sex-ratio to control animal population size. In this project, we will investigate the fitness of sex-reversed individuals and their offspring (trans- generational effects). We will also conduct behavioural experiments for mate choice and intra- and inter-specific aggression in these individuals. Furthermore, we will use computer simulations (individual- based modelling) to integrate all observed parameters to predict outcomes of the application of this theory in the real world. The student will be encouraged to explore their own ideas.

This PhD position (3 years) is open to students, who have completed or are completing their BSc(Hons) or/and MSc (or equivalent), of any citizenship, starting sometime in 2009 (flexible). The successful applicant will be supervised by Dr Mark Lokman, Dr Gerry Closs, and myself (Shinichi Nakagawa) Please check our departmental webpage (<http://www.otago.ac.nz/zoology>). Our department offers an excellent working environment for PhD students. Also s/he will live in a wonderful city of Dunedin, which is surrounded by beautiful wilderness.

We are seeking a highly motivated student with a



proven academic record. If you are interested or want to know more about this PhD, please contact me (shinichi.nakagawa@otago.ac.nz) by email (email subject should say "Trojan fish PhD"). If you would like to apply for this studentship, send me your CV including academic records and names and contacts of 3 referees. The scholarship consists of: a stipend NZD 2,5000 every year for 3 years and fee weavers over 3 years

Shinichi Nakagawa, PhD (Lecturer of Behavioural Ecology) Department of Zoology University of Otago 340 Great King Street P. O. Box 56 Dunedin, New Zealand Tel: +64-3-479-5046 Fax: +64-3-479-7584 <http://www.otago.ac.nz/zoology/staff/academic/-nakagawa.html> shinichi.nakagawa@otago.ac.nz

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## UOtago EvolutionaryBiology 2

A PhD studentship in evolutionary ecology and conservation at University of Otago, New Zealand.

This project uniquely integrates different disciplines V evolutionary biology, conservation biology, behavioural ecology, genetics and endocrinology V to tackle a multitude of questions. The main aim of this project is to test the assumptions of sex chromosome theory using life bearing Poeciliid fish. Trojan sex chromosome theory utilizes hormonal reversal of sex and skewing sex-ratio to control animal population size. In this project, we will investigate the fitness of sex-reversed individuals and their offspring (trans- generational effects). We will also conduct behavioural experiments for mate choice and intra- and inter-specific aggression in these individuals. Furthermore, we will use computer simulations (individual- based modeling) to integrate all observed parameters to predict outcomes of the application of this theory in the real world. The student will be encouraged to explore their own ideas. The scholarship consists of: a stipend NZD 25,000 every year for 3 years and tuition fee waivers over 3 years. This PhD position (3 years) is open to students, who have completed or are completing their BSc(Hons) or/and MSc (or equivalent), of any citizenship, starting sometime in 2009 (flexible). The successful applicant will be supervised by Dr Mark Lokman, Dr Gerry Closs, and myself (Shinichi Nakagawa). Please check our departmental webpage (<http://www.otago.ac.nz/zoology> ). Our department offers an excellent working environment for PhD students. Also s/he will live in the wonderful city of Dunedin, which is surrounded by beautiful scener-

ies. We are seeking a highly motivated student with a proven academic record. If you are interested or want to know more about this PhD, please contact me by email (shinichi.nakagawa@otago.ac.nz; email subject should say fish PhD). If you would like to apply for this studentship, send me your CV including academic records and names and contacts of 3 referees. The initial closing date for the application is 16th January 2009.

Shinichi Nakagawa <shinichi.nakagawa@otago.ac.nz>

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## UOxford ViralEvolution

Suggested Link Heading: Oxford.VirusEvolution

A Ph.D. position is available (October 2009) in the Zoology Department of Oxford University to study the evolution of Endogenous Retroviruses. The project is essentially bioinformatic, but the programming and modelling elements are very much seen as tools rather than aims of the project (I am self-taught), and support in learning them is available. I am more interested in the ability of applicants to think of interesting biological questions and ways in which we might answer them. The studentship is fully funded by the BBSRC and restricted to European Union applicants. The closing date for applications is 16th February 2009. The application procedure at Oxford is byzantine, so please also contact me directly if you are interested.

Project summary and application: <http://www.findaphd.com/search/-showproject.asp?projectid129> Queries: robert.belshaw@zoo.ox.ac.uk or +44 (0)1865 281997

Dr Robert Belshaw Lecturer, Department of Zoology University of Oxford South Parks Road Oxford OX1 3PS Tel.: +44 (0)1865 281997 [http://www.zoo.ox.ac.uk/staff/academics/belshaw\\_r.htm](http://www.zoo.ox.ac.uk/staff/academics/belshaw_r.htm) Robert Belshaw <robert.belshaw@zoo.ox.ac.uk>

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## UPotsdam Biodiversity

Cooperative PhD program of the University of Potsdam and the University of Applied Sciences in Eberswalde at the University of Potsdam "Climate change-proof nature conservation: conservation of biodiversity under

the conditions of rapid environmental change”

The newly implemented PhD program “Climate change-proof nature conservation” invites applications for PhD positions or grants.

The cooperative PhD program has been established at the University of Potsdam and the University of Applied Sciences in Eberswalde at the University of Potsdam to explore and develop sustainable concepts and strategies, that will provide for conservation under conditions of rapid environmental change. The PhD projects will be carried out in close collaboration of the participating universities.

The following projects are open for application:

- Adaptation of large-scale priority setting and planning in nature conservation to global change Based at the FH Eberswalde (Prof. Dr. Ibisch); Requirements: Knowledge of / experience in conservation planning; knowledge of conventional approaches in systematical conservation planning; knowledge of regional planning considering socio-economical processes; proficient handling of GIS and data bases; knowledge of established scenarios and models of environmental change and their results

- Peatlands and wetlands of North-East Germany in climate change: Evaluation of the actual state and experimental analysis of endangering and protection factors for the deduction of biodiversity conservation measures Based at the FH Eberswalde (Prof. Dr. Luthardt); Requirements: very good floristic and basic faunistic knowledge; sound knowledge of general ecology and plant ecology; experience in statistical analysis of quantitative data; proficient handling of GIS and data bases; knowledge of scenario development and modeling

- Subcontinental fens and bogs subject to environmental change: experimental risk analysis of rare specialist and cryophilous plant species Based at the University of Potsdam (Prof. Dr. Joshi); Requirements: sound knowledge of general ecology and plant ecology; enthusiasm for the conduction of ecological experiments; experience in statistical analysis of quantitative data

- Precise description of ecological functions of ecosystem types in North-East Germany and a risk assessment of their functionality under the aspect of climate change. Based at the FH Eberswalde (Prof. Dr. Luthardt); Requirements: sound knowledge of ecology and the specific habitat; special knowledge of specific ecosystem types; proficient handling of GIS and data bases; knowledge of scenario development and modeling

- Static conservation area concepts under climate change: consequences and options for future manage-

ment Based at the University of Potsdam (Prof. Dr. Jeltsch); Requirements: Knowledge of / experience in development and analysis of ecological models; programming skills (preferentially C, C++); knowledge of landscape ecology and scientific nature conservation

- Genetic monitoring of amphibians: development of dynamic conservation concepts based on population structure in time and space Based at the University of Potsdam (Prof. Dr. Tiedemann); Requirements: Skills and experience in molecular genetic laboratory work; good computer skills; knowledge of / interest in field work and nature conservation

Positions are paid according to TVL-13/2 or as a comparable scholarship. Women are strongly encouraged to apply. Equal opportunity regulations apply.

Closing date for applications is January 15, 2009. Please send your application (indicating the preferred project) via e-mail to the coordinator at: [laura.epp@uni-potsdam.de](mailto:laura.epp@uni-potsdam.de)

- Dipl.-Biol. Laura Epp Universität Potsdam Institut für Biochemie und Biologie Evolutionsbiologie / Spezielle Zoologie Karl-Liebknecht-Str. 24-25 (Haus 26, Zi. 2.74) 14476 Potsdam Germany

Tel.: ++49 331 / 977 5250 Fax.: ++49 331 / 977 5070

[lauepp@rz.uni-potsdam.de](mailto:lauepp@rz.uni-potsdam.de) [lauepp@rz.uni-potsdam.de](mailto:lauepp@rz.uni-potsdam.de)

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## UppsalaU MicrobialEvolution

Please post

at the Department of Ecology and Evolution/Limnology, Uppsala University Project description: The major aim of the PhD project is to study the effect of environmental disturbances on the composition of bacterial communities. Particular focus will be placed on the investigation of community assembly patterns and mechanisms in temporal habitats where disturbances, such as draught and other environmental changes, occur frequently. In addition, the project will address the resistance and resilience of bacterial communities and how they are related to the strength and frequency of a disturbance. Approaches will include field studies and lab- as well as field experiments. The project also requires the application of a range of molecular techniques to characterize the bacterial community composition. The results of this project will improve our knowledge about

the regulating factors of microbial diversity and the responses of microbial communities to environmental change and perturbations. The position will be placed within the Limnology programme at the Department of Ecology and Evolution at Uppsala University <http://www.ebc.uu.se/limno/>. Qualifications: We are looking for a highly motivated candidate that is interested in working at the interface between general and microbial ecology. Applicants are requested to have a BSc or MSc in biology or a related field and should have a background in ecology or microbial ecology. Previous experience in the application of molecular methods will be considered an advantage, but is not required. Applications (1 copy) should include a brief description of research interests and past research experience, Curriculum vitae and the name and contact information of 2 personal references. Relevant publications (articles, BSc / MSc thesis or similar) should be attached to the application. Applicants are also asked to indicate the earliest feasible starting date of employment in the application. For further information about the position, please contact Silke Langenheder, e-mail: [silke.langenheder@ebc.uu.se](mailto:silke.langenheder@ebc.uu.se), phone: +46 18 471 6487. The trade union representatives are Anders Grundström, SACO, phone +46 18 471 5380, Carin Söderhäll, TCO/ST, phone +46 18 471 1996 and Stefan Djurström, SEKO, phone: +46 18 471 3315. Local salary guidelines are applicable. Please submit your application to Registrar, UFV-PA 2008/2947 Uppsala University, Box 256, SE-75105 Uppsala, Sweden, or e-mail; [registrator@uu.se](mailto:registrator@uu.se) before January 7, 2009. If an application is sent by fax or e-mail, it has to be completed by a written application within a week's time after the deadline of the application period.

Ramiro Logares <[ramiro.logares@gmail.com](mailto:ramiro.logares@gmail.com)>

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## UStAndrews AnimalGeneClusters

Dear Evoldir,

We are seeking applicants for a PhD position at the School of Biology, University of St Andrews.

### EVOLUTION OF ANIMAL GENE CLUSTERS

There are an increasing number of instances of genes operating in clusters in animal genomes, particularly during development. The Hox gene cluster, that patterns animal anterior-posterior axis development, is the best known example. The rapidly increasing number

of genome sequences provides a valuable resource for understanding these gene clusters, which will be examined to better understand genome evolution and its relationship with animal evo-devo. It is expected that the project will have a strong bioinformatics component, at least in the initial stages, with the prospect for moving into the lab as the project progresses.

Supervisors: Dr David Ferrier and Dr Daniel Barker

Informal enquiries to Dr David Ferrier, [dekf@st-andrews.ac.uk](mailto:dekf@st-andrews.ac.uk)

For further details, including how to apply, please see:

<http://biology.st-andrews.ac.uk/-projectProfile.aspx?psr=79&pid=132> IMPORTANT NOTE ON FUNDING

A successful candidate would receive funding (covering fees and stipend) via a BBSRC Doctoral Training Grant. This funding is ONLY possible for candidates who meet the residence criteria described here:

[http://www.bbsrc.ac.uk/funding/studentships/-studentship\\_eligibility.pdf](http://www.bbsrc.ac.uk/funding/studentships/-studentship_eligibility.pdf) Best regards,

Daniel

– Daniel Barker <http://bio.st-andrews.ac.uk/staff/-db60.htm> The University of St Andrews is a charity registered in Scotland : No SC013532

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

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## UStAndrews EnhancerBioinformatics

Dear Evoldir,

We are seeking applicants for a PhD position at the School of Biology and the Bute medical School, University of St Andrews.

### DISCOVERY AND MODELLING OF ENHANCER BINDING SITES

Genes in the human genome are increasingly well understood, but gene regulation, and in particular enhancers, remain more mysterious. The student will use advanced high-throughput laboratory techniques to discover binding sites of enhancers in the genome. Bioinformatics models of enhancers will be adjusted in the light of this information, so that such binding sites may be predicted computationally with greater accuracy. Both laboratory and bioinformatics approaches

will build on recent developments at St Andrews. This research has implications for genetic diseases of regulatory regions including many kinds of cancer.

Supervisors: Dr Daniel Barker and Dr Jo Parish

Informal enquiries to Dr Daniel Barker, db60@st-andrews.ac.uk

For further details, including how to apply, please see:

<http://biology.st-andrews.ac.uk/-projectProfile.aspx?psr=79&pid=123> IMPORTANT NOTE ON FUNDING

A successful candidate would receive funding (covering fees and stipend). Part of this funding would be obtained via a BBSRC Doctoral Training Grant. Consequently, funding is ONLY possible for candidates who meet the residence criteria described here:

[http://www.bbsrc.ac.uk/funding/studentships/-studentship\\_eligibility.pdf](http://www.bbsrc.ac.uk/funding/studentships/-studentship_eligibility.pdf) Best regards,

Daniel

– Daniel Barker <http://bio.st-andrews.ac.uk/staff/-db60.htm> The University of St Andrews is a charity registered in Scotland : No SC013532

db60@st-andrews.ac.uk db60@st-andrews.ac.uk

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## UWisconsinMadison ConservationGenetics

PhD Position available in Conservation Genetics I am seeking an outstanding student to pursue a doctoral degree in conservation genetics in the Department of Forest and Wildlife Ecology at the University of Wisconsin, Madison. An important responsibility of the successful applicant will be to act as a part-time manager of the molecular lab in the department. The focus of the graduate students research will fall within the general field of the conservation genetics of vertebrates and is dependent on shared interests between myself and the applicant. Current research in my lab focuses on the use of genetic methods to (1) characterize the demographic history of threatened species, and (2) understanding the effects of habitat fragmentation and other factors on the spatio-temporal distribution of genetic variation in threatened species. Funding is in place for three years of graduate student support (\$19,000/year + tuition waiver).

Applicants should possess at minimum a B.Sc., and

preferably a M.Sc., specializing in conservation genetics, molecular ecology, or closely related field. Applicants with a strong background in molecular laboratory methods (PCR, sequencing, cloning, etc.), genetic data analysis, conservation biology, and demonstrated ability to publish in peer-reviewed journals will be given preference. The selected student is expected to enroll in the Department of Forest and Wildlife Ecology in August 2009 for the fall semester. There is potential to begin work as a laboratory technician as early as March 2009. Applicants must apply to the PhD program in the Department of Forest and Wildlife Ecology (<http://forestandwildlifeecology.wisc.edu/grad.htm>) and the UW Graduate School (<http://info.gradsch.wisc.edu/-education/admissions/>).

To apply for the position, please send a cover letter outlining your interests and research background, a curriculum vitae, and contact information of three professional references (name, email, phone, address) as either a PDF or Word file to mpeery@wisc.edu with Conservation Genetics PhD Application in the subject line. Applications will be accepted until January 15, 2009 or until a suitable candidate is found.

For more info, contact: Dr. Zach Peery Department of Forest and Wildlife Ecology University of Wisconsin, Madison Madison, WI 53706 Phone: (831) 771-4139 mpeery@wisc.edu <http://forestandwildlifeecology.wisc.edu/facstaff/peery.html> M ZACHARIAH PEERY <mpeery@wisc.edu>

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## UWisconsinMilwaukee BadgerEvolution

Graduate position (MS/PhD) in landscape genetics of badgers, University of Wisconsin-Milwaukee.

I am seeking a highly motivated and enthusiastic graduate student interested in landscape genetics and its application to wildlife conservation and management. Â This project will employ molecular genetic tools to investigate the landscape genetic structure of American badger populations in Wisconsin. Â This project will include a combination of field, laboratory, and analytical work, and involves collaborations with multiple universities and state and federal agencies. Â The initial phase of the research is best suited to an MS student, though there is potential for expansion into a PhD-level project. Â Successful candidates should have some prior experience with DNA-based genetic

analysis. A Proficiency in ArcGIS and experience in mammal trapping is preferred. Funding in the form of assistantships, research support, and travel grants are available for qualified candidates. Anticipated start date is June or August 2009.

For more information about my lab, visit: <http://www.uwm.edu/People/latch>

To learn more about graduate studies in the Department of Biological Sciences at UWM, visit: <http://www.uwm.edu/Dept/Biology/Docs/Grad/gradindex.html> For more information about the project, or to apply, email a CV (including GPA and GRE scores), letter of interest, and contact information for 3 references to Dr. Emily Latch (latch@uwm.edu). The review of applications will begin immediately and will remain open until the position is filled. Applicants must also apply to UWM Graduate School (deadline Jan 1, 2009) and meet requirements for admission.

latch@uwm.edu latch@uwm.edu

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## UWuerzburg PollinationNetworks

\*PhD position in biodiversity research (3 years, beginning in March 2009)\*

\*Application deadline: January 15th, 2009 \*

\*Task\* As members in a new Bavarian research network (BAYFORKAST) we will investigate the threats posed to plant-pollinator by the ongoing climatic change. The project will be carried out in close cooperation with partners from the universities in Bayreuth and Regensburg. The project primarily necessitates the development of mathematical and spatially explicit simulation models linking theory with empirical data. To get acquainted with the real system± the candidate will, however, participate in field studies of pollinating insects (especially bees, hoverflies, and butterflies) carried out with our partners. These studies will take place along an elevation gradient in the Bavarian national park "Berchtesgadener Land".

\*Profile\* We seek a candidate with a pronounced interest in mathematical and/or computer based modelling of ecological processes. At least a basic knowledge in some programming language (e.g. C, Pascal, Basic, Fortran, R) will be helpful. We expect good communication skills and the ability to work in a team. The candidate should have a master (or comparative level)

in the natural sciences, preferentially in biology. However, candidates from physics, mathematics, or informatics with a strong interest in ecology and evolution may also apply.

The candidate will work at the Field Station Fabrikschleichach (a facility of the University Würzburg, Germany). A drivers licence (and a own car) will be helpful for the field work .

Prof. Dr. H.J. Poethke & PD. Dr. Thomas Hovestadt, Field Station Fabrikschleichach, University of Würzburg Dr. Nico Blüthgen, Department of Animal Ecology Tropical Biology, University of Würzburg

\*Contact:\* Field Station Fabrikschleichach Glashuettenstrasse 5 96181 Rauhenebrach, GERMANY email: station@biozentrum.uni-wuerzburg.de

<http://www.evolutionaryecology.biozentrum.uni-wuerzburg.de/> PD Dr. Thomas Hovestadt Field Station Fabrikschleichach University of Würzburg Glashuettenstrasse 5 OT Fabrikschleichach 96181 Rauhenebrach

E-Mail hovestadt@biozentrum.uni-wuerzburg.de Phone: 0049 931 3182065 (Secretary) 3183083 (direct) Fax: 3183089

Thomas Hovestadt <hovestadt@biozentrum.uni-wuerzburg.de>

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## WashingtonStateU EvolutionaryModeling

Subject: Graduate positions: IGERT Program in Evolutionary Modeling (IPEM)

Graduate Training Program in Evolutionary Modeling We are seeking a self-motivated and creative doctoral student to participate in our NSF-funded IGERT Program in Evolutionary Modeling (IPEM). The program aims to produce professionals versed in modern evolutionary theory and familiar with the most important perspectives and quantitative techniques for studying evolutionary processes and patterns. The program is open to students working on both humans and non-human animals, and emphasizes evolutionary processes of adaptation and diversification in genetic, behavioral, and cultural domains, as well as a set of methods (including computational modeling, game theory, phylogenetic analysis, and other field and laboratory techniques) applicable to analyzing evolutionary processes across these domains. If interested, please see the IPEM

website at <http://ipem.anth.wsu.edu/>. We anticipate supporting several new Ph.D. candidates with IPEM fellowships (2 years) beginning in Fall 2009. Applications are due January 10, and successful candidates will be notified in early Spring.

Participating faculty in biological sciences include:

Jeremiah W. Busch, Plant evolutionary genetics (jwbusch@wsu.edu)

Pat Carter, Evolutionary physiology (pacarter@wsu.edu)

Mark Dybdahl, Coevolution and host-parasite interactions (dybdahl@wsu.edu)

Richard Gomulkiewicz, Evolutionary theory (gomulki@wsu.edu)

Larry Hufford, Plant systematics and evolution (hufford@wsu.edu)

Eric Roalson, Patterns and processes of diversification

in plants (eric.roalson@wsu.edu)

Hubert Schwabl, Behavioral endocrinology (huschwabl@wsu.edu)

Andrew Storfer, Conservation genetics and disease ecology (astorfer@wsu.edu)

Mike Webster (coPI), Avian molecular and behavioral ecology (mwebster@wsu.edu)

Interested applicants should refer to the IPEM website at <http://ipem.anth.wsu.edu/> and contact individual faculty participants that suit your interests. Additional details of biology faculty interests can be found at <http://www.sbs.wsu.edu/faculty/> -

Mark Dybdahl, Assoc Prof School of Biological Sciences  
PO Box 644236 Washington State University Pullman,  
WA 99164-4236

Ph: 509-335-7909 FAX: 509-335-3184 [www.wsu.edu/~dybdahl/](http://www.wsu.edu/~dybdahl/) Mark Dybdahl <dybdahl@wsu.edu>

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### BernU FieldAssist EvolutionaryBiol

Ubern: field assistants bird evolutionary ecology

We are seeking 4 enthusiastic field assistants interested in taking part in 2 field studies in Bern, Switzerland. Applicants will be part of the evolutionary ecology team (Zoological Institute, Bern University). Our study model is a passerine bird, the great tit. The tits are a good model system as they are hole nesting birds,

breeding in forests near Bern, and as they can be easily manipulated. We are part of a 10 people lab team, all working with great tits in natural conditions. We work with about 300 nest boxes for each, disposed in several forests close to Bern. The first study aims to investigate the effect of oxidative stress on sperm quality as well as a potential heritability of these traits in the great tit. This experiment will be conducted by Sylvain Losdat (PhD). The second experiment is interested in the effects of maternal hormones on offspring fitness and will be performed by Katarzyna Podlas (PhD). We will require 2 field assistants for each experiment that will help with all the aspects of the work, including checking nests, ringing the birds, catching adults, performing treatments, and more. Applicants with a Msc in Biology/Ecology and/or with bird handling experience would have an advantage. Supervising for potential Msc analysis and report would be assured by PhD and Post-doc people from the lab. Motivation will play a key role: the work is hard and demanding, may take place in changing weather and requires long hours at times. The study will start at the end of March 2009 until the beginning of June 2009. Fluent English or French speaking is required as well as a valid European driving license.

Applicants can send us a letter + CV and ask for further details or questions on the following email addresses:

\*Sylvain Losdat\* Evolutionary Ecology Group, Zoological Institute University of Berne Baltzerstr. 6 3012 Bern Switzerland Email: [sylvain.losdat@esh.unibe.ch](mailto:sylvain.losdat@esh.unibe.ch) Phone: +41316313020 Mobile: +41774565214

\*Katarzyna Podlas\* Evolutionary Ecology Group, Zoological Institute University of Berne Baltzerstr. 6 3012 Bern Switzerland Email: [podlasova@hotmail.com](mailto:podlasova@hotmail.com) Phone: +41316313020 Mobile: +41774256291

Sylvain Losdat <[sylvain.losdat@esh.unibe.ch](mailto:sylvain.losdat@esh.unibe.ch)>

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## BostonU MarineEvolution

Just in case you missed our earlier announcements in Science, EvoDir, and elsewhere, please see the announcement below.

We will begin review of applications early next week, so there's still time to apply.

The Biology Department at Boston University ([www.bu.edu/biology](http://www.bu.edu/biology)) invites applications for a tenure-track appointment at the Assistant Professor level. We

seek an evolutionary ecologist conducting research in nearshore marine systems at the population, community, and/or ecosystem levels. The successful candidate will also participate in the interdisciplinary Boston University Marine Program ([www.bu.edu/bump](http://www.bu.edu/bump)). Responsibilities will include establishing an independent research program with extramural funding and active participation in undergraduate and graduate teaching.

Please submit a cover letter, curriculum vitae, and statement of research and teaching interests in a single electronic document. E-mail this document and three representative reprints to Dr. Michael Sorenson, Chair, Marine Ecology Search Committee, Department of Biology, Boston University at [biosrch@bu.edu](mailto:biosrch@bu.edu). Also, please arrange for three letters of reference to be sent to the same email address. Review of applications will begin December 5, 2008.

Boston University is an equal opportunity/affirmative action employer.

Michael Sorenson Associate Professor Department of Biology Boston University 5 Cummington St. Boston, MA 02215

(617) 353-6983 FAX: (617) 353-6340

[msoren@bu.edu](mailto:msoren@bu.edu) [msoren@bu.edu](mailto:msoren@bu.edu)

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## BrighamYoungU EvolutionaryBiol

Faculty Opening, Department of Biology, Brigham Young University

Biology Faculty

The Department of Biology is offering a continuing faculty status track position (professional track) to begin in the fall of 2009 (negotiable). Primary duties are managing two biological research facilities V Molecular Genetics Laboratory, the Evolutionary Ecology Laboratories including ecology users of the Isotope Laboratory, and teaching two sections per year of Introductory Biology for non-majors. Candidates must have a Ph.D. in biology or a related discipline, and preference will be given to candidates with expertise in molecular genetics and evolutionary ecology. Excellence in teaching is expected. Interested persons should apply online at <https://yjobs.byu.edu>. Please attach a CV, and statements of teaching and research interests to the completed BYU faculty application form. Applications can also be sent to: Dr. Jack W. Sites, Jr. ([jack\\_sites@byu.edu](mailto:jack_sites@byu.edu)), Search Committee Chair, De-

partment of Biology, Brigham Young University, Provo, UT 84602 V or electronic applications (preferred) to bio@byu.edu.

The review process will begin February 10, 2009 for this position and continue until the position is filled. Faculty application forms can be found at: <https://yjobs.byu.edu>. Additional department and college information is available at website: <http://biology.byu.edu/home>. BYU, an equal opportunity employer, requires all faculty to observe the university's honor code and dress and grooming standards. Preference is given to qualified candidates who are members in good standing of the affiliated church, The Church of Jesus Christ of Latter-day Saints.

"Jerald B. Johnson" <jerry.johnson@byu.edu>

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## CNRS France EvolutionaryBiology

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 Continental Surfaces and Interfaces (which includes landscape ecology), Biodiversity, evolution and biological adaptations: from macromolecules to communities, and Biological systems modelization, bioinformatics. The deadline, regrettably, is January, 6.

THE TYPES OF POSTS (see also <http://www.sg.cnrs.fr/drhchercheurs/concoursch/pdf/-metier-en.pdf>, including salaries): There are chargés de recherche, 2nd and 1st degree, 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 years of experience, respectively. \*However\*, please note that the announced posts of directeurs de recherche do not seem to exist (except in the case of very exceptional applications). These posts are de facto only for promotion of people that already have a position of a chargé de recherche within CNRS. According to my experience already the Chargés 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 becoming increasingly 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 quite 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 6.. 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. I hope we have some funds here at Rennes, but this is not sure.

After having applied \*all\* candidates will be invited to a short presentation and an interview in Paris in spring 2009. 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 of plants) or, alternatively, on the community assembly, diversity and diversification (preferably of arthropods in the canopy). My personal web page (somewhat outdated) is given



below, my team Ecology of Diversification covers further competences in ecophysiology and metabolomics and plant phylogeny.

The host lab here is the UNITE MIXTE DE RECHERCHE ECOSYSTEMES , BIODIVERSITE , EVOLUTION, co-funded by University of Rennes 1 and Centre National de la Recherche Scientifique, with particular expertise in mechanisms of speciation, life history evolution, and adaptation, expertise at the interface between macroevolution and macroecology, expertise in

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

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### DartmouthCollege ResTech PopulationGenetics

The Calsbeek lab at Dartmouth College seeks a part-time research technician for studies of population genetics. The successful applicants duties will include:

- 1) responsibility for microsatellite and sequence data collection,
- 2) general lab management and organization,
- 3) some animal husbandry of lizards.

The position is for 6-9 months, beginning approximately March 2009 with a primary goal of genotyping large numbers of tissue samples for pedigree construction. For more information on the types of research conducted in our lab, please see: <http://www.dartmouth.edu/~calsbeeklab/> The successful applicant will have a bachelors or a masters degree in biology or a related discipline, and will have a strong background in genetics and/or evolution. Other qualifications include excellent organizational skills, the ability to work independently, but with a capacity for interacting in small groups. Previous experience working in a molecular lab environment, particularly with microsatellites, AFLP, SNP, or sequencing, is highly desirable but not required.

Salary will be commensurate with experience. Please send inquiries by email to Ryan Calsbeek ([ryan.calsbeek@dartmouth.edu](mailto:ryan.calsbeek@dartmouth.edu)). Include a CV, contact information for three references and a cover letter

describing your previous experience, why you think you would enjoy the position, and when you would be able to start. Applications will be considered until the position is filled.

Ryan Calsbeek Assistant Professor Department of Biological Sciences Dartmouth College Hanover, NH 03755  
[ryan.calsbeek@dartmouth.edu](mailto:ryan.calsbeek@dartmouth.edu)

Ryan Calsbeek <[ryan.calsbeek@dartmouth.edu](mailto:ryan.calsbeek@dartmouth.edu)>

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### EckInstitute Director DiseaseAndEvolution

DIRECTOR OF OPERATIONS V ECK INSTITUTE FOR GLOBAL HEALTH (EIGH)

The Eck Institute for Global Health (EIGH) seeks applications at the Assistant/Associate Research Faculty level to coordinate all operations of the Institute. The EIGH is dedicated to investigations of human pathogens and their invertebrate and vertebrate vectors, diseases they cause, and their impact on human society, especially in developing regions. The Director of Operations will assume an active role in an aggressive expansion of research and training programs within the EIGH. This expansion also includes creation of core facilities in Genomics and Bioinformatics.

The successful applicant will assume a primary role in coordinating EIGH expansion, with a charge to promote and establish interdisciplinary linkages both within and outside the University of Notre Dame. This individual will guide the expansion of existing international research programs and seek to incorporate social science and human development research into ongoing and expanded EIGH initiatives. Other duties include: work closely with the EIGH Director, university administrators, faculty, students, and other campus Institutes to identify and implement new research and training programs; actively seek new funding opportunities in both research and training; and provide day-to-day oversight of all EIGH activities.

Preferred applicants should have demonstrated experience in biomedical research, be familiar with extramural funding mechanisms, and have strong management skills with evidence of collaborative interactions. Salary and rank are competitive, commensurate with experience and skills. This initial appointment is for 3 years and development of a limited independent research program is possible, with modest startup funds available.

Interested applicants should send a letter of inquiry, Curriculum Vitae, summary of research accomplishments, and 3 letters of reference to: Dr. David Severson, Director Eck Institute for Global Health, 137 Galvin Life Sciences, University of Notre Dame, Notre Dame, IN 46556, USA or by email to [merz.4@nd.edu](mailto:merz.4@nd.edu). Deadline for receipt of applications is 15 January 2009. See the EIGH website ([www.nd.edu/~cghid](http://www.nd.edu/~cghid)) for more information.

The University of Notre Dame is committed to diversity in its staff, faculty, and student body. As such, we strongly encourage applications from members of minority groups, women, veterans, individuals with disabilities, and others who will enhance our community.

The University of Notre Dame is an EEO/AA employer.

Kim Bogold <[merz.4@nd.edu](mailto:merz.4@nd.edu)>

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## Edinburgh ComputationalBiology

The MRC Human Genetics Unit (within the new IGMM) has a vacancy for a new group leader in computational biology in the Biomedical Systems Analysis (BSA) section. The BSA section is a new grouping in the IGMM encompassing groups active in computational genomics, complex trait analysis, population studies and systems-based approaches to understanding developmental genetic networks.

The IGMM (Institute for Genetics and Molecular Medicine) is an exciting development in Edinburgh led by Professor Nick Hastie, CBE FRS FRSE. It brings together the Medical Research Councils Human Genetics Unit and the University of Edinburghs Molecular Medicine Centre and Edinburgh Cancer Research Centre .

Full details at: [http://www.hgu.mrc.ac.uk/StaffInf/Jobs/igmm\\_outstanding\\_scientists\\_08.html](http://www.hgu.mrc.ac.uk/StaffInf/Jobs/igmm_outstanding_scientists_08.html) – Dr Colin A. M. Semple Head of Bioinformatics MRC Human Genetics Unit Institute of Genetics and Molecular Medicine Edinburgh EH4 2XU, UK Tel: +44 (0)131 332 2471 x4034 Fax: +44 (0)131 467 8456 Email: [Colin.Semple@hgu.mrc.ac.uk](mailto:Colin.Semple@hgu.mrc.ac.uk) Web: <http://www.hgu.mrc.ac.uk/Users/Colin.Semple/> [colins@hgu.mrc.ac.uk](mailto:colins@hgu.mrc.ac.uk)

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## FloridaIntIU PlantConservation

PLANT CONSERVATION BIOLOGIST FACULTY POSITION (OPEN RANK) FLORIDA INTERNATIONAL UNIVERSITY AND FAIRCHILD TROPICAL BOTANIC GARDEN

The Department of Biological Sciences at Florida International University and Fairchild Tropical Botanic Garden are seeking an outstanding scientist for an open rank position in plant conservation biology. We seek applicants with a PhD and an exceptional research and publication record. Areas of interest include, but are not limited to, conservation genetics, threatened species management, small population and metapopulation management, protected areas, plant genetic resources, biodiversity and habitat restoration, and tropical ecology. The successful candidate will teach courses within his/her specialty area and develop undergraduate/graduate courses in plant biodiversity and conservation. This is a joint appointment between FIU and Fairchild. The successful candidate will be based at Fairchild and provide input to the establishment of a major new center in tropical plant conservation. Review of applications will begin January 15, 2009; applications will be accepted until the position is filled. To apply send CV, brief description of research accomplishments and objectives, statement of teaching interests, selected reprints, and the names, addresses, and contact information for at least three references to Chair, Plant Conservation Biology Search, Dept. Biological Sciences, FIU, 11200 SW 8th St, Miami, Florida 33199. Florida International University is an Equal Opportunity Educator and Employer.

Contact for further information

Javier Francisco-Ortega, Associate Professor, Department of Biological Sciences, 11200 SW 8th Street, OE Building # 242 (Office), OE Building # 167 (Mail), Florida International University, University Park, Miami FL 33199, USA

Phone: (305) 348-2080 (Office FIU) Fax: (305) 348-1986 (Department Office FIU)

Head of FIU/FTBG Plant Molecular Systematic and Conservation Genetic Laboratory, Center for Tropical Plant Conservation, Fairchild Tropical Botanic Garden, 11935 Old Cutler Road, Coral Gables, Miami FL 33156-4299, USA

Phone: (305) 665-2844 Ext. 3432 (Office at FTBG)  
Phone: (305) 665-2844 Ext. 3423 (Laboratory at FTBG)  
Fax: (305) 665-8032

Email: ortegaj@fiu.edu

Javier Francisco-Ortega <ortegaj@fiu.edu>

– Sheri Church Department of Biology George Washington University 340 Lisner Hall 2023 G Street, N.W. Washington, D.C. 20052

office: 202-994-0274 lab: 202-994-4412 fax:202-994-6100 email: schurch@gwu.edu <http://home.gwu.edu/~schurch/Church.html> schurch@gwu.edu  
schurch@gwu.edu

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## GeorgeWashingtonU MolecularSystematics

The Department of Biological Sciences invites applications for the Louis Weintraub Professor, a tenure-track Assistant or Associate professorship in Molecular Systematics with an appointment date starting in September 2009. We seek a phylogeneticist who uses molecular data to study the phylogenetic relationships among organisms, and whose teaching and research interests will expand and strengthen our department and the Weintraub Program in Systematics and Evolution (see [www.gwu.edu/~clade](http://www.gwu.edu/~clade)). The successful candidate will be expected to develop an externally funded research program and participate in graduate and undergraduate education. Basic Qualifications: A completed Ph.D. in a relevant field and commitment to scholarly research as evidenced by publications in scholarly journals and scholarly works in progress is required. Postdoctoral experience is preferred. To be considered at the associate professor level, the candidate must already be at that rank or have 7 years or more equivalent experience. Review of applications begins January 2, 2009 and will be ongoing until the position is filled.

Application Procedure: Interested candidates should email a letter of application, curriculum vitae, a statement of research and teaching interests, electronic copies of up to three publications, and have three letters of recommendation sent (Assistant Professor applicants) or provide a list of references (Associate Professor applicants) to:

Weintraub Search Committee Chair Department of Biological Sciences 340 Lisner Hall 2023 G Street NW The George Washington University Washington DC 20052  
Email: wsearch@gwu.edu Phone 202-994-6090

Only complete applications will be considered.

The George Washington University is an Equal Opportunity/Affirmative Action Employer. The University Search Committee seeks to attract an active, culturally and academically diverse faculty of the highest caliber.

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## GeorgeWashingtonU PhylogeneticBiogeography

The Department of Biological Sciences invites applications for the Robert Griggs Professor, a tenure-track Assistant or Associate professorship in Phylogenetic Biogeography/Co-evolution with an appointment date starting in September 2009. We seek a phylogeneticist who uses comparative data to study historical biogeography or interactions among species (for example, parasites and their hosts or herbivores and their host plants), and whose teaching and research interests will expand and strengthen our Weintraub Program in Systematics and Evolution (see [www.gwu.edu/~clade](http://www.gwu.edu/~clade)). The successful candidate will be expected to develop an externally funded research program and participate in graduate and undergraduate education. Basic Qualifications: A completed Ph.D. in a relevant field is required and postdoctoral experience is preferred. To be considered at the associate professor level, the candidate must already be at that rank or have 7 years or more experience. Review of applications begins January 2, 2009 and will be ongoing until the position is filled.

Application Procedure: Interested candidates should email a letter of application, curriculum vitae, a statement of research and teaching interests, electronic copies of up to three publications, and have three letters of recommendation sent (Assistant Professor applicants) or provide a list of references (Associate Professor applicants) to:

Weintraub Search Committee Chair Department of Biological Sciences 340 Lisner Hall 2023 G Street NW The George Washington University Washington DC 20052  
Email: wsearch@gwu.edu Phone 202-994-6090

Only complete applications will be considered. The George Washington University is an Equal Opportunity/Affirmative Action Employer. The University Search Committee seeks to attract an active, culturally

and academically diverse faculty of the highest caliber.

– Sheri Church Department of Biology George Washington University 340 Lisner Hall 2023 G Street, N.W. Washington, D.C. 20052

office: 202-994-0274 lab: 202-994-4412 fax:202-994-6100 email: schurch@gwu.edu <http://home.gwu.edu/~schurch/Church.html> schurch@gwu.edu schurch@gwu.edu

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### MaxPlanckInst ExperimentalEvolution

#### INDEPENDENT JUNIOR RESEARCH GROUP

in the field of EXPERIMENTAL EVOLUTION to be hosted at

#### THE MAX PLANCK INSTITUTE FOR EVOLUTIONARY BIOLOGY

We seek an outstanding early-career scientist to lead an independent junior research group working in the area of experimental evolution. Candidates should have a record of internationally recognized research accomplishments. The position is planned to complement the research fields in Evolutionary Ecology, Evolutionary Genetics and Evolutionary Theory at the Institute.

The Institute is located in Plön (Northern Germany) and offers a stimulating research environment dedicated to evolutionary biology. It maintains strong links to the Christian Albrechts University Kiel and the Leibniz Institute for Marine Sciences (IFM-Geomar) in Kiel. The Institute provides state-of-the-art laboratories and equipment, including facilities for genome analysis.

Funding for the group leader position (equivalent to an assistant professor) and associated support is guaranteed for five years with the possibility of extension for up to four additional years. The group will be provided with modern laboratory space, funds for positions for a post-doc, Ph.D. student and technical assistant, and an adequate budget for running costs.

To apply please go to [www.evolbio.mpg.de](http://www.evolbio.mpg.de) and follow the link “Research Group Application”. You will be asked to register and upload (1) a CV including a list of publications, (2) one page summary of your scientific achievements and a two pages statement of your future research plans, and (3) up to three of your most important papers. Also please arrange to have two letters of recommendation uploaded directly by your referees

into the same database.

The deadline for receiving applications is December 31, 2008. Please note that a symposium (scientific presentation of short listed candidates plus interviews) is planned in conjunction with the recruitment of a similar position at the MPI for Chemical Ecology on January 29/30, 2009.

Location: Max Planck Institute for Chemical Ecology, Jena, Germany. The Max Planck Society is an equal opportunity employer, and is very interested in raising the proportion of women in areas where they are underrepresented. Thus applications from female scientists are especially encouraged. Further information can be obtained from: [tautz@evolbio.mpg.de](mailto:tautz@evolbio.mpg.de)

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](mailto:tautz@evolbio.mpg.de)

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### MaxPlanckInstitute EvolutionaryBiodemography

Dear all,

The Max Planck Institute for Demographic Research continues to develop its research activities in the field of Evolutionary Biodemography, and is recruiting to a number of positions. The attached announcement, linking to <http://www.demogr.mpg.de/go/appl-agelife/>, will be appearing soon in Nature, Science etc., and may be of interest to you or to members of your group. Please feel free to distribute this further or to post the text from this e-mail on your web-sites, newsgroups, etc.

Best wishes, David Thomson

<<Gabler-MPI-demoFor-Science.pdf>>

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

Tel. +49 (0)381 2081 229 Fax. +49 (0)381 2081 529

Website: [www.demogr.mpg.de](http://www.demogr.mpg.de) “Thomson, David” <[Thomson@demogr.mpg.de](mailto:Thomson@demogr.mpg.de)>

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## NESCent CommunicationsManager

\*The National Evolutionary Synthesis Center (NESCent)\*

\*Communications Manager, Education & Outreach\*

The National Evolutionary Synthesis Center (NESCent) <http://www.nescent.org/index.php> seeks a highly motivated biologist to serve as Communications Manager for the Centers Education and Outreach program. The Communications Manager will be involved in all aspects of the Centers Education and Outreach activities and will work closely with the Associate Director for Education and Outreach and EOG staff to promote the scientific and educational activities of the Center. The individual will be expected to work with initiatives in the public understanding of science and will work with postdocs, visiting scientists and working groups to help translate NESCent science. We seek an individual with a strong background in Evolutionary Biology or a related field, and with demonstrated experience in science communication, education and outreach.

Expected Qualifications: Ph.D. in biology or related field, with experience in evolutionary biology. We are looking for an individual with experience in science communication, teaching, and/or education and well developed communication skills and leadership potential.

How to Apply: Candidates should submit a letter of application discussing their background and job interests, CV and names of three individuals willing to provide letters of recommendation to [CommMgr@nescent.org](mailto:CommMgr@nescent.org). Applications will be considered until the position is filled; applications received before January 10 will be guaranteed consideration. For more information see our web site at NESCent Employment Opportunities at <http://www.nescent.org/about/employment.php>. Duke University is an Equal Opportunity/Affirmative Action Employer.

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Karen Henry Assistant Director of Research Administration National Evolutionary Synthesis Center 2024 W. Main Street, Suite A200 Durham, NC 27705

email: [khenry@nescent.org](mailto:khenry@nescent.org) telephone: 919-668-4574  
fax: 919-681-8444 <http://www.nescent.org/>

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## NewMexicoStateU GenomicsDirector

Position Available: Director, Genomics and Bioinformatics Facility

New Mexico State University, Biology Department (Req #2008012761)

Date Advertised: December 1, 2008

Targeted Salary \$65,000. Commensurate with education & qualifications.

Contingent upon funding (currently funded for two years). All offers of employment, oral and written, are contingent on the University's verification of credentials, individuals eligibility for employment in the United States and other information required by federal law, state law, and NMSU policies/procedures, and may include the completion of a criminal history check.

Qualifications: Ph.D. degree in Biological Sciences, Computer Science, Mathematics or a related field and three (3) years of experience. Knowledge of programming languages (e.g., C++, Perl, Java, Python, etc.), data management (e.g., SQL), software resources (e.g., scientific libraries and applications), and bioinformatics applications (e.g., sequence analysis, genome mapping, etc.). Knowledge of Unix system administration and the Unix programming environment is advantageous. Ability to communicate clearly, both verbally and in written form, with researchers and clientele. Ability to work collaboratively with scientists and other Facility staff. Leadership skills and initiative suitable for seeking funding opportunities for growth of the Facility.

Examples of Duties: Experimental design and analysis of genomics experiments. The centerpiece of the Facility is a Roche/454 GS FLX emPCR pyrosequencer that will be used for a wide range of genomics experiments and will be operated by other Facility personnel. The candidate will be expected to assist research clientele with designing experiments prior to and analyzing the data subsequent to instrument runs. Typical analyses might include genome assembly, mapping, annotation, mining and linking into existing databases, quantification of genetic variation, metagenomics, and phylogenetics. A thorough understanding of bioinformatics as well as a range of biological sciences is essential to successfully carry out these duties. It is expected that the candidate will keep abreast of research developments

in bioinformatics, genomics, and related fields so as to be able to guide researchers, seek new opportunities, and lead workshops and training activities to disseminate knowledge of techniques. The candidate will also be expected to administer the computer systems associated with the Facility and train users on their use. The candidate will be responsible for supervising and training graduate student assistants.

**Benefits Offered:** Group medical and hospital insurance, group life insurance, long-term disability insurance, state educational retirement, workers' compensation, sick leave, annual leave and unemployment compensation. Opportunity for educational advancement.

**Reply to/Deadline for Applications:** Submit a formal letter of interest, current resume, college transcripts, proof of professional certification(s), and three professional references with names, titles, addresses, daytime phone numbers, and email addresses to:

Brook Milligan Department of Biology New Mexico State University PO Box 30001, MSC 3AF Las Cruces, New Mexico 88003 or as e-mail attachments to: [brook@nmsu.edu](mailto:brook@nmsu.edu)

Review of applications begins 12 January 2009 and the position will remain open until filled. Incomplete application packets will not be considered.

**NMSU IS AN EQUAL OPPORTUNITY/AFFIRMATIVE ACTION EMPLOYER.** Offer of employment is contingent upon verification of individual's eligibility for employment in the United States.

For information about the university and the region, see: <http://www.nmsu.edu/> [phoude@nmsu.edu](mailto:phoude@nmsu.edu)

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## NewMexicoStateU GenomicsManager

**Position Available:** Laboratory Manager, Genome Sequencing Laboratory New Mexico State University, Biology Department (Req # 2008012470) Date Advertised: November 25, 2008 Targeted Salary \$40,000. Commensurate with education & qualifications.

Contingent upon funding (currently funded for two years). All offers of employment, oral and written, are contingent on the University's verification of credentials and other information required by Federal Law, State

Law, and NMSU policies/procedures, and may include the completion of a criminal history check. Qualifications: BS in Biology, Molecular Biology or related field, plus three years experience; or the equivalent combination of education and experience required for the position; MS in Molecular Biology preferred. Strong background in molecular biological laboratory techniques. Experience with qPCR, construction of BAC and normalized cDNA libraries, microarray chip technology, Sanger sequencing, and capillary electrophoresis are advantageous. Ability to communicate clearly, both verbally and in writing, with researchers and clientele. Leadership skills and initiative suitable for seeking opportunities for growth of the Facility.

**Examples of Duties:** Operation, management, and expansion of the NMSU's core Genome Sequencing Laboratory. Daily operation and routine maintenance of a Roche/454 GS FLX emPCR pyrosequencer (training provided), the centerpiece of the Facility. Successful operation of this instrument requires meticulous adherence to protocols. Additional laboratory duties include the preparation of a wide variety of samples for genomic sequencing, and training/supervising graduate student laboratory assistants. Other duties include project management, record-keeping, accounting, and purchasing reagents/ expendables. Must keep abreast of technical advances in genomics in order to advise research clientele in experimental design and seek new applications of genomics technology. Must work collaboratively with team of faculty researchers, bioinformatics specialists, graduate students, and facilities staff. **Benefits Offered:** Group medical and hospital insurance, group life insurance, long-term disability insurance, state educational retirement, workers' compensation, sick leave, annual leave and unemployment compensation. Opportunity for educational advancement. **Reply to/Deadline for Applications:** Submit a formal letter of interest, current resume, and three professional references with names, titles, addresses, daytime phone numbers, and email addresses to:

Peter Houde Department of Biology New Mexico State University Box 30001, MSC 3AF Las Cruces NM 88003 or as e-mail attachments to: [phoude@nmsu.edu](mailto:phoude@nmsu.edu)

Review of applications will begin December 9, 2008 and will continue until the position is filled. Incomplete application packets will not be considered. **NMSU IS AN EQUAL OPPORTUNITY/AFFIRMATIVE ACTION EMPLOYER.** Offer of employment is contingent upon verification of individual's eligibility for employment in the United States.

For information about the university and the region, see: <http://www.nmsu.edu/> [phoude@nmsu.edu](mailto:phoude@nmsu.edu)

phoude@nmsu.edu

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### SmithCollege OneYear TeachingEvolution

One-Year Lecture Position: Genetics, Genomics and Evolution, Smith College

We have authorization to hire a one-year non-tenure-track 0.75 FTE lecturer for the 2009-2010 academic year. The person would team teach both semesters of an introductory course in Genetics, Genomics and Evolution, team teach our 200 level genetics course (Genomics and Genetic Analysis), and offer a 300 level course in their specialty. We hope to find someone who can be affiliated with an existing lab including: Barresi lab - neural development in zebrafish, Katz lab - tree of life/genome evolution in ciliates, Williams lab - molecular biology of filarial parasites. Smith College is an equal opportunity employer encouraging excellence through diversity.

Please contact Bob Merritt (rmerritt@email.smith.edu) or Laura Katz (lkatz@email.smith.edu) for further information. You can find out more about biology at Smith College at: <http://www.science.smith.edu/departments/Biology/lkatz@smith.edu> lkatz@smith.edu

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### Smithsonian FieldAssist PlantMammalEvolution

Field Assistant Position, Rainforest Plant-Mammal Interactions

We have a position for one field assistant to help with NSF funded research on interactions between mammals (agoutis) and palm seeds. This work will focus on radio-tracking both the agoutis as well as the seeds they disperse, but will also include helping with monitoring projects using camera traps and plant surveys. The assistant will work as part of a team that includes post-docs, students, volunteers, and other assistants involving a broad collaboration between the New York State Museum, Princeton University, the Max Plank Institute, University of Groningen, University of Wa-

geningen, and the Smithsonian Tropical Research Institute.

TIME PERIOD: One year, starting late March 2009, with possible extension for a second year.

LOCATION: Barro Colorado Island, a research station in central Panama administered by the Smithsonian Tropical Research institute.

PAYMENT: \$24,000 per year plus benefits through the NY State Museum, one round-trip plane ticket. Assistant will be responsible for their living fees in Panama. Applicants must be a US citizen or have a valid work visa for the United States.

QUALIFICATIONS: Applicant must have a BS or MS degree and experience in field ecology. A background in tropical ecology, radio telemetry, or animal-handling skills would also be beneficial. Applicants must be a US citizen or have a valid work visa for the United States.

APPLICATION DEADLINE: 29 December 2008

TO APPLY: Send a CV, names of 3 references, and a cover letter to rkays@mail.nysed.gov

“Hirsch, Ben” <HirschB@si.edu>

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### UAarhus ThermalAdaptation Evolution

FACULTY OF SCIENCE DEPARTMENT OF BIOLOGICAL SCIENCES Post doctoral position in the Genetic Architecture of Thermal Adaptation in Drosophila The Department of Biological Sciences, Aarhus University, invites applications for a two-to three-year post doctoral position at the Evolutionary Genetics research group, starting from the 1st of February 2009 (or April 2009, if preferred). The Evolutionary Genetics research group/the Aarhus Center for Environmental Stress Research (<http://www.biology.au.dk/aces.en>) has a strong focus on studying thermal adaptation and resistance to environmental stress, and the postdoc is expected to join the research program on adaptation to a climatic gradient, using Drosophila species as a model. The work will start with selection experiments followed by applying various assays and molecular methods to the selection lines, incl. studies of relative resistances and other life history traits, the study of candidate genes using SNPs, gene expression analyses as well as the study of the metabolic profile and performing field tests,

as can be seen from recent publications of the group (<http://www.biology.au.dk/volker.htm>). The postdoc will bring a strong expertise in population genetic and evolutionary ecological studies of model organisms such as *Drosophila*, experience in applying molecular techniques and analyzing the resulting data in an evolutionary context, and should be open to interact with other postdocs and researchers in the group. The work will be done in close cooperation with other researchers in the environmental stress group, particularly Torsten N Kristensen (Torsten.Nygaard@agrsci.dk), and collaborating groups in Aarhus and abroad, with interest of combining evolutionary and physiological approaches to identify mechanisms of adaptation along climatic gradients. Applications must be in English and include a curriculum vitae, a complete list of publications, a statement of future research plans and information about research activities, teaching qualifications and management experience, all in 4 copies (see <http://www.nat.au.dk/default.asp?id=7842&la=UK> for the recommended level of detail). If the applicant wants other material to be considered in the evaluation (publications and other documentation of research and teaching qualifications, as well as management experience) such material must be clearly specified and must either be enclosed in hardcopy (3 copies) or must be available electronically. The Faculty refers to the Ministerial Order No. 92 of 15.02.2008 (<http://science.au.dk/default.asp?id=7839&la=UK>) on the appointment of teaching and research staff at the universities under the Ministry of Science, Technology and Innovation. Salary depends on seniority as agreed between the Danish Ministry of Finance and the Confederation of Professional Unions. Applications should be addressed to The Faculty of Science, University of Aarhus, Ny Munkegade, Building 1520, DK-8000 Aarhus C, Denmark, and marked 212/5-262. The deadline for receipt of all applications is January 5, 2009, at 12,00 noon. For more information please contact Professor Volker Loeschcke, e-mail: [Volker.loeschcke@biology.au.dk](mailto:Volker.loeschcke@biology.au.dk), phone +45 8942 3268. The University of Aarhus has 35,000 students, 8,500 members of staff and a turnover of DKK 4.8 billion in 2008. The university's strategy and development contract are available at <http://www.au.dk/en/-strategy>

– Volker Loeschcke Dept. of Biological Sciences Ecology and Genetics Aarhus University Ny Munkegade, Buildg. 1540 DK-8000 Aarhus C, Denmark

fax: +45 8942 2722 tlf: +45 8942 3268, mobile: +45 2899 2368 email: [volker.loeschcke@biology.au.dk](mailto:volker.loeschcke@biology.au.dk)

Volker Loeschcke <[volker.loeschcke@biology.au.dk](mailto:volker.loeschcke@biology.au.dk)>

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## UArizona Evolutionary Genomics

Below is an advertisement for an open-rank faculty position at the University of Arizona in the general area of Evolutionary Genetics and Genomics.

The Department of Ecology & Evolutionary Biology at the University of Arizona maintains a large group of faculty who are actively working in this area including:

Jeremiah Hackett Joanna Masel Nancy Moran Michael Nachman Howard Ochman Mike Sanderson Matt Sullivan Mike Worobey

We hope that you might bring this ad to the attention of suitable candidates. Thank you very much.

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Evolutionary and Environmental Genomics V University of Arizona

The Department of Ecology and Evolutionary Biology at the University of Arizona seeks to hire at the Assistant, Associate or Full Professor level in the areas of evolutionary and environmental genomics. Candidates' research should show evidence of originality and address significant evolutionary or ecological questions. Approaches can include population genetics, functional and comparative genomics, bioinformatics, field and experimental studies, and can focus on any group of organisms, including microbes. Multidisciplinary research and potential links to other UA programs, such as the initiatives at Biosphere 2 and the BIO5 Institute, are particularly welcomed.

To apply, please submit hard-copy statements of research and teaching interests, complete CV, and up to five reprints of published work via conventional mail, and arrange for three letters of recommendation to be sent to Evolutionary and Environmental Genomics Search Committee, Department of Ecology and Evolutionary Biology, 1041 E. Lowell Street, University of Arizona, Tucson AZ 85721. Review of applications will begin on January 5, 2009. The University of Arizona is an EEO/AA - M/W/D/V Employer.

Department contact: Elaine Mattes  
<[emattes@email.arizona.edu](mailto:emattes@email.arizona.edu)>

Becky Nankivell <[bjn@email.arizona.edu](mailto:bjn@email.arizona.edu)>



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## UArizona EvolutionaryGenomics 2

This is a REVISED announcement.

Evolutionary and Environmental Genomics – University of Arizona

The Department of Ecology and Evolutionary Biology at the University of Arizona seeks to hire at the Assistant, Associate or Full Professor level in the areas of evolutionary and environmental genomics. Candidates' research should show evidence of originality and address significant evolutionary or ecological questions. Approaches can include population genetics, functional and comparative genomics, bioinformatics, field and experimental studies, and can focus on any group of organisms, including microbes. Multidisciplinary research and potential links to other UA programs, such as the initiatives at Biosphere 2 and the BIO5 Institute, are particularly welcomed.

To apply, please submit hard-copy statements of research and teaching interests, complete CV, and up to five reprints of published work via conventional mail, and arrange for three letters of recommendation to be sent to Evolutionary and Environmental Genomics Search Committee, Department of Ecology and Evolutionary Biology, 1041 E. Lowell Street, University of Arizona, Tucson AZ 85721. Review of applications will begin on January 5, 2009. The University of Arizona is an EEO/AA - M/W/D/V Employer.

Elaine Mattes <emattes@email.arizona.edu>

Becky Nankivell <bjn@email.arizona.edu>

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## UBern BioinformaticsTech

The CMPG lab (<http://cmpg.unibe.ch>) is looking for a motivated Programmer and IT Engineer at 80-100% (m/f) to join our young international research group.

Our laboratory is involved in the analysis of genomic data, bioinformatics, and the development of modern statistical genetics tools requiring heavy computations on a Linux cluster.

The candidate will have IT administration responsibil-

ities and participate to the maintenance and the development of dedicated genomic databases, web pages, and computational programs. He/she will be directly involved in current research projects in bioinformatics and provide basic IT support for Linux and Windows users.

Experience/qualifications - Degree in bioinformatics, computer science or equivalent experience - High level programming (C/C++, PHP, Java, Javascript) - Database management (mySQL preferred). - Network and system administration (under Windows and Linux) - Web page design (CMS and dynamic) - Fluency in English

The suitable candidate will also interact with IT administrators of our Institute and of our University.

This permanent position is primarily open for Swiss or EU citizens, or for individuals having a valid working permit in Switzerland. Initial salary will be commensurate with qualifications and experience.

Starting date is on 1st February 2009.

If interested, please send a full CV, a statement of interest and relevant references from previous positions (if applicable) by email to [laurent.excoffier@zoo.unibe.ch](mailto:laurent.excoffier@zoo.unibe.ch)

– Laurent Excoffier

Computational and Molecular Population Genetics (CMPG) Institute of Ecology and Evolution, University of Bern 6, Baltzerstrasse, CH-3012 Bern, Switzerland Tel: +41 31 631 30 31 Fax: +41 31 631 48 88 Email: [laurent.excoffier@zoo.unibe.ch](mailto:laurent.excoffier@zoo.unibe.ch) <http://cmpg.unibe.ch/people/excoffier.htm> Computational Population Genetics Swiss Institute of Bioinformatics (SIB) [http://www.isb-sib.ch/groups/-Computational\\_Population\\_Genetics.htm](http://www.isb-sib.ch/groups/-Computational_Population_Genetics.htm) Laurent Excoffier <[laurent.excoffier@zoo.unibe.ch](mailto:laurent.excoffier@zoo.unibe.ch)>

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## UBern FieldAssist EvolutionaryEcology

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 different 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 read-

ily accept nest boxes making them easy to manipulate and follow from egg laying to offspring fledging. I will require 2 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 2009, and running until around the end of May 2009. 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. [m.coslovsky@students.unibe.ch](mailto:m.coslovsky@students.unibe.ch)

### UBuffalo LabTech CoralEvolution

Laboratory Technician, University at Buffalo - I am looking for an assistant to work on an NSF sponsored project on the population ecology of Caribbean octocorals. Laboratory work will include DNA extraction, PCR, gel quantification, genotyping using a LiCor DNA sequencer, cloning and analysis of genotypic and sequence data. The work also will include maintaining a laboratory database, general laboratory tasks, and supervising students working in the lab. Fieldwork will involve research scuba diving from research vessels or small boats, and will include collecting samples, population surveys and monitoring recruitment experiments.

Applicants must have the appropriate citizenship/visa status to work in the U.S. and should have at least a Bachelor's degree and experience with population genetic and molecular systematic techniques. The assistant must be able to meet University at Buffalo and American Academy of Underwater Sciences (AAUS) standards for certification as a research diver.

Questions regarding the position should be directed to Dr. Howard Lasker ([hlasker@buffalo.edu](mailto:hlasker@buffalo.edu) <<mailto:hlasker@buffalo.edu>> - 716-645-3489 x184)

Additional information can be found at [www.ubjobs.buffalo.edu/applicants/Central?quickFindR391](http://www.ubjobs.buffalo.edu/applicants/Central?quickFindR391) < <http://www.ubjobs.buffalo.edu/applicants/Central?quickFind=52391> >

Applications must be submitted through the Universitys UBJobs website (posting #0800534)-

The Research Foundation is an EEO/AA Employer.

[hlasker@buffalo.edu](mailto:hlasker@buffalo.edu) [hlasker@buffalo.edu](mailto:hlasker@buffalo.edu)

### UParis6 IntegrativeEvolution

An assistant professor position at the Universite Pierre and Marie Curie (UPMC) in Paris, France, is available to work in integrative ecology, i.e. at the interplay between physiology, evolution and ecology. Candidates must hold a PhD diploma in animal ecology, population ecology, behavioral ecology or evolutionary ecology and have solid skills in ecology and animal physiology, and some basic knowledge in French. Those of you who are interested can contact the group leader Manuel Massot by email for further information ([mmassot@snv.jussieu.fr](mailto:mmassot@snv.jussieu.fr)). A full description of the teaching and research experience required (unfortunately in french) is available at <http://jf.legalliard.free.fr/>. The job will start in september 2009 with the gross salary of an assistant professor in France (ca. 2000 a month) but candidates should apply for this position as soon as possible. Indeed, candidates who hold a PhD and would like to apply must first obtain a "qualification" before late december 2008 at the GALAXIE portal (<https://-antares.orion.education.fr/antares/can/index.jsp>). For those who do not know about this french bizerrie, this is the normal procedure to obtain the right to apply for any assistant professor position all over France during four years. If you get the qualification, you will then be able to apply in spring 2009 to this position in our laboratory. Of course, I can provide assistance for those of you who would like to apply from abroad and are highly motivated by the prospect of a position in our research group.

Do not hesitate to contact me!

Best regards, Jean-Francois.

Dr. Jean-Francois Le Galliard <http://-jf.legalliard.free.fr/> CNRS - UMR 7625 Fonctionnement et evolution des systemes ecologiques Universite Pierre et Marie Curie Case 237, Batiment A, 7 Quai St Bernard 75005 Paris FRANCE

CNRS - UMS 3194 Centre de Recherche en Ecologie Experimentale et Predictive (CEREPEP) Station biologique de Foljuif Ecole Normale Superieure Rue du chateau 77140 St-Pierre-les-Nemours

Office (Paris) : +33.1.44.27.26.68 Fax (Paris) : +33.1.44.27.35.16 Office (field) : +33.1.64.28.70.71 Lab (field): +33.1.64.28.69.94

Jean-Francois Le Galliard <galliard@biologie.ens.fr>

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USA Ph:(309) 438-7799 Email: jshajah@ilstu.edu

“Shajahan, Johnny” <jshajah@ilstu.edu>

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### AFLP protocols

Dear Evoldir members,

I am a Postdoctoral fellow, planning to start a new project on population genetics on insect pathogens including fungi & microsporidia. I have a lot of experience with genotyping microsatellites with Genotyper, but I never worked with AFLP. I would appreciate if anyone send me the working protocol for AFLP and also advice me about the instruments/software to buy for AFLP analysis. Please send your reply as soon as possible

Thanks Johnny

Johnny Shajahan 4120, Department of Biological Sciences Illinois State University Normal, IL-61790-4120,

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### Arlequin mismatch answer

Question

I have a question about the calculation of the mismatch distribution using the Arlequin 3.11 software package.

In their article, Schneider and Excoffier (1999), strongly suggest to take into account rate heterogeneity and nucleotide mutation correction models when calculating a mismatch distribution. Especially in the case where the parameters Tau and Theta is going to be used and the validity of inferring a demographic expansion is tested.

However, in Arlequin it seems that the only distance option available is a Pairwise difference with no gamma correction.

Although, I have seen articles that say that they used correction models such as K2P and modified alpha values when calculating mismatch distributions in Arlequin.

Is there a way that one can incorporate these corrections in your data using Arlequin?

Any suggestions will be much appreciated

Thank you

Carina Schlebusch

Answer

I received a reply from one of the developers of Arlequin, which solved my problems. The correction is not available in the Arlequin package but is available on request from the authors

Prof. Excoffier's email is pasted below

Thank you very much

yes, this is correct that no correction for multiple hits is done in Arlequin. However I have a program implementing the computations described in Schneider and Excoffier (1999) that is available upon request Mismatch analysis take much longer time when multiple hits are allowed because we need to do some preliminary computations (h coefficients). However, we have noticed that unless the shape parameter of the gamma distribution of mutation rates was very small (i.e.  $\alpha < 0.2$ ), the estimations were to those resulting from an analysis without any correction.

Some people have asked for it and used it, and you are welcome to do it

Best wishes

laurent

– Laurent Excoffier

Carina Schlebusch <cschlebu@yahoo.com>

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## BIOSYS-2 and FREQPARS

Does anyone know where one can get hold of old phylo-

genetic programmes (specifically BIOSYS-2 and FREQPARS) or at least the executables for these? I have trawled the web and none of the ftps seem to be operational anymore. I am trying to repeat an analysis of some data using BIOSYS-2 that had worked previously (and works fine on BIOSYS-1). I'm beginning to suspect that my executable may be corrupt.

bavin Gouws <g.gouws@ru.ac.za>

---

## Bryophyte phylogeny genes

Dear all,

I am doing a molecular phylogeny of a bryophyte genus and for that purpose I'm looking for informative nuclear regions except ITS region. GapC/Cp as well as GapA/B seem to be promising regions regarding the few literature (e.g. Stone, 2006).

But primers and sequences on NCBI are rare and PCR do not amplify well !

Do you have any advices using these genes for phylogeny purpose ? Do you know other nuclear regions that can fit ?

Thanks in advance, and best wishes for this new year, Amélie

Amélie PICHONET

PhD Student, Teaching Assistant National Museum of Natural History Departement of Systematique and Evolution, Bryology Team Case 39, 57 rue Cuvier 75005 Paris - France Tel : 00 33 1 40 79 31 88 Fax : 00 33 1 40 79 35 94 Email : pichonet@mnhn.fr

pichonet@mnhn.fr

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## Contributions Zoology

Contributions to Zoology - The journal Contributions to Zoology '.. since 1848 ..' solicits high-quality papers in all systematics-related branches of Zoology and Paleontology. Preference will be given to manuscripts dealing with conceptual issues and to integrative papers. Reviews and alpha-taxonomic contributions may

be considered for publication, but acceptance will depend on their high quality and exceptional nature. The journal is published by the National Museum of Natural History Naturalis, Leiden and the Zoological Museum Amsterdam and is freely available online since 1997 at [www.ctoz.nl](http://www.ctoz.nl). Editor-in-Chief: J.W. Arntzen - Leiden Managing Editor: S. Verschoor - Leiden Desk Top Publishing: N. Korenhof - Leiden

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For manuscript preparation and submission see [www.ctoz.nl](http://www.ctoz.nl)

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## CytochromeC primers

Dear Evoldir members,

We wish to PCR amplify the nuclear-encoded cytochrome c gene (known as CYC) from various invertebrates. We have looked for available primers with published sequences, but the results were discouraging. Are there any people working with this gene? Could they provide some primers that could serve as a starting point? All responses and suggestions will be greatly appreciated. Thank you in advance.

Aris

—

ARIS PARMAKELIS, PhD. DEPARTMENT OF ECOLOGY AND TAXONOMY FACULTY OF BIOLOGY NATIONAL & KAPODISTRIAN UNIVERSITY OF ATHENS PANEPISTHMIROUPOLI ZOGRAFOU, GR-15784, ATHENS, GREECE Tel.: ++302107274736 [aparmakel@biol.uoa.gr](mailto:aparmakel@biol.uoa.gr) [parmakel@nhmc.uoc.gr](mailto:parmakel@nhmc.uoc.gr) [parmakel@edu.biology.uoc.gr](mailto:parmakel@edu.biology.uoc.gr) <http://uaeco.biol.uoa.gr/~uameco> <http://www.nhmc.uoc.gr/> Aristeidis Parmakelis <[aparmakel@biol.uoa.gr](mailto:aparmakel@biol.uoa.gr)>

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## Defining identical sequences in an alignment

Dear EvolDir,

I'm having problems with the following and hope you may be able to help.

I would like to identify identical sequences (haplotypes) in an alignment file, which contains ca 700 sequences from the same species, many of which are the same.

I have previously used the program DNAsp on a pc, but am now a mac user. I found DNAsp problematic because the program renames the sequences H1-Hx, so you manually have to find the names of the sequences in the original file, which takes forever and is prone to mistakes when working with 700 sequences. Also, the program does not accept ambiguous nucleotides, which means the input-file has to be reformatted every time one wants to use the program. This is also time consuming and prone to mistakes. As I work with ancient DNA, many sites are initially ambiguous.

So I'm looking for a program for mac which can:

1. define haplotypes in an alignment
2. convert ambiguous bases in the alignment to N
3. provide an output file with the haplotype sequences only (eg in nexus)
4. provide an output with a list of which sequences belong to each haplotype

I hope you may be able to help.

Best regards, Eline Lorenzen

Email: [edlorenzen@bio.ku.dk](mailto:edlorenzen@bio.ku.dk)

Eline Lorenzen Department of Biology University of Copenhagen Universitetsparken 15 2100 Copenhagen Ø Denmark

Eline Lorenzen <[edlorenzen@bi.ku.dk](mailto:edlorenzen@bi.ku.dk)>

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## DiversityProject

Hello, Could you please post the following on EvolDir, subject heading The Diversity Project?

Dear Colleagues,

For the fifth 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 Boston University, Duke University, Old Dominion University and UCLA, students will integrate hands-on field research in the Coral Triangle with cutting edge genetic research. The project will explore the origins marine biodiversity in the Coral Triangle in an effort to improve conservation of this remarkable ecosystems. Students are fully funded for both living and travel expenses. Visit <http://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, 2009. For further information, please contact Dr. Paul Barber ([paulbarber@ucla.edu](mailto: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](mailto:pbarber@bu.edu) <http://people.bu.edu/pbarber/> Paul Barber <[paulbarber@ucla.edu](mailto:paulbarber@ucla.edu)>

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## DNA preservation liquids

G'day folks

I was wondering if folks have any experience with preserving DNA in the field in liquids other than ethanol? My target organisms are fishes, but I'm sure different liquids work on most groups just fine. In some parts of the world ethanol can be very difficult and/or expensive to obtain. Are there any good viable alternatives that can be obtained in third world countries that should be ok that people have experience with? Isopropanol is often available it seems, but I've only seen one report that suggested it should be ok. Also, I guess the isopropanol one would buy in a pharmacy varies depending on who makes it and the country (wikipedia says that in the USA and the UK Isopropyl Rubbing Alcohol is made of ethanol, not isopropanol).

One paper looked at preservation of spiders, and found

RNALater and propylene glycol worked well. Another paper on aphids found acetone was good, as was diethyl ether, and ethyl acetate. I'm not sure though how easy these are to obtain, or safely these can be transported though (RNALater is too expensive to consider).

I also searched the archives, but surprisingly this doesn't seem to be a topic that has come up before.

Thanks Peter Unmack

[peter.mail2@unmack.net](mailto:peter.mail2@unmack.net)

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## Doublesex antibody

Dear Evoldir members,

I am planning to purchase antibody against *Drosophila* doublesex protein from Santa Cruz (cat# sc-15759). So far I can not find any paper using that antibody, so if there is anybody who has tried it with either *Drosophila* or other insects, please let me know how it worked. Thank you very much,

Teiya KIJIMOTO, Ph.D. [tkijimot@indiana.edu](mailto:tkijimot@indiana.edu) Department of Biology Indiana University 915 E. Third Street Myers Hall 150 Bloomington, IN 47405-7107 phone: (812) 856-1783

[tkijimot@indiana.edu](mailto:tkijimot@indiana.edu) [tkijimot@indiana.edu](mailto:tkijimot@indiana.edu)

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## Editor of Phyloinformatics

Jeff Back ([beck@ncbi.nlm.nih.gov](mailto:beck@ncbi.nlm.nih.gov)) at the NCBI is trying to get the now defunct journal "Phyloinformatics" into PubMed Central so it will be available in perpetuity. Before doing this he'd like to make contact with somebody connected with the journal (the editor was Dennis DeGreve, for whom I have no contact details beyond a now defunct email address [editor@phyloinformatics.org](mailto:editor@phyloinformatics.org)).

Does anybody have any contact details for Dennis? It would be great to get Phyloinformatics into PMC.

Regards

Rod

Roderic Page Professor of Taxonomy DEEB, FBLS

Graham Kerr Building University of Glasgow Glasgow G12 8QQ, UK

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[r.page@bio.gla.ac.uk](mailto:r.page@bio.gla.ac.uk) [r.page@bio.gla.ac.uk](mailto:r.page@bio.gla.ac.uk)

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## Evolution of Insects in Urban Environments

Hi all, I'm looking for publications on the evolution (speciation, differentiation, genetic population structure, etc.) of insects in urban environments. One paper that comes to mind is Byrne & Nichols 1999. *Culex pipiens* in London Underground tunnels: differentiation between surface and subterranean populations. *Heredity* 82.

Others are welcome.

Festive greetings! Johan

– Johan Kotze Department of Biological and Environmental Sciences PO Box 65 (Biocenter 3, Viikinkaari 1) FI-00014, University of Helsinki Helsinki, FINLAND  
 Tel: +358 (0)9 191 57918 Fax: +358 (0)9 191 57788 E-mail: [johan.kotze@helsinki.fi](mailto:johan.kotze@helsinki.fi)

Editor-in-Chief, Journal of Negative Results - EEB ([www.jnr-eeb.org](http://www.jnr-eeb.org)) Associate Editor, *Annales Zoologici Fennici* ([www.annzool.net](http://www.annzool.net)) Urban Nature: <http://www.helsinki.fi/bioscience/environmental/urbannature.htm> Urban MSc Programme: [www.helsinki.fi/urban](http://www.helsinki.fi/urban) Globenet: [www.helsinki.fi/science/globenet/](http://www.helsinki.fi/science/globenet/) [johan.kotze@helsinki.fi](mailto:johan.kotze@helsinki.fi) [johan.kotze@helsinki.fi](mailto:johan.kotze@helsinki.fi)

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## Eye evolution

I am pleased to announce that a special issue of *Evolution: Education and Outreach* devoted to the subject of eye evolution is now available free online. It includes articles by several leading eye researchers and is intended to serve as a resource for evolution edu-

cators. The table of contents is provided below along with links to the individual papers. The entire issue is available at <http://www.springerlink.com/content/-m3k441k67q3n/>. *Evolution: Education and Outreach* Volume 1 Issue 4 The evolution of eyes

### Editorial

351. Editorial by Gregory Eldredge and Niles Eldredge <http://www.springerlink.com/content/-u2x507k225172057/fulltext.pdf> 352-354. Introduction by T. Ryan Gregory <http://www.springerlink.com/content/u08256710677h58w/fulltext.pdf> 355-357. Casting an Eye on Complexity by Niles Eldredge <http://www.springerlink.com/content/-u82568h8jj566k42/fulltext.pdf> Original science / evolution reviews

358-389. The Evolution of Complex Organs by T. Ryan Gregory <http://www.springerlink.com/content/-t125078h5p201442/fulltext.pdf> 390-402. Opening the "Black Box": The Genetic and Biochemical Basis of Eye Evolution by Todd H. Oakley and M. Sabrina Pankey <http://www.springerlink.com/content/-p522451641342056/fulltext.pdf> 403-414. A Genetic Perspective on Eye Evolution: Gene Sharing, Convergence and Parallelism by Joram Piatigorsky <http://www.springerlink.com/content/hp5178wmn484t79v/-fulltext.pdf> 415-426. The Origin of the Vertebrate Eye by Trevor D. Lamb, Edward N. Pugh, Jr., and Shaun P. Collin <http://www.springerlink.com/content/n4t036300571k8j4/fulltext.pdf> 427-438. Early Evolution of the Vertebrate Eye-Fossil Evidence by Gavin C. Young <http://www.springerlink.com/content/1876685v14p452k2/fulltext.pdf> 439-447. Charting Evolution's Trajectory: Using Molluscan Eye Diversity to Understand Parallel and Convergent Evolution by Jeanne M. Serb and Douglas J. Eernisse <http://www.springerlink.com/content/-1741pu336457n37u/fulltext.pdf> 448-462. Evolution of Insect Eyes: Tales of Ancient Heritage, Deconstruction, Reconstruction, Remodeling, and Recycling by Elke Buschbeck and Markus Friedrich <http://www.springerlink.com/content/42h1187812186743/-fulltext.pdf> 463-475. Exceptional Variation on a Common Theme: The Evolution of Crustacean Compound Eyes by Thomas W. Cronin and Megan L. Porter <http://www.springerlink.com/content/-t424710h72831147/fulltext.pdf> 476-486. The Causes and Consequences of Color Vision by Ellen J. Gerl and Molly R. Morris <http://www.springerlink.com/content/yk62221178u7w348/fulltext.pdf> 487-492. The Evolution of Extraordinary Eyes: The Cases of Flatfishes and Stalk-eyed Flies by Carl Zimmer <http://www.springerlink.com/content/670x13vk1nwh31g2/-fulltext.pdf> 493-497. Suboptimal Optics: Vision

Problems as Scars of Evolutionary History by Steven Novella <http://www.springerlink.com/content/h4052634m6895781/fulltext.pdf> Curriculum articles

498-504. Bringing Homologies Into Focus by Anastasia Thanukos <http://www.springerlink.com/content/g23113q700811w41/fulltext.pdf> 505-508. Misconceptions About the Evolution of Complexity by Andrew J. Petto and Louise S. Mead <http://www.springerlink.com/content/a7v3307m37236637/fulltext.pdf> 509-516. Losing Sight of Regressive Evolution by Monika Espinasa and Luis Espinasa <http://www.springerlink.com/content/7n0p7j3254952418/fulltext.pdf> Book reviews

548-551. Jay Hosler, An Evolutionary Novelty: Optical Allusions by Todd H. Oakley

— / —

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

**Ghrelin evolution**

Dear colleagues

I am interesting to study ghrelin protein sequence in sturgeon to find its evolutionary relationship with this protein in other animals and also its expression in gonads and its impact on sturgeon reproduction. I would like to introduce scientists who study on ghrelin. I would appreciate receiving reply.

Best wishes Mahtab

mahtab yarmohammadi  
<mahtab\_yarmohammadi@yahoo.com>

**Graduate program training  
timeframe query**

Dear Colleagues,

At Maryland we are reviewing our graduate training programs across the university. As part of this process we are being asked to compare our completion 'benchmarks' for PhD candidacy and PhD defense time frames

with other peer institutions. I have pasted our BEES program responses in below. If you have a moment could you please email me the year your students normally complete their coursework, advance to candidacy, and complete their PhD degrees at you schools?

Thanks in advance! Michele Dudash

Director of the Graduate Program in Behavior, Ecology, Evolution and Systematics

2. Assuming a student is making normal progress to degree in your program, in what year would you expect the student to reach each of the following benchmarks? (Please modify or replace the matrix below to match your programs benchmarks.)

\* University of Maryland BEES program benchmarks.  
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~ biology/dudashlab/dudashlabpage.html BEES program web page: <http://bees.umd.edu> Department of Biology, Room 3202 Biology Psychology Building University of Maryland College Park, MD 20742

~ <http://www.biology.umd.edu/> Office: 301-405-1642

~ Fax: 301-314-9358 Email: mdudash@umd.edu

~ Mailing Address: Department of Biology 1210 Biology-Psychology Bldg. #144 University of Maryland College Park, MD 20742

~ Complete/defend a dissertation proposal Summer Research Address: Mountain Lake Biological Station 240 Salt Pond Road Pembroke, VA 24136

~ <http://www.mlbs.virginia.edu/> Lab phone at MLBS is 540-626-5257 Fax at MLBS is 540-626-5229

~x “Peace and joy of having known them, with the sorrow of the loss less debilitating”

~ mdudash@umd.edu

~ Complete/defend the dissertation

## Graduate program training timeframe query 2

~ Sorry about the first request- the table did not stay formatted. Below is the request with the information in the table in the text below. Thanks again.

~ Dear Colleagues,

~ At Maryland we are reviewing our graduate training programs across the university. As part of this process we are being asked to compare our completion 'benchmarks' for PhD candidacy and PhD defense time frames with other peer institutions.

~ The BEES program has our students completing the majority of their course work at the end of year 2, taking a preliminary exam of general knowledge and defending a research proposal in year 3 as they advance to candidacy in year 3 (after successful completion of their prelim), and completing their degree by the end of year 6.

~x If you have a moment, could you please email me the year your students normally complete their coursework, advance to candidacy, and complete their PhD degrees at you schools?

~ Michele R. Dudash Associate Professor of Biology Director of the Graduate Program in Behavior, Ecology, Evolution and Systematics

~ Thanks in advance! Michele Dudash

~

~ Michele R. Dudash Associate Professor of Biology Director of the Graduate Program in Behavior, Ecology,

~ Dudash lab web page: <http://www.life.umd.edu/>

## Evolution and Systematics

Dudash lab web page: <http://www.life.umd.edu/biology/dudashlab/dudashlabpage.html> BEES program web page: <http://bees.umd.edu> Department of Biology, Room 3202 Biology Psychology Building University of Maryland College Park, MD 20742

<http://www.biology.umd.edu/> Office: 301-405-1642 Fax: 301-314-9358 Email: mdudash@umd.edu

Mailing Address: Department of Biology 1210 Biology-Psychology Bldg. #144 University of Maryland College Park, MD 20742

Summer Research Address: Mountain Lake Biological Station 240 Salt Pond Road Pembroke, VA 24136

<http://www.mlbs.virginia.edu/> Lab phone at MLBS is 540-626-5257 Fax at MLBS is 540-626-5229

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### HIV batch sequence queries

HIV evolution colleagues,

Many of us now require large numbers of HIV sequences with associated clinical and geographic annotations. The best place to get both sequence and annotations has long been the Los Alamos database (<http://www.hiv.lanl.gov/content/-sequence/HIV/mainpage.html>). Unfortunately, the query interface is rather cumbersome to use, and requires some basic understanding of database organization that perhaps not everyone has time to acquire.

I have implemented an alternative interface to the LANL HIV DB that allows the user to input a simple query based on the syntax of the NCBI Entrez query language (for example, "(C)[subtype] (gp120)[gene] (ZA BW)[country]") and retrieves annotated sequences (4019, in this case) in FASTA format direct to your browser window. You can find this tool at <http://fortinbras.us/hivq>. The site is completely free, collects no information from you, and uses no cookies.

If this is your bag, please give it a try, and send along comments to the address indicated at the site.

Best in the new year- Mark Jensen

maj@fortinbras.us

---

### Measuring selection coefficients answers

Here are the responses to my recent enquiry about how best to estimate the magnitude of selection coefficients from longitudinal data on allele frequency. My original query is given below.

Firstly, many thanks to all who responded.

I make no comment on the individual responses but would note that we intend to track the spread of insecticide resistance in large geographic regions; the presumed intense selection and (unfortunate) large mosquito population size makes me inclined to ignore the effects of drift.

\*\*\*\*\*original question\*\*\*\*\*

I want to estimate selection coefficients from a longitudinal series of diploid genotype frequencies. The gene in question encodes insecticide resistance so selection is relatively intense.

I intend to use max. likelihood to fit initial allele frequency, selection coefficient and dominance (i.e.  $P(0)$ ,  $s$  and  $h$  in standard terminology). Given these three parameters we can predict genotype frequencies at any given time point and use the multinomial distribution to get LL of obtaining the observed number of the three genotypes.

So I have two questions

(1) Is this a sensible way of doing it, or are there hidden pitfalls

and/or is there a better way?

(2) Has anyone done it before and published the method so we can cite

it? It seems like it should be a standard type of analysis but we

haven't been able to track a previous one down yet.

(3) Better still, is there a public access programme that we can

download? If not, we'll write our own and make it available.

Comment from myself (you always think of something straight after you've sent the message)

Why check fit to the three genotype frequencies? I'll track allele frequency so why not count the alleles in the three genotypes at each time point and then use the binomial to get LL from the predicted allele frequency. This also avoids having to assume the genotypes are in H-W which may be problematic if selection has already taken place (because, by definition, selection will cause deviations from HW)

A sensible procedure, but with one trap. Remember to condition on your observations, that is, update the initial allele frequency every time you make an observation, and evaluate  $s$  and  $h$  based on each interval of observation.

A. G. Clark used this procedure around 1980 in publications in *Genetics* and *Heredity*, as far as I remember.

/Freddy

Freddy Bugge Christiansen,  
Bioinformatics Research Center (BiRC),  
University of Aarhus,  
C.F. Møllers Alle, Bldg. 1110,  
DK-8000 Århus C.

Dear Ian Hastings,

Regarding your question on Evoldir, could you possibly post the most interesting answers?

I am working at IGC, Portugal in Evolutionary Genetics and I will have data on experimentally evolved populations for which I'll need the same kind of estimations.

Best regards

Ivo Chelo

Ivo M. Chelo, PhD.

Evolutionary Genetics

IGC Instituto Gulbenkian de Ciência

Lisbon, Portugal

Dear Ian,

I am currently working on a very similar issue, and I would be glad to know if you got some feedback on your question. I have a piece of code in R to estimate  $p(0)$  and the relative fitness of 3 possible genotypes using maximum likelihood, and it seems to work (although it is very experimental). The algorithm relies on the assumption that the population size is infinite (no drift), so that all stochasticity comes from sampling. Accounting both for drift and sampling requires much more complex stats, including random effects etc., but it is not impossible (in theory).

In case you are comfortable with R, let me know if you are interested in beta testing my code. Otherwise, I am also curious about existing software that can do the job.

Cheers,

Arnaud Le Rouzic

CEES

Dept. of Biology <[http://www.bio.uio.no/-index\\_en.html](http://www.bio.uio.no/-index_en.html)> <[http://www.bio.uio.no/index\\_en.html](http://www.bio.uio.no/index_en.html)>, P.O. Box 1066 Blindern

0316 Oslo

Norway

I've done it using Bayesian methods: see the attached manuscript. I can send you the BUGS code if you're interested. It should be easy to adapt to your problem.

Bob

[ms is O'Hara 2005 Proc. Roy Soc]

—

Bob O'Hara

Department of Mathematics and Statistics P.O. Box 68  
(Gustaf Hällströmin katu 2b)

FIN-00014 University of Helsinki

Finland

Hi Ian,

John Novembre just made me aware of your posting. You might want to take a look at: <http://www.genetics.org/cgi/content/full/179/1/497> If that method seems to apply to your situation I believe John has a program that he probably wouldn't mind sharing with you.

Best wishes,

Rasmus Nielsen

Ian – A major issue with which you will have to be concerned is sample size. Several years ago, Joel Kingsolver and several coauthors published a series of papers on estimates of selection.

— / —

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

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## Micro software TETRA

Dear Evoldir members

Does anyone know more about TETRA software? I ve read the Mol. Ecol Res article (TETRA: an improved program for population genetic analysis of allotetraploid microsatellite data Wan-Jin Liao, Bi-Ru Zhu, Yan-Fei Zeng, Da-Yong Zhang, Journal: Molecular Ecology Resources, ISSN: 1755-098X, Vol: 8, Issue: 6, Date: 2008, 1260)

TETRA is a improvement of a previous program TETRASAT by S. Markwith that only allowed 15 partial heterozygote samples in microsatellite data.

about it and became enthusiastic however the site indicated to download the software (<http://ecology.bnu.edu.cn/zhangdy/TETRA/TETRA.htm>) gave me a file that when executed looks like a suspicious file (with questions marks in the window, wrong words on buttons like CANCEL instead of CANCEL) I can not get other download. Does any one know about it, where to download or how to install it properly?

Thank you very much Helena

Helena Cotrim, PhD Jardim Botânico da Universidade de Lisboa, Museu Nacional de História Natural. Rua Escola Politecnica 58 1250-102 Lisboa Tel: +351-213 921 882 Fax: +351-213 921841

Helena Cotrim <hmcotrim@fc.ul.pt>

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## Microstellite technical question

Dear Evoldir members,

I have a very technical question about microsatellites motifs and how to read them correctly when sequenced. I explain: If I have a motif (AG)12 it is a dinucleotide so different alleles are at least two base pairs apart (say genotype 120 - 122)

If I have a motif (AGT)12 it is a triucleotide so different alleles are at least three base pairs apart (say genotype 120 - 123)

(AAGA) is a tetranucleotide ...

however, when motifs are of this kind:

(GT)15(AT)3(GT)20 Is it still a dinucleotide?

(CT)12TTCT(GT)18(GA)10 ant this?

(TC)3(TCTG)5 ??

Thanks for your help, it will be very much appreciated

Marco Suárez

evazquez@ecologia.unam.mx

evazquez@ecologia.unam.mx

---

## Ne-Nb query

Dear Evoldir,

I am seeking clarification regarding the correct calculation and interpretation of effective population size (Ne) versus effective number of breeders (Nb) within a closed aquaculture population, and I would be very grateful if anyone is able to assist me with this query.

In a closed population from a single spawning, if calculating Ne from actual data (msat parentage data) using:

$Ne = 4.Nef.Nem / (Nef + Nem)$ ; where  $Nef = (Nf.Kf - 1) / (Kf - 1 + Vkf/Kf)$ ,  $Nem = (Nm.Km - 1) / (Km - 1 + Vkm/Km)$ ,  $Nf =$  Number of female broodstock,  $Kf =$  mean number of progeny per female breeder,  $Vkf =$  variance in progeny number per female, and similarly for male breeders for  $Nm$ ,  $Km$  &  $Vkm$  (Lande & Barrowclough, 1987),

when is it necessary to standardise  $Km$  &  $Kf$  to 2, as per Hedrick et al. 1995 Conservation Biology 9:615-624? Is this only done to avoid potential biases of overestimating progeny variance when dealing with large, simulated datasets (as in this paper)? This paper assumes  $Km = Kf$ , but how is standardisation implemented when  $Km \neq Kf$  (e.g. when uneven broodstock sex ratios are used)? In the literature I have not yet been able to find any such examples of standardisation to 2 when dealing with actual datasets (i.e. not simulations), but if anyone can point me towards some examples it would be great.

Additionally, can anyone confirm, refute or clarify for me that in a closed population containing only one generation (e.g. an aquaculture population), the interpretation of Ne is the same as Nb? My understanding is that it is important to distinguish Nb from Ne in natural populations with overlapping generations, but in this instance when considering a single generation closed aquaculture population, is it incorrect to treat

the Nb of this population as Ne (or vice versa for that matter)?

If anybody is able to shed some light on these queries for me I would be extremely appreciative and grateful.

Thanks for your time.

Cheers,

Curtis Lind. [curtis.lind@jcu.edu.au](mailto:curtis.lind@jcu.edu.au)

Campus Office: Room 4326, Biosciences Complex

email: [aarssen@queensu.ca](mailto:aarssen@queensu.ca) web: <http://biology.queensu.ca/%7Eaarssen/> tel: 613-533-6133  
fax: 613-533-6617 fax: 613-533-6617

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## Nuclear and mitochondrial phylogeny answers

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### NewJournal IdeasEcolEvol

QUEEN'S UNIVERSITY AT KINGSTON ANNOUNCES A NEW JOURNAL:

IDEAS IN ECOLOGY AND EVOLUTION - a new open-access model dedicated to the rapid release of creativity in peer-review publication.

IEE publishes only short forum-style articles that develop new ideas or that involve original commentaries dealing with any topic in the broad domains of ecology and evolution. Articles may have an applied or fundamental focus, they may encompass any level of biological organization, and may involve any taxa, including humans. Articles may address specialized audiences within particular recognized sub-disciplines of ecology or evolution, or they may be broadly pitched to a more general audience, including articles that aim to inform fields of study outside of biology. All articles will share conceptual foundation in the core principles of ecology and evolution studied by biologists.

IEE provides a rapidly published repository for cutting-edge novel thinking and opinion-pieces - combining the speed of blog-style communication with formal peer-review credit. As a reliable source of inspiration, the journal aims to play a leading role in guiding the direction and progress of both future research and public awareness in ecology and evolution.

Please visit the newly launched website: <  
<http://library.queensu.ca/ojs/index.php/IEE>  
><http://library.queensu.ca/ojs/index.php/IEE>

Direct link to the opening editorial: <  
<http://library.queensu.ca/ojs/index.php/IEE/article/view/1949/2053>  
><http://library.queensu.ca/ojs/index.php/IEE/article/view/1949/2053>

Lonnie Aarssen Editor

Lonnie W. Aarssen Professor Dept. of Biology Queen's University Kingston, ON Canada, K7L 3N6

Dear Evoldir members, A few days ago I sent some questions regarding my technical problem on doing phylogenies with both mitochondrial and nuclear markers. I am posting all the answers that I received, since some people are facing the some problem. Thanks so much to all that dedicated some time to answer me!

Obs: For now, I am using the MrBayes approach of partitioning datasets and it is apparently working.

Sibelle Vilaça - [sibelletorres@gmail.com](mailto:sibelletorres@gmail.com)

2008/11/29 <[evoldir@evol.biology.mcmaster.ca](mailto:evoldir@evol.biology.mcmaster.ca)>

Dear Evoldir members,

I am working with mitochondrial and nuclear sequences (cytochrome b and the intron b-fibrinogen 5) to try to delineate population structure and I am trying to do a phylogenetic tree with these two markers. But I am experiencing some problems with how to make an input for some programs (I am currently working with MrBayes and PHYML). For each individual, I have sequences of both nuclear and mitochondrial markers.

Should I analyze these two markers as two datasets? How can I do it?

Should I concatenate them and consider as a single sequence and run a modeltest to determinate the best substitution model?

In a recent paper, Cabanne et al. (2008) concatenated the nuclear and mitochondrial sequences, and used the IUPAC ambiguity code for the polymorphic sites. Since I know the phase of my nuclear sequences, is there a way that I can use it in the phylogeny with the mitochondrial data?

Any comments would be of great help.

Sibelle  
- Sibelle Torres Vilaça Laboratório de Biodiversidade e

Evolução Molecular ICB-UFMG Av. Antonio Carlos, 6627 CP 486 - Sala L3-244 31270-010 Belo Horizonte, MG, Brasil Tel: +55 31 3409-2566

sibelletores@gmail.com

Dear Sibelle

You should analyse your data separately. The markers are not linked, thus will not be co-inherited. The true tree for these markers would be highly reticulated. You will also need to account for the fact that there are 2 alleles for the nuclear gene. If you have heterozygous individuals, then PHASE is a very good software to deal with this. Cheers Brent

Sibelle, Both the programs you mention allow you to partition a single data set and use different parameters for each partition in a combined analysis. That seems a good way for you to proceed here. Check the respective manuals for details, but it's not difficult. You can also analyze them together under a single model. Using a gamma distribution of site rates can cover much of the difference among partitions, and the results would not be useless. And this would allow you to use some fast likelihood programs like RAxML and GARLI. In MrBayes, at least, you can't run partitioned analyses using different basic models; only the parameters can vary among partitions. But all other models are special cases of GTR + I + G, so MrBayes will approximate whatever model is appropriate for each partition. Here, for comparison, is a MrBayes block that does partitioned analysis of a mitochondrial data set, by codon position.

```
begin mrbayes;
lset nst=6 rates=invgamma; charset 1position = 1-10858\3;
charset 2position = 2-10859\3; charset 3position = 3-10860\3
partition by_position 3:1position, 2position, 3position;
set partition = by_position; unlink shape=(all);
unlink revmat=(all); unlink pinvar=(all);
unlink statefreq=(all); showmodel; mcmc ngen=100000
samplefreq=1 printfreq=100 savebrlen=yes nchains=4;
quit; end;
```

Regards, John H.

Hi,

If the two genes independently show different models to use from model testing, it would be inappropriate to concatenate them as a single sequence. Good luck with your analysis.

David Liberles University of Wyoming

It depends on your data, but it's likely that you'll want to partition each gene by codon position and run a separate model on each. Below is an example from a dataset I have, with three genes (28S, EF1a, and wingless). It's possible, however, that making this many partitions will create problems with too many parameters. There's a program called Tracer ([tree.bio.ed.ac.uk/software/tracer/](http://tree.bio.ed.ac.uk/software/tracer/)) that will

help check if there are problems (based on MrBayes output). One nice thing about it is that you can do the run with it fully partitioned and look at how the parameters converged in the different partitions, so if they are similar (for example, if first and second positions are both extremely slow-evolving) you might want to combine them in order to reduce the parameters. The paper by Praz et al. 2008 (*Mol. Phyl. Evol.* 49(1):185-197) gives a good explanation of using it. Here's how partitioning is done for a MrBayes block:

```
BEGIN mrbayes;
charset 28S=1-1599 1600; charset EF101-2176
2428-2703 3017-3268; charset EF1nt101-2174\3 2428-
2701\3 3017-3266\3; charset EF1nt202-2175\3 2429-
2702\3 3018-3267\3;
```

— / —

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

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## Software BAPS upgrade available

BAPS software for population genetic analyses is upgraded to version 5.2. This version contains a number of bug fixes and new features (compared to generation 4.X) which are described in detail in the new paper:

Corander J, Marttinen P, Sirén J, Tang J. Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. *BMC Bioinformatics*, 2008, in press.

The BAPS website now finally contains a detailed manual describing the new features. The software is downloadable from: <http://web.abo.fi/fak/mmf//mate/jc/-software/baps.html> NB! If you have already used the version 5.0 or 5.1, the runtime component need not be re-installed when upgrading to v5.2. For details, see the software download pages.

Best, Jukka

bayesian@luukku.com

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## Software FigTree v1.2 released

FigTree v1.2 is now available for download from its web-

site:

<http://tree.bio.ed.ac.uk/software/figtree/> What is FigTree?

FigTree is designed as a graphical viewer of phylogenetic trees and as a program for producing publication-ready figures. It was written as a companion program to BEAST < <http://beast.bio.ed.ac.uk/> > but it can be used to generate trees from other programs as well.

Mac OS X, Linux/UNIX and Windows versions are available

FigTree requires a Java Virtual Machine to run. Many systems will already have this installed. It requires at least version 1.5 of Java to run (see README file for details). Mac OS X version 10.4 or better (Tiger and Leopard) will already have a suitable version of Java installed. I am sorry but FigTree simply doesn't run on older versions of Mac OS X.

Features Cross-platform graphical tree display. Three different tree styles: rectangular, polar and radial. Display of node heights, branch lengths, support values and other annotations. Node height range bars if available. Collapse of clades into triangles. Colouring of branches and tip labels. Colouring by annotation (for example, support values). Quick search for tip labels or partial tip labels. Printing and export as PDF and other graphics formats.

What is new in version 1.2?

Added a 'highlight' button which provides a block colouring for a clade.

Added a continuous colour gradient option to the 'Colour By' control in the Appearance panel. Use setup to activate (at present it disables the 'Width By' option).

Added a 'Name' annotation that can be used to edit taxon names. It can also be used to name clades (and these are displayed for collapsed clades).

Added a new drop down find panel that is activate by Find in the Edit menu or the find icon in the tool bar.

Font sizes and a few other options can now be set in the 'Preferences' box. These act as defaults for new windows.

Can be run in command line mode to convert tree files into graphics formats (useful for workflows and web-server applications).

Bug Fixes: Fixed a problem with branch annotations being applied to the wrong branches when the tree is re-rooted.

"Colour By" colours were reversed from those suggested in the Setup dialog.

The "Colour By" setup didn't work as expected if Auto-Range was turned off.

Made the control palette panels slightly more compact.

Andrew Rambaut Institute of Evolutionary Biology University of Edinburgh Ashworth Laboratories Edinburgh EH9 3JT EMAIL - [a.rambaut@ed.ac.uk](mailto:a.rambaut@ed.ac.uk) TEL - +44 131 6508624

[a.rambaut@ed.ac.uk](mailto:a.rambaut@ed.ac.uk) [a.rambaut@ed.ac.uk](mailto:a.rambaut@ed.ac.uk)

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## Systematics Research Fund

SYSTEMATIC RESEARCH FUND IS OPEN FOR APPLICATIONS

The SRF fund is jointly administer by the councils of the Linnean Society of London and the Systematics Association.

Applications of all nationalities are welcome, and need not be members of either the Systematics Association or the Linnean Society of London.

Typical activities supported include contributions to fieldwork expenditure, the purchase of scientific equipment or expertise (e.g. buying time on analytical equipment), specimen preparation (including the cost of temporary technical assistance), and contributions to publication costs. Projects of a more general or educational nature will also be considered, provided that they include a strong systematics component. Typical activities not supported include attendance at scientific meetings and contributions to student maintenance or tuition fees. The fund does not provide payments for Bench Fees. Projects already substantially funded by other bodies may be disadvantaged.

Successful projects are selected by a panel of six systematists who represent a wide range of conceptual interests and taxonomic groups. The value of any single award will not exceed £1500.

Applications may be submitted after 1 October but must be received before the 31 December of the same year, to be eligible for funds approved in the following calendar year. Decisions will be posted March-April of the year subsequent to submission.

Please read the "Guidelines for applying for SRF funding" before completing the online application form below. Please note that only applications made using the form below are acceptable.



Application forms are accessible at:

<http://www.linnean.org/index.php?id=3D331> or

<http://www.systass.org/awards/>-

T.A.Richards@exeter.ac.uk

T.A.Richards@exeter.ac.uk

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## Toad DNA extraction

Dear colleagues,

I'm following a protocol method for DNA extraction using phenol like I read in some papers in order to obtain DNA of the amphibian specie \*Bufo calamita\* (anuran) using samples in ethanol 80%. The problem with ethanol 80% is that I don't have so much DNA and I need to prove the primers with sufficient and good DNA before to use samples in ethanol. So I try to obtain DNA using a freezing animal but I have problems for obtained a purification DNA. I want to find an efficient protocol. Thanks.

- NEUS OROMÍ i FARRÚS

Departament de Producció Animal (Fauna Silvestre)  
Escola Superior d'Enginyeria Agrària Universitat de Lleida tel. 97370 2902/2888, 620743942 neusoromi@gmail.com/noromi@prodan.udl.cat >

Neus OromíFarrús <neusoromi@gmail.com>

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## UWyoming SummerRes Bioinformatics

Please forward to any students who might be interested:

Bioinformatics and Computational Molecular Biology Undergraduate Summer Research Program University of Wyoming The University of Wyoming is proud to offer summer research opportunities to external undergraduate students to engage in research in bioinformatics and computational molecular biology in Laramie. The summer research program will last from May 26, 2009 to August 7, 2009 and will include a stipend of \$3500 for the period.

The program in previous years included students from Amherst College, Oberlin College, Grinnell College, Ju-

niata College, SUNY-Buffalo, and CUNY.

Several labs that will host bioinformatics/computational molecular biology students include:

\* Alex Buerkle: Statistical genetics and models of adaptation and speciation

\* Mark Gomelsky: Statistical analysis of microarray data; microbiology

\* Jan Kubelka: Protein folding

\* David Liberles: Comparative genomics and molecular evolution

\* Anne Sylvester: Comparative genomics of maize

\* Dan Wall: Genetics of bacterial motility

\* Naomi Ward: Metagenomics and Microbial Genomics

\* Cynthia Weing: Environmental Genetics and Adaptation in Plants

To apply, send a resume and statement of research interests to liberles@uwyo.edu, arrange to have 2 letters of recommendation sent directly by the letter writer to liberles@uwyo.edu, and arrange to have an official transcript sent to:

David Liberles Department of Molecular Biology Dept. 3944 University of Wyoming Laramie, WY 82071

Applications will be evaluated on a rolling basis starting on February 2, 2009.

<http://www.wyomingbioinformatics.org/-SummerSchool/> "David A. Liberles"  
<liberles@uwyo.edu>

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## Weighting by subst rate

Dearall,

I would like to ask if there is a way (software)to assign different weights to each locus based on substitution rates.

Thanks in advance,

Daniel

Daniel Toffoli Ribeiro Laboratório de Genética de Populações e Evolução Universidade Federal de São Carlos <http://www.ufscar.br/~evolucao/> tel: ++55 (16)33518787

Daniel Toffoli Ribeiro <toffolidan@yahoo.com.br>

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## PostDocs

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### AlbertEinstein EvolutionarySystemsBiol

Post Doctoral Research Fellow in Evolutionary Systems Biology

Department of Systems & Computational Biology,  
Albert Einstein College of Medicine

Postdoctoral research position is available in Evolutionary Computational/Systems Biology. The program's focus is the study of gene networks as they pertain to complex traits and their evolution.

Applicants could have skills in any of several areas of evolutionary, computational or systems biology. We encourage applicants from any of these and related

fields. We particularly encourage applicants interested in model organisms and with strong background in theoretical and computational biology.

The position is available immediately and for the duration of 1-3 years; Salary (starting at \$37K, plus benefits) will be commensurate with experience. EOE

If interested, please send your curriculum vitae, list of publications, research proposal, and arrange for at least three letters of reference sent to:

Prof. Aviv Bergman Department of Systems & Computational Biology Albert Einstein College of Medicine Jack and Pearl Resnick Campus 1300 Morris Park Avenue Bronx, NY 10461

E-mail: SysBio@aecom.yu.edu (Subject: Post Doctoral Fellowship)

Many thanks, Vanessa

Vanessa Castellina Administrative Coordinator to Aviv

Bergman, Ph.D., Founding Professor and University Chairman of the Department of Systems & Computational Biology

Albert Einstein College of Medicine of Yeshiva University Price Center, Room 153 1300 Morris Park Avenue Bronx, NY 10461 T: 718-678-1115 F: 718-678-1018 Email: [vcastell@acom.yu.edu](mailto:vcastell@acom.yu.edu)

Vanessa Castellina <[vcastell@acom.yu.edu](mailto:vcastell@acom.yu.edu)>

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## ArizonaStateU EvolutionaryGenetics

A postdoctoral position is available for research in evolutionary genetics at Arizona State University (ASU). The funding is available for two years, with good possibility of a year extension. The successful applicant is expected to (i) generate sequencing, SNP, and/or microsatellite data from malarial parasites and (ii) perform phylogeography and evolutionary genetic analyses using software commonly available. Overall, the project involves the analysis of malaria parasite genomic data for inferring parasite demographic structure and evolutionary events involving the evolution of adaptive genetic variation. These problems will be addressed in the broad context of adaptive multi-locus evolutionary dynamics under temporally and spatially heterogeneous selection. He or she in this position will collaborate closely with both Dr. Ananias Escalante (evolutionary genetics of malaria parasites) and Dr. Yuseob Kim (theoretical population genetics) of the School of Life Sciences in ASU. The applicant should be proficient in evolutionary genetics and be able to perform statistical data analysis of DNA sequence/microsatellite variation. This position offers the opportunity of interacting with a multidisciplinary group of professionals at ASU, U. of Washington, The Pennsylvania State University, and malaria endemic countries. Knowledge in malaria biology or infectious diseases is not required. Candidates must have earned a Ph.D. in biology or a related field at the time of appointment.

To apply send a CV that includes a list of 3-4 professional references and contact information, a personal statement, and one or two selected publications by email to [Ananias.Escalante@asu.edu](mailto:Ananias.Escalante@asu.edu) or by mail to: Ananias Escalante, School of Life Sciences, Arizona State University, PO Box 874501, Tempe, AZ 85287-4501. Informal inquiry is encour-

aged. The initial deadline for receipt of applications is February 1, 2009, with applications reviewed weekly thereafter until the search is closed. Arizona State University is an affirmative action, equal opportunity employer committed to excellence through diversity.

Ananias. A. Escalante, PhD Associate Professor School of Life Sciences Arizona State University PO Box 874501, Tempe AZ 85287-4501 E-mail: [Ananias.Escalante@asu.edu](mailto:Ananias.Escalante@asu.edu) Phone: (480) 965-3739 Fax: (480) 965-6899 <http://sols.asu.edu/faculty/aescalante.php> Ananias Escalante <[Ananias.Escalante@asu.edu](mailto:Ananias.Escalante@asu.edu)>

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## Cairns 2 PlantSystematics

CSIRO-JCU postdoctoral fellowships at the Australian Tropical Herbarium

Two exciting postdoctoral (3-year) fellowships in plant systematics (broadly interpreted) are available at the Australian Tropical Herbarium (ATH), Cairns, Australia ([www.ath.org.au](http://www.ath.org.au)).

The Australian Tropical Herbarium (ATH) is a joint venture partnership researching tropical Australian plant and fungal biodiversity and evolution. We seek two outstanding postdoctoral researchers to contribute to a dynamic research team. You will employ contemporary, and where appropriate develop innovative methods in the study of the origins, radiations and relationships of tropical plant and/or fungal groups of Australasian relevance. Your expertise in the collection and analysis of morphological and/or genetic data will lead to high impact research outcomes. Specific projects to be undertaken will be negotiated with the successful applicants and will reflect both the applicants expertise and interests, and the ATHs research themes.

The ATH offers an unrivalled herbarium and spirit specimen collection of Australian tropical plants, full systematics research and field facilities including a new state of the art molecular biology laboratory. These positions are offered jointly by two of the partners in the ATH joint venture: the CSIRO and JCU. The CSIRO (Commonwealth Science and Industrial Research Organisation, [www.csiro.au](http://www.csiro.au)) is Australia's national science agency and one of the largest and most diverse research agencies in the world. James Cook University (JCU: [www.jcu.edu.au](http://www.jcu.edu.au)) is ranked among the worlds top 50 (and Australias top 2) most highly cited research institutions for Environment/Ecology (ESI Database,

Thomson Reuters).

Situated on James Cook University's Cairns campus, ATH staff enjoy an enviable tropical lifestyle in a thriving modern city with an international airport, and ready access to the natural laboratories of the World Heritage-listed Wet Tropics rainforests, tropical savannas and the Great Barrier Reef.

Enquiries to: Professor Darren Crayn, telephone +61 (0)7 4042 1859, e-mail [darren.crayn@jcu.edu.au](mailto:darren.crayn@jcu.edu.au) Employment Type: Appointments will be full-time for a fixed-term to 27 January 2012 subject to a probationary period. Salary: Academic Level A - AU\$59,478 - \$63,733 per annum. Commencing salary will be in accordance with qualifications and experience. Benefits include generous employer superannuation contribution and attractive options for salary packaging. Applications close on 16 January 2009. For more information including how to apply, visit <http://cms.jcu.edu.au/jobs/research/JCUPRD.041973> Darren Crayn <[darren.crayn@jcu.edu.au](mailto:darren.crayn@jcu.edu.au)>

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## DublinCityU MammalianProteinEvolution

Hi Folks,

I am looking for candidates to apply for a Post Doctoral funding scheme running in Ireland.

The scheme will fund the successful candidate for 3 years in the area of mammalian protein evolution.

If you are interested please contact me directly: [mary.oconnell@dcu.ie](mailto:mary.oconnell@dcu.ie)

Best wishes

Mary

– Dr Mary J. O'Connell, Bioinformatics and Molecular Evolution Group leader, School of Biotechnology, Dublin City University, Glasnevin, Dublin 9.

Phone: +353 1 700 5112 Fax: +353 1 700 5412 Email: [mary.oconnell@dcu.ie](mailto:mary.oconnell@dcu.ie)

[mary.oconnell@dcu.ie](mailto:mary.oconnell@dcu.ie)

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## DukeU MadagascarPhylogeography

Postdoctoral Position:

We seek a postdoctoral associate to oversee and coordinate all aspects of geospatial analysis relating to the investigation of speciation patterns and distribution of vertebrate species in Madagascar. The research is part of an NSF-funded project in collaboration with the Field Museum of Natural History and the University of Antananarivo, Madagascar. Phylogenetic and biogeographic analysis of Malagasy vertebrates, each with unique life-history and dispersal characteristics, are being conducted to identify areas of high endemism potentially associated with underlying geological features, and also to test for the role that rivers have played in generating patterns of vertebrate diversity and distribution. The postdoctoral associate will focus on Geographical Information System (GIS) analyses which will serve as the integrative platform for synthesizing specimen occurrence data with phylogenetic analyses.

The Yoder Lab is located in Duke's Biological Sciences Building where we are a member of the highly dynamic and interactive Department of Biology. All lab projects aim to investigate the geological and geographic forces that drive patterns of vertebrate distribution and endemism in Madagascar. Madagascar has been designated as one of the most critical geographic priorities for conservation action, retaining less than 10% of the natural habitats that existed before human colonization. Field inventory activities focus on the herpetofauna and mammals occurring at the survey sites. The lab also has a significant focus on capacity-building through the education and training of both American and Malagasy students.

Qualifications:

The successful applicant will have completed their Ph.D. and is expected to have expertise in ecological niche modeling (ENM), using some or all of the following GIS tools: OpenModeller, BIOCLIM, GARP, MODIS, Maxent, etc. The successful candidate will be highly organized, mature, enthusiastic, and motivated.

Conditions:

This position is funded for two years. Salary is competitive, and the position will carry full benefits. The position will be given to the most qualified applicant, though a start date of February 1, 2009 or sooner is

highly desired.

To Apply:

Send current CV, publications, and list of references to:

Anne D. Yoder, Professor Departments of Biology & BAA Duke University, Box 90338 Durham, NC 27708 ph: 919-660-7275 fax: 919-660-2793 anne.yoder@duke.edu <http://www.biology.duke.edu/-yoderlab/> Director, Duke Lemur Center 919-489-3364, ex. 223 <http://lemur.duke.edu/> Anne Yoder <anne.yoder@duke.edu>

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## DukeU PopulationGenomics

The Noor laboratory at Duke University seeks post-doctoral applicants to help with one or both of two projects. The first project is a collaborative, NIH-funded research project to help examine the nature of the association of fine-scale recombination rate and nucleotide diversity, divergence, and codon bias in a *Drosophila* species. Related papers listed below. Efforts will include computational analyses of multiple new full-genome-resequenced and fine-scale linkage maps as well as some molecular lab benchwork. This funding is collaborative with Rich Kliman and Laurence Loewe. Basic computational skills required, preferably specifically on analyses of DNA sequences.

The second project is to examine patterns of sex chromosome evolution and sexual selection in an unrelated species for which a new genome sequence assembly is being obtained. This species has homomorphic sex chromosomes, and the sex-determining region is associated with an active mobile element. Again, basic computational biology skills and basic molecular lab skills required.

If interested in one or both projects, please contact Mohamed Noor (noor@duke.edu). DO NOT send attachments- just send statement of intent and experience in text of e-mail. Anticipated timing is spring/summer of 2009, but this is potentially negotiable.

References related to Project 1: Kulathinal, R. J., S. M. Bennett, C. L. Fitzpatrick, and M. A. F. Noor. 2008. Fine-scale mapping of recombination rate in *Drosophila* refines its correlation to diversity and divergence. *Proceedings of the National Academy of Sciences USA*, 105: 10051-10056. doi:10.1073/pnas.0801848105

Noor, M. A. F. 2008. Connecting recombination, nu-

cleotide diversity, and species divergence in *Drosophila*. *Fly*, 2: 255-256

Noor, M. A. F. 2008. Mutagenesis from meiotic recombination is not a primary driver of sequence divergence between *Saccharomyces* species. *Molecular Biology and Evolution*, 25: 2439-2444. doi:10.1093/molbev/msn186

Cirulli, E. T., R. M. Kliman, and M. A. F. Noor. 2007. Fine-scale crossover rate heterogeneity in *Drosophila pseudoobscura*. *Journal of Molecular Evolution*, 64: 129-135

Mohamed A. F. Noor noor@duke.edu Professor & Associate Chair Tel: 919-613-8156 Biology Department Lab: 919-613-8193 Box 90338 FAX: 919-660-7293 Duke University Durham, NC 27708 USA <http://www.biology.duke.edu/noorlab/> noor@duke.edu noor@duke.edu

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## Edinburgh ComputationalBiology

The IGMM (Institute of Genetics and Molecular Medicine, Edinburgh, UK) has openings for researchers at an early stage of their career who wish to develop an independent research programme within a world class research environment. We welcome interest from individuals with research interests in any of the IGMM priority areas including computational biology.

Successful candidates will have a PhD, an established track record of research achievement and publication and will have demonstrated the potential to obtain grant funding from competitive sources. You will be provided with excellent research and infrastructure facilities. You will be encouraged to secure independent funding in the form of a personal fellowship or career development fellowship, although pump-priming support of up to 2-3 years will be available to exceptional candidates. Salary will be in the range of £29,704-£35,469 (UE07 scale) dependent on qualifications and experience. There will be running expenses of up to £12,000 per annum.

Full details at: [http://www.hgu.mrc.ac.uk/StaffInf/-Jobs/igmm\\_outstanding\\_scientists\\_08.html](http://www.hgu.mrc.ac.uk/StaffInf/-Jobs/igmm_outstanding_scientists_08.html) - Dr Colin A. M. Semple Head of Bioinformatics MRC Human Genetics Unit Institute of Genetics and Molecular Medicine Edinburgh EH4 2XU, UK Tel: +44 (0)131 332 2471 x4034 Fax: +44 (0)131 467 8456 Email: Colin.Semple@hgu.mrc.ac.uk Web: <http://www.hgu.mrc.ac.uk/Users/Colin.Semple/> col-

ins@hgu.mrc.ac.uk colins@hgu.mrc.ac.uk

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## EmoryU 2 Drosophila Speciation

Two Post-Doc Positions in Speciation Gene and Meiotic Drive in *Drosophila* in Emory University

Two post-doc positions funded by NIH (pending final approval) are available at April 1, 2009 in the lab of Yun Tao at Emory University on mapping, cloning and molecularly characterizing genes involved in meiotic drive and speciation in *Drosophila simulans*. The start date is flexible from January to middle summer, 2009. The initial appointment will be one year but extendable up to four years. The goals of the project are (1) to characterize two meiotic drive systems (Winters and Durham) in *D. simulans*; (2) to characterize the speciation genes between *D. simulans* and *D. mauritiana*; (3) to trace the molecular evolution of the genes involved in meiotic drive and speciation; and (4) finally to test the theory that meiotic drive is a major mechanism leading to speciation.

Some background of the project can be found in the three publications (Tao et al. 2001 PNAS 98: 13183-8; Tao et al. 2007a PLoS Biology 5 (11): e292; Tao et al. 2007b PLoS Biology 5(11); e293. )

Candidates for these two positions should have demonstrated expertise in one or more of the following areas: *Drosophila* genetics, standard molecular biology lab techniques, small RNA, bioinformatics, molecular evolution, evolutionary genetics (experimental or theory). Candidates are expected to be highly motivated (i.e., pursuing an academic career), independent, eager to learn new skills and explore new intellectual territories. Successful applicants are encouraged to develop new and independent research projects in the broad field of evolutionary genetics, particularly in genetic conflicts and speciation.

Interested applicants should contact Yun Tao (y tao3@emory.edu; 404-727-0815) with a cover letter, CV, a one-page statement of career development (i.e., research interests), and the names of three or more references.

Yun Tao Assistant Professor Department of Biology  
Emory University 1510 Clifton Rd. Atlanta, GA 30322  
y tao3@emory.edu 404-727-0815

Yun Tao <y tao3@emory.edu>

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## EmoryU EvolutionOfVision

Postdoctoral Positions at Emory University

The Long-term goal of our research is to elucidate 1) the molecular basis of spectral tuning of visual pigments and 2) the evolutionary mechanisms of dim-light and color vision of organisms to various light environments. To solve these central unanswered questions in phototransduction and evolutionary genetics simultaneously, we perform gene cloning and mutagenesis analyses, cell culture-based functional assays, evolutionary genetic and synthetic biological analyses, and quantum chemical analyses for various vertebrate species.

Selected References:

Shi, Y. and Yokoyama, S. (2003) Molecular analysis of the evolutionary significance of ultraviolet vision in vertebrates. PNAS 100: 8308-8313.

Yokoyama, S., Tada, T., Zhang, H. and Britt, L. (2008) Elucidation of phenotypic adaptations: molecular analyses of dim-light vision proteins in vertebrates. PNAS 105: 13480-13485. Altun, A., Yokoyama, S. and Morokuma, K. (2008) Spectral tuning in visual pigments: An ONIOM(QM:MM) study on bovine rhodopsin and its mutants. J. Phys. Chem. B 112: 6814-6827.

Yokoyama, S. (2008) Evolution of dim-light and color vision pigments.

Annu. Rev. Genomics Hum. Genet. 9: 259-282.

Currently, we are looking for recent graduates who are well versed in experimental molecular biology/genetics and are interested in evolution. If you are interested, please send CV to Shozo Yokoyama (Email:syokoya

Shozo Yokoyama, Ph. D. Asa G. Candler Professor of Biology Department of Biology Emory University 1510 Clifton Road Rollins Research Center Atlanta, GA 30322 Tel:404-727-5379 FAX:404-727-2880 Email:syokoya@emory.edu

Shozo Yokoyama <syokoya@emory.edu>

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## EmoryU Host-parasite interactions

Post-Doctoral Position, Host-parasite interactions  
Emory University, Atlanta, GA USA  
Laboratories of Drs. Jacobus de Roode and Nicole Gerardo

A postdoctoral position is available for research on the coevolutionary interactions between monarch butterflies, their parasites and their larval host plants. The project would focus on identifying the molecular basis of host resistance to parasitism, and involve a combination of functional genomics, experiments and field-work. The postdoc would assemble sequences derived from 454 sequencing of cDNA, annotate genes using existing genome databases of insects and protozoan parasites, and implement statistical analyses to compare the transcriptome of infected and uninfected individuals. He/she would also carry out experiments to study the expression of candidate resistance genes in infected and uninfected monarchs, and in monarchs reared on different host plant species. Additional projects may focus on the population genetics and co-phylogenies of monarchs and their parasites in natural populations.

This is a joint project between the laboratories of Jacobus de Roode and Nicole Gerardo. Both labs combine field work, experimentation and molecular genetics to study host-parasite coevolution, and address questions related to virulence evolution, mutualism, and the molecular evolution of host resistance. The labs are part of Emory's Population Biology, Ecology and Evolution program, which has a strong focus on host-parasite interactions and molecular genetics. For more information on the labs and program, see: <http://www.biology.emory.edu/research/deRoode/> <http://www.biology.emory.edu/research/Gerardo/> [www.biomed.emory.edu/PROGRAM\\_SITES/PBEE/](http://www.biomed.emory.edu/PROGRAM_SITES/PBEE/) Candidates must have a strong background in bioinformatics, with emphasis in functional genomics and gene annotation, and should have an interest in evolutionary biology and host-parasite interactions. The postdoc is also expected to take part in the training of graduate and undergraduate students.

The position will be available for 1 year initially, with the possibility of a 1-2 year extension. Salary will be based on experience and will follow NIH guidelines; benefits will be provided. Applications should be sent by 20 January 2009 (to [jderood@emory.edu](mailto:jderood@emory.edu)), and be accompanied by a short research statement, a CV and the names of 3 referees. The postdoc would ideally start no later than April 2009.

For more information, please contact Jacobus de Roode on [jderood@emory.edu](mailto:jderood@emory.edu) or 404 727 2340.

Jaap de Roode PhD Assistant Professor  
Department of Biology  
Emory University  
1510 Clifton Road  
Atlanta Georgia 30322  
USA  
Office: 404 727 2340  
Cell:

+1 404 200 5540  
E-mail: [jaapderoode@hotmail.com](mailto:jaapderoode@hotmail.com)  
<http://www.biology.emory.edu/research/deRoode/jaapderoode@hotmail.com>

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## EmoryU HostParasiteInteractions

Post-Doctoral Position, Host-parasite interactions  
Emory University, Atlanta, GA USA

Laboratories of Drs. Jacobus de Roode and Nicole Gerardo

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<http://www.biology.emory.edu/research/deRoode/>  
<http://www.biology.emory.edu/research/Gerardo/>  
[www.biomed.emory.edu/PROGRAM\\_SITES/PBEE/](http://www.biomed.emory.edu/PROGRAM_SITES/PBEE/)  
Candidates must have a strong background in bioinformatics, with emphasis in functional genomics and gene annotation, and should have an interest in evolutionary biology and host-parasite interactions. The postdoc is also expected to take part in the training of graduate and undergraduate students.

The position will be available for 1 year initially, with

the possibility of a 1-2 year extension. Salary will be based on experience and will follow NIH guidelines; benefits will be provided. Applications should be sent by 20 January 2009 (to [jderood@emory.edu](mailto:jderood@emory.edu)), and be accompanied by a short research statement, a CV and the names of 3 referees. The postdoc would ideally start no later than April 2009.

For more information, please contact Jacobus de Roode on [jderood@emory.edu](mailto:jderood@emory.edu) or 404 727 2340.

[jderood@emory.edu](mailto:jderood@emory.edu) [jderood@emory.edu](mailto:jderood@emory.edu)

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## FloridaStateU RodentPhylogenetics

Post-doctoral position in rodent phylogenetics and diversification.

A NSF-funded position is available beginning spring or summer 2009 in the lab of Scott Stepan at Florida State University on molecular and morphological diversification of the muroid rodents. Position will initially be for one year with possible extension of up to three additional years. The project will involve using multiple nuclear genes to infer the phylogeny of the most diverse clade of mammals, the rodent superfamily Muroidea, macroevolutionary patterns of diversification in morphology, and comparative quantitative genetics. Successful applicants will have opportunities to develop independent research questions involving systematics, molecular evolution, biogeography, macroevolutionary trends, and adaptive radiations.

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

Post-doc applicants should have a Ph.D. in evolution, systematics, or related field and be proficient in PCR, DNA sequencing, and phylogenetic analysis. Subsequent years will include 3D digitization of museum specimens and possibly computational projects. Salary will start at \$38,000 and start date is negotiable. Review of applications will begin Jan. 10 and continue until the position is filled. Additional information on the Stepan Lab is available from <http://bio.fsu.edu/~steppan/>, on the Ecology and Evolution group at <http://www.bio.fsu.edu/ee/index.html>, and the Department (for graduate application, etc...) at <http://www.bio.fsu.edu/>. Applicants should submit a cover letter, CV, short statement of research interests,

and the names of three or more references.

For more information, contact, Dr. Scott Stepan; e-mail: [stepan@bio.fsu.edu](mailto:stepan@bio.fsu.edu); phone: (850) 644-6536; fax: (850) 644-9829.

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

[stepan@bio.fsu.edu](mailto:stepan@bio.fsu.edu) phone: 850.644.6536 fax: 850.644.9829

<http://bio.fsu.edu/~steppan> <http://www.bio.fsu.edu/faculty-steppan.php> Ecology and Evolution Group at FSU: <http://www.bio.fsu.edu/ee/index.html> [stepan@bio.fsu.edu](mailto:stepan@bio.fsu.edu) [stepan@bio.fsu.edu](mailto:stepan@bio.fsu.edu)

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## Italy AnimalConservationGenetics

Title: Post doc in Animal Conservation Genetics

Research Centre: The research carried out at the Environment Department of Edmund Mach Foundation encompasses both ecological and molecular studies. It focuses on the functional integrity and biodiversity of aquatic (mainly plankton, diatoms and salmonid fishes) and land taxa (mainly vertebrate fauna and their parasites, higher plants including annual species and forest trees) that are subject to anthropic pressure and global climate changes. The ACE-SAP (Alpine Ecosystems in a Changing Environment: Biodiversity Sensitivity and Adaptive Potential) Major Proposal is a collaborative project funded by the Autonomous Province of Trento involving three regional institutions (Edmund Mach Foundation, Natural History Museum of Trento, Civic Museum of Rovereto) and one external partner (University of Davis, California).

Description: We are seeking a highly motivated and independent individual to carry out a research project on the conservation genetics of *Salmo carpio*. The successful candidate will be responsible of assessing the genetic diversity of *Salmo carpio* populations. Both neutral and potentially adaptive markers will be employed. Population genetics, demographic and ecological studies will be carried out to provide conservation guidelines for this species. The position, initially granted for a time span of 23 months, may be renewed and upgraded depending on the successful completion of the project.

IT knowledge: Standard packages (e.g. Microsoft Office, web browser); DNA editing software; population genetics/evolutionary specific software (e.g. Arlequin,



Structure, PAUP\*, MEGA).

More information and application:

[http://www.fondazioneedmundmach.it/-sperimentazione\\_context2.jsp?ID\\_LINK=3139&area=6](http://www.fondazioneedmundmach.it/-sperimentazione_context2.jsp?ID_LINK=3139&area=6)

Deadline for application: 31st December 2008

Daniele Barbacovi Fondazione Edmund Mach Research Centre - Human Resources Office Via Mach 1, 38010 S. Michele all'Adige (TN) - Italy Phone +39 0461 615542 - Fax + 39 0461 650956 Skype daniele.barbacovi\_crfem <http://www.fondazioneedmundmach.eu>

[daniele.barbacovi@iasma.it](mailto:daniele.barbacovi@iasma.it) [daniele.barbacovi@iasma.it](mailto:daniele.barbacovi@iasma.it)

Phylip, Mega), and analysis of nucleotide variability (DNAsp, Arlequin); The capacity to use Perl script and Shell Linux o VBA macro will be considered as a plus.

More information and application:

[http://www.fondazioneedmundmach.it/-sperimentazione\\_context2.jsp?ID\\_LINK=3141&area=6](http://www.fondazioneedmundmach.it/-sperimentazione_context2.jsp?ID_LINK=3141&area=6)

Deadline for application: 31st December 2008

Daniele Barbacovi Fondazione Edmund Mach Research Centre - Human Resources Office Via Mach 1, 38010 S. Michele all'Adige (TN) - Italy Phone +39 0461 615542 - Fax + 39 0461 650956 Skype daniele.barbacovi\_crfem <http://www.fondazioneedmundmach.eu> [risorseu-manecentricerca@iasma.it](mailto:risorseu-manecentricerca@iasma.it)

## Italy Microbial Adaptation

Title: Post doc in Microbial Molecular Ecology

Research Centre: The research carried out at the Environment Department of Edmund Mach Foundation encompasses both ecological and molecular studies. It focuses on the functional integrity and biodiversity of aquatic (mainly plankton, diatoms and salmonid fishes) and land taxa (mainly vertebrate fauna and their parasites, higher plants including annual species and forest trees) that are subject to anthropic pressure and global climate changes. The ACE-SAP (Alpine Ecosystems in a Changing Environment: Biodiversity Sensitivity and Adaptive Potential) Major Proposal is a collaborative project funded by the Autonomous Province of Trento involving three regional institutions (Edmund Mach Foundation, Natural History Museum of Trento, Civic Museum of Rovereto) and one external partner (University of Davis, California).

Description: We are seeking a highly motivated and independent individual to carry out a research project within the frame of the major proposal ACE-SAP which requires culturing under controlled conditions and the genetic characterisation of cyanobacteria, aimed towards the study of adaptive traits related to cellular floating. The successful candidate will be responsible of sampling, selection of suitable molecular markers for selected cyanobacterial species. The position, initially granted for a time span of thirty months, may be renewed and upgraded depending on the successful completion of the project.

IT knowledge: Software for processing and aligning nucleotide sequences (Staden Package, Phred, Bioedit, ClustalW, T-Coffee), for phylogenetic analysis (Paup,

## Italy Plant Conservation Genetics

Title: Post doc in Plant Conservation Genetics / Phylogeny

Research Centre: The research carried out at the Environment Department of Edmund Mach Foundation encompasses both ecological and molecular studies. It focuses on the functional integrity and biodiversity of aquatic (mainly plankton, diatoms and salmonid fishes) and land taxa (mainly vertebrate fauna and their parasites, higher plants including annual species and forest trees) that are subject to anthropic pressure and global climate changes. The ACE-SAP (Alpine Ecosystems in a Changing Environment: Biodiversity Sensitivity and Adaptive Potential) Major Proposal is a collaborative project funded by the Autonomous Province of Trento involving three regional institutions (Edmund Mach Foundation, Natural History Museum of Trento, Civic Museum of Rovereto) and one external partner (University of Davis, California).

Description: We are seeking a highly motivated and independent individual to carry out a research project on the phylogeny/conservation genetics of selected, endemic taxa. The successful candidate will be responsible of sampling, selection of suitable molecular markers and phylogenetic reconstruction for three angiosperm taxa with uncertain taxonomy (within the *Erysimum*, *Brassica* and *Aquilegia* genera). Upon taxonomic status confirmation, population genetics, demographic and ecological studies will be carried out to provide conservation guidelines for the most interesting species. The position, initially granted for a time span of three years, may be renewed and upgraded depending on the successful completion of the project.

IT knowledge: Software for sequence processing, alignment and editing (e.g. Staden Package, Phred, Bioedit, ClustalW). Programs for population genetics/evolutionary analyses (e.g. Arlequin, Structure, Phylip). The ability to write/use Perl, Linux Shell scripts or VBA macros and the use of software for phylogenetic analyses (Paup, Phylip, Mega) are considered as optional qualifications in the selection.

More information and application:  
[http://www.fondazioneedmundmach.it/sperimentazione.context2.jsp?ID\\_LINK=3140&area=6](http://www.fondazioneedmundmach.it/sperimentazione.context2.jsp?ID_LINK=3140&area=6)  
 Deadline for application: 31st December 2008

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 daniele.barbacovi@iasma.it daniele.barbacovi@iasma.it

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IT Knowledge: Software for sequence processing, alignment and editing (e.g. Staden Package, Phred, Bioedit, ClustalW, T-Coffee). Programs for population genetics/evolutionary analyses (e.g. Arlequin, Structure, Phylip). The ability to write/use Perl, Linux Shell scripts or VBA macros and the use of software for phylogenetic analyses (Paup, Phylip, Mega) are considered as optional qualifications in the selection.

More information and application:  
[http://www.fondazioneedmundmach.it/sperimentazione.context2.jsp?ID\\_LINK=3142&area=6](http://www.fondazioneedmundmach.it/sperimentazione.context2.jsp?ID_LINK=3142&area=6)  
 Deadline for application: 31st December 2008

Daniele Barbacovi Fondazione Edmund Mach Research Centre - Human Resources Office Via Mach 1, 38010 S. Michele all'Adige (TN) - Italy Phone +39 0461 615542 - Fax + 39 0461 650956 Skype daniele.barbacovi\_crfem <http://www.fondazioneedmundmach.eu> risorseu-manecentroricerca@iasma.it

## Italy PlantMolecularBiodiversity

Title: Post doc in Plant Molecular Biodiversity

Research Centre: The research carried out at the Environment Department of Edmund Mach Foundation encompasses both ecological and molecular studies. It focuses on the functional integrity and biodiversity of aquatic (mainly plankton, diatoms and salmonid fishes) and land taxa (mainly vertebrate fauna and their parasites, higher plants including annual species and forest trees) that are subject to anthropic pressure and global climate changes. The ACE-SAP (Alpine Ecosystems in a Changing Environment: Biodiversity Sensitivity and Adaptive Potential) Major Proposal is a collaborative project funded by the Autonomous Province of Trento involving three regional institutions (Edmund Mach Foundation, Natural History Museum of Trento, Civic Museum of Rovereto) and one external partner (University of Davis, California).

Description: We are seeking a highly motivated and independent individual to carry out a research project on adaptation of alpine plant species to abiotic stress. The successful candidate will be responsible of sampling and isolation of candidate genes from natural populations of Brassicaceae species aimed at the dissection of the molecular mechanisms underlying adptation to high altitude habitats. The position, initially granted for a time span of three years, may be renewed and upgraded

## LavalU CapelinPopulationGenetics

An 18 month postdoctoral position will be available starting in spring, 2009 in the laboratories of Julian Dodson and Julie Turgeon, at Laval University in Québec City. A postdoctoral fellow very familiar with AFLP development and analysis is needed to conduct a study of the population structure of a small pelagic forage fish, the capelin (*Mallotus villosus*), in the estuary and Gulf of St. Lawrence. We will also be looking for evidence of introgression among historical lineages (see Dodson et al. 2007. *Trans-Arctic dispersals and the evolution of a circumpolar marine fish species complex, the capelin*. *Molecular Ecology* 16: 5030-5043). This project is part of the scientific program of CHONe, the Canadian Healthy Oceans Network (NSERC, Canada). Please send a letter of motivation, a CV and three letters of reference to Professor Julian Dodson, Département de biologie, Pavillon Vachon, local 3044, 1045 Ave. de la Médecine, Université Laval, Québec, Qc G1V 0A6 or to [julian.dodson@bio.ulaval.ca](mailto:julian.dodson@bio.ulaval.ca) <<mailto:julian.dodson@bio.ulaval.ca>> .

Annual salary = 40K (or generous supplement and extension of fellowship to two years for scholarship holders)

Prof. Julian J. Dodson, Département de biologie, Pavillon Vachon, local 3044 1045 Ave. de la Médecine, Uni-

université Laval, Québec, Qc G1V 0A6

julian.dodson@bio.ulaval.ca  
<mailto:julian.dodson@bio.ulaval.ca>

www.bio.ulaval.ca/labdodson/ < <http://www.bio.ulaval.ca/labdodson/> >

Julian.Dodson@bio.ulaval.ca  
lian.Dodson@bio.ulaval.ca

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## Leuven Belgium Evolutionary Genomics

POST-DOCTORAL POSITION IN EVOLUTIONARY BIOLOGY AND GENOMICS:

ADAPTIVE EVOLUTION OF MARINE FISHES

Research context:

Our team studies the intraspecific evolution of the fish genome and its interactions with parasites and the environment. At the moment adaptive evolution is being studied in key ecological and economic fishes (e.g., Raeymaekers et al. 2007; Maes et al. 2007; Souche et al. 2007; Chistiakov et al. 2008).

Assignment:

We have an open call for a 12-month postdoctoral fellowship in fish evolution to be funded by the Belgian Federal Science Policy (BELSPO) at the Katholieke Universiteit Leuven. The immediate task involves the in depth analysis of large-scale pyrosequencing (454) runs (annotation and polymorphism detection). Subsequently, the aim is to set-up and screen a SNP array for European eel and common sole for neutral and adaptive signatures.

Profile:

The candidate (Ph.D. in (molecular) biological sciences, bioinformatics or biochemical sciences with excellent skills in genomics, bioinformatics and programming) will extract and interpret information from a large genetic dataset. The successful candidate originates from the following countries: non-EU Eastern Europe, new states issuing from the Russian Federation, non-EU Mediterranean region, Central and Southern Africa, Central and Southern America, India and Vietnam (see also <http://www.belspo.be/'belspo/-home/calls/postdoc.en.stm>).

WE OFFER:

You will join an expert team in ecological genetics and environmental genomics. A fully equipped medium throughput DNA lab, including a capillary sequencer, is operational. Salary is according to Belgian government standards (1800-2200 /month net). There is a possibility to extend the duration of the grant with complementary national funding opportunities. Leuven (<http://www.leuven.be>) is a pretty historical university city with a very high and pleasant standard of living. The historic university, founded in 1425 (<http://www.kuleuven.be/en>), has a top research and teaching standard.

Interested?

Send your CV, two letters of reference and a letter of motivation before 31 December 2008 to:

Dr. Filip Volckaert Katholieke Universiteit Leuven Laboratory of Animal Diversity and Systematics Ch. Deberiotstraat 32 B-3000 Leuven, Belgium Phone: +32 16 32 39 66 Fax: +32 16 32 45 75 E-mail: [filip.volckaert@bio.kuleuven.be](mailto:filip.volckaert@bio.kuleuven.be) URL: <http://bio.kuleuven.be/dev> Disclaimer: [http://www.kuleuven.be/cwis/email\\_disclaimer.htm](http://www.kuleuven.be/cwis/email_disclaimer.htm) Filip Volckaert <[Filip.Volckaert@bio.kuleuven.be](mailto:Filip.Volckaert@bio.kuleuven.be)>

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## Lyon Phylogenetic Algorithms

A 18 months post-doctoral position is available to work on “integrative algorithms for multi-gene phylogenetics” in the BBE laboratory of the University of Lyon, France (<http://lbbe.univ-lyon1.fr/?lang=en>).

The work will be conducted by Vincent Daubin from the Bioinformatics and Evolutionary Genomics Group and Eric Tannier, from the Baobab group. The subject is in the scope of the two groups, molecular evolution on one side and combinatorial algorithmics on the other.

The successful candidate will have a strong background in Bioinformatics, Algorithmics and/or Statistics and good programming skills. A good understanding of evolutionary biology is also required. He/she will have to interact with both biologists and computer scientists in the context of a larger project funded by the ANR (National Research Agency) which objective is to propose efficient algorithms to infer species and genes trees through the modelling of genome evolution mechanisms. This project is in collaboration with biology and computer science labs in Montpellier, France.

The BBE lab offers a highly stimulating scientific en-

vironment, and Lyon is a beautiful, history rich, lively city.

Please send a CV and motivation letter to Vincent Daubin (daubin@biomserv.univ-lyon1.fr) and Eric Tannier (Eric.Tannier@inria.fr).

Keywords: Algorithmics, Phylogenetics, comparative genomics, tree reconciliation, parallel computing

– Vincent Daubin Bioinformatique et Génomique Evolutive | Bioinformatics and Evolutionary Genomics Laboratoire Biométrie et Biologie Evolutive | Biometry and Evolutionary Biology Dept. 43 Bld du 11 Novembre 1918 69622 Villeurbanne cedex FRANCE

Phone: 33+ 4.26.23.44.74 Fax: 33+ 4.72.43.13.88

Vincent Daubin <daubin@biomserv.univ-lyon1.fr>

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## Max-Planck Nematode Population Genetics

MAX-PLANCK INSTITUT FÜR ENTWICKLUNGS-  
BIOLOGIE

Max-Planck Institute for Developmental Biology

The Department for Evolutionary Biology (Director Ralf J. Sommer) invites applications for a Postdoctoral Position on Nematode Population Genetics.

The Department has an active research program in evolutionary ecology and evolutionary developmental biology studying the nematode model organism *Pristionchus pacificus*, the genome of which has recently been sequenced (Dieterich et al., Nature Genetics, 40, 1193-1198 (2008)).

An overview of our research can be obtained in *BioEssays* 28, 651-659 (2006).

*Pristionchus* nematodes live in close association with scarab beetles and feed on microbes that grow on the carcass of the dead beetle. Our model species, *P. pacificus* is cosmopolitan and we have currently more than 100 wild isolates representing an enormous resource for natural variation. Mutation accumulation lines have been generated for several strains.

We want to initiate a population genetic analysis in *P. pacificus*. Access to large-scale sequencing facilities, including next generation sequencing technology, is available.

Experience in population genetics is absolutely re-

quired.

The position is for two years with a possible extension for one more year.

Funding would be available from 1. April 2009.

Closing date for applications: 15. December 2008

Please submit applications to:

Ralf J. Sommer

Dept. for Evolutionary Biology

Max-Planck Institute for Developmental Biology

72076 Tübingen, Germany

Ralf.sommer@tuebingen.mpg.de

<http://www.eb.tuebingen.mpg.de/dept4/home.html>

<http://www.pristionchus.org>

<http://www.pristionchus.org/> <

dmerrill@k-state.edu

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## SheffieldU Modeling Bird Populations

A Post Doc position in quantitative genetics and agent-based modeling on a long term bird population, Sheffield University, UK

Brief outline: The post-holder will assist with an analysis of components of fitness using our long-term data on house sparrows on Lundy Island, UK. Applicants should have a PhD (or equivalent experience) in quantitative genetics or evolutionary ecology and have experience of advanced statistical methods. Analytical work involves quantitative genetics and individual-based modelling. The successful candidate will be required to undertake fieldwork for a maximum of up to three months during the year. The project is currently funded until December 2011. The post is available immediately, initially, for one year.

Report to: Terry Burke, Professor of Molecular Ecology

Main Duties and Responsibilities - Analyse a multi-generation pedigree for the Lundy house sparrow population, using the MasterBayes R package to conduct paternity analysis and quantitative genetic analysis - Investigate the fitness consequences of mate choice - Investigate the fitness consequences of reproductive effort - Use animal model and quantitative genetic methods to investigate the genetic basis of individual traits (especially parental care) - Use individual-based modelling

to model how variation in paternal care is maintained in this population in conjunction with extra-pair paternity - Undertake fieldwork for a maximum of three months per year - Develop statistical models to estimate phenotypic and genetic correlations - Undertake further analyses as required - Collate and present the results and conclusions in talks and publications - Actively manage and organise a new Access database.

Planning and Organising - Collate information and organise samples for analysis by the project's technician

Resource Management Responsibilities - Recruit, organise, train and direct field assistants when required - Assist with the supervision and training of project and PhD students

#### Further Information

This post is fixed-term, with a start date of 1 February 2009 or as soon as possible thereafter, initially for a period of 12 months.

Informal enquiries: Informal enquiries may be directed to Terry Burke T.A.Burke@sheffield.ac.uk, or by telephone on +44 (0) 114 222 0096.

Salary: £27,999 per annum.

Terms and conditions of employment: Will be those for Grade 7 staff.

Closing date: 05/01/08

Health assessment: Please note that due to the duties of this post, the appointee will be required to complete a satisfactory health assessment from the University Staff Occupational Health Service.

The University of Sheffield is committed to achieving excellence through inclusion

shinichi.nakagawa@otago.ac.nz

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## UAlberta BeetlePopulationGenomics

Post-Doctoral Position: Population Genomics of the Mountain Pine Beetle System

Department of Biological Sciences - University of Alberta Position duration ? until Dec 31, 2009 with a strong possibility of extension Closing date ? open until filled

The Department of Biological Sciences has an opening for a Post Doctoral Fellow in the area of Population Ge-

nomics. You will become an integral member of a fast moving, multidisciplinary team researching the Mountain Pine Beetle (MPB) infestation in Western Canada. This research will be conducted in the laboratory of Dr. Felix Sperling and will involve collaboration with other project researchers. The successful candidate will possess a doctoral degree in molecular biology, quantitative genetics, bioinformatics, or a closely related field. Knowledge and experience in single nucleotide polymorphism (SNP) identification, re-sequencing and typing, or association and QTL analysis is required. Related experience with insects and/or plants is preferred. You will be responsible for:

- 1) Identification of candidate genes with potential adaptive significance for interacting biological organisms in the MPB infestation from project EST libraries;
- 2) In silico identification and validation of SNPs within candidate genes;
- 3) Genotyping and association and QTL analysis of interacting biological organisms using identified SNPs
- 4) Supervising research personnel in a laboratory setting.

Interested individuals should submit an application package (cover letter and curriculum vitae) and arrange to have three sealed letters of reference forwarded to the address below. In accordance with University of Alberta Policy, applicants should have no more than three years' post doctoral experience. Salary is commensurate with experience. Electronic applications are preferred.

Matt Bryman Project Manager The Tria Project: Mountain Pine Beetle System Genomics CW 405 Biological Sciences Building University of Alberta Edmonton, AB T6G 2E9 Email: mbryman@ualberta.ca

We thank all applicants for their time and effort, but only those selected for an interview will be contacted.

#### Additional Information

Dr. Felix Sperling is a Professor in the Department of Biological Sciences and specializes in population genetic surveys, species delimitation and related analyses in insects, including bark beetles. ([http://www.biology.ualberta.ca/faculty/-felix\\_sperling/](http://www.biology.ualberta.ca/faculty/-felix_sperling/)) Department of Biological Sciences ? <http://www.biology.ualberta.ca> Postdoctoral Fellows Office - <http://www.postdoc.ualberta.ca> mbryman@ualberta.ca

Postdoctoral Positions Available: Research Associate Arizona Research Laboratories, University of Arizona, Tucson, AZ

NIH-Training Program: Postdoctoral Excellence in Research and Teaching (PERT) The Postdoctoral Excellence in Research and Teaching (PERT) Program is a comprehensive program which offers up to three years of support to outstanding candidates seeking advanced postdoctoral research training, teacher training and student mentorship opportunities in preparation for an academic career in biomedical and life sciences. Funded by NIGMS through an IRACDA (Institutional Research and Career Development Award) training grant, the PERT program also seeks to increase the number of well-qualified underrepresented minority students entering competitive careers in biomedical research, as well as to foster ties between research-intensive institutions and minority-serving institutions.

PERT trainees may select from over forty-two faculty research mentors at the University of Arizona, representing a broad range of disciplines in biomedicine, bioengineering, genetics, biochemistry, neurobiology, evolutionary biology, molecular/cellular biology, physiology and behavior. The program stresses the use of model organisms for biomedical and life sciences research. The program is administered through the Arizona Research Laboratories Center for Insect Science and is partnered with a Minority Serving Institution, Pima Community College, (<http://www.pima.edu/-program/biology/>). Starting salary, based on the NIH NRSA scale, will be \$36,996 for program participants with less than one year of postdoctoral experience. An annual allowance for research supplies and travel is also included. Positions are dependent upon continued funding. Additional information about the Center for Insect Science and the PERT program is available at <http://cis.arl.arizona.edu/PERT>. Qualifications: Applicants must have, as of the beginning date of the appointment, a Ph.D. in a related field from an accredited institution and must be U.S. citizens or permanent residents. Applicants should have no more than two previous years of postdoctoral experience at the time of application. In addition, candidates must be able to start the position on or before July 1, 2009 Application: All applicants must apply electronically through the University of Arizona's Career Track website at: <https://www.uacareertrack.com>, citing job # 42298. All applications are to include:

–a letter of interest with a statement explaining how the PERT program will assist the applicant in his/her research and career goals. –a CV –a three to six page research proposal developed with the intended PERT faculty research mentor describing the project to be

undertaken during the training period –three letters of reference –a letter of support from the intended faculty research mentor

Potential applicants are encouraged to contact relevant Program Faculty as soon as possible to discuss research projects and the application process. Original letters of reference and the letter from the proposed faculty research mentor should be mailed to: PERT, Center for Insect Science, 1007 E. Lowell Street, University of Arizona, Tucson, AZ 85721-0106.

Emailed letters will be accepted only if accompanied by an electronic signature. The letter of interest, CV and research proposal should be submitted online through the UA Career Track website listed above.

Review of applications begins February 20, 2009, at 8:00 a.m. As an equal opportunity and affirmative action employer, the University of Arizona recognizes the power of a diverse community and encourages applications from individuals with varied experiences and backgrounds. Please contact Teresa Kudrna for more information, [tkudrna@email.arizona.edu](mailto:tkudrna@email.arizona.edu), 520-621-4923.

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Teresa Kudrna Program Coordinator, PERT Program Center for Insect Science 1007 E. Lowell Street, Room 227 Tucson, AZ 85721 Telephone: 520-621-4923 Fax: 520-621-2590 Email: [tkudrna@email.arizona.edu](mailto:tkudrna@email.arizona.edu)

Teresa Kudrna <[tkudrna@email.arizona.edu](mailto:tkudrna@email.arizona.edu)>

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## UBasel BehaviouralEvolution

POSTDOCTORAL POSITION IN BEHAVIOURAL EVOLUTION ? We are looking for a postdoctoral scientist interested in behavioral/social evolution. The research of our group focuses on the evolution of family interactions by family conflicts and parent-offspring co-adaptation, and we explore experimentally the functions and inheritance of interacting parent and offspring behavioral phenotypes. The research is carried out using a (sub-)social insect species, the European earwig *Forficula auricularia* (Dermaptera). Earwig females provide food to their early instar nymphs and protect them against predation. Their offspring interact with their mothers to influence food provisioning, and they compete among each other. Our previous work showed that insect progeny solicit from their caring parents by chemical signalling (pheromones), and part of the

project involves analyses and quantification of offspring chemical signals using GC/MS.

**BACKGROUND ?** Applicants should have a PhD and a strong background and interest in behavioral ecology and/or evolutionary quantitative genetics. Experience with behavioral experimentation/observation/quantification is required. Experience with GC/MS for analyses of chemical cues is not a requirement, but a plus.

**RESEARCH GROUP AND INSTITUTE ?** Our research group is part of the Zoological Institute at the University of Basel, which hosts various groups that interact on a daily basis, share a common interest in evolutionary questions and work on diverse research topics and study systems including host-parasite interactions (Prof. Ebert), speciation (Prof. Salzburger), immune system evolution (Prof. Du Pasquier), sex-allocation (Dr. Scharer), and sexual selection and bird song (Dr. Amrhein).

**POSITION AND APPLICATION ?** The postdoctoral position is funded through a Swiss National Science Foundation (SNF) research grant. Starting date is negotiable, but the position is available from 1. May 2009 onwards for up to three years. Please send your application documents (preferably by e-mail) including CV, publication list, a one-page statement of research interest, and contact details for three potential referees to:

Prof. Mathias Kolliker (Ass Prof SNF), University of Basel, Zoological Institute, Evolutionary Biology, Vesalgasse 1, 4051 Basel. E-mail: [mathias.koelliker@unibas.ch](mailto:mathias.koelliker@unibas.ch); internet: [www.evolution.unibas.ch/koelliker](http://www.evolution.unibas.ch/koelliker). Applications received before \*\*20. January 2009\*\* will be given full consideration.

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

Math-

netics, 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 2009. 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 (Brad Shaffer) 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://www.cpb.ucdavis.edu>.

**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, 2009. 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](mailto:gradcoordinator@ucdavis.edu).

DEADLINE: January 20, 2009

Stephanie Macey-Gallow

Center for Population Biology

Stephanie

[<smaceygallow@ucdavis.edu>](mailto:smaceygallow@ucdavis.edu)

Macey-Gallow

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## UCaliforniaDavis PopulationBiology

EFFECTIVE: December 5, 2008

DEADLINE: January 20, 2009

**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 ge-

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## UCaliforniaLosAngeles TheoPopGenetics

Post-doctoral Position available in:

STATISTICAL AND THEORETICAL POPULATION GENETICS

In the research group of: John Novembre Dept of Ecology and Evolutionary Biology Interdepartmental Program in Bioinformatics University of California - Los Angeles

A two-year postdoctoral position is available in the research group of John Novembre. The focus of the postdoctoral fellow will be on the development of innovative statistical methodology for the analysis of genomic-scale population genetic data. The exact project is flexible; however on-going projects address human population structure and ancestry inference, the impacts of population structure on genome-wide association studies, adaptive variation in structured populations, and generally developing approaches for interpreting large-scale observations of genetic variation from model and non-model organisms.

At UCLA, the fellow will benefit from interactions with a strong group of statistical geneticists and empiricists using high-throughput approaches for measuring and analyzing genetic variation. The fellow will be able to work with and learn from an active community of researchers within the department's EcoEvo Theory Group (<http://www.eeb.ucla.edu/ecoevotheory/>), as well as UCLA's Bioinformatics, Biomathematics, Biostatistics and Human Genetics programs.

Preference will be given to applicants who have experience in the following fields: computational biology, statistical genetics, evolutionary genetics, computer science, or applied mathematics. Proficiency in programming (using any language) is required (although preferably candidates will have experience with various tools, e.g., C++, R/Matlab, python/perl).

The expected start date is negotiable, and the salary will be competitive and based on level of experience.

If interested, please send a cover letter, curriculum vitae, as well as contact information for three references to [jnovembre@ucla.edu](mailto:jnovembre@ucla.edu).

Applications should arrive before January 21st, 2009 to guarantee consideration.

– John Novembre, Assistant Professor <http://www.eeb.ucla.edu/Faculty/Novembre/> Dept of Ecology and Evolutionary Biology Interdepartmental Program in Bioinformatics University of California, Los Angeles 621 Charles E Young Dr South Box 951606 Los Angeles, CA 90095-1606 Phone: 310-825-4065

[jnovembre@gmail.com](mailto:jnovembre@gmail.com)

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UCatholicLouvain  
ButterflyEvolution

Job offer for a postdoc at the Universite catholique de Louvain (UCL), Louvain-la-Neuve, Belgium:

“Behavioural ecology of butterfly movements: a matter of perception?”

We are looking for a postdoctoral researcher who could join us for a period of 12 months starting in Jan-Mar 2009 (exact starting date is negotiable). We aim to develop new and stimulating behavioural research on the significance of perceptual range within a context of insect dispersal in fragmented landscapes. Butterflies are used as model system for a series of experiments in the lab and in the field. Earlier work on speckled woods (*Pararge aegeria* L.) has suggested intriguing differences in the response distance to target habitat in individuals from continuous forest and individuals from fragmented agricultural landscape (Merckx & Van Dyck 2007. *Anim. Behav.* 74: 1029-1037). We want to better understand the nature of environmental cues butterflies respond to during traveling across the landscape matrix. Therefore we want to develop a challenging evolutionary ecological research program with a strong emphasis on perceptual differences relative to landscape type. We will also explore some eco-physiological aspects. Another postdoc will also join our team to work in this field, so it will be a collaborative project. There will be frequent interactions with the lab-members of other lines of research. You will earn a postdoc grant from our University (UCL).

Candidates should have excellent CV (i.e., several publications in outstanding behavioural, ecological, conservation or evolutionary journals, experience with observational and experimental behavioural research). Only researchers who have been outside Belgium for at least the last two years can apply for this position.

You will work within a cluster of two young research teams at the Biodiversity Research Centre of the Université catholique de Louvain (UCL) in Belgium. The Behavioural Ecology and Conservation Group headed by Hans Van Dyck ([www.ecol.ucl.ac.be/ecco/en](http://www.ecol.ucl.ac.be/ecco/en)) and the Quantitative Conservation Biology Group headed by Nicolas Schtickzelle ([www.uclouvain.be/quant-cons-biol](http://www.uclouvain.be/quant-cons-biol)). Van Dyck's lab addresses several issues within the broad field of evolution in anthropogenic landscapes



(combining behavioural ecology, life history biology, thermal ecology, landscape ecology and conservation). Schtickzelle's lab addresses conservation issues using quantitative approaches like population viability analysis. Both labs have a common and complementary interest in the process of dispersal and in resource-based habitat approaches. Our university is in the French-speaking part of Belgium (Louvain-la-Neuve, close to Brussels). Lab meetings and other scientific meetings are in English, some knowledge of French would be easy.

If you are interested, please send an e-mail message in which you explain why you would like to join us and attach your CV (including a full publication list and a reference person) as a separate document.

Please submit your file no later than December, 25th 2008.

Prof. Hans Van Dyck, Behavioural Ecology & Conservation Group ([hans.vandyck@uclouvain.be](mailto:hans.vandyck@uclouvain.be)) Prof. Nicolas Schtickzelle, Quantitative Conservation Biology Group ([nicolas.schtickzelle@uclouvain.be](mailto:nicolas.schtickzelle@uclouvain.be))

Prof. Nicolas Schtickzelle Research Associate (FNRS) & Lecturer

Quantitative Conservation Biology Biodiversity Research Centre Universite catholique de Louvain Croix du Sud 4 B-1348 Louvain-la-Neuve Belgium

phone : +32 10 47 20 52 fax : +32 10 47 34 90 office: building Carnoy, room C.157

[nicolas.schtickzelle@uclouvain.be](mailto:nicolas.schtickzelle@uclouvain.be)  
[/www.uclouvain.be/quant-cons-biol](http://www.uclouvain.be/quant-cons-biol)  
[nicolas.schtickzelle@uclouvain.be](mailto:nicolas.schtickzelle@uclouvain.be)  
[las.schtickzelle@uclouvain.be](mailto:las.schtickzelle@uclouvain.be)

<http://>  
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## UGeorgia EvolutionaryBiology

The Computational Systems Biology Lab (<http://csbl.bmb.uga.edu>) of the University of Georgia is seeking applications for a Post Doctoral Associate position to work on developing computational tools and a database for horizontal gene transfer prediction and analysis in microbial genomes in a new NSF "Tree of Life" project. The successful applicant should have a Ph.D degree in computational biology, evolutionary biology, or computer science with a good understanding of biology, and should have substantial experience in computer programming and knowledge in database development. Previous experience in phylogenomics tool

development will be a big plus. Interested applicants should contact Prof. Ying Xu via [jy@uga.edu](mailto:jy@uga.edu).

[yanbin.yin@gmail.com](mailto:yanbin.yin@gmail.com)

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## UNebraskaLincoln Bioinformatics MolEvol

\*\* Repost due to the delay in the university's job opening web site \*\*

POSTDOCTORAL POSITION in Bioinformatics and Molecular Evolution at University of Nebraska-Lincoln

A postdoctoral position is available in the Etsuko Moriyama lab at the University of Nebraska-Lincoln. The research project emphasizes developing methods for protein classification and functional prediction, molecular evolutionary analyses of protein functions, and elucidating evolutionary and molecular mechanisms of duplicated proteins and their functional divergence. We are currently targeting protein families including G-protein coupled receptors and nuclear receptors. The scope, however, will be expanded to other families.

Our lab has very interdisciplinary research environment. We regularly collaborate with researchers in many different fields. The postdoc will have opportunities to collaborate with researchers with diverse backgrounds, from computer science, bioinformatics, structural biology, molecular evolution, population genetics, to genomics and molecular biology.

Preference will be given to applicants who have experience in any combination of the following fields: computer science (especially machine learning), multivariate statistical analysis, bioinformatics (especially protein classification and structural analysis), comparative genomics, and molecular evolution (especially for protein functions). Strong background in biology is highly desired. Proficiency in programming (using any language) is required. Experience in MySQL database development/management will be appreciated.

To apply, go to [employment.unl.edu](http://employment.unl.edu) and click on Search Job Openings and complete the Faculty/Administrative application for Requisition #080977. Then also directly send a cover letter, CV, and names and contact information for three references to [emoriyama2@unl.edu](mailto:emoriyama2@unl.edu). The position becomes available on January 5, 2009, and will be supported for 2 years or longer depending on funding situation.

Applications will be reviewed as they arrive. Please feel free to contact me with any questions.

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, PhD Associate Professor School of Biological Sciences & Center for Plant Science Innovation University of Nebraska-Lincoln 403 Manter Hall Lincoln, NE 68588-0118

Email: emoriyama2@unl.edu Phone: 402-472-4979, Fax: 402-472-2083 (SBS business office)

Moriyama Lab web page: <http://bioinfolab.unl.edu/-emlab/index.html> SBS faculty page: <http://www.biosci.unl.edu/faculty/moriyama/-index.shtml> emoriyama2@unlnotes.unl.edu emoriyama2@unlnotes.unl.edu

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## UOulu ConservationGenetics

Conservation genetics postdoc position in the Department of Biology at the University of Oulu, Finland.

The postdoc will conduct collaborative research with the senior and various graduate students concerning the conservation and evolutionary genetics of large carnivores in Finland and Russian Karelia. The objectives of our research are to investigate within and between population genetic variation, effective population sizes, social structure and amount of inbreeding in large carnivores in these areas. In addition we are investigating the association between genetic diversity, gene expression and fitness characters of the studied individuals, and also possibility of adaptive variation in some candidate genes.

The post-doc is expected to have a solid background in DNA techniques, and good organizational skills. The position requires Ph.D. in genetics, molecular biology or related fields. Experience in investigating adaptive variation and/or gene expression is appreciated.

The initial contract period would be for one year (2009) with the possibility for additional year of funding (2010). The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish Universities. In addition, the appointee will be paid a salary component based on personal work performance: the total salary

will vary between 2775 - 3078 EUR per month (before the deduction of taxes and health and retirement benefit).

Informal inquiries should be addressed to Jouni Aspi (Jouni.aspi@oulu.fi) or Minna Ruokonen (Minna.Ruokonen@oulu.fi). Further information on our research can be obtained from our web page: [www.flcrp.org](http://www.flcrp.org). Applications should include a CV, statement of research interests and email addresses of two references. Applications should be sent as to Jouni.aspi@oulu.fi. This search will remain open until the position is filled.

Jouni.Aspi@oulu.fi

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## UOulu PineAdaptiveVariation

Post doc position in genetics of adaptive variation in Scots pine, for at least two years is available in the plant genetics research group at Oulu (<http://cc.oulu.fi/~genetwww/plants/>). The group works on the demographic history and genetics of climatic adaptation in Scots pine and *Arabidopsis lyrata*, and on the genetics of speciation.

This project examines the genetic basis of variation in timing of growth and cold tolerance, using studies of sequence variation, phenotypic (and gene expression) responses to environmental effects, and association genetics. Comparative approaches between species are possible with collaborating groups.

The candidates should have a Ph.D and experience/interest in population genetics/genomics, and/or quantitative genetics of the physiological variation. The post doc will interact in Oulu with Ph.D. students/post docs in related projects, and within the European project NOVELTREE (where other groups work on related topics). The starting date of the position is flexible, preferably early in 2009.

The Department of Biology has the plant growth and DNA work facilities needed for the project.

The salary is based on the Finnish Universities scales for teaching and research personnel, which include a component based on personal work performance.

The application should include a CV, a publication list, a statement of research interests and a short description of the motivation for applying for this position, and the names of two references.

The applications should be sent to Outi.Savolainen@oulu.fi, preferably by e-mail, before December 15, (or until position is filled). For further information, please contact Outi.Savolainen@oulu.fi

Outi Savolainen Department of Biology PO Box 300 FIN-90014 University of Oulu Finland phone +358-8-5531782 mobile+358-405168900

Outi Savolainen <outi.savolainen@oulu.fi>

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### UParisSud ComparativeGenomics

COMPARATIVE GENOMICS OF UNCULTURED ARCHAEA - 3-YEAR POSTDOCTORAL POSITION AT THE UNIVERSITY OF PARIS-SUD (FRANCE)

A 3-year postdoctoral contract funded by the French “National Research Agency ANR” is available from January 2009 to participate in the research project EVOLDEEP (Evolutionary and population genomics of deep-sea uncultivated microorganisms) coordinated by Purificación López-García. Work will be carried out in the “Microbial diversity and evolution” team in the University of Paris-Sud at Orsay (<http://www.esu-psud.fr/spip.php?rubrique7>), which is located 25 km south from Paris, 30 min by suburban train.

The project aims at reconstructing and comparing complete genome scaffolds of uncultured deep-sea planktonic archaea (both crenarchaeota and euryarchaeota) from genome fragments archived in metagenomic fosmid libraries in our lab. The work will include the identification of archaeal fosmids from fosmid end sequences in existing libraries that will be completely sequenced, providing the basis for scaffold genome assembly. Genome scaffolds will be annotated and analysed, with especial attention to comparative analyses in order to make inferences about the metabolism and the evolution (phylogeny, population genomics, recombination, horizontal gene transfer) of these uncultured archaeal lineages.

The net salary will be around 2000 euros (including social security and medical assistance) depending on the applicant’s experience.

We are seeking motivate candidates with good experience in genome assembly, annotation and comparative genomics. Skills in programming and database management will be appreciated.

Interested candidates should contact us as soon as pos-

sible, providing a CV, a cover letter and the names of at least two referees:

Purificación López-García Unité d’Ecologie, Systématique et Evolution - CNRS UMR8079 Université Paris-Sud 11, bâtiment 360, 91405 Orsay Cedex, France E-mail: [puri.lopez@u-psud.fr](mailto:puri.lopez@u-psud.fr) <http://www.esu-psud.fr/spip.php?rubrique7> “puri.lopez” <[puri.lopez@u-psud.fr](mailto:puri.lopez@u-psud.fr)>

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### UPompeuFabra Barcelona Metagenomics

A three-year postdoc position is available at the Institute of Evolutionary Biology (IBE), UPF-CSIC, Barcelona (<http://www.upf.edu/bioevo/>; [www.prbb.org](http://www.prbb.org)), under the supervision of Francesc Calafell. The successful candidate will join a project in skin metagenomics: we are analyzing by ultrasequencing the microbial communities in human skin by themselves and in relation to the onset of psoriasis. We are looking for a Ph.D. in bioinformatics, genetics, or evolutionary biology, with a strong background in sequence analysis: assembly, alignment, tree construction, evolutionary analysis of sequences. Programming in PERL and other languages is a requirement. We seek a positive, analytical, proactive persone who feels comfortable working in a team.

Please send by January 15th a CV, a letter of intent and two references to:

Francesc Calafell Unitat de Biologia Evolutiva Departament de Ciències Experimentals i de la Salut Universitat Pompeu Fabra Doctor Aiguader 88 08003 Barcelona Catalonia Spain

Tel: +34-93-316.08.42 Fax: +34-93-316.09.01 e-mail: [francesc.calafell@upf.edu](mailto:francesc.calafell@upf.edu)

Francesc Calafell <[francesc.calafell@upf.edu](mailto:francesc.calafell@upf.edu)>

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### UppsalaU 10 EvolutionGenomics

10 POST-DOCS TO UPPSALA CENTRE FOR EVOLUTION AND GENOMICS

The Uppsala Centre for Evolution and Genomics

(<http://www.uceg.uu.se>), located at the Uppsala University Evolutionary Biology Centre (<http://www.ebc.uu.se>), has been established through a 10-years Centre of Excellence Grant from the Swedish Research Council. The objective is to perform cutting-edge basic research in the interphase of evolution and genomics, studying the genomics of phenotypic diversity in natural populations. Key questions include, for example, the genetic background to local adaptation, speciation, large-scale morphological evolution and host-parasite interactions. The Centre has an affiliated post-graduate school program (<http://www.ebc.uu.se/gradschool/>), which offers courses and activities for PhD students in this area. Director of the Centre is Professor Hans Ellegren.

The Centre has various possibilities to recruit students as well as more senior researchers and general inquiries about such possibilities can be sent to the Director (Hans.Ellegren@ebc.uu.se). We now seek 10 highly motivated post-docs to take an active role in a number of projects relating to bioinformatics, evolutionary biology, genomics and molecular evolution. Specifics about each position are given below, together with contact information to the responsible group leader.

To apply for any of these positions, please email a statement of interest and research goals (2 pages max), CV and list of publications to the host for the position you are interested in, according to below. In addition, you should arrange to have 2 referees email letters of recommendation to the host. If you are interested in more than one position, please contact each host. Evaluation of applications will start by the end of January 2009 and will continue until the positions are filled. Starting date will be decided with the successful candidates.

Summary of job titles (details follow below)

Speciation genetics

Speciation genomics

Molecular evolution in social amoebas

Vertebrate development

Glycosaminoglycans in the evolution of bilaterians

Behavioural genomics

Genetics of plant adaptation

Bacterial evolutionary genomics

Ecological genetics of adaptive variation in *Arabidopsis lyrata*

Genetics of adaptive variation in *Primula*

Speciation genetics

A postdoc position is available to study the genetics

of speciation using a natural hybrid zone of pied and collared flycatchers on the Swedish islands of Oland and Gotland. We already have a pedigree including more than 10.000 individual birds (collected during the last 30 years) and a large number of genetic markers available. This opens the possibility of genetic approaches ranging from traditional quantitative genetics to genome-wide association studies. The aim is to answer central questions on the process of speciation from a genomic perspective. For example, are the genes coding for ecological and sexual isolation the same genes that are causing genetic incompatibility? The project would be suitable for someone with a strong interest in evolutionary biology in general and in speciation or genetic related questions in particular. Previous experience in quantitative genetics, QTL-mapping or bioinformatics would be advantageous. Candidates should be able to work independently and have good organizational skills.

Host: Anna Qvarnström  
([Anna.Qvarnstrom@ebc.uu.se](mailto:Anna.Qvarnstrom@ebc.uu.se))

Speciation genomics

Massive parallel sequencing provides outstanding possibilities for detecting the genetic basis of adaptation, including those genome characteristics that underlie speciation. Besides offering a route toward the identification of speciation genes or genomic island of speciation, the new technologies can be used to address the relative importance of structural versus regulatory differences in adaptive population divergence. The two songbird sister species pied and collared flycatcher are important ecological models for studies of speciation and life history evolution. We are seeking an ambitious bioinformatics post-doc who, using a combination of data from high-throughput short (Illumina Solexa) and medium (Roche 454) next generation sequencing approaches, will analyse transcriptome as well as full genome sequences from these species, with the ultimate aim of identifying regions involved in their reproductive isolation. The successful candidate needs to have a background in molecular evolution and be well acquainted with the handling of large-scale DNA sequence data.

Host: Hans Ellegren ([Hans.Ellegren@ebc.uu.se](mailto:Hans.Ellegren@ebc.uu.se))

Molecular evolution in social amoebas

A postdoctoral research position is offered to study molecular evolution in social amoebae (*Dictyostelia*). *Dictyostelids* are

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To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evodir.html>

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## UPretoria FishPhylogenetics

Postdoctoral research fellowship opportunity 2009: South Western Indian Ocean (SWIO) marine fish phylogenetics and colonisation history

The Molecular Ecology and Evolution Programme (MEEP), Department of Genetics, University of Pretoria and the South African Institute for Aquatic Biodiversity (SAIAB), a Facility of the National Research Foundation, are operating a joint research project under the African Coelacanth Ecosystem Programme (ACEP). This flagship programme of the South African Department of Science and Technology aims to investigate biodiversity, ecosystem processes and oceanography in the South Western Indian Ocean.

A postdoctoral research fellowship of R120 000 per year is available, commencing in 2009. Within the broader project examining marine fish differentiation and connectivity at multiple spatial and temporal scales, our team seeks to use a phylogenetic and phylogeographic approach to determine relationships and intraspecific structuring at different scales in a number of selected coastal/estuarine-linked, pelagic and deep water fish species in the SWIO. A few selected species will also be investigated on a finer ecological scale to assess the constraints of SWIO oceanography and species biology on gene flow. We further aim to integrate genetic data into oceanographic modelling to improve understanding of ecosystem processes in the SWIO.

Prospective candidates should have a background in zoology, ichthyology or the broad biological sciences and must have obtained their PhD within the past five years. Previous phylogenetic and phylogeographic experience is required. Interested candidates are welcome to contact Paulette Bloomer, Ofer Gon, Gavin Gouws or Monica Mwale for further information.

Applications: Interested researchers are invited to submit their academic records and CVs, including the contact details of three referees and a brief description (1 - 2 pages) detailing their interest in the current project, their research interests and experience, and their career goals. Applications should be received no later than 5 January 2009. The fellowship will commence as early as possible in 2009 and will initially be for one year,

but with the prospect of renewal for a further one to two years.

Contact details: Molecular Ecology and Evolution Programme, Dept of Genetics, UP (<http://web.up.ac.za/>) SAIAB <http://www.saiab.co.za> Prof. Paulette Bloomer - Tel +27 12 420 3259, fax +27 12 362 5327 e-mail: [paulette.bloomer@up.ac.za](mailto:paulette.bloomer@up.ac.za) Mr. Ofer Gon - Tel: +27 46 603 5828, e-mail [o.gon@ru.ac.za](mailto:o.gon@ru.ac.za) Dr. Gavin Gouws - Tel: +27 46 603 5843, e-mail: [g.gouws@ru.ac.za](mailto:g.gouws@ru.ac.za) Dr. Monica Mwale - Tel +27 46 603 5842, e-mail: [m.mwale@ru.ac.za](mailto:m.mwale@ru.ac.za) - Carel Oosthuizen Faculty of Agricultural and Natural Sciences Department of Genetics Molecular Ecology and Evolution Programme Room 7-27, Agricultural Sciences Bldg University of Pretoria Pretoria Republic of South Africa Tel: 27 12 420 4402 Fax: 27 12 362 5327 Email: [co@tuks.co.za](mailto:co@tuks.co.za)

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[s98077814@tuks.co.za](mailto:s98077814@tuks.co.za)

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## UPretoria PopulationGenetics

Postdoctoral fellowship opportunity: University of Pretoria (Jan-Dec 2009)

Applications are invited for a postdoctoral opportunity jointly offered by the Veterinary Genetics Laboratory (VGL, Faculty of Veterinary Science) and the Molecular Ecology and Evolution Programme, Department of Genetics (Faculty of Natural and Agricultural Sciences) at the University of Pretoria (UP).

The aim of the fellowship is to provide a strong research link between the two groups and their associated staff and postgraduate students. We are interested in the phylogeography and population genetics of wildlife species in South Africa and the application of these

data to wildlife forensic and management questions. Through collaboration with the newly established Veterinary Wildlife Centre we are also interested in how population dynamics and individual genetic variability may affect susceptibility to and the spread of wildlife diseases such as bovine TB. Current projects include: the identification of African wild cat x domestic cat hybrids; optimization of microsatellite genotyping from faecal DNA to enable population genetic studies of elusive species; development of standardized panels of nuclear DNA markers for wildlife species. In line with the UP postdoctoral policy we wish to provide an outstanding young researcher with an opportunity to develop their research skills at UP and to transfer new skills to UP.

**Funding:** The post-doctoral fellowship consists of a tax-free bursary of R150 000 sponsored by the VGL. A contribution will also be made to relocation costs and for attendance of one international conference. Candidates will not be allowed to work or provide formal services for additional remuneration in the form of a salary.

**Requirements:** Only candidates (up to 35 years of age) with a PhD may apply and should not have attained their qualification more than seven years prior to their appointment as a post-doctoral fellow. Candidates should preferably not have obtained their most recent advanced degree at UP, or be linked to UP in any other manner, just before taking up the fellowship. A PhD in Genetics/Zoology/Veterinary Science/Wildlife Management with expertise in DNA technologies such as DNA sequencing, microsatellites and SNP's and the associated population genetics analytical approaches is required.

**Application procedure and deadlines:** The application form below as well as three referees reports must please be submitted to Dr Cindy Harper (cindy.harper@up.ac.za) by the 19th of January 2009. A short list of candidates will be selected for interviews. The final award of the fellowship will require approval by the Faculty Research Committee.

UNIVERSITY OF PRETORIA

FORMAT FOR SUBMISSION OF CV

DATE OF SUBMISSION:

#### 1. BIOGRAPHICAL SKETCH

1.1 GENERAL INFORMATION Surname: Maiden name (if applicable) First names: Title: Gender: Citizenship: Date of birth: Age: E-mail address: Institution most recently affiliated with: Position: Postal Address: Telephone number: Fax number:

#### 1.2 ACADEMIC QUALIFICATIONS OBTAINED

(List all) Degree/Diploma Field of study HE Institution Year/Obtained Distinctions

1.3 RESEARCH / RELEVANT WORK EXPERIENCE TO DATE (if applicable) Name of institution Capacity and/or type of work Period

2. RESEARCH OUTPUT (ensure proper referencing)

2.1 Publications in peer-reviewed / refereed journals

2.2 Publications in peer-reviewed / refereed journals (submitted)

2.3 Books and/or chapters in books

2.4 Published full-length conference papers / keynote addresses

2.5 Non-refereed scientific publications or popular scientific articles

2.6 Technical/policy reports

2.7 Patents

#### 3. OTHER SCHOLARLY, RESEARCH-BASED CONTRIBUTIONS

3.1 Participation in conferences, workshops and short courses - specify type of contribution

3.2 Teamwork and collaboration with others

3.3 Membership in national and international bodies List all the scientific associations or societies to which you belong. Specify your involvement.

3.4 Visits to universities or research institutes as researcher

#### 4. BRIEF STATEMENT OF MAJOR SCHOLARLY CONTRIBUTION FROM PHD (MAX 500 WORDS)

Signature

PLEASE SUPPLY THE FOLLOWING FORM TO THREE ACADEMIC REFEREES FOR COMPLETION AND RETURN TO Dr Harper (Cindy.harper@up.ac.za) by the 19th of January 2009

Letter of Reference

Name of post-doctoral fellow (to be completed by applicant) Title of the project:(to be completed by applicant) Short summary of the project:(to be completed by applicant):

Name:(to be completed by the referee) Institution:(to be completed by the referee) Association with post-doctoral fellow:(to be completed by the referee) Evaluation of the relevance and suitability of the fellow's research experience to the proposed project:(to be completed by the referee)

Comments on the intellectual capabilities, skills and ex-

pertise he/she

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To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evodir.html>

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## UWyoming Phylogenetics

Postdoctoral position in phylogenetics

A postdoctoral position in the Liberles Group at University of Wyoming is available to work on mechanistic models for the gene tree/species tree reconciliation problem. The successful candidate should have extensive experience with programming and statistics as well as knowledge of the phylogenetics field and interest in evolution. Send CV to [liberles@uwyo.edu](mailto:liberles@uwyo.edu).

The successful candidate will have a Ph.D. in a relevant biological or quantitative field with complementary experience in biology (phylogenetics/evolution)/statistics/programming.

“David A. Liberles” <[liberles@uwyo.edu](mailto:liberles@uwyo.edu)>

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## Vienna PopulationGenetics

A postdoctoral position is available, for research into the genetics of speciation in *Antirrhinum*. The project would focus on a hybrid zone between subspecies that differ in floral morphology: plants would be genotyped for major genes that determine flower pattern, and for multiple microsatellite markers. The aim is to find why the subspecies remain distinct, and how they diverged from each other. This is a joint project between Nick Barton at the Institute of Science and Technology (I.S.T. Austria), and Enrico Coen, at the John Innes Institute in Norwich. The postdoc would be based at I.S.T., and would be responsible for experimental design and data analysis; she/he would take part in fieldwork in the Pyrenees.

The Institute of Science and Technology is a new multidisciplinary research institute, located in the

Wienerwald, just outside Vienna (<http://www.ist-austria.ac.at>); the working language is English. There are close links with other population genetics groups at the University of Vienna and at the Veterinary University.

The position will be available for three years, with the possibility of an extension; the salary scale starts at 44,100 p.a. Applicants should have a Ph.D. in a relevant area, with good quantitative and computing skills, and an interest in evolutionary biology. For further details, please contact [nick.barton@ist-austria.ac.at](mailto:nick.barton@ist-austria.ac.at). Applications should be sent by January 15th, and should include a CV, a statement of research interests, and names of referees. I.S.T. Austria encourages women to apply, and child-care facilities are available.

[nick.barton@ist-austria.ac.at](mailto:nick.barton@ist-austria.ac.at)

[nick.barton@ist-austria.ac.at](mailto:nick.barton@ist-austria.ac.at)

[ist-austria.ac.at](http://www.ist-austria.ac.at)

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## WashingtonStateU 2 EvolutionaryModeling

We are looking for two postdoctoral scientists interested in developing mathematical models of ecological and evolutionary processes in communities. Although the specific questions to be addressed are open, the basic aim is to derive systems of differential or difference equations from a description of interactions among phenotypically variable individuals for a variety of ecological interactions (such as competition, predation, and mutualism) to model the joint population and evolutionary dynamics of communities. The work is part of an ongoing collaboration between Scott Nuismer, Richard Gomulkiewicz, and Michael Doebeli to develop a theoretical framework for coevolution between multiple species.

One position will be based in the joint research group of Richard Gomulkiewicz (Washington State University; Pullman) and Scott Nuismer (University of Idaho; Moscow), and the other will be based in the research group of Michael Doebeli (University of British Columbia; Vancouver). Applicants should have a Ph.D, a background in evolutionary biology or ecology, and an interest in developing and analyzing mathematical models of biological processes. For more information please contact Scott Nuismer, Richard Gomulkiewicz or Michael Doebeli.

Cheers, Scott

Scott Nuismer Associate Professor Department of Biological Sciences University of Idaho Moscow, ID 83844  
Phone: (208) 885 4096 FAX: (208) 885 7905 [http://-](http://www.webpages.uidaho.edu/~snuismer/Nuismer-Lab/)

[www.webpages.uidaho.edu/~snuismer/Nuismer-Lab/](http://www.webpages.uidaho.edu/~snuismer/Nuismer-Lab/)  
Scott Nuismer <[snuismer@uidaho.edu](mailto:snuismer@uidaho.edu)>

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## WorkshopsCourses

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### BodegaMarineLab Phylogenetics Mar7-13

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

March 7-13, 2009

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 construction of phylogenetic trees is becoming a methodology that is well-defined, with broad agreement on the central issues and questions. A nearly standard set of topics is now taught as part of the curriculum at many colleges and universities. On the other hand, application of phylogenetic methods to interesting problems outside of systematics is an area of special excitement, innovation, and controversy, and perspectives vary widely.

In March, 2009, for the tenth year, we will teach a workshop for graduate students interested in applying phy-

logenetic methods to diverse topics in biology. The one-week course will be an intensive exploration of problems to which modern phylogenetic tools are being applied. We cover a range of topics in biogeography, ecology, conservation biology, phylogenomics, functional morphology, macroevolution, speciation, and character evolution. The course starts with recent advances in phylogenetic methodology, and then focuses on methods and tools that can be brought to bear on these “applied” issues in the context of a given phylogeny.

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

#### Specific Topics to be Covered

\* Finding, evaluating and interpreting phylogenetic trees; phylogenetic databases \* Recent advances in tree reconstruction: Bayesian inference; stochastic optimization strategies; divide-and-conquer methods; Garli; gene-tree species tree resolution \* Analysis of character evolution–theory: parsimony, likelihood and Bayesian approaches; null models and statistical testing \* Analysis of character evolution–form and function of complex character systems \* Phylogeography; coalescent methods for inferring migration rates and patterns \* Phylogenetic comparative methods \* Phylogenetic perspectives on biodiversity and conservation biology \* Data mining of sequence databases for phylo-



genetic analysis \* Estimation of divergence times from sequence data, analysis of diversification rates \* Ecological Phylogenetics, biogeography

Instructors for the main workshop.

\* Peter Wainwright \* Brad Shaffer \* Brian Moore \* Michael Donoghue \* Bruce Rannala \* Jonathan Eisen \* Rich Glor \* Justen Whittall \* Greg Pauly \* Samantha Price \* Stephen Smith \* 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 reconstruction will be assumed.

Admission and Fees. Students will be admitted based on academic qualifications and appropriateness of research interests. The course fee is \$450. This includes room and board at BML for duration of the course (arriving March 7, leaving March 14) and transportation from Davis to BML.

Application Deadline. Applications are due by January 4, 2009. Please send a completed application form (available at [http://bodegaphylo.wikispot.org/-2009\\_Course\\_Announcement](http://bodegaphylo.wikispot.org/-2009_Course_Announcement)) and one letter of recommendation from your major advisor. Applications should be sent via email as PDFs to [pqspinks@ucdavis.edu](mailto: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 9 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 email:[pqspinks@ucdavis.edu](mailto:pqspinks@ucdavis.edu)

[pqspinks@ucdavis.edu](mailto:pqspinks@ucdavis.edu) [pqspinks@ucdavis.edu](mailto:pqspinks@ucdavis.edu)

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## Lyon Comparative Genomics Jan12-23

Dear all,

We would like to announce that the registration to the European course on comparative genomics at ENS Lyon (France) from January 12 to 23th, 2009 is now open.

Our course is a two weeks-long series of lectures and round tables on topics such as - Gene and genome dupli-

cation - The evolution of non-coding DNA - Evolutionary genomics of the origin of humans - Sex chromosomes and sex determination - Phylogenomics - Bacterial genomics and the origin of life - Genomics of speciation - Transposable elements and the evolution of new genes - The origin of genome architecture - The future of genomics.

Speakers include: M Lynch, K Wolfe, D Charlesworth, L Duret, N Galtier, M Gouy, M Scharl, E Douzery, E Rocha, JN Volff, H Kaessmann, E Green, L Quintana Murci, A Huttenhofer, M Robinson-Rechavi, A Widmer, W Salzburger, B Jordan.

We will accept 35 students.

Registration is free but required. The students will have to make their own arrangements for accomodation, meals and travel.

Registration will be closed on December 17 and results will be released on December 19.

Find registration form and more details at [http://lbbe-dmz.univ-lyon1.fr/spip\\_cg/](http://lbbe-dmz.univ-lyon1.fr/spip_cg/) With best regards,

Gabriel Marais and Jean-Nicolas Volff

-

Dr Gabriel Marais

Bioinformatics and Evolutionary Genomics Biometry and Evolutionary Biology Dpt. (UMR 5558) University of Lyon 1 Mendel's building, 16 rue Raphael Dubois 69622 Villeurbanne cedex France

Tel: (+33) (0) 4 72 43 29 09 Fax: (+33) (0) 4 72 43 13 88

Email: [marais@biomserv.univ-lyon1.fr](mailto:marais@biomserv.univ-lyon1.fr) Web site: <http://lbbe.univ-lyon1.fr/> Gabriel Marais <[marais@biomserv.univ-lyon1.fr](mailto:marais@biomserv.univ-lyon1.fr)>

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## MountainLakeBioStation Evolutionary Biol Summer

ANNOUNCING: MLBS Summer 2009 Field Course and REU Opportunities Mountain Lake Biological Station MLBS.org

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 17th year. Work at MLBS focuses on field-based ecology, evolution, physiology, and behavior. Learn more about the programs, complete an on-line applications, or download a flier to post: Courses web page:

<http://mlbs.org/courses.html> REU web page: <http://mlbs.org/REU.html> Fliers to Distribute or Post:

[http://mlbs.org/download/MLBS\\_Poster.pdf](http://mlbs.org/download/MLBS_Poster.pdf) [http://mlbs.org/download/MLBS\\_Courses.pdf](http://mlbs.org/download/MLBS_Courses.pdf) [http://mlbs.org/download/MLBS\\_REU\\_Poster.pdf](http://mlbs.org/download/MLBS_REU_Poster.pdf) Please forward this information to colleagues or students you think might be interested. Thanks for your help! Best wishes, happy and safe holidays.

\*\*\*\* Learn all about Mountain Lake opportunities at MLBS.org \*\*\*\*

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skype: flightofthesandor web:

[virginia.edu/biology/faculty/nagy.htm](http://virginia.edu/biology/faculty/nagy.htm) MLBS web page: [mlbs.org](http://mlbs.org)

"Nagy, Eric" <[enagy@virginia.edu](mailto:enagy@virginia.edu)>

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## RiodeJaneiro MolecularSystematics Mar16-22

Advanced methods for phylogenetic analysis of molecular sequences

The web-site and application procedure for our EMBO-funded molecular systematics course to run in Rio de Janeiro (2009, March 16-22) is now open (although some parts are still under construction).

The web site is at <http://cwp.embo.org/wpc09-02/-application.html> Please do not direct enquiries to me.

I hope to see some of you in Rio next year.

Martin Embley

Dr. T. M. Embley Professor of Evolutionary Molecular Biology & Royal Society Wolfson Research Fellow Institute for Cell and Molecular Biosciences Framlington

Place Newcastle University NE2 4HH UK

Tel 0191 222 7702 Fax 0191 222 7424

University Home page:

<http://www.ncl.ac.uk/camb/staff/profile/-martin.embley> New Lab Webpage:

<http://www.ncl.ac.uk/microbial.eukaryotes/> Take a look at our Molecular Systematics course Web Page - it is also available in down-loadable (powerpoint) format:

<http://bioinf.ncl.ac.uk/molsys> Martin.Embley@ncl.ac.uk Martin.Embley@ncl.ac.uk

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## USalzburg Phylogeography Feb12-20

Phylogeographical Analysis - Workshop and PhD/Master course (course Nr.: 437.112)

Phylogeography literally combines phylogeny with biogeography and investigates the geographic distribution of intra- or interspecific genetic variation. Observed patterns reflect the biogeographical and evolutionary history of a species or a species complex. Phylogeographic studies address questions about colonization pattern, historical range contractions or expansions in reaction to past climate change or other environmental influences, ice age refugia or hybridization. The phylogeographic approach has become increasingly important in taxonomic research as well as in the field of conservation biology. Methodologically, phylogeography combines elements of population genetics, phylogeny and historical biogeography. Despite its original focus on genetic lineages and sequence data, also allele frequencies and other types of genetic data are frequently used. In this course we will introduce the theoretical basis of phylogeography, genetic markers used, and data analysis. The main part will be a computer course in analysing and interpreting phylogeographic data based on model datasets and/or data sets of students.

â Where: University of Salzburg, Faculty of Natural Sciences, Hellbrunnerstrasse 34, 5020 Salzburg, Austria  
â When: Thursday 12. 2. 2009 â Friday 20. 2. 2009  
Course fee: 150 â-(excluding food&hotel)

Course leaders: â Dr. Dorothee Ehrich (University of Tromsø, Norway) works on molecular ecology and phylogeography of arctic animals and plants. â Dr. Andreas Tribsch (University of Salzburg, Austria) works

on the evolution and phylogeography of alpine and arctic-alpine plants.

Salzburg situated is ca. 150 km east of Munich and 300 km west of Vienna. The city can be reached via: â Train â Salzburg Airport (with Austrian, Lufthansa, Norwegian, SAS, Ryanair, Tuifly, Swiss, etc.) [Alternatively Linz airport (ca. 90 minutes by train) or Munich airport (ca. 160 minutes by train)]

The course is limited to 25 participants. Minimum attendance is 15 participants. Please send a short application (including title of master/PhD thesis, motivation for participation, etc.) and questions to andreas.tribsch@sbg.ac.at until January 7th, 2009. Notification of acceptance: January 13th.

With regards, Andreas Tribsch

Dr. Andreas Tribsch University of Salzburg, Department of Organismic Biology, /Ecology and Diversity of Plants Hellbrunnerstrasse 34, A-5020 Salzburg, Austria tel.: ++43/662/80445504, andreas.tribsch@sbg.ac.at

Dorothee Ehrich <Dorothee.Ehrich@ib.uit.no>

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## Wittenberg Germany EvolGenetics Apr2-4

workshop on:

Evolutionary Genetics - the impact of next generation

sequencing technologies

02.4. - 04.4.2009 in Lutherstadt Wittenberg (Tagungszentrum LEUCOREA)

Frühjahrsakademie der Gesellschaft für Genetik (GfG)

confirmed speakers include: Christian Schlötterer, Vienna; Philip Rosenstiel, Kiel; Michael Hofreiter, Leipzig; Christopher Wheat, Helsinki; Jan Korbel, Heidelberg; Yun Song, Berkeley; Frank Chan, Stanford; Tina Harr, Chicago/Plön; Philip Johnson, Berkeley

The workshop is aimed at advanced PhD students, postdocs and established scientists in the field. It includes lectures by international speakers and discussion rounds. One goal of the meeting is to identify the specific challenges that arise in the context of the huge amount of data that can be expected from next generation sequencing projects. A second goal is to identify authors for a special volume of Molecular Ecology with the working title "Next generation molecular ecology" which is planned to cover application of high throughput sequencing techniques for ecological and evolutionary questions (to be published in 2009).

Organization: Diethard Tautz (MPI for Evolutionary Biology, Plön) and Wolfgang Stephan (University of Munich)

Participation fee 200 euro (includes accomodation and meals), limited to 60 participants. If you are interested, please send an email to:

gfg-fa2009@evolbio.mpg.de

to get further details.

tautz@evolbio.mpg.de tautz@evolbio.mpg.de

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## Instructions

Instructions: To be added to the EvoDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvoDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope),

but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email `evoldir@evol.biology.McMaster.CA`. Do not include encoded attachments and do not send it as Word files, as HTML files, as  $\LaTeX$  files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be 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 preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by  $\LaTeX$  do not try to embed  $\LaTeX$  or  $\TeX$  in your message (or other formats) since my program will strip these from the message.