

---

# E v o l D i r

July 1, 2008

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

---

## Forward

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

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

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



Forward .....	1
Conferences .....	2
GradStudentPositions .....	10
Jobs .....	22
Other .....	37
PostDocs .....	55
WorkshopsCourses .....	71
Instructions .....	74
Afterward .....	74

---

## Conferences

<p>Edinburgh QuantGenetics Jun17-22 ..... 2</p> <p>Halifax EvolutionaryProtistology Jul21-26 deadlines3 3</p> <p>IrvineCA MEEGID IX Oct30-Nov1 2 .....3</p> <p>KansasCity EcologicalGenomics Nov14-16 .....3</p> <p>Marseilles 12thEvolutionaryBiology Sep24-26 deadline 4</p> <p>Oia Spain SnailEvolution Sep2-7 ..... 4</p> <p>Paris Recomb ComparativeGenomics Oct13-15 ..... 5</p> <p>Pompeii AncientDNA Oct19-22 ..... 6</p> <p>Porto Portugal 11thGABBA Jun13 2 .....6</p> <p>StonyBrookU Darwin2009Celebration Nov5-9 update</p>	<p>UBath Sex and asex Sep5 ..... 7</p> <p>UGeorgia WeedAdaptation Sep11-13 ..... 8</p> <p>UMinnesota Evolution 2008 Jun20-24 photos ..... 8</p> <p>URennes PopulationGenetics Aug25-28 .....9</p> <p>UStAndrews ComparativeGenomics June13 .....9</p> <p>UZurich SpermCompetition in honor of Paul Ward Oct25 ..... 9</p> <p>Vienna Cat-VirusEvolution Aug24-27 AbstractDead- line ..... 10</p>
---	---

---

### Edinburgh QuantGenetics Jun17-22

Preliminary Announcement and note for your diaries:

Fourth International Conference on Quantitative Ge-  
netics: Understanding variation in complex traits

Edinburgh 17-22 June 2012

<http://www.icqg4.org.uk/> Variation in quantitative and other complex phenotypes underpins most important traits in human health and disease, agriculture, natural populations and evolution. The genomics revolution has provided the tools to start the dissection of such traits, enhancing both their understanding and exploitation. This has led to an explosion of interest and new studies across all of biology.

The aim will be to present and discuss state-of-the-art results, theoretical developments, understanding and methodology across the whole range of quantitative genetics - the genetic analysis and interpretation of data on complex traits - and to provide a stimulating conference in an attractive locale. Topics will include statistical methods for parameter estimation, including analysis of trait, genomic and functional genomic data; methods for QTL and gene identification; genetic control of complex traits; prediction of breeding value and individual risk, and interpretation of evolutionary change.

The meeting will pertain to and span results from, for example, humans, livestock, crops, micro-organisms and natural and experimental populations of all species.

The conference will be held at the Edinburgh International Conference Centre, and sponsored by the UKs Genetics Society (<http://www.genetics.org.uk/>). It follows previous successful meetings at Iowa State University in Ames, North Carolina State University in Raleigh, and Zhejiang University in Hangzhou, China (<http://www.icqg.org/>).

Information on the web will be updated in due course. Meanwhile, for further information please contact a member of the pro-tem local organising committee: Bill Hill ([w.g.hill@ed.ac.uk](mailto:w.g.hill@ed.ac.uk)) (Chair), Lutz B<sup>1</sup>nger, DJ de Koning, Chris Haley, Loeske Kruuk and Alan Wright.

– Prof W G Hill Institute of Evolutionary Biology  
School of Biological Sciences University of Edinburgh  
West Mains Road Edinburgh, EH9 3JT

e-mail: [w.g.hill@ed.ac.uk](mailto:w.g.hill@ed.ac.uk) Phone: +44-(0)131-650 5705  
Fax: +44-(0)131-650 6564

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

“W.G.Hill” <[w.g.hill@ed.ac.uk](mailto:w.g.hill@ed.ac.uk)>

---

## Halifax Evolutionary Protistology Jul21-26 deadlines3

\*PROTIST2008\* is this year's combined meeting of ISEP (the International Society for Evolutionary Protistology) and ISOP. It will be held July 21-26 in Halifax, Canada.

The final deadline for registration is July 1!

If you are planning to come, and have not yet registered, you should do so ASAP! - you will also need to organise your accommodation ASAP.

We have an excellent scientific program prepared. The abstracts for all presentations, including the plenary addresses and symposium talks, are now available on the meeting website.

Visit <https://protist2008.dal.ca/> now for on-line registration and all other details.

Alastair Simpson Sina Adl

Alastair.Simpson@Dal.Ca

veterinary or agronomical relevance. Special emphasis will be given to health problems of particular interest to Mediterranean and tropical countries: AIDS, malaria, tuberculosis, sleeping sickness, leishmaniasis, ebola, bird flu, chikungunya, cattle and crop pathogens.

Abstract submission deadline: July 30, 2008

Keynote Speakers: Francisco J. Ayala, University of California, Irvine (Evolution of Malaria; Darwin's Revolution) Robin Bush, University of California, Irvine (Influenza Evolution) Koussay Dellagi, Centre for Research and Surveillance of Emerging Diseases in the Indian Ocean, Tunisia (Chikungunya Epidemics) Apollinaire Djikeng, J. Craig Venter Institute, Rockville, Maryland (Viral Genomics) Henry Harpending, University of Utah, Salt Lake City (Infectious Diseases and Human Evolution) Annie Rimoin, University of California, Los Angeles (Implementing Active Surveillance of Human Monkeypox in the Democratic Republic of Congo) Michel Tibayrenc, Institut de Recherche pour le Developpement, France (Integrated Evolutionary Epidemiology: Where are We Now?) Nathan Wolfe, University of California, Los Angeles (Viral Forecasting)

Register at [http://www.th.ird.fr//site\\_meegid/-menu.htm](http://www.th.ird.fr//site_meegid/-menu.htm) Denise Chilcote for F.J. Ayala and M. Tibayrenc

"Francisco J. Ayala" <fjayala@uci.edu>

---

## IrvineCA MEEGID IX Oct30-Nov1 2

October 30 - November 1, 2008 9th International Congress on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID IX)

Principal Organizers: Michel Tibayrenc (Institut de Recherche pour le Developpement, France) Francisco J. Ayala (Ecology and Evolutionary Biology, University of California, Irvine)

Location: UC Irvine Student Center, University of California, Irvine A major event in genetics and the evolution of infectious diseases. Topics include: genetics, genomics, proteomics, population biology, mathematical modeling, and bioinformatics. Papers can report on the host, the pathogen (viruses, parasitic protozoa, helminths, fungal organisms, and prions), or the vector for vector-borne diseases. Papers considering co-evolution phenomena are particularly encouraged. All infectious models can be considered, including those of

---

## KansasCity EcologicalGenomics Nov14-16

ECOLOGICAL GENOMICS SYMPOSIUM

NOVEMBER 14 - 16, 2008

KANSAS CITY on the Plaza

Plan now to attend the 6th Annual "Genes in Ecology, Ecology in Genes" Symposium on November 14, 15, & 16, 2008, in Kansas City. We will convene in the Intercontinental Hotel on the beautiful Country Club Plaza on Friday at 6:00 p.m. and conclude on Sunday at noon.

Ecological Genomics is a field at the interface of ecology, evolution and genomics that seeks to place the functional significance of genes and genomics into an ecological and evolutionary context. Featured speakers for the 2008 Symposium include the following:

. Kathleen Donohue, Organismic & Evolutionary Biol-

ogy, Harvard University

. Michael B. Eisen, Molecular and Cell Biology, University of California, Berkeley

. William Jeffery, Biology, University of Maryland at College Park

. Carol Eunmi Lee, Zoology, University of Wisconsin, Madison

. Bryant F. McAllister, Biological Sciences, University of Iowa

. Patrick C. Phillips, Biology, University of Oregon

. Thorsten B. H. Reusch, Leibniz-Institute for Marine Sciences, Kiel, Germany

. Ralf J. Sommer, Evolutionary Biology, Max Planck Institute for Developmental Biology, Tuebingen, Germany

. Stephen M. Welch, Agronomy, Kansas State University

. Mark Young, Plant Sciences and Microbiology, Montana State University-Bozeman

A poster session will be held on Friday night and Saturday. Poster topics should be related to the field of Ecological Genomics. A limited number of submitted poster abstracts will be selected for oral presentations.

Information will be posted on our website, [www.ecogen.ksu.edu](http://www.ecogen.ksu.edu) < <http://www.ecogen.ksu.edu/> > , as details are finalized. Please share this announcement with colleagues and students who are interested in learning more about the field of Ecological Genomics. If you have questions, please contact us at (785) 532-3482 or [ecogen@ksu.edu](mailto:ecogen@ksu.edu).

Funding for this symposium is provided by Targeted Excellence at Kansas State University.

Ecological Genomics Institute Directors:

Dr. Loretta Johnson

Dr. Michael Herman

Kansas State University, Division of Biology

by

Doris Merrill, Program Coordinator Ecological Genomics Institute Kansas State University, Division of Biology 116 Ackert Hall, Manhattan, KS 66506-4901 (785) 532-3482, [dmerrill@ksu.edu](mailto:dmerrill@ksu.edu) [www.ecogen.ksu.edu](http://www.ecogen.ksu.edu) < <http://www.ecogen.ksu.edu/> >

[dmerrill@k-state.edu](mailto:dmerrill@k-state.edu) [dmerrill@k-state.edu](mailto:dmerrill@k-state.edu)

---

## Marseilles 12th Evolutionary Biology Sep24-26 deadline

Dear All,

We inform you that the deadline for the registration of the 12th Evolutionary Biology Meeting at Marseilles is on June 30th.

We are please to inform you that the first accepted abstracts of the 12th Evolutionary Biology Meeting at Marseilles are announced on are our website: <http://sites.univ-provence.fr/evol-cgr> . Best wishes,

Axelle Pontarotti

Universite EGEE <[Egee@univ-provence.fr](mailto:Egee@univ-provence.fr)>

---

## Oia Spain Snail Evolution Sep2-7

Dear All,

This e-mail is to inform you that the next International Symposium on Littorinid Biology and Evolution (<http://webs.uvigo.es/isolbe/>) will be held in the Talaso Hotel at Oia (NW Spain) during 2-7th September 2008. This meeting will deal with any topic related to biology and evolution of littorinid snails, and related marine gastropods. Two expert researchers will open the daily sessions as invited speakers (Dr. B.R. Silliman and Dr. J.A. Coyne), and both oral and written contributions will be welcome. The meeting has been traditionally multi disciplinary and very friendly, and it is a good opportunity for students and young scientists to share their work. There will be also three concurrent workshops aiming to train young scientists in different methods related to littorinid research:

I. Morphometric and taxonomic techniques (P. Conde-Padín & E. Rolán-Alvarez). II. Evolutionary software for analysis of mating behavior (A. Carvajal-Rodríguez and E. Rolán-Alvarez). III. Sequence data analysis (D. Posada and H. Quesada).

The deadline for inscription and abstract submission is the 15th of July. All needed information is in the WEB page (see above).

Best, Emilio Rolán-Alvarez

Emilio Rolán-Alvarez <rolan@uvigo.es>

---

## Paris Recomb Comparative Genomics Oct13-15

Dear EvolDir,

It is our pleasure to announce the Sixth Annual RECOMB Satellite Meeting on Comparative Genomics and issue this call for submissions. We are looking forward to another great meeting, this year in Paris, France. We have an exciting group of confirmed keynote speakers, and anticipate a vibrant series of “late breaking talks” selected from the paper and poster submissions. Please consider submitting your own work for papers, posters, and talks. Submission details can be found below and on the conference website: <http://igm.univ-mlv.fr/RCG08> Best Regards, Craig Nelson & Stephane Vialette (PC Co-chairs) Jens Lagergren, Aoife McLysaght, & David Sankoff (Steering Committee)

RECOMB-CG, 2008 October 13-15, 2008 Ecole Normale Supérieure, Paris, France <http://igm.univ-mlv.fr/RCG08> CONFIRMED KEYNOTE SPEAKERS Olga Troyanskaya (Princeton University) Aviv Regev (Broad Institute) Trisha Wittkop (University of Michigan) Chris Ponting (University of Oxford) Laurent Duret (Université Claude Bernard)

KEY DATES Paper submission deadline June 18, 2008 Notification of paper acceptance July 14, 2008 Final manuscript due July 24, 2008 Poster submission deadline September 22, 2008 Workshop October 13-15, 2008

### CALL FOR PAPERS

Papers should be submitted via the EasyChair system. Submissions must be received in electronic form by 11:59pm (Paris local time), June 16th, 2008.

Submissions should be no longer than 12 single-spaced A4 pages with 1.25-inch margins all around, everything included (title, authors, addresses, abstract, references, figures, tables), in at least a 10-point font. An optional short appendix may contain details or additional data to be consulted at the discretion of the program committee. Note that authors of accepted papers will have to reformat them for the proceedings using the Springer LNCS style, which has even wider margins. It may save the authors' some work if this format is used from the

outset. The submission must include the corresponding author's email address.

Papers submitted for review should represent original, previously unpublished work. At the time the paper is submitted to the conference, and for the entire review period, the paper should not be under review by any other conference or scientific journal.

Note that accepted papers will be considered as preliminary work, and may be submitted to a journal publication after notification of acceptance.

Successful submissions will be invited for a 20-minute presentation, and the paper will be printed in the conference proceedings, which will be published by Springer in the “Lecture Notes in Bioinformatics” series.

Address any questions to the program committee chairs: Craig E. Nelson (Craig.Nelson@uconn.edu) Stephane Vialette (vialette@univ-mlv.fr)

### THEME AND SCOPE

Rapid DNA sequencing technologies have fueled an explosion in genome level data. RECOMB-CG is devoted to the development and utilization of computational methods for the comparative exploration of genome structure, function, and evolution. Both theoretical and applied contributions are welcome, and papers that combine new techniques with new knowledge derived from their application are highly encouraged.

Submissions should include genome wide analyses informed by comparative data. Topics of interest include but are not limited to:

Algorithms for comparative genomics Genome rearrangements Ancestral genome reconstruction Multiple genome alignment Genome sequence comparison Modeling genome evolution Identification, classification, and evolution of non-coding motifs Comparative genomics for genome annotation Gene and genome duplication Evolution of gene families Identification of highly conserved and rapidly evolving sequences Gene tree reconciliation Comparative genomics and epigenetics Comparative genomics and proteomics Comparative genomics and gene expression Comparative genomics and adaptation

### CONFERENCE CHAIRS

Craig E. Nelson (Molecular & Cell Biology - Univ. of Connecticut, USA) Stephane Vialette (IGM - Univ. Paris-Est, France)

### STEERING COMMITTEE

Jens Lagergren (Stockholm Bioinformatics Centre and CSC, KTH, Sweden) Aoife McLysaght (University of

Dublin, Ireland) David Sankoff (University of Ottawa, Canada)

#### PROGRAM COMMITTEE

Lars Arvestad (Royal Institute of Technology, Sweden) Veronique Barriel (Museum national d'histoire naturelle, France) Anne Bergeron (Universite du Quebec a Montreal, Canada) Guillaume Blin (Universite Paris-Est, France) Guillaume Bourque (Genome Institute of Singapore, Singapore) Jeremy Buhler (Washington University in Saint Louis, USA) Pierre Capy (Universite Paris-Sud, France) Cedric Chauve (Simon Fraser University, Canada) Avril Coghlan (Sanger Institute, UK) Miklos Csuros (Universite de Montreal, Canada)

— / —

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>

### Pompeii AncientDNA Oct19-22

9th International Conference on Ancient DNA and Associated Biomolecules Pompeii, Italy, 19-22 October 2008 - [www.ancientdna9.it](http://www.ancientdna9.it) Extended deadline for abstract submission: 20 June 2008!

The "9th International Conference on Ancient DNA and Associated Biomolecules" will be held in Pompeii, one of the world's most intriguing archaeological sites, from 19 to 22 October 2008.

Don't miss this opportunity of participating in this unique event!

Online registration available at [www.ancientdna9.it](http://www.ancientdna9.it)

For further information please visit the meeting website [www.ancientdna9.it](http://www.ancientdna9.it) or contact the Organising Secretariat: Scientific Communication srl, E-mail: [info@ancientdna9.it](mailto:info@ancientdna9.it)

#### Main Topics

Preservation, isolation and analysis of ancient DNA and other ancient biomolecules

Methods of extraction and purification of ancient biomolecules from ancient materials

PCR and sequencing of ancient DNA

Prevention and causes of sample contamination

Authenticity of putative ancient DNA

Hereditary and infectious diseases in past populations

Population genetics, DNA profiling, sexing, methods and application

Identification of species

Forensic applications

Evolution

Human migrations

Domestication

New and emerging technologies

[kim.carney@shaw.ca](mailto:kim.carney@shaw.ca) [kim.carney@shaw.ca](mailto:kim.carney@shaw.ca)

### Porto Portugal 11thGABBA Jun13

2

Dear all,

Since the attachment with the poster didn't follow through, we are sending you the program of the 11th GABBA (Graduate Program in Areas of Basic and Applied Biology) Annual Symposium written in the bottom of this email. Remember that this year, this event will take place on June 13th at Porto, Portugal.

The main subject will be 'Homeostasis: The struggle for equilibrium?'. We have gathered world-wide recognized scientists in their fields to discuss different aspects of this fascinating topic. See in the bottom all the details. You can also find this information at [gabba.up.pt](http://gabba.up.pt). Registrations are FREE and will be accepted until 9th June.

Please spread the word!

Hope to see you all there,

Best regards,

The students of the 11th Edition of the GABBA Program

#### PROGRAM

8:45 Registration

9:30 Welcome: Homeostasis and a common reader

Maria de Sousa

GABBA Coordinating Committee

ICBAS | IBMC | Porto, Portugal

10:00 Modelling cellular homeostasis

Virgilio Lew

Cambridge University | Cambridge, United Kingdom

10:45 Coffee Break

11:15 Maintaining genomic stability through cell division: a problem of dynamics, regulation and homeostasis

Claudio Sunkel

ICBAS | IBMC | Porto, Portugal

12:00 Living dangerously at the edge of the chromosomes: how do telomeres hide from DNA repair and checkpoint detection

Miguel Godinho Ferreira

Instituto Gulbenkian de Ciência | Lisboa, Portugal

12:45 Lunch

14:30 "Quorum sensing" mechanism controls the number of IgM-secreting B cells

António Freitas

Institut Pasteur | Paris, France 15:30 Differentiation and Physiology of T Lymphocytes

Benedita Rocha

Necker Institute | Paris, France

16:15 Coffee Break

16:45 Social evolution in microbes: do cellular societies display evolutionary homeostasis?

Kevin Foster

Harvard University | Cambridge, USA

17:30 Applying the concept of Homeostasis to the study of human behaviour: Driving Behaviour as a model

Cândido da Agra and Carla Sofia Cardoso

Escola de Criminologia | Faculdade de Direito da Universidade do Porto | Porto, Portugal

18:15 Round Table

patricy@hotmail.com

---

**StonyBrookU**  
**Darwin2009Celebration Nov5-9**  
**update**

All,

the Darwin '09 meeting at Stony Brook now has a complete list of speakers, which you can check at <http://-darwin09.org/> The site will be open for registration as soon as we will get confirmation of full funding.

Cheers, Massimo Pigliucci

~~~ Prof. Massimo Pigliucci 650 Life Science Bldg. Stony Brook University Stony Brook, NY 11794 1-631-632-1097 genotypebyenvironment.org platofootnote.org "Truth springs from argument amongst friends." - David Hume

massimo.pigliucci@gmail.com

---

## UBath Sex and asex Sep5

THE EVOLUTION OF SEX AND ASEXUAL REPRODUCTION

Genetics Society Autumn Meeting, University of Bath, UK, Sept. 5th 2008

Scientific organisers: Laurence Hurst (Bath) and Roger Butlin (Sheffield)

To accompany the presentation of 2008 Mendel Lecture by Professor Matthew Meselson and the 2008 Balfour Lecture by Daven Presgraves, The Genetics Society is organizing a one day conference on THE EVOLUTION OF SEX AND ASEXUAL REPRODUCTION. This will be held at the University of Bath, UK on Friday 5th September.

While the maintenance of sex and recombination remains an intellectual challenge, the long term persistence of some asexuals is equally puzzling. What if anything can be learnt about the former issues by studying the latter and vice versa? There are multiple contrasting approaches to these problems: theoretical versus empirical approaches, genetical verses ecological explanations, field versus laboratory systems. This meeting will bring together all of these strands in current research.

For more details and registration go to: [http://-www.genetics.org.uk/autumn\\_2008,\\_one\\_day\\_meeting](http://-www.genetics.org.uk/autumn_2008,_one_day_meeting)

Speakers:

Christina Burch (North Carolina, USA)

Jukka Jokela (Zurich, Switzerland)

Peter Keightley (Edinburgh, UK)

Ryszard Korona (Krakow, Poland)

Dunja Lamatsch (Mondsee, Austria)

Thomas Lenormand (Montpellier, France)

Mike Lynch (Indiana, USA)

Stefan Scheu (Darmstadt, Germany)

Featuring:

2008 Mendel Medal winner, Matthew Meselson (Harvard, USA)

2008 Balfour Lecture by Daven Presgraves (Rochester, New York)

Laurence D. Hurst Royal Society Wolfson Research Merit Award Holder Professor of Evolutionary Genetics Department of Biology and Biochemistry University of Bath Bath Somerset, UK BA2 7AY

tel: +44 (0)1225 386424 fax: +44 (0)1225 386779 email: l.d.hurst@bath.ac.uk

Laurence Hurst <l.d.hurst@bath.ac.uk>

---

## UGeorgia WeedAdaptation Sep11-13

Agricultural Weeds: Bridging the Gap Between Evolutionary Ecology and Crop Science

<http://www.plantbio.uga.edu/weeds> Sept 11th -13th, 2008

We are pleased to announce a 2-day conference designed to stimulate conversation between evolutionary ecologists and applied scientists that study weed adaptation to the agricultural system. The goal is to foster new, integrative thinking about the process of weed domestication to agriculture and the evolution of 'weediness.'

Topics include: Weed adaptation to the agricultural system, transgene movement from crops to wild species, parasitic weeds, weed shifts and weedy species of future interest

We will be hosting presentations from the following speakers as well as a poster session for registrants. There will be a poster abstract competition for graduate students and post-docs with the award being \$500 travel/housing relief. See the website for details.

Confirmed speakers:

Regina Baucom, University of Georgia John Burke, University of Georgia Shu-mei Chang, University of Georgia Matt Estep, University of Georgia

Jonathan Gressel, Weizmann Institute of Science, Israel (KEYNOTE) Jodie S. Holt, University of California, Riverside (KEYNOTE) Joel Kniskern, University of Chicago Paul Neve, University of Warwick, UK Kenneth Olsen, Washington University Allison Snow, Ohio State University Neal Stewart, University of Tennessee, Knoxville John Stinchcombe, University of Toronto Patrick Tranel, University of Illinois at Urbana-Champaign Lidia Watrud, Research Ecologist, Western Ecology Division, U.S. EPA William Vencill, University of Georgia Theodore Webster, University of Georgia - Tifton campus Cynthia Weinig, University of Minnesota

This conference will be held at the University of Georgia in Athens, GA. For registration and more information, please see:

<http://www.plantbio.uga.edu/weeds/> Conference organizers:

Regina Baucom, [gbaucom@uga.edu](mailto:gbaucom@uga.edu) John Burke, [jmburke@plantbio.uga.edu](mailto:jmburke@plantbio.uga.edu) Shu-mei Chang, [chang@plantbio.uga.edu](mailto:chang@plantbio.uga.edu) William Vencill, [wvencill@uga.edu](mailto:wvencill@uga.edu)

This conference is supported by the Office of the Provost at the University of Georgia, as well as both the Plant Biology and Crop and Soil Sciences departments.

– John M. Burke, Ph.D. Tel: 706.583.5511 Fax: 706.542.1805 <http://www.theburkelab.org/> University of Georgia Department of Plant Biology Miller Plant Sciences Athens, GA 30602

[jmburke@uga.edu](mailto:jmburke@uga.edu) [jmburke@uga.edu](mailto:jmburke@uga.edu)

---

## UMinnesota Evolution 2008 Jun20-24 photos

Members of ASN, SSB. SSE:

Please submit your photos of anything with an evolution theme to be shown at the annual joint meeting of our societies in Minnesota (6/20-6/24). Photos will be judged at the All-Society banquet and cash awards of 100, 50, and 25 US dollars or equivalent will be given to the top three entrants. The photos may contribute to the SSE web site.

Please submit one photo as a power point slide with a figure legend of 2-3 lines written in Ariel font (or similar) of font size 24. Legend should begin with your



name followed by a colon, e.g., Alice Smith: Photos must be on a white background.

Please submit electronically by Tuesday noon June 17th to Charles B. Fenster, EVP SSE: [cfenster@umd.edu](mailto:cfenster@umd.edu)

with subject header: Photo for Joint Meeting

Thank you,

Charlie Fenster, EVP SSE

Charles B. Fenster Associate Professor Executive Vice President, Society for the Study of Evolution Department of Biology BIOLOGY/Psychology Bldg. Room 3210

University of Maryland College Park, Maryland 20742 USA phone: 301 405 1640 fax: 301 314 9358

<http://www.life.umd.edu/biology/fensterlab/> Charles Fenster <[cfenster@umd.edu](mailto:cfenster@umd.edu)>

---

## URennes PopulationGenetics Aug25-28

Rappel !

Bonjour

La date limite des inscriptions pour le colloque « Petit Pois Dérivé » qui se tiendra à Rennes à Agrocampus, du 25 au 28 août 2008 \*est fixée au 15 juin !\*

Toutes les informations utiles ainsi que les formulaires d'inscription sont sur le site du colloque : <https://colloque.inra.fr/ppd2008> . cordialement

—————  
This is a reminder,

Hi

The deadline for the registrations for the conference “Petit Pois Dérivé” holds in the University of Rennes (AgroCampus) from August 25 to August 28, is June 15th.

All the informations as well as registration forms can be found on the conference website: <https://colloque.inra.fr/ppd2008> . Sincerely.

Isabelle Baumgarten <[Isabelle.Baumgarten@agrocampus-rennes.fr](mailto:Isabelle.Baumgarten@agrocampus-rennes.fr)>

---

## UStAndrews ComparativeGenomics June13

Dear Evoldir,

Comparative Genomics - last chance to register

The Scottish Bioinformatics Forum meeting “Comparative Genomics” will be in St Andrews, Scotland, on 13th June 2008. If you wish to attend, please register as soon as possible.

For full details and conference program, see:

< [http://www.sbforum.org/events.php?e\\_id=41](http://www.sbforum.org/events.php?e_id=41) >

Thank you,

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)

---

## UZurich SpermCompetition in honor of Paul Ward Oct25

Dear colleagues interested in sexual selection and sperm competition

This is the first announcement of our planned

Symposium on sexual selection, sperm competition and cryptic female choice in honor of our friend and colleague Paul Ward, who died of cancer earlier this year,

Saturday 25 October 2008 (the day of his 50th birthday) at the University of Zurich, Switzerland.

A tentative list of speakers include:

Tim Birkhead, Sheffield, UK Geoff Parker, Liverpool, UK Leigh Simmons, Perth, AUS Tim Carr, Bath, UK David Hosken, Exeter, UK Nina Wedell, Exeter, UK Tom Tregenza, Exeter, UK Oliver Martin, Norwich, UK Rhonda Snook, Sheffield, UK Luc Bussière, Stirling, UK Klaus Peschke, Freiburg, D Tracy Ivy, Rochester, USA Scott Pitnick, Syracuse, USA Scott Sakaluk, Illinois, USA Ann-Katrin Eggert, Illinois, USA

Everybody is welcome to attend, and more information will follow in due time. Please forward this message to anybody interested, and reserve the date.

Best regards,

Dr. Wolf Blanckenhorn Zoological Museum University of Zurich-Irchel Winterthurerstrasse 190 CH-8057 Zurich

Phone: +41 44 635.47.55 Fax: +41 44 635.47.80 E-mail: wolf.blanckenhorn@zm.uzh.ch

[http://www.zm.uzh.ch/zmneu/forschung/-blanckenhorn\\_wolf.html](http://www.zm.uzh.ch/zmneu/forschung/-blanckenhorn_wolf.html) <http://www.esf.org/-thermadapt> Prof. Wolf Blanckenhorn Zoologisches Museum Universität Zürich-Irchel 34 (Gebäude)-J (Stock) -98 (Büro) Winterthurerstrasse 190 CH-8057 Zürich

Tel: +41 (0)44 635.47.55 Fax: +41 (0)44 635.47.80 E-mail: wolf.blanckenhorn@zm.uzh.ch

[http://www.zm.uzh.ch/zmneu/forschung/-blanckenhorn\\_wolf.html](http://www.zm.uzh.ch/zmneu/forschung/-blanckenhorn_wolf.html) <http://www.esf.org/-thermadapt> wolfman@zm.uzh.ch

---

### Vienna Cat-VirusEvolution Aug24-27 AbstractDeadline

Reminder - Abstract deadline on June 6th, 2008!!!

9th International Feline Retrovirus Research Symposium - Vienna, August 24th - 27th 2008

Dear Colleague

On behalf of the organizing committee for the 9th International Feline Retrovirus Research Symposium to be held in Vienna, Austria, August 24-27, 2008, I am pleased to invite you and members of your group to submit abstracts of your latest work. The conference promises to be an innovative and exciting blend of retroviral research, advances in the cat as a model of infectious disease, cat genomics and viral and host evolution.

Felids and their associated retroviruses offer an unique opportunity to study evolution of both pathogenic and apathogenic viruses as well as endogenous retroviruses and the co-adaptation of their respective hosts. The scientific committee therefore also specifically encourages contributions from researchers interested in feline and viral evolution.

Submitted abstracts will be reviewed by the scientific committee and assigned to oral or poster presentations (your preference would be helpful) and the best of these would receive partial or full financial support for attendance. A significant amount of the budget will be allocated for this, so we really would encourage abstract submission.

Please visit the conference website at <http://www.retrovirus.at> for additional information, submission of abstracts, and registration. Please note the deadline for abstracts is June 6, 2008 and an early registration discount deadline is at the same date. Please feel free to contact the local organizing committee (office@retrovirus.at) with any questions.

Best wishes,

Dieter Klein

Steinrigl Adolf Stefan <Adolf.Steinrigl@vu-wien.ac.at>

---

## GradStudentPositions

|                                           |    |                                                   |    |
|-------------------------------------------|----|---------------------------------------------------|----|
| CardiffU MolecularEvolution .....         | 11 | Senckenberg GlobalChangeGenetics .....            | 14 |
| DalhousieU HostParasite .....             | 11 | TrinityCollege BioinformaticsGeneExpression ..... | 15 |
| Europe 9 speciation .....                 | 11 | UBern SticklebackAdaptation .....                 | 15 |
| Frankfurt PlantSystematicsEvolution ..... | 12 | UCollegeCork StatisticalGenetics .....            | 15 |
| IowaStateU 2 CropPestEvolution .....      | 13 | UCopenhagen InsectSocietyEvolution .....          | 16 |
| NHM Oslo 3 Biosystematics .....           | 13 | UJena ComparativeMorphometry .....                | 16 |

|                                           |    |                                             |    |
|-------------------------------------------|----|---------------------------------------------|----|
| UKonstanz MateChoiceMHC .....             | 17 | USouthampton EvolutionaryNeuroscience ..... | 20 |
| UKonstanz VertPhylogenomics .....         | 18 | UtahStateU EiderPopulationDynamics .....    | 21 |
| UParisSud PhylogeneticQueryLanguage ..... | 18 | Vienna PopulationGenetics .....             | 21 |
| UppsalaU SnailEvolution .....             | 19 |                                             |    |

---

## CardiffU MolecularEvolution

Dear all, I am forwarding the mail below from a colleague looking for a PhD student. If you are interested or know of potential students, please contact him directly as I am only forwarding the information. Best wishes, Lounès Chikhi

I am looking for a first class student interested in doing a PhD developing and applying molecular markers to predators of fruit tree pest in orchards in the South of France. He or she must be bilingual, French and English. It would involve a mixture of molecular work in my labs and fieldwork in France and is a great opportunity for a student interested in molecular evolution. Do you know of anyone who might be suitable?

Many thanks,

Bill Symondson

Dr William O.C. Symondson Reader in Invertebrate Molecular Ecology Cardiff School of Biosciences Cardiff University Biomedical Sciences Building Museum Avenue Cardiff CF10 3US UK

Tel: 029 20 875151 Fax: 029 20 874116

Email: Symondson@Cardiff.ac.uk

—

Lounès Chikhi Chargé de Recherche CNRS UMR CNRS Evolution et Diversité Biologique, Toulouse chikhi@cict.fr

NOUVELLE ADRESSE (01/10/2007 AU 30/09/2008):

Population and Conservation Genetics Group Instituto Gulbenkian de Ciência Rua da Quinta Grande, 6 P-2780-156 Oeiras, Portugal Tel: +351 21 446 46 71 Fax: +351 21 440 79 70 chikhi@igc.gulbenkian.pt

chikhi@cict.fr

---

## DalhousieU HostParasite

I am seeking a highly motivated PhD student to join a large project examining micro-evolutionary processes in Trinidadian guppies. The broader project examines guppy evolution in the context of varying parasite and predator regimes. The PhD project will examine the role of molecular genetic diversity at both neutral and potentially non-neutral genetic loci in these processes, and will integrate closely with ecological experiments and parasitological work conducted at McGill and in Trinidad. This is a great opportunity to conduct fascinating research, work closely with a team of scientists at Dalhousie and McGill Universities, network with a broader group of scientists from across North America &#8211; and do field work in the northern rainforests of Trinidad. If interested, e-mail Paul Bentzen for further details.

Paul Bentzen Professor,

DFO Chair in Fisheries Resource Conservation Genetics

Department of Biology,

Dalhousie University

Halifax, NS, B3H 4J1

tel: 902-494-1105 e-mail:Paul.Bentzen@dal.ca fax: 902-494-3736 web:<http://pblabs.biology.dal.ca> Paul Bentzen <paul.bentzen@dal.ca>

---

## Europe 9 speciation

SPECIATION: A Marie Curie Initial Training Network

Nine 'Early-stage researcher' positions are expected to be available, for 3 years in each case, starting in the autumn of 2008. ESR will register for a PhD degree in one of the 4 partner universities: Sheffield (UK), Jyväskylä (Finland), Groningen (The Netherlands) and St Andrews (UK).

We anticipate projects in the following areas (lead supervisors):

1.1 Genetic incompatibilities and the evolution of reproductive barriers between allopatric *Drosophila* popula-

tions (Anneli Hoikkala/Maaria Kankare, Jyvaskyla) 1.2 Genetics and genomics of prezygotic isolation in *Nasonia* (Leo Beukeboom/Louis van de Zande, Groningen) 1.3 Genetics of reproductive isolation in grasshopper hybrid zones (Roger Butlin, Sheffield) 2.1 The role of sexual selection in the evolution of reproductive isolation (Rhonda Snook, Sheffield) 2.2 Genetics and genomics of song preference in *Drosophila* (Mike Ritchie, St Andrews) 3.1 Modes of speciation and diversity patterns (Franjo Weissing/Leo Beukeboom, Groningen) 3.2 Variation in developmental mode and divergence in *Pygospio* and *Littorina* (Emily Knott, Jyvaskyla) 3.3 The genetic basis of variation in reproductive diapause in *Drosophila montana* (Anneli Hoikkala/Maaria Kankare, Jyvaskyla) 3.4 The genetic basis of variation in reproductive diapause in *Nasonia vitripennis* (Leo Beukeboom/Louis van de Zande, Groningen)

For further information and details of how to apply, please see <http://speciation.group.shef.ac.uk/-itn> or contact the Coordinator, Roger Butlin ([r.k.butlin@sheffield.ac.uk](mailto:r.k.butlin@sheffield.ac.uk))

Roger K Butlin Professor of Evolutionary Biology

Animal and Plant Sciences University of Sheffield Western Bank Sheffield S10 2TN UK

Tel. +44 (0)114 2220097 FAX +44 (0)114 2220002

[r.k.butlin@sheffield.ac.uk](mailto:r.k.butlin@sheffield.ac.uk)

---

## Frankfurt Plant Systematics Evolution

### Job announcement

The Department of Botany and Molecular Evolution at the Senckenberg Research Institute and Natural History Museum in Frankfurt (Germany) invites applications for

1 PhD studentship in Systematics, Evolution and Biogeography of Plants

Salary: approx. 29,400 gross per annum (employment according to German BAT BL IIa/2), funded by the Deutsche Forschungsgemeinschaft (DFG)

Duration: 2008-2011 (36 months)

Starting date: September 1st/October 1st, 2008

Essentials:

We look for a highly motivated candidate holding a

Master's degree (or equivalent) in a relevant subject with proven expertise in molecular systematics techniques (DNA extractions, PCR, sequencing) and plant morphology. You will demonstrate interest in plant systematics, broader questions in evolutionary botany and plant biogeography studies. Good communication skills, the ability to work independently and the willingness to conduct fieldwork in South America/Southeastern Asia are essential. A working knowledge of English, and possibly also Spanish, are highly desirable.

Job duties:

You will combine existing DNA sequence data with new data collected and produced during the project to reconstruct evolutionary relationships for different taxa in the economically important pantropical plant family Meliaceae (mahogany family, Sapindales). These multi-gene phylogenetic trees will be set in a temporal context by fossil calibrations or constraints. You will compare morphological features of selected fossil taxa to those of their putative living relatives. Together with information on the geographical and ecological attributes of species and knowledge about the geological history of the distributional areas, you will answer questions about the timing and setting of divergence events and the association of divergence events with habitat niche requirements. You will be expected to contribute to teaching at undergraduate levels.

The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply.

Equally qualified severely handicapped applicants will be given preference.

Applications should be emailed to Dr. Alexandra Muellner ([alexandra.muellner@senckenberg.de](mailto:alexandra.muellner@senckenberg.de)) as a single pdf and include:

- 1) a cover letter outlining relevant background and work experience
- 2) a full curriculum vitae, including a list of publications
- 3) copies of educational certificates
- 4) names and addresses of two referees.

For informal enquiries please contact Dr. Alexandra Muellner ([alexandra.muellner@senckenberg.de](mailto:alexandra.muellner@senckenberg.de)).

Closing date for applications: August 3rd, 2008.

Dr. Alexandra Nora Muellner

Senckenberg Research Institute, Department of Botany and Molecular Evolution, Grunelius-Moellgaard Labo-

ratory, Senckenberganlage 25, D-60325 Frankfurt am Main, Germany.

Tel. +49-(0)69-97075-1158, Fax +49-(0)69-97075-1137

<http://www.senckenberg.de/>

mueller\_alexandra@yahoo.de

---

## IowaStateU 2 CropPestEvolution

Graduate Positions at Iowa State University

Two graduate assistantships (M.S. or Ph.D.) are available in the Department of Entomology at Iowa State University (< <http://www.ent.iastate.edu/> ><http://www.ent.iastate.edu/>) to study ecological and evolutionary aspects of interactions between agricultural pests and crop plants with the goal of enhancing pest management and sustainability of agriculture. Students may pursue degrees in entomology, or in ecology and evolution through the University's interdepartmental program in Ecology and Evolutionary Biology (< <http://www.grad-college.iastate.edu/EEB/> ><http://www.grad-college.iastate.edu/EEB/>). Degrees also may be earned in both areas of study simultaneously. Interested individuals should send a cover letter describing research interests and career goals, the names and contact information of 3 references, and a curriculum vitae to Aaron Gassmann ([aaronjg@iastate.edu](mailto:aaronjg@iastate.edu)). Although electronic applications are preferred, application materials also may be mailed to Department of Entomology, 110 Insectary, Iowa State University, Ames, IA 50011.

Aaron Gassmann <[aaronjg@iastate.edu](mailto:aaronjg@iastate.edu)>

---

## NHM Oslo 3 Biosystematics

Dear EvoDir,

I would like to forward the announcement for 3 PhD positions, also available at the following link: <http://www.admin.uio.no/opa/ledige-stillinger/2008/-vit/3Ph.DfellowshipsBiology-08-9783.html> 3 Ph.D. student fellowships in biosystematics/evolutionary biology available at National Centre for Biosystematics (NCB), Natural History Museum, University of Oslo (UiO)

The National Centre for Biosystematics (NCB) (<http://www.nhm.uio.no/ncb/>) is a strategic, interdisciplinary research facility at the Natural History Museum (NHM), which aims to perform research in modern systematics and biodiversity on a high international level. The NCB integrates research groups working on plants, fungi and animals, which to a large extent utilize similar molecular genetic tools in their research. The NHM has a modern DNA laboratory with all necessary facilities and has access to a pyrosequencing instrument at the UiO. The Ph.D. students will work in an interdisciplinary and stimulating research environment together with other Ph.D. students, postdocs and guest researchers. The fellowships will include research stays abroad. The fellowships are connected to the following projects:

(1) Cryptic speciation in arctic plants

This project will follow up recent discoveries in arctic *Draba*, showing that there are many cryptic biological species within what has traditionally been regarded as well-defined, single taxonomic species. This project will investigate the generality of this kind of cryptic speciation in arctic plants. It will test whether such speciation is connected to inbreeding or other factors by comparing diploid species with different reproductive systems, different ecological characteristics, and from different taxonomic groups. The Ph.D. student will use a combination of classic biosystematic approaches and development of new DNA markers from pyrosequencing to address the association between development of reproductive barriers and total genomic differentiation. The project will also address biogeographic aspect of speciation and include field work in various regions, probably in Alaska, Svalbard, mainland Norway, and the Alps. The Ph.D. student will work closely together with other scientists studying the genetic mechanisms involved in speciation.

(2) Barcoding of DNA preserved in permafrost for reconstruction of past vegetation and climate

This project is connected to the ongoing EU project ECOCHANGE (2007-2011), where NCB has developed a barcoding database for 850 arctic vascular plant species. This reference database is used for species identification based on pyrosequencing of ancient DNA preserved in permafrost. The Ph.D. student will be part of the international ECOCHANGE team and develop new DNA markers for further resolution of some important vascular plant genera and initiate the development of a similar barcoding system for mosses. The project involves research stays in other European countries to develop expertise in pyrosequencing, bioinformatics, and analysis of ancient DNA.

(3) Sexual selection, genetic differentiation and reproductive isolation in birds. Previous studies have identified highly divergent patterns of genetic and morphological differentiation, and varying degree of reproductive isolation, in three species in the avian sub-family Saxicolinae (the bluethroat *Luscinia svecica*, the common redstart *Phoenicurus phoenicurus* and the common stonechat *Saxicola rubicola*). This project will investigate genetic and morphological differentiation within this sub-family in detail, using a combination of field experiments, molecular methods and measurements of study skins in museum collections. The project consists of three main parts: (1) molecular phylogeny of Saxicolinae, (2) phylogeography in the three mentioned species within this sub-family, and (3) experimental investigation of the role of a sexually selected character in subspecies discrimination within one of these species (the bluethroat). The research fellow will visit the largest natural history collections in Europe to collect morphological data and samples for DNA analyses, and perform field experiments at NHM's field station in Åvre Heimdalen, Oppland, Norway.

Applicants must hold a Master's degree (or equivalent) in biology, preferably with a broad practical and theoretical background in molecular genetic methods.

The purpose of the fellowship is research training leading to the successful completion of a PhD degree. When evaluating the application, emphasis will be on applicant's academic and personal prerequisites to carry out the project.

The fellowships are financed for four years, with a compulsory work load of 25%.

The University of Oslo wishes to attain a more equal gender distribution



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>

## Senckenberg GlobalChangeGenetics

Senckenberg.GlobalChangeGenetics

Graduate position:

A PhD position is available in global change biology/population genetics at the Department of Limnol-

ogy & Conservation, Senckenberg Research Institute and Natural History Museum, Germany.

Current models suggest that global warming will lead to massive species extinctions in the near future. It is expected that certain traits increase susceptibility towards changing climate, including reduced dispersal, low genetic diversity, small population size, isolation and low tolerance towards temperature changes. In Europe, several cold-adapted species of plants and animals persist as isolated glacial relicts in high altitudes. Many of these species combine several, if not all of the above-listed factors and may thus be among the first species to become extinct if global temperature shows further increase. The PhD candidate will develop and apply genetic markers (e.g., microsatellites, AFLP, sequence data) to investigate genetic population structure in cold-adapted, montane species in central European mountain ranges. In particular, research will focus on patterns of gene flow and isolation among populations, inbreeding levels within isolated relict populations, and to identify conservation units. Besides the molecular part, field work and controlled laboratory experiments on temperature and general stress tolerance will be conducted. The study is not focused on a certain taxonomic group; research will thus likely comprise both plant and animal species. We are looking for a highly motivated student with a strong interest in biodiversity, conservation and population genetics. The candidate is expected to have some experience in the laboratory, ideally with the application of microsatellite markers and/or DNA sequencing. Knowledge of German language is no precondition, but we expect the willingness to learn some German during the stay. A valid international drivers licence is required for field sampling. The Senckenberg Research Institute and Natural History Museum (head quarter in Frankfurt am Main) is among the largest natural history museums in Europe and has a longstanding tradition in high quality biodiversity research. The Department of Limnology & Conservation is located at the research station Gelnhausen. The station has all facilities required for this research (fully equipped molecular lab, laboratories for sample sorting and microscopical analysis, field equipment). Gelnhausen is a quaint town in close proximity to Frankfurt am Main. The city has a picturesque historic Old Town with several historic sites from the medieval times and is surrounded by beautiful mountain ranges. Frankfurt am Main, an international city with a rich and diverse cultural life and unique international transport connections, can be reached within 30 minutes by car or train. In order to apply, please send an application sheet, CV, publication list and contact data of two references per email to:

Dr. Carsten Nowak Senckenberg Research Institute & Natural History Museum Research station Gelnhausen, Dep. Limnology & Conservation Email: [cnowak@senckenberg.de](mailto:cnowak@senckenberg.de) [www.senckenberg.de](http://www.senckenberg.de) Applications will be considered until the position is filled.

Senckenberg wishes to increase the share of women in areas where they are underrepresented, and strongly encourages women to apply. Senckenberg has an affirmative action policy for the disabled and especially encourages them to apply.

[cnowak@senckenberg.de](mailto:cnowak@senckenberg.de) [cnowak@senckenberg.de](mailto:cnowak@senckenberg.de)

---

### TrinityCollege BioinformaticsGeneExpression

PhD Studentship: Gene expression in a host-parasite system

A 3-year PhD studentship is available to study the interaction between a nematode and its bumble bee host at the gene expression level. The project will be supervised by Dr Mark Brown (Trinity College Dublin), Dr Seirian Sumner (Institute of Zoology, London) and Professor Mark Blaxter (University of Edinburgh) and will involve a combination of parasitological, next-generation sequencing, quantitative-PCR, and bioinformatic analysis.

The position is open to EU citizens. The ideal applicant will have (or be expecting) a 1st or 2:1 honours degree (or equivalent) in Genetics or Biology, with evidence of good laboratory and quantitative skills, and an interest in evolutionary biology. The position will start on 1st October 2008 and will involve working in Ireland and the UK. Requests for further information and applications (a CV, cover letter and names of 2 academic referees) should be made to Mark Brown ([mabrown@tcd.ie](mailto:mabrown@tcd.ie)). This is an open-ended application process - applications will be considered immediately as they are received and once a suitable candidate has been found the position will be closed.

Trinity College Dublin([www.tcd.ie](http://www.tcd.ie)) is Ireland's premier university. The School of Natural Sciences ([www.tcd.ie/naturalscience](http://www.tcd.ie/naturalscience)) has a thriving research environment, with particular strengths in ecology, evolution, gene expression and parasitology.

This position is funded by Science Foundation Ireland under its Research Frontiers Programme.

Mark JF Brown, MA (Oxon), PhD, FTCD Senior Lecturer in Zoology Department of Zoology School of Natural Sciences Trinity College Dublin Dublin 2 Ireland tel: +353 (0)1 896 1627 fax: +353 (0)1 677 8094 email: [mabrown@tcd.ie](mailto:mabrown@tcd.ie) web: <http://www.tcd.ie/Zoology> [mabrown@tcd.ie](mailto:mabrown@tcd.ie)

---

### UBern SticklebackAdaptation

An M.Sc. opportunity is available in the Institute of Zoology at the University of Bern, Switzerland.

Project: Rapid adaptation and differentiation among populations of threespined sticklebacks which have colonised and spread throughout Swiss freshwater systems within the last century. This project will focus on estimating heritabilities of various morphological traits that diverge between populations from different habitat types, and directly measure selection in experimental settings.

This project will contribute to a larger ongoing study of Swiss sticklebacks that examines morphological, morphometric, genetic and ecological aspects of this invasion.

Interested candidates may contact Dr. Arjun Sivasundar for detailed project information.

Admission procedure, credit requirements etc. can be found on the webpage of the masters program in ecoogy and evolution at

<http://www.ecolevol.unibe.ch/lenya/mscee/live/-index.html> Start date: Immediate

For more information contact Dr. Arjun Sivasundar (email: [arjun.sivasundar@aqua.unibe.ch](mailto:arjun.sivasundar@aqua.unibe.ch))

[arjun.sivasundar@aqua.unibe.ch](mailto:arjun.sivasundar@aqua.unibe.ch)

---

### UCollegeCork StatisticalGenetics

Science Foundation of Ireland funded PHD studentship position (3 years), University College Cork.

Statistical genetics of *Helicobacter pylori* - anthropological genetics in the fast lane.

This project will involve adapting and developing the “copying model” that has been applied to human genetic data (see PLoS Genet 4 e1000078), in order to analyze DNA sequence data obtained from a large collection of the bacteria from around the world. Previous analyses has shown that the bacteria has a similar history of migration to that of the humans that carry them, while evolving at a much faster rate. See e.g. Science 299, 1582-1585, PNAS 101, 4746-4751, Nature 445,915-918. This project will exploit unpublished data from hundreds of additional isolates from diverse ethnic groups, including several hundred strains taken from Siberians. Candidates should have a good mathematical training and some interest in one or more of evolutionary biology/anthropology/genetics. The project will be supervised by Daniel Falush using data generated in the laboratories of Mark Achtman and others. Previous experience has shown that the unique properties of *H. pylori* make it an ideal system within which to develop novel genetic analysis tools that can subsequently be applied to a wide variety of organisms and questions. The position is open to students of any nationality and comes with a stipend of 20,000 Euros per year + student fees. Applicants should contact d.falush@ucc.ie with a CV and the names of 2 referees.

“Falush, Daniel” <D.Falush@ucc.ie>

---

### UCopenhagen InsectSocietyEvolution

#### 3 PhD FELLOWSHIPS, CENTRE FOR SOCIAL EVOLUTION, COPENHAGEN

The Centre for Social Evolution (CSE) at the University of Copenhagen has 3 vacancies for Ph.D. fellowships to study aspects of social evolution in insect societies, starting on the 1st November or 1st December 2008.

CSE has six major research programs, which focus on mating system evolution, information and recognition, social parasitism, disease, invasive ants and the evolution of symbiotic interactions. Any of these topics is eligible, and interdisciplinary combinations are encouraged, but one position will be filled in the information and recognition field. See <http://www.bi.ku.dk/CSE/> for further details of CSE<sup>1</sup>'s research, for staff and post-doctoral and Ph.D. fellows involved, and for relevant publications.

Depending on the topic concerned, successful candidates will be supervised by one or several of the CSE senior staff: Jacobus J. Boomsma, Patrizia d'Ettorre, David R. Nash and Jes S. Pedersen. Collaborative work with CSE<sup>1</sup>'s partner group at the faculty of Life Sciences, directed by Jørgen Eilenberg, is also a possibility.

Candidates should possess an M.Sc. or equivalent degree in evolutionary biology, population biology, animal behaviour or a related field, and should preferably have demonstrated their excellence by at least one publication. Experience with DNA techniques, immunity assays, modelling and/or chemical analysis (e.g. GC-MS), and a good knowledge of relevant evolutionary theory will be an advantage.

Candidates who would like to be considered for one of these posts are invited to send a CV, PDFs of published or accepted manuscripts, and a one-page declaration of interest, outlining what kind of questions they would like to address, how these would fit in with CSE<sup>1</sup>'s ongoing research, and how their educational background and expertise would enable them to embark on this work in a focused and productive way, by e-mail, to:

Bettina Markussen Secretary, Centre for Social Evolution Department of Biology, University of Copenhagen Universitetsparken 15, DK-2100 Copenhagen, Denmark e-mail: BENMarkussen@bio.ku.dk

For informal inquiries please contact CSE<sup>1</sup>'s director, Professor Jacobus J. Boomsma (JJ-Boomsma@bio.ku.dk) or, for the earmarked “information and recognition” fellowship, Dr. Patrizia d'Ettorre (pdettorre@bio.ku.dk).

The deadline for receipt of documents is 15 August 2008. Declarations of interest and CV's will be reviewed by a committee of senior members of CSE to identify candidates that will be invited for interview and to submit a full Ph.D. proposal.

Patrizia D Ettorre <pdettorre@bio.ku.dk>

---

### UJena ComparativeMorphometry

Applications are invited for a PhD-student position in the Independent Junior Research Group “Neuroimaging” at the University of Jena, Germany.

The focus of the group is on developing new methods for computational brain morphometry and on their ap-



plication to the study of structural brain plasticity from both medical and evolutionary perspectives. The focus of the PhD position is on schizophrenia research and patient classification using computational morphometry but there is room for adapting the project to the interests and skills of the incumbent (e.g. towards comparative morphometry).

The candidate should have a Master's degree in Psychology, Mathematics, Computer Science, Neuroscience, Physics, Biology or a related area and be willing to collaborate intensively with people from other fields in this list. Experience in anatomical MRI (data acquisition, processing, statistics) and programming skills (Matlab, C/C++) are desirable.

The successful candidate will join the Independent Junior Research Group "Neuroimaging" (Dr. Christian Gaser) at the department of Psychiatry. The department has excellent research facilities including an on-site, research-dedicated Siemens Tim Trio 3T MRI scanner.

Salary will be according to the German public service scale EG 13/2 TV-L (PhD Student, i.e. 50%). The appointment is initially for 2 years with an option of extension up to 4 years and is available immediately. Applications will be considered until the position is filled.

To apply, please email CV, statement of research interests, and contact information of potential references to

Christian Gaser, Ph.D. Assistant Professor of Computational Neuroscience Department of Psychiatry Friedrich-Schiller-University of Jena Jahnstrasse 3, D-07743 Jena, Germany e-mail: christian.gaser [at] uni-jena.de <http://dbm.neuro.uni-jena.de> .

daniel.mietchen@googlemail.com

---

## UKonstanz MateChoiceMHC

PhD position in Fish ecology, behaviour and evolution at the Limnological Institute, University of Konstanz - Germany

In the research group of Jasminca Behrmann-Godel we are looking for a PhD student. The position is part of a DFG project (German science foundation) and is funded for preliminary 16 months (an extension to a total of 3 years is possible).

Aim of the project is to investigate the influence of

MHC (major histocompatibility complex) gene variability on social behaviours like mate and shoal choice in perch (*perca fluviatilis*/ L). In a preliminary study, we have identified MHC genes in perch and designed specific primers to amplify a high number of MHC class II alleles. This information will be used to set up an individual genotyping method using e.g. SSCP (single strand conformation polymorphism) or DGGE (denaturing gradient gel electrophoresis) in combination with cloning and sequencing of MHC alleles. Individually genotyped perch will then be tested in behavioural experiments to investigate the influence of MHC allele variability on mate choice or shoal choice decisions. Thus the project combines modern molecular genetic techniques with behavioural experiments on wild caught and laboratory bred fish.

Our research group is a part of the fish ecology group of Prof. Reiner Eckmann at the Limnological Institute of the University of Konstanz. The Limnological Institute provides a pleasant and exciting research environment. Besides a small molecular genetics lab, it has an aquarium facility, outdoor mesocosms for semi natural studies and offers best conditions for any kind of fishing and aquatic research in Lake Constance.

Further information on our research can be obtained from our web page: <http://www.uni-konstanz.de/-FuF/Bio/forsch/limno/fishecology/> . Besides research, PhD students are expected to assist in undergraduate teaching and supervision. The University of Konstanz is one of the nine excellent universities in Germany, selected in 2007.

Applicants should have a master's degree (MA or Diplom) in biology/zoology and research experience in evolutionary biology with good expertise in molecular genetics and lab work. Practical skills in the work with fish are helpful but not compulsory. Interested students should email their applications containing a CV, statement of research interests and email addresses of two references. Review of applications will commence on July 20<sup>th</sup> 2008. Starting date is August/September 2008. Applications should be sent as one pdf file to [Jasminca.Behrmann@uni-konstanz.de](mailto:Jasminca.Behrmann@uni-konstanz.de) <<mailto:Jasminca.Behrmann@uni-konstanz.de>>.

Cheers, Jasminca Behrmann-Godel

Jasminca Behrmann-Godel <[jasminca.behrmann@uni-konstanz.de](mailto:jasminca.behrmann@uni-konstanz.de)>

---

## UKonstanz VertPhylogenomics

Ph.D. positions available in Vertebrate Phylogenomics/Evo-Devo at the University of Konstanz - Germany

In the research group of Shigehiro Kuraku Ph.D., we are looking for two new Ph.D. students (3 years). These new positions are funded by the [\\$B!F\(BYoung Scholar Fund\\$B!G\(B](#) and the [\\$B!F\(BKonstanz Research School - Chemical Biology\\$B!G\(B](#) of the University of Konstanz (<http://www.chembiol.uni-konstanz.de/>). This graduate school is funded by the [\\$B!H\(Bexcellence initiative\\$B!I\(B](#) of the German government. The University of Konstanz is one of the nine excellent universities in Germany, selected in 2007.

Large-scale DNA sequence resources are becoming available for early vertebrates, such as cyclostomes and chondrichthyans. Successful candidates are expected to contribute to the project entitled [\\$B!F\(BBioinformatic analysis to elucidate processes of genome evolution in early vertebrates\\$B!G\(B](#). By designing and establishing a computational pipeline for data mining in available genomic/EST sequences of early vertebrates, we aim to identify genomic traits [gains/losses of protein-coding genes and non-coding RNAs (e.g. miRNAs)] that have been acquired during early vertebrate evolution and have contributed to the establishment of basic architecture unique to the phenotypes of vertebrates.

Further information on our research can be obtained from our web page: <http://www.evolutionsbiologie.uni-konstanz.de/index.php?section=88>. As the field of this project, [\\$B!F\(BVertebrate Phylogenomics/Evo-Devo\\$B!G\(B](#), says, our study has a highly interdisciplinary nature. Applicants are expected to have an interest, knowledge and skills in either molecular evolution, molecular phylogenetics, genome evolution, or Evo-Devo. Experience in the laboratory in addition to skills in bioinformatics (e.g. Linux, Perl, etc.) would be a plus. Note that applicants without such specific interests and background are not considered any further.

Our research group is a part of the laboratory of Prof. Axel Meyer, which studies the evolution of teleost genomes. We provide an inspiring atmosphere for studying vertebrate genome evolution as a whole, with an international laboratory in which English is the first language spoken: Knowledge of German is not required.

Interested students with an MA degree should email their applications containing a CV, statement of research interests and email addresses of two references. Review of applications will commence on June 23rd 2008. Starting dates are flexible, but must be before the end of this year. Applications should be sent as one pdf file to [shigehiro.kuraku@uni-konstanz.de](mailto:shigehiro.kuraku@uni-konstanz.de).

Shigehiro Kuraku Ph.D. Assistant Professor Department of Biology University of Konstanz Universitätsstrasse 10, 78457 Konstanz, Germany Tel: +49 7531 88 2763 Fax: +49 7531 88 3018

[shigehiro.kuraku@uni-konstanz.de](mailto:shigehiro.kuraku@uni-konstanz.de)  
[shigehiro.kuraku@uni-konstanz.de](mailto:shigehiro.kuraku@uni-konstanz.de)

---

## UParisSud PhylogeneticQueryLanguage

I sent an email entitled "Postdoctoral opportunity at the University of Paris Sud (deadline is June 10th)" last Friday to Dr. Golding's email address to be posted on the EvolDir site. I am really sorry: I made a mistake both in the title and in the body of the message, it was a PhD opportunity and not a postdoctoral opportunity.

Could you please ignore my precedent message (about the postdoc) and post this new message (PhD opportunity) on the EvolDir site as soon as possible (the deadline is June 10th)? Thank you so much in advance for your precious help and again sorry for the mistake.

With best regards,

Sarah Cohen-Boulakia

Sarah Cohen-Boulakia Assistant Professor University of Paris Sud 11 Computer science department, Bioinformatics group Orsay 91405 cedex France +33 1 69 15 32 16

We propose a PhD opportunity in the group of Professor Ch. Froidevaux at the University of Paris-Sud on the following theme: Towards a language to query phylogenetic data

Please send a motivation letter, a resume, and the name of collaborators/advisors able to recommend your application by June 10th, 2008 to Christine Froidevaux ([chris@lri.fr](mailto:chris@lri.fr)) and Sarah Cohen-Boulakia ([cohen@lri.fr](mailto:cohen@lri.fr))

More information is available below and at <http://www.lri.fr/~cohen/phylo.html> \* Advisors Sarah Cohen-Boulakia (Assistant Professor), Christine

Froidevaux (Professor) \* Collaborators Bernard Labeledan, Olivier Lespinet (Institut de Genetique et de Microbiologie, Universite Paris-Sud, Orsay, France) Val Tannen (University of Pennsylvania, USA) \* Location Bioinformatics group at LRI (Laboratoire de Recherche en Informatique), Universite Paris-Sud, Orsay, France

\* Topic Understanding the relationships between different species may have consequences both at practical level (e.g., history of a pathogen agent involved in a disease), and at fundamental level (e.g., construction of the tree of life: finding the history of all organisms). The study of evolution requires various and numerous pieces of data such as morphological characteristics of a set of specimens or, more importantly, genomic and proteomic sequences of a group of species, functional and structural annotations. For several years now, there has been an avalanche of data available. Combining and integrating masses of phylogenomics data is of paramount importance for better understanding evolution.

\* Background More specifically, this subject is part of two projects, pPOD and Microbiogenomics.

\*\* On the one hand, pPOD is an international project, in which data are collected throughout the world by research groups having distinct interests (specialized on different groups of species). Data collected by those various groups are available in a variety of formats (relational, tabulated files, and so on.).

\*\* On the other hand, partners of the the French project "ANR masses de donnees" Microbiogenomics study evolution by building phylogenetic trees based on families of proteins, part of their data is currently stored in flat-files format (trees) and within a relational warehouse (sequences, annotations). In both projects, phylogeneticists need to ask complex questions involving all the data, both produced and consumed by the various steps of the generation and analysis of phylogenetic trees, including the trees themselves or families of trees. Examples of queries include: What are the differences between those two trees? If I modify the alignment by adding gaps, what would be the impact on the final generated tree; or

"Among the available trees, what are the subtrees whose proteins are all involved in a given metabolic pathway? Which are the protein modules appearing in trees in which a given group of species is monophyletic; or

\* Work The aim of this work is to enable various phylogeneticists to make use of all these data in a unified way, in the context of a relational database. One of the main challenges lies in that the relational model does

not fit with hierarchical (tree-based) data.

As a first step, queries frequently asked by major pPOD and Microbiogenomics partners should be identified. Queries may be increasingly complex and can be expressed using different kinds of language (relational algebra, SQL and so on). In particular, queries may involve families of trees, comparison and clustering algorithms, and topological features of the trees.

A classification of queries should then be proposed.

The third step would consist in exploring the limitations of current relational standards (latest versions of SQL) to represent phylogenetic data and express queries. This study should provide the building blocks for a more expressive high-level query language.

More information on the pPOD project: <http://-phylodata.seas.upenn.edu> More information on the Microbiogenomics project: <http://microbiogenomics.upenn.edu>

— / —

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

## UppsalaU SnailEvolution

Uppsala University hereby declares the following position to be open for application

PhD-position in Evolutionary Ecology

at the Department of Ecology and Evolution, Population and Conservation Biology, Evolutionary Biology Center

Description of the project: Adaptation to extreme climate change in a community of brackish water snails.

The aim of the project is to study rapid evolution in response to extreme climate in the snail guild of the Baltic Sea. The study will combine laboratory and field experiments with genetic and physiological studies. The purpose is to investigate the genetic response to increased environmental temperatures in a system that provides a very good opportunity to study the link between population-level response to selection and the underlying genetic change.

The project will be supervised by Anssi Laurila (EBC, Uppsala University) in cooperation with Jukka Jokela

(ETH Zurich) and Jesper Sorensen (Aarhus University).

We are looking for a highly motivated candidate with a Masters Degree within ecology, evolutionary biology or equivalent, who can work independently. Familiarity with field work on aquatic ecology and knowledge on molecular or physiological ecology, experimental design, and/or statistics will be advantageous. Good knowledge of the English language and a driving licence are a requirement.

The application should include a letter summarising motivation, research interests and relevant experience, a complete CV, publication list (if available), an academic transcript (list of grades in university courses), and names and contact information of two references, preferably all as one pdf-file.

For more information, please contact Anssi Laurila, phone +46 18 471 6493, e-mail [Anssi.Laurila@ebc.uu.se](mailto:Anssi.Laurila@ebc.uu.se). Union representatives are: Anders Grundström, SACO, phone +46 18 471 5380, Carin Söderhäll, TCO/ST phone +46 18 471 1966 and Stefan Djurström, SEKO, phone +46 18 471 3315.

The application should be sent to: Registrar, UFV-PA 2008/1547, Uppsala University, P.O Box 256, SE-751 05 Uppsala, Sweden, fax + 46 18 47120000 or e-mail: [registrator@uu.se](mailto:registrator@uu.se) no later than July 3, 2008. An application by fax or e-mail must be followed by a letter containing the original document, at the latest one week after application deadline.

Anssi Laurila Population and Conservation Biology/ Department of Ecology and Evolution Evolutionary Biology Center Uppsala University Norbyvägen 18D 75236 Uppsala Sweden

Tel. +46-18-4716493

<http://www.popbiol.ebc.uu.se/>

[anssi.laurila@ebc.uu.se](mailto:anssi.laurila@ebc.uu.se) [anssi.laurila@ebc.uu.se](mailto:anssi.laurila@ebc.uu.se)

---

## USouthampton EvolutionaryNeuroscience

A PhD mutlidisciplinary studentship is available in the School of Biological Sciences, University of Southampton, UK. The project will use a combination of bioinformatics and neuroscience to investigate the affects of alcohol on nematodes from an evolutionary perspective.

Details below:

**BACKGROUND.** There is an urgent need to better understand the biological mechanism that underpins addiction. Alcohol is recognised amongst the most harmful addictive drugs and, despite its simple structure, acts through complex interactions between molecular, cellular and systems level targets. This studentship will investigate the acute and chronic impact of ethanol through use of the nematode, *Caenorhabditis elegans*, as a model organism. Many of the mammalian molecular and cellular targets implicated in the action of alcohol are conserved in this organism and we have established a range of relevant behavioural and electrophysiological assays. This project will build a database of ethanol and its targets which, using evolutionary bioinformatics, will be used to predict key molecular targets of ethanol action for experimental investigation in *C. elegans*. Mutants lacking the ethanol target will be screened for modified response to acute or chronic ethanol treatment, defining in teractions and providing insight into neural substrate of ethanol's action, which can then be modelled or directly applied in the more complex organization that underlie alcohol (and likely other addictive drugs) in the mammalian brain.

**TRAINING.** The work recognises that the modern neuroscientist requires broad exposure to several sub-disciplines. The Studentship will actively encourage the acquisition of such skills and provides an opportunity to develop skills at the interface between bioinformatics and experimental biology. Further, the studentship will be supported by the School of Biological Sciences Graduate School, which has a broad portfolio of general and specialised training required in the modern workplace.

**FUNDING.** The Gerald Kerkutt Charitable Trust provides funding for 3/4 years and provides opportunity to apply for support for further specialist training consummate with the projects requirement for a broad and integrative training. This is a fully funded studentship with a student stipend set at the same level as a research council studentship (currently £12,940 per annum).

**REQUIREMENTS.** Applicants should be UK/EU students with a degree of 2-1 or higher in a relevant discipline (e.g. Neuroscience / Physiology/ Pharmacology/ Biochemistry/ Molecular Biology / Genetics) and a curiosity and enthusiasm for research. Laboratory experience (e.g. final year project) is essential, with a strong preference for some experience of neuroscience. The candidate must also have an interest in, and aptitude for, computers.

**CONTACT.** Interested students should contact Dr Richard Edwards ([r.edwards@soton.ac.uk](mailto:r.edwards@soton.ac.uk)), Professor

Lindy Holden-Dye (lmhd@soton.ac.uk) or Dr Vincent O'Connor (voconno@soton.ac.uk). We will be looking to interview and appoint to the position by mid July to start in October 2008.

APPLICATION DEADLINE: Monday July 7th 2008. Interested and motivated applicants should apply through the University of Southampton School of Biological Sciences graduate entry (email: sbs-gradi@soton.ac.uk)

STARTING DATE: October 1st 2008.

Dr Richard Edwards Senior Research Fellow (Bioinformatics) School of Biological Sciences University of Southampton Building 62, Room 6047, Boldrewood Campus Southampton SO16 7PX Tel: +44(0)23 8059 4344 email: r.edwards@southampton.ac.uk [www.southampton.ac.uk/biosci](http://www.southampton.ac.uk/biosci)  
R.Edwards@soton.ac.uk

---

## UtahStateU EiderPopulationDynamics

Title: Common Eider Population Dynamics - M.S. Position

School: Utah State University, Logan, UT

Departments: The Department of Wildland Resources and the Ecology Center <http://www.cnr.usu.edu/departments/departments/wild/wild> <http://www.usu.edu/ecology/> In collaboration with the Hudson Bay Project <http://research.amnh.org/~rfr/hbp/> Description of research: Common Eider (*Somateria mollissima*) populations around the world are declining, raising concern amongst managers, conservation groups, and native communities. Because of global warming and earlier thawing of the Arctic icepack, Polar Bears (*Ursus arctos*) are now coming to shore earlier than they used to. This will lead to increased predator-prey interactions between bears and eiders, and could increase the frequency of catastrophic egg depredation for coastal eider colonies, as well as decrease survival of nesting females. Although Common Eiders have evolved a bet-hedging life history to cope with some reproductive failure (i.e., they delay first reproduction, live long, and are highly iteroparous), it is not known how increased exposure to polar bears (and potentially other predators) will affect eider populations.

The student will monitor Common Eider reproductive

biology, as well as predator-prey interactions with Polar Bears and other potential predators, over 2 field seasons near La Pérouse Bay, Manitoba. The objective of this project is to develop a generalized population model for Common Eiders using published data, historical data from the La Pérouse Bay study, and the students own data. The student will then use perturbation analysis to examine how changes in the frequency distribution of reproductive success and breeding-season survival of nesting females affect Common Eider populations.

Stipend: Selected applicant must qualify for one of the following fellowships offered by USU to cover two years of research stipend. Tuition costs will also be covered. <http://www.usu.edu/graduateschool/financial/fellowships.cfm> [http://www.cnr.usu.edu/files/uploads/quinney\\_masters\\_brochure\\_2008-2009.pdf](http://www.cnr.usu.edu/files/uploads/quinney_masters_brochure_2008-2009.pdf)

Qualifications: Applicants should have a background in Wildlife, Ecology, or related discipline. Preference will be given to applicants who have experience with waterfowl research and a strong quantitative background. Applicants must meet the requirements for at least one of the fellowships listed above.

Application: Applications can be sent via e-mail to Dr. David N. Koons: david.koons@usu.edu. Applications must include 1) a cover letter describing your research background and interest in the position, 2) your CV, and 3) copies of transcripts and GRE scores. A small pool of applicants will then be asked to apply for the fellowships listed above and provide letters of recommendation.

Last Date to Apply: Until position is filled. Preferred starting date is 4 January 2009.

david.koons@usu.edu david.koons@usu.edu

---

## Vienna PopulationGenetics

The Vienna Population Genetics PhD program has just opened a new call:

[http://i122server.vu-wien.ac.at/pop/PhD/-phd\\_start.html](http://i122server.vu-wien.ac.at/pop/PhD/-phd_start.html) the available topics are:

- Detecting the signature of selection in structured populations
- Variation in life history traits in natural *D. melanogaster* populations
- Adaptation of *Drosophila* to temperature
- Functional characterization of intron variation
- Genetic basis of segregating morphological variation in *Drosophila*

deadline for receipt of applications: 19.9.2008

Christian Schlötterer Institut für Populationsgenetik  
Veterinärmedizinische Universität Wien Josef Bau-  
mann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-  
250775693 [http://i122server.vu-wien.ac.at/pop/-  
pop-gen.html](http://i122server.vu-wien.ac.at/pop/-pop-gen.html) christian.schloetterer@vu-wien.ac.at  
christian.schloetterer@vu-wien.ac.at

---

## Jobs

|                                                               |    |                                              |    |
|---------------------------------------------------------------|----|----------------------------------------------|----|
| Bodo Norway MarineEvolutionaryBiology .....                   | 22 | Smithsonian TropResInst DeputyDirector ..... | 30 |
| Brisbane Bioinformatics .....                                 | 23 | Sydney 2 BehaviourEvolution .....            | 30 |
| ChicagoBotanicGarden VicePresident .....                      | 23 | Taipei 4 EvolutionaryBiology .....           | 31 |
| France CNRS ATIP EvolutionaryBiology .....                    | 24 | UBern ResTech Fish .....                     | 31 |
| FranklinMarshallCollege temp Teaching .....                   | 25 | ULausanne PlantEvolution .....               | 32 |
| HopkinsMarineStation ResTech MarineConservation               | 25 | UMaryland Genomics bioinformatics .....      | 33 |
| KansasStateU ResTech PlantEvolutionaryGenet ...               | 26 | UNewBrunswick MarineProtistanDiversity ..... | 34 |
| NationalGeographic TheGenographicProject .....                | 26 | USGS WestVirginia Tech MolEvolution .....    | 34 |
| NESCent AsstDirScience .....                                  | 27 | USouthampton ChairBiologicalComputing .....  | 35 |
| Netherlands PlanktonEvolution .....                           | 28 | USussex ResTech SocialWasps .....            | 35 |
| NorthCarolinaStateU PlantMolecularSystematics ..              | 29 | UVienna TheoreticalEpidemiology .....        | 36 |
| NorthernArizonaU MicrobialGenomics FacilityMan-<br>ager ..... | 29 | Washington MuseumTech .....                  | 36 |

---

### Bodo Norway MarineEvolutionaryBiology

Dear colleagues

Even though the ad doesn't say so explicitly, evolution-  
ary biologists and behavioral ecologists are strongly  
encouraged to apply!

Professor/qualification fellowship in Marine ecology -  
Professor/professorstipendiat i marin økologi

The Faculty of Biosciences and Aquaculture seeks ap-  
plicants for the position of a full Professor in marine  
ecology with interest for aquaculture related issues.  
The candidate should be a well-established, professor-  
competent scientist having proven expertise in marine  
ecology. Research interests can include environmental  
requirements of intensive or extensive aquaculture. The

appointee should have a Ph.D in biology, postdoctoral  
and/or academic experience including supervision of  
doctoral students and a strong publication record, the  
potential to establish competitive, externally funded re-  
search programmes, and be willing to participate in in-  
terdisciplinary, collaborative research enhancing the ex-  
isting programmes. A strong commitment to teaching  
and supervision of MSc and PhD studies are important.  
Deadline 4. August 2008.

Follow the link for more information

[http://www.hibo.no/index.php?ID=3D11386&lang=  
3Dnor&displayitem=3D605&module=messageboard](http://www.hibo.no/index.php?ID=3D11386&lang=3Dnor&displayitem=3D605&module=messageboard)

Cheers,

Jarle Tryti Nordeide

Faculty of Biosciences and Aquaculture  
Bodø University College NO-8049 Bodø,  
Norway E-mail: Jarle.Nordeide@hibo.no  
<mailto:Jarle.Nordeide@hibo.no> Phone: (+47) 7551

7331 or 7551 7350 URL: <http://tryti.wordpress.com/>  
< <http://tryti.wordpress.com/> >

Jarle.Nordeide@hibo.no

---

## Brisbane Bioinformatics

### SENIOR RESEARCH FELLOWSHIP IN BIOINFORMATICS

The Queensland Institute of Medical Research (QIMR) is one of the largest medical research institutes in the southern hemisphere, with programs in areas such as cellular and molecular sciences, epidemiology and population health, cancer biology, biotechnology, infectious diseases and vaccine development. Situated on the Herston campus in Brisbane, it is closely affiliated with the major Queensland universities and teaching hospitals in Brisbane.

The Institute has excellent research infrastructure including genomics platforms and next generation sequencing. In addition to its basic research activities, QIMR operates a Good Manufacturing Practice (GMP) facility and is associated with a phase I clinical trials company (Q-Pharm).

QIMR is seeking to enhance its scientific Faculty by offering a Senior Research Fellowship to an individual with outstanding ability in the area of Bioinformatics, Computational Biology or a related discipline. The successful applicant will be required to provide strategic leadership in Bioinformatics at the Institute and develop collaborative links with scientists across a range of disciplines. In addition to the Fellowship salary, scientific funding will be provided to the successful applicant to assist him/her to establish their own research program within the existing divisions of the Institute.

The successful applicant will be expected to obtain competitive grants to support their own research program within 5 years. It is anticipated that the Fellow will be eligible to hold an adjunct university appointment.

A Competitive Fellowship Package commensurate with qualifications and experience will be offered. The package will include salary, on-costs and travel. Attractive salary packaging and superannuation options also apply.

Further Information is available from Professor Martin Lavin, Assistant Director on (07) 3362 0341 or [martin.lavin@qimr.edu.au](mailto:martin.lavin@qimr.edu.au)

Applications should include curriculum vitae, proof of qualifications, a 5 year plan for research (no more than 5 pages) and the names and contact details of five professional referees.

Please quote reference number 60/08 and send applications to: [vacancies@qimr.edu.au](mailto:vacancies@qimr.edu.au) or: Human Resource Officer, Queensland Institute of Medical Research, PO Royal Brisbane Hospital, QLD, 4029.

Applications Close: 5:00pm Friday 5 September 2008

Kind Regards

Melanie Anderson Human Resource Assistant Queensland Institute of Medical Research 300 Herston Road Ph: (07) 3362 0370 Fax:(07) 3362 0111

Peter M. Visscher Queensland Statistical Genetics Queensland Institute of Medical Research 300 Herston Road Herston, Queensland 4006, Australia tel. +61 7 3362 0166 fax. +61 7 3362 0101 <http://genepi.qimr.edu.au> < <http://genepi.qimr.edu.au/> > [peter.visscher@qimr.edu.au](mailto:peter.visscher@qimr.edu.au)

[Peter.Visscher@qimr.edu.au](mailto:Peter.Visscher@qimr.edu.au)

---

## ChicagoBotanicGarden VicePresident

Also see add at: <http://www.chicagobotanic.org/jobs/-index.php> THE CHICAGO BOTANIC GARDEN IS SEEKING:

Vice President, Academic Affairs

Reporting to the President and CEO, the Vice President of Academic Affairs is responsible for leading the development of the academic programs of the Chicago Botanic Garden, including the Joseph Regenstein, Jr. School of the Botanic Garden, the Plant Science and Conservation research efforts, and the Lenhardt Library, and supervises the Directors of those programs. The position also supervises an administrative assistant. The Vice President of Academic Affairs will guide the expansion of the Garden's plant science and conservation efforts to become an international center for research in rare and endangered plant biology, ecological restoration, plant evolution, horticultural ecology, and soil science. The Vice President of Academic Affairs will guide the growth of the Regenstein School of the Botanic Garden so that the knowledge of the Garden's scientists, professional horticulturists, and graduate students can be shared with a large and grow-

ing audience of novice and advanced students enrolled in the Regenstein School of the Botanic Garden, and guide the growth of the Lenhardt Library to become an outstanding information resource for Garden staff, members, visitors, and the botanic and horticulture professions. This position will serve as a member of the Garden's senior management team, and will help develop the Garden's strategic direction, annual operating goals, and budgets and resource allocations, including the supervision of a \$3.5 million annual operating budget. The person hired in this position will collaborate closely with Institutional Advancement to generate raised and earned revenue to support research, the School and Lenhardt Library. The Vice President of Academic Affairs serves as liaison with the Academic Affairs Committee of the Board of the Garden.

#### Candidate Profile:

We seek a leader with vision, scientific reputation, proven administrative and managerial experience in complex organizations, responsibility for substantial budgets, and experience in similar organizations. The ideal candidate will hold a Ph.D. in Botany or related field, with leadership recognition in his/her academic field. The candidate's university faculty and/or research experience should qualify him/her for adjunct associate or adjunct full-professor standing at Northwestern University and teaching courses through the Botanic Garden/Northwestern partnership is welcomed and encouraged, although the vice president's first year will most likely be completely occupied with senior administrative leadership responsibilities.

The position requires a high level of interpersonal and communication skills with the ability to work with internal and external constituencies equally well. The successful candidate will be results-oriented with strong political, analytical, organizational, budgeting, and grant-writing skills. He/she must be a well-spoken, creative and energetic individual who functions well within a team environment that includes cross-department coordination.

It is expected that candidate will have a passion for the people and programs associated with a botanical garden as well as high integrity and moral values that complement the culture of the Chicago Botanic Garden. This person will be a poised individual who is supportive, diplomatic, personable, able to manage multiple priorities, and is extremely comfortable with public speaking and relating to the media.

#### Mission of The Chicago Botanic Garden:

The mission of the Chicago Botanic Garden is to promote the enjoyment, conservation and understanding

of plants and the natural world.

#### Background:

The Chicago Horticultural Society was founded in 1890 to promote gardens and gardening. Today the Society has emerged as a leader in plant science and conservation, dedicated to training today's plant scientists and managing the nationally renowned Chicago Botanic Garden. A 385-acre living museum, the Garden is built on nine islands that house a collection of more than 2.3 million plants in 23 specialty gardens, three native habitats, six miles of shoreline, and 81 acres of waterways. It is one of the few botanic gardens accredited by the American Association of Museums.

The Garden's mission commits it to generate knowledge about plants, to share that knowledge widely, and to educate those who will continue to generate new knowledge and safeguard our biological heritage. In fulfillment of these commitments, the Garden has spent the last three decades developing a large, scientifically based plant collection that, along with a growing library, forms the foundation of the research and education activities. At the same time, the Garden leadership has assembled an extraordinary pool of talent and expertise, including some of the nation's foremost plant scientists.

— / —

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>

---

## France CNRS ATIP Evolutionary Biology

Centre National de la Recherche Scientifique ATIP PROGRAMMES (Actions Thématiques et Incitatives sur Programme) Call for Team leaders 2008-2009 The "Département des Sciences du Vivant" (Life Sciences Division) of the CNRS, offers an opportunity to scientists at the end of their postdoctoral training for developing an innovative independent research project while setting up their own group within a CNRS laboratory. Successful applicants will receive a three year grant (150 k for equipment and consumables), the possibility of hiring a postdoctoral fellow for two years, at least 50 m<sup>2</sup> of lab space and, whenever possible, technical assistance. At the end of the three years, the ATIP team



leaders may compete for a two year extension through the "ATIP Plus" programme. Eight programmes concern specific research areas (Evolutionary Biology, Biodiversity and ecosystem dynamics, Cell biology and Immunology, Developmental biology, Genetics, Microbiology, Systems biology, Neurobiology; from molecular to cognitive neurosciences, Structure-function relationships - dynamics of biomolecules and their assemblies), and one (ATIP "Blanche") is open to any project of high scientific quality related to Life Sciences. Applications from scientists presently working in a foreign country are particularly encouraged. Applicants must be less than 40 years old, or have defended their PhD thesis within the last ten years (exception may be made for women with children). At the beginning of the ATIP contract, applicants need not hold a permanent position within a French research organisation such as CNRS, INSERM or University. In this case, the CNRS will hire the team leader, and salaries will amount ~3,500 per month. However, he/she must apply for and obtain such a tenured position in order to be eligible for a possible two year extension ("ATIP Plus" programme). Applications for tenured positions are independent from the ATIP programme and have to be submitted in parallel. Applicants are not allowed to join a laboratory in which they have been PhD student or postdoctoral fellow for years. Application forms and more detailed information are available either directly or through the web site of the CNRS: <http://www.cnrs.fr/infoslabos/-atip/lifeatip.htm>. Applications must be written in English and addressed before October 1st, 2008 to: Jean HOUMARD - Chargé de Mission CNRS - Département des Sciences du Vivant 3, rue Michel Ange - F-75794 Paris Cedex 16. E-mail: [sdv-atipe@cnrs-dir.fr](mailto:sdv-atipe@cnrs-dir.fr)

Dr. Jean Houmard Chargé de mission Département Sciences du Vivant CNRS 3, rue Michel-Ange 75794 Paris cedex 16 Tél. 33 (0)1 44 96 40 29 Fax 33 (0)1 44 96 53 60

Jean Houmard <[sdv-atipe@cnrs-dir.fr](mailto:sdv-atipe@cnrs-dir.fr)>

---

### FranklinMarshallCollege temp Teaching

EVOLUTION/POPULATION  
BIOLOGY/ECOLOGY

The Biology Department of Franklin & Marshall College invites applications for TWO VISITING ASSISTANT PROFESSOR positions, beginning January

2009. The first position is for spring semester 2009 and academic year 2009-10; the second is for spring semester 2009 only. Teaching responsibilities in spring semesters will include lectures and laboratories in an evolution-centered, introductory course that includes Mendelian genetics and ecology. The first position will also involve teaching an upper-level lecture/laboratory course in evolution, behavioral ecology, or population biology in Fall 2009. Candidates should have a Ph.D. and demonstrated strength in teaching and research. Franklin & Marshall College has a tradition of excellence in science and student research. A new life sciences building opened in August 2007. Please send a letter of application, a statement that includes plans for actively engaging undergraduates through teaching, curriculum vitae, and undergraduate and graduate transcripts to Prof. D. Ardia, Department of Biology, Franklin & Marshall College, Lancaster, PA 17604-3003. Applicants should also have 3 reference letters sent directly to Prof. Ardia. Review of applications begins August 8, 2008. Electronic submissions cannot be accepted. Telephone: 717-291-3949; Fax: 717-358-4548; e-mail: [dardia@fandm.edu](mailto:dardia@fandm.edu); website: <http://www.fandm.edu/-biology.xml> Franklin & Marshall College is a highly selective liberal arts college with a demonstrated commitment to cultural pluralism. Equal Opportunity Employer

Please consider the environment before printing this e-mail or any other unimportant document

Dan Ardia Assistant Professor of Biology Franklin & Marshall College P.O. Box 3003 (for couriers: 415 Harrisburg Ave.) Lancaster, PA 17604 1-717-291-3949 Fax 1-717-358-4548 [daniel.ardia@fandm.edu](mailto:daniel.ardia@fandm.edu) <http://edisk.fandm.edu/daniel.ardia/index.html> [daniel.ardia@fandm.edu](mailto:daniel.ardia@fandm.edu) [daniel.ardia@fandm.edu](mailto:daniel.ardia@fandm.edu)

---

### HopkinsMarineStation ResTech MarineConservation

Part-time (75% FTE), benefits eligible, research technician position at in Steve Palumbi's lab at Stanford University's Hopkins Marine Station, in Pacific Grove, CA. Under the direction of the Principal Investigator the technician will assist with research related to genetic characterization of populations of marine vertebrates and invertebrates in the context of ongoing research into marine conservation and management. The primary responsibilities of the technician will include collecting larvae and adult specimens, extracting DNA

and documenting genetic variation. This will require the use (or development) of many research skills using a variety of molecular genetic tools. In addition, the technician will participate in a variety of research activities including: field monitoring of multiple sites in central California, animal care, and laboratory maintenance. There is potential for extension of the technician position to other research projects as well as the possibility of co-authorship of at least one resulting publication.

**QUALIFICATIONS:** The successful applicant will be highly organized, have attention to detail, be able to work as an independent part of a team, have a basic understanding of and facility with standard computer software programs, and have practical experience with a variety of standard molecular tools (for example, DNA extraction, PCR, gel electrophoresis, DNA sequencing, etc). In addition to these basic requirements, we desire an applicant with an interest in marine ecosystems and their ecological functioning.

Starts approximately 8/1/08

To apply contact: Tim Knight email:  
trknight@stanford.edu  
trknight@stanford.edu

---

### KansasStateU ResTech PlantEvolutionaryGenet

#### RESEARCH TECHNICIAN, PLANT EVOLUTIONARY GENETICS

There is an opening for a research technician in the Ungerer laboratory in the Division of Biology at Kansas State University. The technician will participate in ongoing research projects in the area of plant evolutionary genetics and additionally serve in the role of laboratory manager. Specific job tasks will include basic laboratory work (DNA/RNA extraction, PCR, primer design, and DNA sequencing), greenhouse work (plant care), ordering/tracking of supplies and reagents, and participation in the training of undergraduate students. Minimum requirements include a B.S. or B.A. degree in biology or related field, 1-2 years experience in molecular biology (laboratory skill set described above), basic computer skills (e.g., word processing and spreadsheets), and familiarity with, or willingness to learn, basic growth chamber/greenhouse plant care. For additional information contact Mark Ungerer at mcungere@ksu.edu.

To apply, send by email a cover letter and C.V., and have 3 letters of recommendation sent to the address below. Review of applications will begin July 7, 2008 and continue until the position has been filled. Kansas State University is an equal opportunity employer.

Mark Ungerer Division of Biology Kansas State University Manhattan KS 66506 Office: 785.532.5845 Email: mcungere@ksu.edu

mcungere@ksu.edu mcungere@ksu.edu

---

### NationalGeographic TheGenographicProject

#### Genographic Fellows Program

National Geographic has partnered with IBM to carry out one of the most important and far reaching global research projects in the history of the National Geographic Society, The Genographic Project.

The Project announces the creation of the Genographic Fellows Program. These short-term fellowships (3-6 months, with the possibility of renewal) will be filled by researchers working on specific problems of interest, as determined through consultation with the Fellow and the Projects scientific team. Reporting to the Project Director, Dr. Spencer Wells, each fellow will pursue focused analytical research during his or her tenure. Applications will not be accepted for sampling or laboratory work. The goal of the Fellows program is to analyze the growing Genographic database, which currently contains over 200,000 records from public participants and indigenous and traditional peoples.

Successful applicants will typically have a PhD in population genetics, experience in computational analysis of genetic data, and familiarity with mitochondrial DNA and Y-chromosome phylogeography. In rare circumstances a successful applicant may not have received a PhD, but will have distinguished him or herself through insightful analyses of genetic genealogy data. Each fellow will have the option (pending mutual agreement) of working at National Geographic headquarters in Washington, DC, at one of Genographics 11 regional and associate centers, or at his or her home institution while on sabbatical leave. Salary will be commensurate with experience.

The successful candidate will have the opportunity to focus on the development and/or implementation of computational techniques for the analysis of human

DNA data, to interact with participating faculty, post-docs and students in the various interdisciplinary research groups and centers around the world.

Highly motivated individuals interested in population genetics and human evolution are encouraged to apply. Two fellowships will be awarded in 2008, to commence in the second half of this year. Applications should include a current CV, a description of the proposed research topic not to exceed two pages, and two letters of recommendation from colleagues familiar with the candidates work.

For more information about the project please visit: <http://www.nationalgeographic.com/genographic>

Responsibilities: - Identify and pursue specific questions of interest in consultation with the project's scientific team.

- Perform computational analysis of the current Genographic database, which currently contains over 200,000 records from public participants and participating indigenous and traditional communities.

- Assist the Project Director in designing research projects and in the publication process drawing on findings coming out of the research database analysis.

- Survey the scientific literature regularly for relevant articles, stories and papers.

Successful candidates will have the following qualifications: - PhD in human Population Genetics or related field. In rare circumstances a successful applicant may not have received a PhD, but will have distinguished him or herself through insightful analyses of genetic genealogy data.

- Experience in computational analysis of genetic data, and familiarity with mitochondrial DNA and Y-chromosome phylogeography.

- Research experience (first-authored publications in populations genetics would be an advantage).

Skill Requirements: - be proficient in the use of software packages for phylogenetic and population genetics analysis (Network, Arlequin, Batwing, etc...)

- Highly motivated, with strong ability to work independently.

- Fluency in English essential and a working knowledge of at least one other language is helpful.

- Interest in anthropology and/or linguistics would be an advantage.

An overview of research topics and relevant papers already published by the Genographic Project can be found at: <https://www3.nationalgeographic.com/>-

[genographic/resources.html](http://www.nationalgeographic.com/genographic/resources.html)

For more information and to apply, please visit <http://www.nationalgeographic.com/jobs>. (Fellow, Genographic, Job ID #3504). Review of applications will begin immediately and continue until the position is filled.

David F. Soria Hernanz, Ph.D. Research Fellow The Genographic Project 1145 17th Street NW Washington DC Tel 202 775 6137

[DSoria@ngs.org](mailto:DSoria@ngs.org)

---

## NESCent AsstDirScience

The National Evolutionary Synthesis Center ([www.nescent.org](http://www.nescent.org) < <http://www.nescent.org> >), NESCent, is a national Center sponsored by the NSF to promote synthetic activities in evolutionary biology.

The Center seeks a full time Assistant Director for Science. The Assistant Director will assist the Director and Associate Director for Science and Synthesis in promoting the scientific activities of the Center and will be involved in all scientific activities of the Center. Specific tasks will include coordinating the reporting functions of the Center, including developing assessment tools and surveys; working with informatics staff to implement reporting modules of the administrative database; and working with Directors and other senior staff in preparing grant applications, annual reports and documents for site visits and advisory boards. The individual will also help to oversee the logistics of the proposal review system, and to coordinate other Center activities, including Darwin Day and other symposia and workshops. The individual filling this job should have a Ph.D. in evolutionary biology or related field, several years of postdoctoral experience and an interest in developing experience in administrative activities.

Candidates should submit a letter of application discussing their background and interests, a CV and names of three individuals willing to provide letters of recommendation to AcademicJobsOnline < <https://academicjobsonline.org/ajo/Duke/NESCent> > Applications will be considered until the position is filled; applications received before July 15 will be guaranteed consideration. For more information see our web site at NESCent Employment Opportunities < <http://www.nescent.org/about/employment.php> >. Duke University is an Equal Opportunity/Affirmative Action

Employer.

Karen Henry <khenry@nescent.org>

## Netherlands PlanktonEvolution

The Netherlands Institute of Ecology (NIOO) is offering young, talented researchers, tenure-track positions. These staff members are expected to develop their own line of research within a particular field. NIOO's career policy is characterised by flexible personnel management with a focus on the individual. Academic achievements are leading for the successful tenure-track procedure. The NIOO offers the candidate excellent research facilities and ample opportunities for professional development and supplementary training and education.

The appointment will be on a temporary basis for a maximum of 6 years. On completion of 5 years of employment there will be an assessment of performance based on established criteria. If the outcome of the assessment is positive, the researcher will be promoted to the rank of senior researcher with tenure.

TENURE-TRACK POSITION FOR AN EXPERIMENTAL/EVOLUTIONARY PLANKTON ECOLOGIST

Vacancy number CL-AFW-08416

Job description: The position: The position is part of the department of Aquatic Food Webs (AFW) that aims to elucidate how evolutionary principles, ecological mechanisms and abiotic factors govern the dynamics and structure of lake food webs. We focus on interacting ecological and evolutionary mechanisms that underlie the major patterns and processes in freshwater food webs. The new position will strengthen the present ecological and theoretical lines of research of the department.

Personal profile: The successful candidate should be an ecologist with i) preferably expertise in planktonic food web interactions and ii) with considerable expertise in experimental and evolutionary ecology. The candidate must be able to cover evolutionary questions and genomic tools within aquatic food web studies. The candidate should hence have a proven interest in these topics. The candidate's experience should reflect the broad range of methodologies used by the department, i.e. ranging from the field (e.g. mesocosms) to the laboratory (e.g. chemostats), and is expected to develop a genomic (e.g. gene expression profiling) research line.

The candidate must be capable of requiring and supervising externally acquired PhD students.

Requirements:

The successful candidate has the following qualifications:

A Ph.D. degree and preferably two years postdoctoral experience abroad;

Excellent research and organisational qualities, and a good publication record;

The ability to successfully acquire external research financing.

Appointment: The appointment will be on a temporary basis for a maximum of 6 years. The appointed scientist will be evaluated after 3 and on completion of 5 years of employment there will be an assessment of performance based on established criteria. Based on the assessment the researcher will be promoted to the rank of senior researcher with tenure.

Salary: The salary will depend on qualifications and work experience from EUR 3129 gross per month up to a maximum of EUR 4284.- gross per month (scale 11 CAO-NU) for a full-time job.

Information: Please contact the head of department Prof. Dr. E. van Donk (e.vandonk@nioo.knaw.nl) or Dr. W.M. Mooij (w.mooij@nioo.knaw.nl). More information can be found on the NIOO website ([www.nioo.knaw.nl](http://www.nioo.knaw.nl) <<http://www.nioo.knaw.nl/>>).

Applications: Please send your application including complete curriculum vitae and the vacancy number to Prof. Dr. H.J. Laanbroek, NIOO, Centre for Limnology, P.O. Box 1299, 3600 BG Maarssen, the Netherlands or by e-mail to [m.albers@nioo.knaw.nl](mailto:m.albers@nioo.knaw.nl). The closing date for application is June 22th 2008.

Prof. dr. Ellen van Donk Netherlands Institute of Ecology - Centre for Limnology (NIOO-KNAW) Rijksstraatweg 6, 3631 AC, Nieuwersluis P.O.Box 1299, 3600 BG Maarssen The Netherlands Tel: +31 (0)294 239353/239300 Fax: +31 (0)294 232224 Email: [e.vandonk@nioo.knaw.nl](mailto:e.vandonk@nioo.knaw.nl) <<mailto:e.vandonk@nioo.knaw.nl>> Website:

[www.nioo.knaw.nl](http://www.nioo.knaw.nl) <[file://www.nioo.knaw.nl/](http://www.nioo.knaw.nl/)> Personal website: [www.nioo.knaw.nl/ppages/evandonk](http://www.nioo.knaw.nl/ppages/evandonk) <<https://webmail.cl.nioo.knaw.nl/exchweb/bin/redir.asp?URL=http://www.nioo.knaw.nl/ppages/evandonk>> <<http://www.creamofscience.org/en/page/keur.view/-16003.keur>> for (downloading) pdf's of my publications

"Donk, Ellen van" <[E.vandonk@nioo.knaw.nl](mailto:E.vandonk@nioo.knaw.nl)>

---

## NorthCarolinaStateU PlantMolecularSystematics

### Job Description

Position Title: Research Specialist Department of Plant Biology, North Carolina State University Raleigh NC USA

We are seeking qualified applicants for a Research Specialist position to join a plant molecular systematics and evolution lab. Research areas of the lab encompasses plant systematics, biogeography, conservation genetics, and evolutionary developmental genetics. Main duties of the position are to manage the day-to-day operations of the lab and assist the principle investigator in all ways possible to thrive the program (including generating and analyzing data, assisting in grant and manuscript writing, providing technical and safety training to new lab personnel, and managing budget, etc.). In addition, this position will also provide general facilities support for departmental research programs in Gardner Hall at NCSU. These include managing and the overseeing the centralized deionized water system, departmental autoclave, and critical shared equipment, as well as coordinating with the departmental facilities liaison on issues related to research facilities, electrical and water interruptions, and other research-related facilities issues.

Requirements: Degree in BS degree in Biology or Plant Biology is required. A degree in MS in plant biology is preferred. Additional requirements include research background in evolutionary biology and techniques in gene isolation, qRT-PCR, in-situ hybridization, gene transformation, protein analysis, genome sequencing, gene cloning, and southern hybridization. Research experience in plant molecular systematics, plant development and evolution, population genetics, and phylogeography are preferred. Qualified applicants should be self-motivated, well-organized, have effective written and verbal communication skills in English, and be able to work as a part and leader of a team.

Salary or range: \$41,000 for 12 months Start Date: Aug. 1st 2008 Contact: jenny\_xiang@ncsu.edu

Jenny Xiang

Qiu-Yun (Jenny) Xiang, Ph.D. Associate Professor Department of Plant Biology North Carolina State University Gardner Hall 2215 Raleigh, NC 27695-7612

USA Phone: 919-515-2728 Fax: 919-515-3436 Home-page: <http://www4.ncsu.edu/~qyxiang> Jenny Xiang <jenny\_xiang@ncsu.edu>

---

## NorthernArizonaU MicrobialGenomics FacilityManager

“BSL-3 Select Agent Research Project Coordinator/Project Director

The Center for Microbial Genetics and Genomics on the campus of Northern Arizona University in Flagstaff, Arizona, is seeking a BSL-3 Select Agent Biocontainment Facility manager for a new BSL-3 Facility to be operational in June 2008. The Facility consists of ca. 1800sqft of Select Agent BSL3 laboratory space and ca. 4500sqft of non-Select Agent BSL2 laboratory space. The Center is a large and growing Research facility with over 50 Faculty, Staff and Students working on multiple research projects focused on understanding the evolution of microbial pathogens, with a strong emphasis on Biodefense. The Center also has close ties with the Translational Genomics (TGEN) Microbial Pathogen Facility, also located in Flagstaff. Reporting to the Center Assistant Director, the incumbent, working closely with the NAU RO and an Assistant Facility Manager, will oversee daily operation of the Select Agent Facility to enable high quality scientific research, biosafety, regulatory compliance and fiscal soundness. Responsibilities include development, implementation and oversight of policies and SOP systems required to operate the facility and manage personnel. Preference will be given to candidates experienced with the operation and management of biosafety level 3 laboratories. The position will require approximately fifty percent effort managing the facility, with the balance devoted to scientific research on relevant projects. This position will be filled at either a Research Project Coordinator or Project Director level, depending upon the academic level and work experience of the successful candidate.

For more information and application instructions, please go to <http://hr.nau.edu/m/content/view/620/-476/>, vacancy #557656, or contact James Schupp at James.Schupp@nau.edu.”

+

Jim Schupp <James.Schupp@nau.edu>

---

## Smithsonian TropResInst DeputyDirector

### IS SEARCHING FOR A DEPUTY DIRECTOR

The Smithsonian Tropical Research Institute (STRI), headquartered in the Republic of Panama, seeks an excellent scientist with extensive administrative and research experience to serve as Deputy Director. The Deputy will assist the Director in fostering and evaluating staff research programs, and administrative and outreach support activities, by providing leadership and guidance to staff, fellows, students and visiting scientists. The Deputy also has significant liaison roles with Panamanian government authorities, national education institutions and civil society.

STRI is a unit of the Smithsonian Institution that is primarily devoted to fundamental research in tropical sciences, including animal behavior, anthropology, archaeology, botany, ecology, evolution, geology, molecular biology, paleontology, plant physiology, and soils science; additional programs center on conservation biology and applied ecology (see <http://www.stri.org>).

STRI maintains modern research laboratories, a library, administrative and support centers in Panama City, several major facilities for marine and terrestrial field research in Panama, a 100' research vessel, and canopy access cranes. STRI coordinates a global network of forest-dynamics plots through its Center for Tropical Forest Sciences/SI Global Earth Observatories. In collaboration with other institutions, STRI also participates in the operation of large research facilities in Brazil and Kenya. STRI employs approximately 40 scientists and 300 technical and support personnel, and annually hosts more than 1000 scientific visitors. STRI is committed to advanced scientific training through rigorous Fellowship and Internship Programs, and via cooperative programs with leading educational institutions.

Applicants should have a Ph.D and research experience in a relevant field of science, and a record of excellence in scientific administration. Fluency in Spanish, and familiarity with Latin America, is desirable.

Interested candidates should submit a curriculum vitae; a summary of administrative experience and accomplishments; a summary of scientific research interests; a vision statement on the future of tropical biology and

related fields; and the names and contact information of five potential referees. Annual salary and benefits are commensurate with experience.

Review of applications will begin in August 2008 and continue until the position is filled. Please send applications electronically to the Director of STRI, c/o Ms. Luz Latorraca, Office of Human Resources at: [LatorraL@si.edu](mailto:LatorraL@si.edu). Address inquiries concerning the position to Dr. William Wcislo, Acting Deputy Director, at: [WcisloW@si.edu](mailto:WcisloW@si.edu)

STRI is an equal opportunity employer and appointments are made regardless of nationality.

“Bilgray, Adriana” <[BilgrayA@si.edu](mailto:BilgrayA@si.edu)>

---

## Sydney 2 BehaviourEvolution

The Centre for the Integrative Study of Animal Behaviour at Macquarie University (Sydney, Australia) is seeking to fill two permanent academic positions (Level C/D) from four areas:

Neuroethology Sensory Ecology Performance Physiology Quantitative Genetics

Ref. 21359 / 21360 Animal Behaviour Macquarie's CORE in Animal Behaviour builds on established strength in the analysis of mechanism and function (<http://galliform.bhs.mq.edu.au/~cisab/>). We wish to add breadth to our research program by making additional appointments in two of four target areas.

This is an ideal opportunity for imaginative scientists who are prepared to challenge existing paradigms and wish to work in a stimulating collaborative environment.

Applications are invited from:

Neuroethologists interested in examining topics such as sensory processes or the way patterns of natural behaviour develop or are encoded in an organism

Sensory Ecologists examining how perceptual abilities and computational processing shape social behaviour

Performance Physiologists investigating the capacity of individuals for functionally critical behaviour, with the goal of understanding constraints and processes

Quantitative Geneticists studying the heritability of behaviour and/ or experimentally driving evolution in model systems.

Essential criteria Applicants must have:

\* PhD or equivalent \* International scientific reputation  
\* Outstanding record of peer-reviewed publication with high impact \* History of success in attracting external research funding \* Ability to recruit and supervise postgraduate students \* Research interests that complement those of existing staff

Desirable criteria Preference will be given to applicants with:

\* Ability to communicate and interact effectively with students, staff and the community \* Excellence in teaching, particularly in upper-level courses designed to expose undergraduates to new research findings \* Proposed research program that can be accommodated within existing infrastructure.

Base salary range \$(Aus) 84,413 - \$(Aus) 111,773, plus 17% employer superannuation contribution.

Enquiries: Chris Evans on +61 (0)2 9850 9230 or email [chris.evans@mq.edu.au](mailto:chris.evans@mq.edu.au)

Closing date: June 30, 2008.

Macquarie University is an Equal Opportunity Employer with a commitment to diversity and social inclusion. We encourage applications from Indigenous Australians; people with a disability; those from culturally and linguistically diverse backgrounds; and women (particularly for senior and non-traditional vacancies).

N.B. only those applications submitted via the Macquarie University Online Recruitment System will be accepted.

For further information please visit [www.research.mq.edu.au/excellence](http://www.research.mq.edu.au/excellence) Explanatory notes The Australian academic scale has five levels (A-E). The usual starting appointment for a recent PhD is Level A. Staff with some years of postdoctoral experience typically begin at Level B. Level C is hence roughly analogous to the North American rank of Associate Professor, while Level D corresponds approximately to the lower steps in the full Professor scale.

Simon Griffith Centre for the Integrative Study of Animal Behaviour Macquarie University Sydney, NSW 2109, Australia. phone: +61 9850 4186 fax: +61 2 9850 9231 <http://galliform.bhs.mq.edu.au/~simon/> [simon.griffith@mq.edu.au](mailto:simon.griffith@mq.edu.au) [simon.griffith@mq.edu.au](mailto:simon.griffith@mq.edu.au)

---

## Taipei 4 Evolutionary Biology

The Biodiversity Research Center, Academia Sinica, Taipei, Taiwan is in an expansion mode, with four tenure-track openings now (open-rank but junior scientists preferred) and more openings in the near future. It has recently recruited a new director, Wen-Hsiung Li, who is also the James Watson Professor at University of Chicago. Information on the center's research activities can be found on the web at <http://-biodiv.sinica.edu.tw/en2007/>. The center currently has several active PIs in marine ecology, especially in the West Pacific marine ecology. It invites applications for two positions in marine ecology. The impact of climate change on marine ecosystems is particularly encouraged, but other areas of ecology will also be considered. The center is also strong in molecular and genomic evolution and has recently set up a sequencing core with one 454 and one Solexa machine. The Academia Sinica wants to establish a strong program in microbial genomics and the center is now inviting applications for two positions in microbial diversity. For each position, a Ph.D. with a minimum of two years of relevant postdoctoral research experience is preferred. The positions will be open until filled; however, the first review will be conducted before or on August 1. An applicant should submit the names and e-mail addresses of three references along with CV (including a list of publications), representative papers (pdf files), and a statement of past achievements and future research interests to Ms. Miao-Suey Lin ([zomslin@gate.sinica.edu.tw](mailto:zomslin@gate.sinica.edu.tw)).

[wli@uchicago.edu](mailto:wli@uchicago.edu)

---

## UBern ResTech Fish

RESEARCH TECHNICIAN - INSTITUTE OF ECOLOGY & EVOLUTION, UNIVERSITY OF BERN, SWITZERLAND

Aquarium facility manager and molecular lab technician

The Division of Aquatic Ecology and Macroevolution at the Institute of Ecology & Evolution (former Zoology), University of Bern, Switzerland seeks a research tech-

nician to maintain its new tropical fish breeding and experimental facilities in Bern, and to perform benchwork in its genetics lab.

Job description:

50%: Maintenance of the fish breeding and experimental facility. Since this facility is new, duties will include initial setup of the aquarium system. The technician will be responsible for the running of the system as a whole, for the health and well-being of the fish housed in the facility, and for the implementation of experimental breeding schemes.

30%: Molecular lab work. One of the foci of our division is research on the genetics of speciation and adaptation in fish, and the responsibilities of the technician will include bench work for the collection of genetic data, such as DNA extraction, PCR, sequencing, fragment analysis, RNA extraction, RT-PCR.

10% Provision of assistance to scientific staff and students in laboratory techniques

10%: Ordering of supplies and consumables, arranging repair and maintenance of equipment, and book-keeping.

Candidate profile:

The successful candidate will have a strong desire to participate in and contribute to scientific research in the field of evolutionary biology.

- Pre-existing expertise in maintaining a large aquarium facility is a plus, but an interest in being trained in the same is a requisite.
- Knowledge of basic molecular lab techniques: At least basic familiarity with some or all of the above mentioned techniques is a plus.
- The candidate will be systematic and orderly in record keeping. Detailed and accurate records of all aquarium and lab-related activities are required for scientific and accounting purposes.
- Fluency in German will be advantageous.
- The successful candidate must have a driver's license and driving record that qualifies her/him to drive university vehicles

Pay details:

Payment is according to University of Bern salary scheme

Contact:

Interested candidates may apply electronically with a covering letter and CV to Professor Ole Seehausen [ole.seehausen@aqua.unibe.ch] before 30th of

June 2008. We will consider applications until the position is filled.

Ole Seehausen Institute of Ecology & Evolution University of Bern Baltzerstr. 6, CH-3012 Bern & Centre of Ecology, Evolution and Biogeochemistry Eawag, Seestrasse 79 CH-6047 Kastanienbaum

<http://www.fishecology.ch> Ole.Seehausen@eawag.ch

---

## ULausanne PlantEvolution

Assistant (tenure track) or Associate Professor in Plant Evolution, Lausanne, Switzerland

The University of Lausanne invites applications for an assistant (tenure track) or associate professorship. All areas of plant evolution will be considered and research programs taking an experimental approach are particularly welcome. The position will be in the Department of Ecology and Evolution (<http://www.unil.ch/-dee>) which has a long track record of excellence in research. The Department of Ecology and Evolution has approximately 20 research groups, 40 postdoctoral researchers and 50 PhD students working on a wide range of different fields, including:

â Evolution of Insect Societies â Biology and Ecology of Ants â Evolution of Host-Parasites Interactions â Speciation and Phylogeny â Evolutionary Biology of Learning and Memory â Evolutionary Genetics and Ecology of Social Life â Plant Biosystematics and Population Genetics â Mating Systems and Population Genetics â Ecology and Evolution of Dispersal â Evolution and Maintenance of Genetic Colour Polymorphism â Ecology and Evolution of Symbiotic Organisms â Evolutionary Bioinformatics â Evolutionary Biology and Ecology: - Evolutionary Conservation Biology

In addition, to collaboration within the Department there are many possibilities for collaboration with other departments that are located in the same building or nearby, such as Plant Molecular Biology, Genomics and Microbiology. The Department also runs the very successful masters program "Behavior, Evolution and Conservation" (<http://www.unil.ch/bec>) and is the coordinating institute of an inter-university doctoral program "Ecology and Evolution" (<http://www.unil.ch/-ee>) between 5 Swiss universities.

A generous start-up package and state-of-the-art research infrastructure will be available within an environment which favors collaborations. The University



of Lausanne is situated on a campus on the shores of Lake Geneva that provides an attractive and stimulating environment for research and a high standard of living.

The successful candidate should have an excellent record in Plant Evolution and is expected to develop an internationally recognized research program funded by external sources. Teaching duties include an undergraduate class in botany. The appointee will supervise Masters and PhD students and participate to other training activities of the Department. The job description is available on the Web at the address [www.unil.ch/fbm/page2295\\_fr.html](http://www.unil.ch/fbm/page2295_fr.html). Applications, including a curriculum vitae with a complete list of publications in which the five most significant are identified, a brief statement of research program and teaching philosophy, and the names of three referees, should be sent by 22.08.2008 to Prof. Francioli, Dean of the Faculty of Biology and Medicine, University of Lausanne, Rue du Bugnon 21, CH-1005 Lausanne, Switzerland.

Women are encouraged to apply.

For further information, contact [ian.sanders@unil.ch](mailto:ian.sanders@unil.ch) or [jerome.goudet@unil.ch](mailto:jerome.goudet@unil.ch).

Ian R. Sanders Professor of Evolutionary Biology Dept. of Ecology & Evolution University of Lausanne Biophore Building 1015 Lausanne Switzerland

Tel (direct): +41 21 692 4261 Tel (Secretary): +41 21 692 4260 Fax: +41 21 692 4265 Email: [ian.sanders@unil.ch](mailto:ian.sanders@unil.ch)

[http://www.unil.ch/dee/page7238\\_en.html](http://www.unil.ch/dee/page7238_en.html)

Sanders <[Ian.Sanders@unil.ch](mailto:Ian.Sanders@unil.ch)>

Ian

team of collaborative investigators with a broad spectrum research program related to the genomics of infectious disease agents, human microbial metagenomics, functional genomics, and bioinformatics. The impact of the IGS team on the field of genomics has been substantial, with more than 500 publications during the past 15 years that have been cited more than 30,000 times.

Within the Institute are two state-of-the-art resource centers: the Genomics Resource Center (GRC), a high-throughput, state-of-the-art core laboratory supporting the scientific programs of IGS and external collaborators with multiple DNA sequencing, genotyping, and array platforms and the Informatics Resource Center (IRC) which provides genome assembly, annotation, and data analysis services.

IGS is recruiting additional faculty members to join its interdisciplinary scientific team. We are looking for highly collaborative investigators at all stages of their careers that have a track record in the application of large-scale approaches to the study of biological systems. We are looking to complement our existing expertise, and applicants with funded research programs in comparative genomics, statistical genomics, human genetic variation, and systems biology are encouraged to apply. There are many opportunities for collaborations with colleagues in IGS and across the School of Medicine in both basic and translational research in cardiovascular disease, cancer biology, and infectious disease and participation in graduate and medical education.

IGS is in a period of rapid expansion with many new research appointments anticipated in the next five years. To view detailed job descriptions for open IGS positions see our website at <http://www.igs.umaryland.edu> All faculty and postdoctoral applicants should submit curriculum vitae, statement of research interest and names of three references to [IGS-jobs@som.umaryland.edu](mailto:IGS-jobs@som.umaryland.edu)

Consideration of candidates will begin upon receipt of applications and will continue until the positions are filled. AA/EOE/ADA

[www.hr.umaryland.edu](http://www.hr.umaryland.edu)

[carollee@wisc.edu](mailto:carollee@wisc.edu)

[carollee@wisc.edu](mailto:carollee@wisc.edu)

---

## UMaryland Genomics bioinformatics

UNIVERSITY OF MARYLAND School of Medicine  
INSTITUTE FOR GENOME SCIENCES

The newly created Institute for Genome Sciences (IGS) at the University of Maryland, School of Medicine seeks to fill several Faculty, Postdoctoral Fellow and Bioinformatics positions.

The Institute is led by Claire M. Fraser-Liggett, Ph.D., one of the world's preeminent genome scientists and previous Director and President of the Institute for Genomic Research (TIGR). The Institute for Genome Sciences houses an interdisciplinary, multi-departmental

---

## UNewBrunswick MarineProtistanDiversity

### Position in Marine Protistan Diversity

The Department of Biology, University of New Brunswick (Fredericton), seeks applicants for a tenure-track position at the Assistant-Associate Professor level in Marine Protistan Diversity. The successful candidate will develop a strong research program examining genomic diversity from evolutionary and environment perspectives, emphasizing comparative genomics and protistan diversity at the species to genomics level in marine heterotrophic and/or phototrophic protists. Specific research areas include, but are not limited to: exploring species diversity through molecular biology; evolution of organelles and organismal attributes; genome structure and function; and diversity with regards to biochemical and cellular processes. The candidate will be expected to mentor undergraduate and graduate students, as well as postdoctoral fellows, and teach undergraduate and graduate courses appropriate to departmental need and the candidates expertise. The successful candidate must have a track record in research that will be highly competitive in attracting external research funding and HQP. The position is associated with the Canadian Institute for Advanced Research (CIFAR) and its newly established Integrated Microbial Biodiversity (IMB) program. The successful applicant will join a network of international researchers as a Scholar in the CIFAR IMB Program (information on this program can be found at [www.cifar.ca](http://www.cifar.ca)). The applicant will also contribute to the Marine Environmental Barcoding component of the international Barcode of Life, a project aimed at investigating protistan biodiversity in the ocean with molecular techniques. The successful candidate will join an internationally recognized group of researchers at UNB working on protistan molecular biology, comparative genomics, bioinformatics and biodiversity (CEMAR: [www.unb.ca/ceamar](http://www.unb.ca/ceamar)). Additional research strengths in the Department of Biology include aquatic ecology and fish biology, conservation biology, and evolutionary biology. Information about Biology at UNB is available at [www.unb.ca/fredericton/science/biology](http://www.unb.ca/fredericton/science/biology).

A PhD and relevant postdoctoral experience is required.

The closing date for applications is August 4, 2008. To apply, send a letter describing your research and teaching interests, a curriculum vitae with names, addresses, and e-mail contacts for three referees, representative publications, and a statement of teaching philosophy to:

Dr. Gary W. Saunders Chair & Professor, Dept. of Biology Canada Research Chair in Molecular Systematics & Biodiversity Coordinator, Centre for Environmental

& Molecular Algal Research (CEMAR) Director & Algal Curator, Connell Memorial Herbarium University of New Brunswick Fredericton, NB, Canada, E3B 5A3 F: 506 453-3583 <http://www.unb.ca/ceamar/> All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. Applicants should indicate current citizenship status. This position is subject to budgetary approval.

THE UNIVERSITY OF NEW BRUNSWICK IS COMMITTED TO THE PRINCIPLE OF EMPLOYMENT EQUITY

Gary Saunders <[gws@unb.ca](mailto:gws@unb.ca)>

---

### USGS West Virginia Tech MolEvolution

A full-time Biological Technician I position available to perform contract work for the U.S. Geological Survey Leetown Science Center (LSC). The work supports Dr. Tim King's Laboratory in the LSC Aquatic Ecology Branch's molecular ecology and evolution research program focusing on the conservation genetics of threatened and endangered species. The position is based at the LSC in Kearneysville, West Virginia. Qualified individuals must possess a bachelor's degree (or equivalent) in Biology and knowledge of general molecular genetics techniques used to extract, purify, quantify, electrophorese, and hybridize total genomic DNA or RNA from tissue samples. The qualified candidate will demonstrate experience with all aspects of good laboratory techniques such as data recording, and be able to enter and analyze experimental data using spreadsheets, graphics, and word-processing software. The individual will assist Dr. King and work closely with other Government and contractor staff by supporting some or all of the following tasks depending on the individual's specific qualifications:

- ? Perform laboratory analyses, laboratory experimentation, and data sampling to support AEL investigations of genetic variability of fish, mammals, reptiles, amphibians, and mollusks.
- ? Extract, purify, and quantify total genomic DNA or RNA from tissue samples using fluorometric techniques.
- ? Amplify specific DNA segments by the polymerase chain reaction (PCR) technique.
- ? Quantify digests of amplified regions with restriction enzymes.
- ? Support electrophoretic analysis of total genomic DNA, PCR products, and restrictase digests of DNA preparations, and general proteins.

Clone digested genomic DNA and PCR products. ? Perform DNA sequencing using automated sequencers, e.g., Applied Biosystems 3130XL. ? Maintain a daily work journal of tasks accomplished. The position may require light field work and infrequent related travel. Attendance at relevant training courses in molecular biological techniques may be offered/required at the Center. Base wage: \$21.36 per hour, 40 hours per week.

IAP World Services offers comprehensive benefits including competitive compensation, medical, dental, 401(k), and other employee selected benefit options. Qualified candidates must be able to perform normal office duties, use general office systems, and operate computer equipment. IAP World Services is an Equal Opportunity Employer. Individuals with the above experience and qualifications are requested to submit a resume via the IAP World Services website at [www.iapws.com/careers](http://www.iapws.com/careers) or contact Dr. King.

Tim King, Ph.D. Aquatic Ecology Branch Leetown Science Center U.S. Geological Survey 11649 Leetown Road Kearneysville, West Virginia 25430 Phone: 304.724.4450 Facsimile: 304.724.4424 Personal Mobile: 304.582.4622

“People acting in a group can accomplish things which no individual acting alone could even hope to bring about.” - Franklin Delano Roosevelt

tlking@usgs.gov tlking@usgs.gov

---

## USouthampton ChairBiologicalComputing

[http://www.jobs.ac.uk/jobs/RN211/-Chair\\_in\\_Biological\\_Computing/](http://www.jobs.ac.uk/jobs/RN211/-Chair_in_Biological_Computing/) Chair in Biological Computing School of Electronics and Computer Science & Institute for the Life Sciences

Ref No. 2379-08-E

This joint appointment is an opportunity for an established researcher with an outstanding track record to build and lead a world class activity at the life sciences interface. You will be able to demonstrate a substantive engagement with both computational and biological research questions in an area such as synthetic biology, evolutionary modelling, integrative systems biology, or computational neuroscience.

We are seeking an exceptional individual with the vision and energy to help drive forward our ambitious agenda

and address the next generation of research challenges. You will have demonstrated a record of internationally recognised research achievement at the life sciences interface, as well as the ability to build and drive successful research activity at the highest level.

This appointment will complement and strengthen existing ECS/IfLS research in areas such as Adaptive Behaviour, Artificial Intelligence, Biological Computing Substrates, Evolutionary and Ecological Modelling, Microbial Ecosystems, Proteomics, Theoretical Biology and Theoretical Neuroscience, bringing together mathematical modelling, simulation modelling, wet lab and field experimentation, and devices.

Information about ECS can be found at <http://www.ecs.soton.ac.uk> < <http://www.ecs.soton.ac.uk/> > and the IfLS at <http://www.ifls.soton.ac.uk> < <http://www.ifls.soton.ac.uk/> >

Informal enquiries can be made in the first instance to Professor Harvey Ruttos@ecs.soton.ac.uk <<mailto:hos@ecs.soton.ac.uk>>

The closing date for this appointment is 12 noon on 15 August. Interviews will take place on 10 October.

Tom Hebborn <[teh07r@ecs.soton.ac.uk](mailto:teh07r@ecs.soton.ac.uk)>

---

## USussex ResTech SocialWasps

UNIVERSITY OF SUSSEX School of Life Sciences Department of Biology & Environmental Science Ref: 261 Technician in Molecular/Behavioural Ecology of Social Systems Salary Scale: Grade 6 £25,135-£28,290

We seek a self-motivated person with an interest in animal behaviour/entomology for a 28-month NERC-funded post in the research group of Professor Jeremy Field at Sussex University, UK (<http://www.sussex.ac.uk/biology/profile115853.html>). The aim of the project is to understand helping decisions in primitively eusocial insects, using *Polistes* paper wasps as a model. In particular, to separate the effects that kin selection and direct fitness benefits have on behaviour, and to investigate the role of inheritance in promoting helping. The major part of the work will be microsatellite genotyping, with initial training provided as required. There will also be a range of other labwork, and there may be an opportunity to take part in fieldwork in Spain.

The successful applicant will have a degree or equiv-

alent in a relevant subject and an interest in animal behaviour/entomology. Experience with animal social systems (especially social insects), and experience of molecular techniques, behavioural ecology/entomology and fieldwork would be useful, but it is not necessary to have experience in all of these areas. An ability to speak Spanish would also be useful.

The start date is 1 September 2008 or as soon as possible thereafter. The appointment will be made at the lower end of the salary scale.

Informal enquiries: e-mail [j.field@sussex.ac.uk](mailto:j.field@sussex.ac.uk)

Closing date for applications: 11 July 2008

Interviews will be held between 16 and 25 July 2008

For full details and how to apply see <http://www.sussex.ac.uk/jobs>

Applications should be sent to: [lifescirecruitment@sussex.ac.uk](mailto:lifescirecruitment@sussex.ac.uk), and should include a statement of the earliest date on which the applicant would be available to start work, plus a CV with the contact details (including email addresses) of 2-3 referees who would be available to provide references before interview

The University of Sussex is committed to equality of opportunity

[jf94@sussex.ac.uk](mailto:jf94@sussex.ac.uk) [jf94@sussex.ac.uk](mailto:jf94@sussex.ac.uk)

---

## U Vienna Theoretical Epidemiology

The Veterinary University of Vienna is offering a tenured full time position for a theoretical epidemiologist.

In addition to a solid background in epidemiology, the prospective post holder should be familiar with computer programming, statistical and epidemiological software packages. A proven record of research and teaching is expected. The future post holder should be willing to secure extramural funding and to contribute to statistics and epidemiology teaching.

The Vienna Research Area offers a vibrant research environment including a strong, still expanding population genetics/evolutionary biology group (Reinhard Bürger, Ulf Dieckmann, Thomas Flatt, Andreas Futschik, Arndt v. Haeseler, Joachim Hermisson, Alistair McGregor, Michael Kopp, Claus Rüffler, Karl Sigmund, Christian Schlötterer, Claus Vogl).

applications should be send to: [gertrud.krupka@vu-](mailto:gertrud.krupka@vu-wien.ac.at)

[wien.ac.at](mailto:wien.ac.at) using the reference "öffentliches Veterinärwesen: wissenschaftlicher Mitarbeiter-Epidemiologie"

DEADLINE: 23.6.08

Christian Schlötterer Institut für Tierzucht und Genetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-250775603 fax: +43-1-250775693  
<http://i122server.vu-wien.ac.at/pop/-pop-gen.html> christian.schloetterer@vu-wien.ac.at  
[christian.schloetterer@vu-wien.ac.at](mailto:christian.schloetterer@vu-wien.ac.at)

---

## Washington MuseumTech

NMFS-SC-2008-0018

Museum Technician, ZA-1016-II

Salary Range: 39,330.00 - 68,875.00 USD per year

Open Period: Wednesday, June 04, 2008 to Wednesday, June 25, 2008

If interested, please contact: U.S. Department of Commerce DOC/NOAA/Workforce Management Office NMFS/Ecosystems Client Service Division Norfolk, VA 23510 Fax: 000-000-0000 For questions about this job: Candy Burke Phone: 757-441-6877 Fax: 000-000-0000 Email: [candy.burke@noaa.gov](mailto:candy.burke@noaa.gov) USAJOBS Control Number: 1239578

Series & Grade: ZA-1016-2/2 Position Information: Full-time

Duty Locations: 1 vacancy - Washington DC Metro Area, DC

Who May Be Considered: - All qualified U.S. Citizens; - Permanent federal employees in a competitive position, or in an excepted service position covered by an interchange agreement, or former federal employees eligible for reinstatement; - Veterans eligible for veterans' preference or separated from the armed forces under honorable conditions after three years or more of continuous military service (VEOA); - 30% disabled veterans; handicapped and other applicants eligible for non-competitive appointment under special appointing authorities - Career Transition Assistance Plan (CTAP) and Interagency Career Transition Assistance Plan (ICTAP) eligibles.

Job Summary: NOAA's National Marine Fisheries Service (NMFS) is dedicated to stewardship of our na-

tion’s living marine resources, and habitat through scientific research, management, and enforcement. NMFS provides effective stewardship to benefit the nation through domestic and international programs supporting coastal communities that depend upon the resources, while providing recreational opportunities and safe and healthy seafood to consumers. This position is located at the National Marine Fisheries Service, Northeast Fisheries Science Center, National Systematics Laboratory in Washington, DC.

**Key Requirements:** Applications will be accepted only from United States citizens. Must apply on-line through “USAJOBS”. See the “How to Apply Section”. Must meet the specialized experience requirements. Must meet time-in-grade/band requirement by the applicable closing date.

**Major Duties:** The incumbent will serve as a Museum Technician (Zoology) for the National Systematics Laboratory. Incumbent will provide assistance to the Director of the National Systematics Laboratory and staff zoologists. Performs a wide range of technical duties in connection with systematics research on fishes and invertebrates. Assists the Director with fulfilling administrative requirements of the NSL. Assists in a variety of duties involving the physical duration and technical management of NSL specimens and the National Collection of Fishes and Invertebrates. Participates in handling ethanol and formalin preserved zoological specimens, handling of incoming shipments of new acquisitions; shipping of specimens; sorts and identifies specimens. Prepares specimen catalog data for entry into computer, catalogs specimens, files new and returned specimens in the appropriate collection; participates in routine maintenance of collections. Assists and supports taxonomic research. Conducts literature searches; examine specimens, measures and/or counts taxonomic characteristics; records and analyzes data,

and assists with specialized sampling (X-Raying, tissue sampling and processing). Participate in NOAA and other cruises to collect specimens.

**Qualifications:** Applicants must meet all qualification requirements by the closing date of this announcement. Qualification requirements in the vacancy announcement are based on the U.S. Office of Personnel Management (OPM) Qualification Standards Handbook, which contains federal qualification standards. This handbook is available on the Office of Personnel Management website located at <http://www.opm.gov/-qualifications> .Applicants must have one year of specialized experience equivalent to the next lower grade level(GS-05) or pay band(ZP-1) in the Federal service or specialized non-federal experience. Specialized experience is experience that equipped the applicant with the particular knowledge, skills, and abilities to perform successfully the duties of the position, and that typically is in or related to the duties of the position to be filled. Specialized experience is knowledge of natural history museum technician work practices; knowledge in preservation of museum collections; skill in the examination and measurement of specimens; ability to use a variety of software programs such as Microsoft Office, Photoshop, EndNote, and scanning software; ability to research scientific literature citations, order and organize reprints; OR One full academic year of related graduate level education; OR Superior Academic Achievement (SAA). If you are qualifying for this position based on Superior Academic Achievement (SAA), you must meet ONE of the following: 1) CLASS

— / —

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>

---

## Other

|                                  |                                           |
|----------------------------------|-------------------------------------------|
| Aligning Dloops ..... 38         | Bioperl SynNonSyn Sites ..... 40          |
| Aligning Dloops answers ..... 38 | Conservation intervention papers ..... 40 |
| AntiEvolution Law in LA ..... 39 | DNA Fluorometer ..... 41                  |

|                                                     |    |                                                |    |
|-----------------------------------------------------|----|------------------------------------------------|----|
| Embedding Insects Sectioning .....                  | 41 | RNAlater expiration date .....                 | 49 |
| Evolution lab practicals .....                      | 41 | Roommate Evolution 2008 2 .....                | 49 |
| Evolution roommate 4 .....                          | 42 | Rotting fruit samples for Caenorhabditis ..... | 49 |
| Evolution roommate 5 .....                          | 42 | Sequencing problems answers .....              | 50 |
| Evolution roommate 6 .....                          | 42 | SNPs from bulk samples .....                   | 50 |
| Evolution roommate 7 .....                          | 42 | Software BayesianSerialCoalescence .....       | 50 |
| Evolution roommates .....                           | 42 | Software DAMBE and VISTA .....                 | 51 |
| Fst vs Rst differences .....                        | 43 | Software DAMBE update .....                    | 51 |
| HardyWeinberg Bonferonni .....                      | 43 | Software SitewiseTreefinder .....              | 51 |
| KinshipRelatedness help request .....               | 43 | Software Spidermonkey .....                    | 52 |
| Kipyatkov email .....                               | 44 | SouthAfrica FieldVolunteers .....              | 52 |
| Lepidoptera group .....                             | 44 | spiking RealTimePCR .....                      | 53 |
| MolEvolSoftware Parallel .....                      | 44 | Teaching evolution .....                       | 53 |
| Opponents new strategy .....                        | 45 | UV for sterilization answers .....             | 53 |
| Panama Treefrogs .....                              | 46 | Windows bootstrap software .....               | 54 |
| Population genetics simulation software answers ... | 46 | Windows bootstrap software solved .....        | 55 |
| RennesU ConsequencesPhylogeneticDiversity .....     | 47 |                                                |    |
| Request for stuffed CottonTopTamarin .....          | 48 |                                                |    |

---

## Aligning Dloops

Dear all of you in EvolDir,

I am just wondering if any of you have experienced to align hypervariable sites in mitochondrial genome. (such as control region=D loop) I know many of you have carried out to align by eyes and hands. I also did same way but it is very hard to find out homologous region to be aligned in control region among different genera within same tribe. I've tried to use Clustal W for obtaining references. The results turned out complicated and not appropriate for analysis of constructing trees. How do you deal with this kinds of variable sites when aligning?

Any comments would be greatly appreciated.

Best wishes, Annie

¾ÈÁÈ <safety76@paran.com>

---

## Aligning Dloops answers

Dear Brian,

Here is all the answers that I want to put onto.

Thanks Junghwa An

I have tons of experience aligning very diverse sequences from lentiviruses and other viruses (as well as the complete mitochondrial genomes of vertebrates). Clustal is a "toy" compared to HMMer, MAAFT and other tools for multiple sequence alignment. Write back, and I will give you help.

Brian Foley, PhD HIV Databases <http://hiv.lanl.gov>  
(505) 665-1970

Sorry, I saw the typo just as I hit the send button <http://align.bmr.kyushu-u.ac.jp/mafft/software/> – Brian Foley, PhD HIV Databases <http://hiv.lanl.gov>  
(505) 665-1970

Hi Annie, It can be a hard job to align control region sequences between different species! You did not write with which species you work. I worked mainly with sequences of fishes and it is hardly possible to align between different species. I worked on intraspecific phylogenies and tried to find outgroups. Even within the same Genera of e.g. Sprattus or Mullus I could not align sequences. Though, for some groups it is still possible and I always do this to design new primers (where I look for conserved elements). I can recommend you a paper that deals with the appropriateness of the control region for interspecific phylogenies of fishes (they also describe how they aligned):... Lee W-J, Conroy J, Howell WH and Kocher TD (1995) Structure and Evolution of Teleost Mitochondrial Control Regions. Journal of Molecular Evolution, 41, 54-66. To manually align sequences, and most probably you have to do that as you might have to deal with duplications of part of the sequences and many large indels, I always start with the central conserved region. If you have sequences of the tRNA-Pro at the 5' end and/or the tRNA-Phe at the

3'end it is not as good to start from there. You should be aware that these are the most variable regions and very often are not homologous due to large indels right at the beginning/end of the control region. It's also good to search for conserved sequence blocks and fix those. Have a look at this publication:... Saccone C, Pesole G and Sbisà E (1991) The main regulatory region of mammalian mitochondrial DNA: Structure-function model and evolutionary pattern. *Journal of Molecular Evolution* 33, 83-91. When you have many different species you should also be aware of the strong variation within a species, which can strongly influence your alignment. I would not recommend this region for interspecific phylogenies unless you have no other choice. When I had to deal with outgroup sequences for intraspecific phylogenies I deleted the hypervariable (5' or 3') ends and tried to use the central conserved region only, but there was not enough variation within the species to evaluate the "oldest haplotype" as this was dependant from how much I deleted. All my phylogenies stayed unrooted. Maybe this is what you can do for your interspecific phylogenies: just use the central conserved region. Another thing that might help is downloading additional sequences of related species from Genbank and use them to improve the alignment. I hope this will help you somehow and if you have any questions don't hesitate to write back.

All the best, Paul

Hello, The control region and especially its HVR can be really problematic to align in divergent taxa. It can contain repetitive sequences or just have received many substitutions. In mammals it's removed from alignments even in closely related taxa (recently diverged). In fish it's more conserved and can actually be used in phylogenetic reconstruction at the genus level (see Doukakis's papers). Douzery has published on the cervid control region. I would remove it from the analysis. The rest of the mitochondrial genome sequence should be more informative at this scale anyway. In cases of difficult to align sequences (indels, varying length, etc), a simultaneous alignment and phylogeny method can be employed to integrate across alignment and tree space. POY, BaliPhy, and StatAlign are programs implementing these methods.

Best, sergios

Sergios-Orestis Kolokotronis, PhD Coordinator, DNA Barcoding Initiative for Conservation 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 7648 koloko@amnh.org <http://koloko.net> Hi Annie

You can exclude sites (across all taxa) if there are some

too variable to be aligned. When you know what sites (bp) you are excluding you can just add that command to your tree-building command set in PAUP or Mr-Bayes or whatever you are using. You should report this in your methods.

good luck, Kathryn

Hi,

Try Bali-Phy and BEAST. They might be good for D-loop stuff. Read attached: Rokas, then Wong, then Lunter, then redelings. BEAST will

— / —

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>

## AntiEvolution Law in LA

Please read the following forwarded email about evolution education in Louisiana.

From: "Barbara Forrest" <barbara.forrest@gmail.com> Date: June 18, 2008 11:08:42 AM PDT Subject: Help needed immediately for Louisiana

You all no doubt know what is happening down here. We have the point at which the only possible measure we have left is to raise an outcry from around the country that Gov. Jindal has to hear. He won't respond, but we have to at least make some noise. What is happening in Louisiana has national implications, much to the delight of the Discovery Institute.

SB 733, the LA Science Education Act, has passed both houses of the legislature and the governor has indicated that he intends to sign it. But we don't have to be quiet about this. There is something that you and everyone else you know who wants to help can do: The LA Coalition for Science has posted a press release and an open letter to Jindal asking him to veto the bill. <http://lasciencecoalition.org> .

It is time for a groundswell of contacts to Jindal, and \*this must be done immediately\* since we don't know when he will sign the bill. The vote in the legislature is veto-proof, so any request for Jindal to veto the bill \*must stress that the governor can make this veto stick

if he wants it to stick\*. Please contact everyone you know and ask them to contact the governor's office and ask him to veto the bill. If you have a blog, blog this. If you have friendly contacts in your address book, please ask them to also contact the governor's office.

The contact information is at the LCFS link above. We want people all over the country to do this, as many as possible. Here are the talking points:

Point 1: The Louisiana law, SB 733, the LA Science Education Act, has national implications. So far, this legislation has failed in every other state where it was proposed, except in Michigan, where it remains in committee. By passing SB 733, Louisiana has set a dangerous precedent that will benefit the Discovery Institute by helping them to advance their strategy to get intelligent design creationism into public schools. Louisiana is only the beginning. Other states will now be encouraged to pass such legislation, and the Discovery Institute has already said that they will continue their push to get such legislation passed.

Point 2: Since Gov. Jindal's support for teaching ID clearly helped to get this bill passed in the first place, his decision to veto it will stick if he lets the legislature know that he wants it to stick.

Point 3: Simply allowing the bill to become law without his signature does not absolve the governor of the responsibility for protecting the public school science classes of Louisiana. He must veto the bill to show that he is serious about improving Louisiana by improving education. Anything less than a veto means that the governor is giving a green light to creationists to undermine the education of Louisianachildren.

I have given you the talking points here. You can pull additional ones from the LCFS press release and our online letter.

Now let's get them out! Contact the governor. Then contact your friends, and ask them to contract the governor and to ask all of their friends to do the same. We need to create a huge network of e-mails asking people to do this. Where they live does not matter at this point. What is happening in Louisiana has implications for everyone in the nation.

Barbara

Michael Zimmerman Office of the Dean College of Liberal Arts and Sciences Butler University Indianapolis, IN 46208

Tel: 317.940.9224 Fax: 317.940.8815 mz@butler.edu

—

Dr. Daniel I. Bolnick Assistant Professor Section of

Integrative Biology One University Station C0930 University of Texas at Austin Austin, TX 78712

512-471-2824 fax 512-471-3878 danbolnick@mail.utexas.edu

danbolnick@mail.utexas.edu

---

## Bioperl SynNonSyn Sites

Dear EvolDir members, I would like to identify 4-fold synonymous and non-synonymous positions in a set of aligned sequences for which I already possess a GFF file. Does anyone has a perl script that I could use to identify readily these positions? That would save me time! Thanks infinitely,

Juliette

Juliette de Meaux Research Group Leader

Dept Genetics and Plant Breeding Max Planck Inst. for Plant Breeding Res. Carl-von-Linné Weg 10 50829 Cologne

Tel: +49 (0) 221 50 62 465 e-mail: demeaux@mpiz-koeln.mpg.de

<http://www.mpiz-koeln.mpg.de/english/research/-koornneefGroup/demeaux/index.html>

demeaux@mpiz-koeln.mpg.de demeaux@mpiz-koeln.mpg.de

---

## Conservation intervention papers

Dear EvolDir members,

I am looking for papers or reports that document the effectiveness of conservation or routine management interventions published in either Portuguese or Spanish in South or Central American journals.

I welcome any information on papers/reports or useful journals.

Thank you in advance

Ursula

– Ursula María Ramírez Escobar Departament de Genètica Facultat de Biologia Universitat de Barcelona



Avda Diagonal, 645 Barcelona 08071. SPAIN Tel: (34) 93 402 16 32 Fax : (34) 93 411 09 69

Ursula Ramirez Escobar <ursulare@gmail.com>

---

## DNA Fluorometer

Quantifying DNA Concentration Using Modulus Fluorometer -

Hi I was wondering if anyone uses or has used the Modulus Fluorometer by Turner Biosystems to quantify how much DNA they get from an extraction. I found a protocol for using the Quant-iT<sup>®</sup> PicoGreen(R) dsDNA Kit, but I wanted to know if there was another method that people prefer or get accurate results from. Any suggestions or comments are much appreciated. Thanks,

Patrick Barry University of Alaska Fairbanks School of Fisheries and Ocean Science Juneau Ak, 99801

pat barry <patdbarry@gmail.com>

---

## Embedding Insects Sectioning

Dear Colleagues,

My lab is trying to do a little internal anatomy on ants, through embedding and sectioning via microtome, but we are having problems with the embedding method. More specifically we cannot get the embedding medium to solidify enough. We've been using two different durcupan based methods, one from Oppelt et al. 2007, Naturwissenschaften. Even a near doubling of the hardener component leaves our blocks at best like licorice. E.g. too soft. We chose the durcupan method out of concern for getting a block of the right hardness for our ants (hard on the outside due to the exoskeleton, but very soft inside).

I personally have no experience in such work, unfortunately, and those social insect researchers I know to have done such work all are based in Europe. Would there happen to be any Lab in NY or close by (PA, MA) doing embedding and sectioning of any sort of arthropod (preferentially) that could possibly be willing to have my MS student come and simply watch how you

do things with whatever method is working for you for a day or two? We would very much appreciate it.

Best,

Else Fjerdingstad

Else J. Fjerdingstad, Ph.D. Assistant Professor

Department of Biology Queens College, City University of New York 65-30 Kissena Boulevard Flushing, NY 11367, U.S.A.

Office: NSB E-118 Tel: +1 718 997 3421 Laboratory: NSB E-133/135D, Tel: +1 718 997 3472 Fax: +1 718 997 3445 E-mail: Else.Fjerdingstad@qc.cuny.edu

[http://qcpages.qc.cuny.edu/Biology/fac\\_stf/-Fjerdingstad/fjerdingstad.html](http://qcpages.qc.cuny.edu/Biology/fac_stf/-Fjerdingstad/fjerdingstad.html)

else.fjerdingstad@qc.cuny.edu

else.fjerdingstad@qc.cuny.edu

---

## Evolution lab practicals

Dear all

We are teaching a new introductory evolution course for first semester students. In addition to our regular lectures, we have a weekly practical slot of 3-4 hours. In this context we are looking for suggestions for practicals on ANY subtopic within the realm of EVOLUTION that we could perform with up to 100 students in ONE room, without hoardes of teaching assistants being available.

I would be grateful for ANY suggestions!

Thanks in advance and best,

Dr. Wolf Blanckenhorn Zoological Museum University of Zurich-Irchel 34 (building)-J (floor) -98 (office) Winterthurerstrasse 190 CH-8057 Zurich

Phone: +41 44 635.47.55 Fax: +41 44 635.47.80 E-mail: wolf.blanckenhorn@zm.uzh.ch

[http://www.zm.uzh.ch/zmneu/forschung/-blanckenhorn\\_wolf.html](http://www.zm.uzh.ch/zmneu/forschung/-blanckenhorn_wolf.html) <http://www.esf.org/-thermadapt> wolfman@zm.uzh.ch wolfman@zm.uzh.ch

---

## Evolution roommate 4

Greetings Evoldir members,

I am a grad student attending the Evolution conference and am looking for someone (female) who has a room to share or would like to find something with me. Please email me if you are interested. My email is: mdo@nsm.umass.edu

Thanks, Mary Doherty Graduate Program in Organismic and Evolutionary Biology University of Massachusetts 611 North Pleasant Street Amherst, MA 01002

mdo@nsm.umass.edu mdo@nsm.umass.edu

---

### Evolution roommate 5

Greetings Evoldir,

I'm looking for a roommate for the Evolution Meetings in Minneapolis. I have a double room reserved at the Radisson University Hotel from Jun 20 thru 25th, and am looking for someone to split costs with. It should be about \$70 per night each.

If you're interested, please contact me at geyerl@si.edu.

Regards, Laura Geyer

– Laura B. Geyer, PhD Lessios Lab Manager/Research Associate Smithsonian Tropical Research Institute geyerl@si.edu lbgeyer@gmail.com (preferred)

>From the US: Smithsonian Tropical Research Institute Attn: Laura Geyer - Naos Unit 948 APO AA 34002-0948

703/487-3770. ext. 8730

Internationally: Instituto Smithsonian de Investigaciones Tropicales Att: Laura Geyer - Naos Apartado 0843 - 03092 Balboa, Ancón Panamá, República de Panamá

(+507) 212-8730

Fax: (+507) 212-8790 or (+507) 212-8791

GeyerL@si.edu

---

### Evolution roommate 6

Hello EvolDir,

I have a room with 2 beds booked at the Days Inn University Hotel for the upcoming 2008 Evolution Meeting in Minnesota. If anyone's still looking for accom and would like to split the cost, please drop me a line.

Booking details: Arrival: Fri 20 June 2008 Check out: Tues 24 June 2008 Room cost: \$139 + tax per night (total)

Thanks, Steve Arnott

sarnott@stanford.edu

---

### Evolution roommate 7

Hi,

I am looking for someone to share my double dormitory room. This is almost last minute. But I found a roommate a month ago and she just emailed me that she would not attend the meeting.

So, call me or email me if you are interested in it or someone else you know might be interested in it. Cell phone:314-302-3532

Thanks.

– Guoqin Yu Schaal Lab EEPB program Washington University in St. Louis St. Louis, MO. 63130

Phone (Lab): 314-935-6815 Cell phone:314-302-3532 Website: <http://www.biology.wustl.edu/faculty/schaal/website/Homepage.htm> yu guoqin <yuguoqin2001@gmail.com>

---

### Evolution roommates

Greetings Evoldir members,

I am a grad student attending the Evolution conference and am looking for one to two female roommates to share a hotel room. I have already booked a room with 2 double beds (with option for a rollaway) at the Holiday Inn Metrodome, from June 19-June 24. The cost of the room is \$119.00 per night, divided by two or three.

If anyone is interested, let me know! My email is: belchrl@auburn.edu

Thanks, Rebecca Hunter

belchrl@auburn.edu belchrl@auburn.edu

---

### Fst vs Rst differences

hello, im working population genetic using microsatellite and using genealex for analysis. i used it several times. but now this time i encounter with big problem. in fst test i can separate two populations but in rst they dont have difference with each other. if you work with this program , please help me.

roggi safari <roggi\_safari@yahoo.com>

---

### HardyWeinberg Bonferonni

Dear colleagues,

I am a new phd student and my research area is human genetics and especially genetics of human diseases. I would like to ask you something about the Bonferonni correction. I have p-values of Hardy-Weinberg equilibrium lower than 0.05 ( $p < 0.05$ ) in one control population for 3 SNPs. I would like to apply the Bonferonni correction in this population. I have seen in the literature different approaches for Bonferonni correction eg multiplying the observed p-values with total number of tests (SNPs \* populations) or dividing the statistically significant value of 0.05 with the total number of tests (SNPs \* populations tested in the study).

Which is the most suitable way for that?

Thank you in advance,

Konstantinos Rouskas, Msc School of Biology Aristotle University of Thessaloniki Thessaloniki, Greece e-mail: rouskas@bio.auth.gr

Konstantinos Rouskas <rouskas@bio.auth.gr>

---

### KinshipRelatedness help request

Hi all,

I am just beginning to analyze several populations for relatedness/kinship. We have collected 57 individuals (we believe this to be most of not all the individuals of this species in this area) and genotyped them at 10 loci. For now I am only examining this one population, but we have others. We sampled at two different time periods in this population. These individuals are a fossorial rodent and we have information about which burrow they were caught in, their sex, and age. Based on the field work and radio-telemetry we can infer some maternal/pup relationships. However, I have run Kinship and Relatedness without any of the field inferred data.

I ran multiple hypotheses in Kinship:

- a) Hypothesis = full sib to unrelated  $rm = 0.5$ ,  $rp = 0.5$  with null hypothesis =  $rm = 0.0$ ,  $rp = 0.0$
- b) H = full sib to half-sib  $rm=0.5$ ,  $rp=0.5$  and  $Hn = rm = 0.5$ ,  $rp = 0.0$
- c) H = half-sib to unrelated  $rm = 0.5$ ,  $rp = 0.0$  and  $Hn = rm = 0.0$ ,  $rp = 0.0$

I also tried looking at "parentage"

- d) H = maternal/offspring to unrelated  $rm = 1.0$ ,  $rp = 0.0$  and  $Hn = rm = 0.0$ ,  $rp = 0.0$
- e) H = paternal/offspring to unrelated  $rm = 0.0$ ,  $rp = 1.0$  and  $Hn = rm = 0.0$ ,  $rp = 0.0$
- f) I ran Relatedness in Kinship for pairwise r values

So several confusing things resulted from comparing these results. 1) the results files for maternal/offspring and paternal/offspring (d) and e) above) both have the same exact results. The results files look exactly the same including pairwise relationships that are significant?! Any thoughts about this?

2) We have several instances where inferring relationships are very difficult. For example: pairwise kinship between individuals 1 and 2 were significant at the 0.001 level under test a) and c) above but not significant under test b)???? Also the relatedness value between these two individuals is 0.08. From comparing tests a), b), and c) I might conclude that these two are half-sibs but the relatedness score does not support that, right?

3) One last question, in the Kinship manual on page 9 it states "Note that Kinship cannot distinguish between types of relationships that would have the same r values (such as mother-offspring vs. maternal half-siblings)". I am confused by this if you can test  $rm = 0.5$ ,  $rp = 0.0$  as maternal half-sibs and run another test as  $rm = 1.0$ ,  $rp = 0.0$  doesn't this distinguish? Or is it on the output end that it cannot distinguish, meaning both relationships might be found to be significant

when tested?

I am sure these are simple questions for some but I could sure use some help and guidance. I have been doing a lot of reading and I have concluded that the case may be that we are asking too much of our data and all we can say is that these individuals are closely related rather than distinguish first- and second-order or parentage relationships and/or we may need to go to CERVUS for parentage. I have also concluded that we may be better off adding the relationships we inferred from the field into Kinship to get the best possible answer. So, is there anyway to distinguish half-sibs from full-sibs reliably? No one knows the breeding system in these rodents and we would like to detect multiple paternity if possible. Thanks to any of you who take the time to read this much less answer me. I hope there is someone who can light the way out of the darkness that are these statistics!

– Toni Piaggio, Ph.D. APHIS Fellow, Research Molecular Biologist USDA/ National Wildlife Research Center 4101 LaPorte Ave. Fort Collins, Colorado 80521

ph. 970-266-6142 work e-mail:  
Toni.J.Piaggio@aphis.usda.gov

Toni Piaggio <batchaser@gmail.com>

---

### Kipyatkov email

Dear Colleagues, As my email is returned when sent to the only address I could find for Prof. Vladilen Kipyatkov, social insect researcher at St Peterburg, I was wondering if anyone might have a more recent email address for him. While I can and do find his home page on the web, it is in Russian... and I do unfortunately not understand...

Thanks much in advance, Else Fjordingstad

Else J. Fjordingstad, Ph.D. Assistant Professor Department of Biology Queens College, City University of New York 65-30 Kissena Boulevard Flushing, NY 11367 Office: NSBE-118 Tel: +17189973421 Laboratory: NSBE-133/135D, Tel: +17189973472 Fax: +17189973445 E-mail: Else.Fjordingstad@qc.cuny.edu

<http://qcpages.qc.cuny.edu/Biology/fac=5Fstf/Fjordingstad/fjordingstad.html>

else.fjordingstad@qc.cuny.edu  
else.fjordingstad@qc.cuny.edu

---

### Lepidoptera group

Dear Lepidopterists et al.,

In order to make communication about common issues more effective, LepGen (a Lepidoptera genetics and genomics list serv managed by Marian Goldsmith) and ButterflyBase (a Lepidoptera genome database curated by Alexie Papanicolaou) are preparing a community registry. The first purpose is to populate LepGen with as many interested parties as possible. The second purpose is to create a searchable online database of all laboratories working with Lepidoptera in order to facilitate collaborations, exchange of ideas, and strengthen our community.

Naturally, membership is open to any laboratory, regardless of whether or not their primary research is on moths and butterflies or other organisms.

If you have 10-15 minutes to spare please go to [http://butterflybase.org/community/lepgen\\_registry.php](http://butterflybase.org/community/lepgen_registry.php) to fill out this very short survey. During the survey, you can also opt to register with LepGen, which will continue to serve as the main mode of communication among our group.

If you are not registered with LepGen, completing it as soon as possible will make sure you don't miss any important announcements.

Many thanks!

Marian Goldsmith Biological Sciences Department University of Rhode Island Kingston, RI 02881-0816, USA  
Email: mki101@uri.edu Tel: 1-401-874-2637; FAX: 1-401-874-4256

Alexie Papanicolaou Entomology Max Planck Institute for Chemical Ecology Hans Knoell Str 8 Jena 07745 Germany  
Email: apapanicolaou@ice.mpg.de

Alexie Papanicolaou <apapanicolaou@ice.mpg.de>

---

### MolEvolSoftware Parallel

Has anyone compiled a list of Phylogenetics and Population Genetics software that can be compiled for parallel computing?

Thanks,

– Mariana Mateos, Ph.D. Assistant Professor and Sloan Faculty Mentor Section in Ecology and Evolutionary Biology Department of Wildlife and Fisheries Sciences Texas A&M University 320B Heep Laboratory Building 2258 TAMUS College Station, TX 77843-2258 Phone: 979-847-9462 Fax 979-845-4096 Email: [mmateos@tamu.edu](mailto:mmateos@tamu.edu) <http://wfsc.tamu.edu/mateoslab/> Mariana Mateos <[mmateos@tamu.edu](mailto:mmateos@tamu.edu)>

## Opponents new strategy

Opponents of Evolution Adopting New Strategy By LAURA BEIL Published: New York Times June 4, 2008

DALLAS Opponents of teaching evolution, in a natural selection of sorts, have gradually shed those strategies that have not survived the courts. Over the last decade, creationism has given rise to “creation science,” which became “intelligent design,” which in 2005 was banned from the public school curriculum in Pennsylvania by a federal judge.

Now a battle looms in Texas over science textbooks that teach evolution, and the wrestle for control seizes on three words. None of them are “creationism” or “intelligent design” or even “creator.”

The words are “strengths and weaknesses.”

Starting this summer, the state education board will determine the curriculum for the next decade and decide whether the “strengths and weaknesses” of evolution should be taught. The benign-sounding phrase, some argue, is a reasonable effort at balance. But critics say it is a new strategy taking shape across the nation to undermine the teaching of evolution, a way for students to hear religious objections under the heading of scientific discourse.

Already, legislators in a half-dozen states Alabama, Florida, Louisiana, Michigan, Missouri and South Carolina have tried to require that classrooms be open to “views about the scientific strengths and weaknesses of Darwinian theory,” according to a petition from the Discovery Institute, the Seattle-based strategic center of the intelligent design movement.

“Very often over the last 10 years, we’ve seen antievolution policies in sheep’s clothing,” said Glenn Branch of the National Center for Science Education, a group

based in Oakland, Calif., that is against teaching creationism.

The “strengths and weaknesses” language was slipped into the curriculum standards in Texas to appease creationists when the State Board of Education first mandated the teaching of evolution in the late 1980s. It has had little effect because evolution skeptics have not had enough power on the education board to win the argument that textbooks do not adequately cover the weaknesses of evolution.

Yet even as courts steadily prohibited the outright teaching of creationism and intelligent design, creationists on the Texas board grew to a near majority. Seven of 15 members believe in the notion of intelligent design, and they have the blessings of Gov. Rick Perry < [http://topics.nytimes.com/top/reference/timestopics/people/p/rick\\_perry/index.html?inline=nyt-per](http://topics.nytimes.com/top/reference/timestopics/people/p/rick_perry/index.html?inline=nyt-per) >, a Republican.

What happens in Texas does not stay in Texas: the state is one of the country’s biggest buyers of textbooks, and publishers are loath to produce different versions of the same material. The ideas that work their way into education here will surface in classrooms throughout the country.

“ ‘Strengths and weaknesses’ are regular words that have now been drafted into the rhetorical arsenal of creationists,” said Kathy Miller, director of the Texas Freedom Network, a group that promotes religious freedom.

The chairman of the state education board, Dr. Don McLeroy, a dentist in Central Texas, denies that the phrase “is subterfuge for bringing in creationism.”

“Why in the world would anybody not want to include weaknesses?” Dr. McLeroy said.

The word itself is open to broad interpretation. If the teaching of weaknesses is mandated, a textbook might be forced to say that evolution has an “inability to explain the Cambrian Explosion,” according to the group Texans for Better Science Education, which questions evolution.

The Cambrian Explosion was a period of rapid diversification that evidence suggests began around 550 million years ago and gave rise to most groups of complex organisms and animal forms. Scientists are studying how it unfolded.

Evolution as a principle is not disputed in the scientific mainstream, where the term “theory” does not mean a hunch, but an explanation backed by abundant observation, and where gaps in knowledge are not seen as grounds for doubt but points for future understanding.

Over time, research has strengthened the basic tenets of evolution, especially as advances in molecular genetics have allowed biologists to read the history recorded in the DNA of animals and plants.

Yet playing to the American sense of fairness, lawmakers across the country have tried to require that classrooms be open to all views. The Discovery Institute has provided a template for legislators to file “academic freedom” bills, and they have been popping up with increasing frequency in statehouses across the country. In Florida, the session ended last month before legislators could take action, while in Louisiana, an academic-freedom bill was sent to the House of Representatives after passing the House education committee and the State Senate.

— / —

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>

---

## Panama Treefrogs

Dear colleagues,

We are seeking an Intern for research this fall at the Smithsonian Tropical Research Institute on ecology, evolution and behavior of red-eyed treefrogs, as part of a collaborative project with Karen Warkentin and James Vonesh. This position is open to recent graduates as well as undergraduate students. It does not have nationality restrictions and we encourage applications from Latin Americans. Funding covers monthly stipend, plus travel and housing expenses. The position could start in mid-August 2008 at the earliest, or in September, and would be for three months. The application deadline is July 15th.

More information on the project and application process is posted on the Warkentin Lab website, [people.bu.edu/kwarken](http://people.bu.edu/kwarken).

Please inform young scientists you believe would benefit from this experience of the opportunity.

Thank you, Karen Warkentin

Karen Warkentin <[kwarken@bu.edu](mailto:kwarken@bu.edu)>

---

## Population genetics simulation software answers

(I resend this message, as it does not seem to have been delivered the first time).

Thanks to all who replied to my question about metapopulation genetics simulation software. The original question was:

Can anybody suggest a software package for individual based metapopulation genetics simulation of diploid organisms under different population sizes, migration rates, migration models and extinction-recolonisation rates. The program should be able to output genetic parameters at every generation (or every ten-hundred generations). EasyPop does not seem to have an option of incorporating extinction-recolonisations.

The software packages suggested:

SimuPop - to be programmed in Python Rmetasim and Kernelpop - to be programmed in R Mendelsac-countant Nemo quantiNemo simcoal2 Ecogenetics - being developed

The packages simcoal2 and quantiNemo appear to be relatively easy to use, although in simcoal2 (and simcoal) making the input file work can sometimes be difficult. I am currently experimenting with these two packages and you are welcome to contact me a little later, if you want to learn more about my experience.

Regards, Asta

\*\*\*

Original replies From: Paul Craze  
[<mailto:P.Craze@sussex.ac.uk>]

It depends exactly what you want and how quickly you need it. Over the next few months I'm going to be developing a program to do something similar to what you describe and I could always try incorporating the kind of things you need (as well as making it more user-friendly than programs I write just for my own use!). Anyway, it might be an option to think about if it turns out there is no off-the-shelf software that'll do what you need.

\*\* there are not much simulation softwares enabling many evolutionary scenarios. EasyPop is indeed a good one to start, two others are also useful (also never used them myself), namely

Mendelsaccountant (<http://mendelsaccountant.info/>) and SimuPop ([http://simupop.sourceforge.net/-index.php?option=3Dcom\\_content&task=-3Dview&id=14&Itemid=49&PHPSESSID=-079f19c6d701054b662d66903326dcd](http://simupop.sourceforge.net/-index.php?option=3Dcom_content&task=-3Dview&id=14&Itemid=49&PHPSESSID=-079f19c6d701054b662d66903326dcd)).

Please forward me the responses you get, as I am interested to hear if any new programs exist or is in development.

\*\* try rmetasim and kernalpop. See Allan's website (<http://linum.cofc.edu/software.html>). it does exactly what you are attempting

\*\* I have developed software to do just this. There are two R packages on CRAN that implement 1) patchy sites with a migration matrix and 2) continuous space (potentially broken into patches). The former is called rmetasim the latter, kernelpop. Both are lots more flexible than easypop, but with flexibility comes complexity. You need to use R to use the packages, though I'd argue that learning R would be useful for lots of other things as well. \*\*

Regarding individual based modeling software- give Nemo a look. It isn't quite as ready out of the box as you are looking for, but it can do everything you are look for it to do.

\*\*

quantiNEMO does exactly what you are looking for. We just (yesterday) have it accepted by Bioinformatics. Extinction - recolonization can be simulated in two ways, either by setting an extinction rate for the populations, but in this case the extinction is random, or you specify the extinction explicitly by setting temporarily the carrying capacity of a patch to zero. The program itself and an extensive manual can be found at <http://www2.unil.ch/popgen/software/quantinemo/>.

\*\* Nemo is an individual-based, genetically and spatially explicit simulation software. You can use it to model any kind of metapopulation structure with extinction/colonization, explicit sex- specific dispersal matrices (or island/stepping stone/lattice models), extended choice of mating systems, etc. It implements neutral genetic markers and deleterious mutations, for examples of two genetic traits that are already implemented.

You can save the results at any pace you want during the simulation. The stats you can save for the neutral markers are F-stats (Gst & Theta), coancestries, heterozygosities, allelic diversity, Nei's D, etc. Plus you can save the population genotypes in FSTAT file format for subsequent analysis.

Nemo is a command line tool. It's free and dis-

tributed under the GNU General Public License. You can download the source, documentatoin, and binaries (executable files) for Mac and Windows at the following URL: [http://sourceforge.net/project/showfiles.php?group\\_id=3D161751](http://sourceforge.net/project/showfiles.php?group_id=3D161751) \*\* SimuPOP is able to do it, but you have to program it in Python. The

— / —

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>

---

## RennesU

### ConsequencesPhylogeneticDiversity

Dear all

I have a thesis subject to offer within the contest for PhD candidates of Ecole Doctorale Vie Agro Santé at Rennes University (best candidates receive a fellowship for the thesis of their choice). Candidates should preferably have a master from this academic year and candidates have to be in the upper two thirds of the ranks of their year (if such ranking exists).

Please find more information below (in English, but note that presentations in front of the committee will have to be given in French). Thank you for distributing this offer in your labs.

Best regards

Andreas

—

Thesis subject in the contest of Doctoral School Vie-Agro-Santé at Rennes (France):

Phylogenetic diversity of vegetation consequences for trait evolution and ecosystem functioning

Research team / Research Unit: Ecology of Diversification (ATIP Action Thématique du CNRS within Research Unit ECOBIO-Ecosystems, Biodiversity, Evolution)

Supervisor: Andreas Prinzing

Before applying / for all further information: please contact [andreas.prinzing@univ-rennes1.fr](mailto:andreas.prinzing@univ-rennes1.fr) to explain you what you need for an application in France.

Applications at < <http://www.vas.univ-rennes1.fr/> > <http://www.vas.univ-rennes1.fr> (deadline June 20)

## Context:

It is increasingly appreciated that functional traits of plant species drive the functioning of ecosystems and the services ecosystems provide to humans. Functional traits are the result of millions of years of evolution, with different traits prevailing in different phylogenetic lineages, and local plant communities can be assembled from many or few lineages. At the scale of island floras it has been shown that phylogenetic structure of floras indeed effects functioning, from trait evolution to ecosystem level processes. We suggest that the same applies to local communities in different types of environments: Phylogenetic diversity of plant communities may determine their functioning. Moreover, phylogenetic diversity may respond to anthropogenic impacts, in particular ongoing nitrogen pollution. Phylogenetic diversity may thus be a common denominator to detect impacts of humans and understand their consequences on ecosystem services. We are going to study three major aspects, each of them being new to science. For each of the aspects a wealth of data and material is already available within a CNRS-funded Action Thématique (ATIP) project on the Ecology of Diversification.

## Sujet

## Hypotheses

(Q.1) Evolutionary consequences of phylogenetic diversity of communities: Do a species functional traits depend on whether its neighbors are phylogenetically closely or distantly related? Closely related plant species may compete more strongly, and exchange more natural enemies, than distantly related species. In that case, a species should shift its traits more strongly where it co-exists with closely related species, and it should be better defended against natural enemies. (Q.2) Ecosystemic consequences of phylogenetic diversity of communities: Is phylogenetically diverse plant litter decomposed more quickly than phylogenetically clustered litter? (Q.3) Anthropogenic drivers of phylogenetic diversity of communities: Does nitrogen pollution change the phylogenetic diversity of plant communities and of decomposers in the plant litter? Nitrogen is a key resource in ecosystems that is currently in over-supply across much of the Bretagne region and the rest of Europe, triggering increased competitive displacements of species.

## The major steps of the thesis

For (Q.1) we will study early successional communities, meadows (profiting from an already established prime biodiversity experiment at Jena with already established cloning and cultivation) and in late successional communities, forests (profiting from a research

project on oak crowns situated within phylogenetically more or less closely related canopies).

For (Q.2) we will explore how the phylogenetic position of plant species correlates to the phylogenetic position of their decomposers, using meta-analyses of published studies. We will also study whether litter of phylogenetically diverse plant communities is colonized by phylogenetically diverse sets of decomposers, and whether decomposition and nitrogen mineralization is quicker in such communities, based on unique data bases for the Région Bretagne. Moreover, we will establish, for the first time, experimental litter communities across multiple phylogenetic scales.

For (Q.3) we will consider data bases of Région Bretagne combined with assessments of phylogenetic structure and speed of decomposition. We will use geostatistical approaches to test how a surplus input of nitrogen across the Bretagne shifts the phylogenetic structure of the vegetation, and its related decomposer faunas. This will permit to test contrasting theories on

— / —

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>

---

## Request for stuffed CottonTopTamarin

Dear evolDir members,

a colleague of mine, Thiago Carvalho, at the Instituto Gulbenkian de Ciência in Lisbon, is organizing an exhibition entitled “Darwin’s Evolution”, which will also have a Linnaeus module. Linnaeus had a live cotton top tamarin (*Saguinus oedipus*) as a pet (there is even a portrait of his monkey!). He (my friend, not Linnaeus) would be interested in using a stuffed cotton top tamarin. If anybody is aware of any individual that could potentially be sent and lent for that use, that would be great. For any question (will they harm the poor animal?), please do not hesitate to either contact me ([chikhi@igc.gulbenkian.pt](mailto:chikhi@igc.gulbenkian.pt)) or him ([tcarvalho@igc.gulbenkian.pt](mailto:tcarvalho@igc.gulbenkian.pt)). This is relatively urgent since the exhibition will be run at the Gulbenkian Museum in Lisbon, from February to June of next year.

thank you in advance for your help, Lounes



PS: the animal should already be stuffed. If possible.

–

Lounès Chikhi Chargé de Recherche CNRS UMR  
CNRS Evolution et Diversité Biologique, Toulouse  
chikhi@cict.fr

NOUVELLE ADRESSE (01/10/2007 AU 30/09/2008):

Population and Conservation Genetics Group Instituto  
Gulbenkian de Ciência Rua da Quinta Grande, 6 P-  
2780-156 Oeiras, Portugal Tel: +351 21 446 46 71 Fax:  
+351 21 440 79 70 chikhi@igc.gulbenkian.pt

“\”Lounès Chikhi (IGC)\”  
<chikhi@igc.gulbenkian.pt>

---

### RNAlater expiration date

Hi all,

I have some tubes with unused RNAlater that date back to March 2007. They were stored at room temperature. According to the product documentation, RNAlater is storable for only about a year. Does anyone have any experience of using RNAlater that has been stored for longer than a year? Given the price of the chemical I hoped to be able to use the old vials, but of course I don't want to risk to lose samples just because I'm stingy... Any advice or experiences would be greatly appreciated!

Cheers, Michi

– Michael Tobler Department of Wildlife and Fisheries  
Sciences Texas A&M University 2258 TAMU College  
Station, TX 77843-2358, USA

Phone: 001-405-664-4820 Website: <http://www.sulfide-life.info/mtobler>  
Humans are not the pinnacle of evolutionary progress but only an aberrant side branch of fish evolution. - Moyle

michi.tobler@gmail.com

---

### Roommate Evolution 2008 2

Hello Evoldir people,

I have just realized that I reserved a double room in

Yudof Hall for the Evolution conference but only need one bed. I'd be happy to share the room with a fellow female evolutionary biologist who's still in need of a place to stay. We'd split the cost of the suite (\$96 / 2) and I have the place booked for Friday the 20th to Tuesday the 24th.

Please contact me if you're interested at [lgc@rice.edu](mailto:lgc@rice.edu)

Have a great day,

Lesley Campbell

Lesley Campbell <[lgc1@rice.edu](mailto:lgc1@rice.edu)>

---

### Rotting fruit samples for Caenorhabditis

Dear all,

This is a call for rotting fruit samples from all around the world (especially outside Western Europe and US-Canada) to find *Caenorhabditis* species.

*Caenorhabditis* nematodes proliferate in rotting fruits that have fallen on soil below their tree (and are also found on snails, isopods, etc. that probably carry them to the fruits - cf. Barriere and Felix, Genetics 2007). Curiously pretty much the same as *Drosophila* and yeasts.... In the past years, 8 new *Caenorhabditis* species were found - in China, Portugal, US, Ghana, India, La Reunion and Guyana. With other colleagues, we also study the distribution and genetic structure of the different species, so we are also interested in getting the “old” ones, like *C. elegans* or *C. briggsae*. From the recent surge in new species since we sample rotting fruits, we are probably very far from exhausting the diversity of species around the world.

If you or someone you know are living or traveling outside of “Western” Europe (mostly France/UK/Germany; even Ireland, Italy or Scandinavia need sampling!) and US/Canada, I would be interested that you sample rotting fruits /vegetables/flowers (either wild or cultivated, below their tree). Samples of about 10-20 ml are good. They need to travel in aerated containers so that they don't start fermenting and depleting the oxygen, for example in plastic bags or 10-50 ml tubes which are not airtight (cap slightly unscrewed, or small hole in it). I could get worms out after 2-3 weeks of travel, provided they are not heated too much.

Note there is a prize for finding a sister species

to *C. elegans* (cash + the right to propose a name). <http://www.wormbase.org/mt/wormbase/archives/2007/09/11/10.14.02/> If you send the key sample, you'll get it....

Thank you to those who will bring/send me samples! French customs are not a problem to import live material. I can give you my fedex number if convenient. Don't hesitate to contact me if you have questions: felix@ijm.jussieu.fr.

With all my best wishes, Marie-Anne – Marie-Anne Felix Institut Jacques Monod, Tour 43, 2 place Jussieu, 75251 Paris Cedex 05, France Tel: +33-1-44-27-40-88; Fax: +33-1-44-27-52-65 (5th floor, corridor 43-42) <http://ijm2.ijm.jussieu.fr/-ijm/recherche/equipes/nematode> STRAINS: <http://www2.ijm.jussieu.fr/worms/search.php> Marie-Anne Felix <felix@ijm.jussieu.fr>

---

## Sequencing problems answers

Dear all,

A couple of months ago I sent an email reporting rather frustrating sequencing problems. It appears we have found the source: The UV light box for cutting bands!

When we narrowed down the problem to the gel cutting stage we proceeded by sequencing directly from a purified PCR product (even though we often get unspecific bands). The sequences were mostly ok, of course this protocol was no good for cloning. During our further investigations we found out that someone changed the light bulb around the time we had the first problems. Although the bulb hasn't been replaced yet it appears that cutting bands from Ethidium bromide gels is more productive than a cheap cyber green stain that we have started using in February. We also keep the UV exposure to an absolute minimum!

Anyway, thank you all for the many suggestions. And to the couple of people who reported similar problems: Go and check you UV light bulb!

Best wishes, Birgit

Birgit Meldal, PhD Division of Transfusion Medicine Department of Haematology University of Cambridge National Blood Service Center Long Road Cambridge CB2 2PT

Tel: +44 (0) 1223 548049 E-mail: bhmm2@cam.ac.uk

bhmm2@cam.ac.uk

---

## SNPs from bulk samples

hello

has anybody experience in applying and analysing SNPs from bulk samples, i.e. samples that contain more than one individual? i am looking for relevant literature and advice on methods and analysis.

with best regards, christian rellstab

Dr. Christian Rellstab Centre of Excellence in Evolutionary Research Department of Biological and Environmental Science P.O.Box 35 FI-40014 University of Jyväskylä Finland

christian.rellstab@jyu.fi

---

## Software BayesianSerialCoalescence

Subject: Bayesian Serial Coalescence

We have released a new version of Serial SimCoal with bayesian analysis capabilities. This means that rather than specifying set parameter values for the model simulations, users can now specify a prior distribution of values, and compare the simulation results to actual data to derive posterior probability distributions for those parameters. Like previous versions, this program is backwards compatible with all prior versions of SimCoal and will run input files created for those versions (including those written by Excoffier, not by us). Users can specify population structure, historical events, and use samples of many different ages (aDNA supported). Data can be microsat, RFLP or sequence. Summary statistics of each run are returned, along with parameter values.

The package is available for MacOS and PC, and can be found along with the users manual and source code at <http://iod.ucsd.edu/simplex/ssc/BayeSSC.htm>

We hope you find this useful! The Serial SimCoal Development Team Christian Anderson (contact: senka@ucsd.edu) Yvonne Chan Uma Ramakrishnan Liz Hadly

Christian Anderson <senka@ucsd.edu>

---

## Software DAMBE and VISTA

Dear All,

I just tried DAMBE on the Windows VISTA platform and did not experience any problem. Those who have experienced problems please let me know the details.

Here is what I did:

1. Upgraded to Windows VISTA from a PC with Windows XP and DAMBE already installed. After upgrading to VISTA, DAMBE runs fine.
2. Did a clean installation of Windows VISTA on a PC and then installed DAMBE 5.0.15 at [http://dambe.bio.uottawa.ca/-dambe\\_installation\\_instructions.asp](http://dambe.bio.uottawa.ca/-dambe_installation_instructions.asp). I experienced no problem during installation. I run functions with sequence alignment, distance-based, maximum parsimony and maximum likelihood phylogenetic methods and encountered no problem. (There is one point during installation when I was asked if I should allow the DAMBE installation to run. I click the 'Allow' button and everything went fine.)

One minor difference between Windows XP and Windows Vista is that Microsoft XML parser is part of the VISTA so one does not need to click and install msxml6.msi.

(I will begin to register DAMBE users so that I do not have to email updates to the entire EvolDir).

Best Xuhua

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

---

## Software DAMBE update

Dear All,

Due to popular requests, I have just added to DAMBE

the genetic distance based on the GTR (General time reversible) substitution model. To use it, open an aligned sequence file in virtually any standard format, click 'Phylogenetics|Distance methods|Nucleotide sequences'. In the dropdown list box labelled 'Genetic distance', choose 'GTR' (the default is TN93), and click the 'Run' button.

I have also modified the interface slightly and improved the format of the output.

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

---

## Software SitewiseTreefinder

Another unpaid TREEFINDER version is online at:

[www.treefinder.de](http://www.treefinder.de) TREEFINDER is a software to compute phylogenetic trees from molecular sequences.

New features are:

- user-definable substitution model: MAP - computation of sitewise rates - automatic generation of data partitions

MAP is a class of general time-reversible substitution models mapping characters to states as defined by the user. Multiple characters may represent one state. MAP definitions, such as e.g. MAP["AGPST", "C", "DENQ", "FWY", "HKR", "ILMV"], can be stored in variables and then be used as building blocks of more complex models. All parameters can be estimated. The MAP can be fed into any function that takes substitution models, including tree reconstruction, hypothesis testing, model selection, sequence simulation.

The computation of sitewise rates replaces the old rate profile tool.

Based on the sitewise rates one can now divide a sequence alignment into partitions of slower and faster evolution.

Please note that I am still not being paid for my work and that I had no income for years. I wonder if somebody finds TREEFINDER worth offering me a compensation, a wage, a position, a perspective. I wonder if I should continue or stop the Treefinder project, this

programming work is not really fun if one is excluded from life.

Gangolf Jobb

Gangolf Jobb <gangolf@treefinder.de>

---

## Software Spidermonkey

Dear Evoldir,

We would like to introduce the community to Spidermonkey, a new web application that we are hosting at <http://www.datamonkey.org>. Spidermonkey uses phylogenetic and Bayesian network methods to detect co-evolving sites in an alignment of nucleotide, codon, or protein sequences. Inference of site coevolution is based on the overlap of substitution events in the tree. Substitutions are inferred by maximum likelihood reconstruction of ancestral sequences, which can be resampled in order to quantify uncertainty in reconstruction.

Spidermonkey is completely free and operates on our 80-processor Linux cluster. It is based on methods that we also distribute freely as a stand-alone application within our open-source phylogenetic software package HyPhy (<http://www.hyphy.org>).

For further details, please refer to <http://www.datamonkey.org/help/spidermonkey.php>.

Sincerely yours, - Art Poon.

---,--- Dr. Art FY Poon \_\_\_/ '--- Division of Comparative Pathology and Medicine \_\_\_/ \---- Department of Pathology \--- University of California, San Diego  
apoon@biomail.ucsd.edu apoon@biomail.ucsd.edu

---

## SouthAfrica FieldVolunteers

Volunteer needed as field assistants for the project:

Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

>From mid August onwards

Project: We study the reasons of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habi-

tat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students with a BSC/Vordiplom or equivalent are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o' clock), and stops its activity with dusk (19 o' clock). Work during nights might also be necessary. Work in the field will be done for 5-6 days a week. Applicants must be able to manage extreme temperatures (below 0 at night, sometimes over 40C during days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small group.

Work of field assistants: Trapping and marking of mice and rats; radio-tracking to determine home ranges and nest sites; direct behavioral observations in the field; experiments and observations with captive specimen under natural weather conditions; maintenance and cleaning of the research station.

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 750 (around 65 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 2000 or 170 Euro/month). Including extras, you should expect costs of about 250 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: Currently we are looking for one volunteer to start middle of August, two volunteers to start beginning of September and two to star beginning of December. Volunteers are expected to stay at least 2 months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to [carsten.schradin@zool.uzh.ch](mailto:carsten.schradin@zool.uzh.ch).

More information under [www.stripedmouse.com](http://www.stripedmouse.com) Contact via e-mail: [carsten.schradin@zool.uzh.ch](mailto:carsten.schradin@zool.uzh.ch)

Dr. Carsten Schradin Research Assistant, Zoological Institute, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel: +41 - (0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

Carsten Schradin <[carsten.schradin@zool.uzh.ch](mailto:carsten.schradin@zool.uzh.ch)>

---

### spiking RealTimePCR

Dear EvolDir members,

I am using real-time PCR to quantify gene expression in non-model species (*Apodemus* sp., *Marmosops* sp.). RNA is extracted from spleen and liver samples stored in RNA-later. Currently I try to find and validate appropriate house-keeping genes. To control for reverse transcription efficiencies I wanted to spike my samples with an artificial RNA. I transcribed a known sequence successfully into RNA via T7 transcription and added it into my RT-reaction, but unfortunately I failed to amplify this reference in my real-time PCR with specific primers.

What I am asking for is experiences with spiking. Is there someone who has a good artificial external reference he can recommend or a good protocol, tips or tricks that might help?

Thanx and all the best!

Jan

Jan Axtner Evolutionary Genetics Leibniz Institute for Zoo- and Wildlife Research (IZW) Alfred-Kowalke-Str. 17 10315 Berlin Germany

phone: +49 30 5168 711

fax: + 49 30 5126 104 e-mail: [axtner@izw-berlin.de](mailto:axtner@izw-berlin.de) <<mailto:axtner@izw-berlin.de>>

"Axtner, Jan" <[axtner@izw-berlin.de](mailto:axtner@izw-berlin.de)>

---

### Teaching evolution

I am going to the Evolution meetings this year after a very long hiatus, and would enjoy talking with any of my peers that also teach evolution at a small liberal arts college. I would be very interested in discussing the particular challenges and opportunities associated with, or sharing ideas and strategies for, teaching evolution and doing research in a small liberal arts college setting. We could even entertain forming a loosely organized group (support group?) to discuss these issues on a more routine basis. If anyone is interested in meeting, please feel free to send me your name and contact information so we can try to connect; or if enough people respond I will figure something out so we can all get together during the conference.

Thanks in advance, and I look forward to meeting you this June.

S. Shawn McCafferty Assistant Professor Biology Department Wheaton College Norton, MA 02766

S Shawn McCafferty <[smccaffe@wheatonma.edu](mailto:smccaffe@wheatonma.edu)>

---

### UV for sterilization answers

I received a number of answers regarding the UV sterilisation of PCR and extraction reagents. Many people advocated the use of filter tips and small aliquots of reagents but the actual use of UV received a variety of responses;

I used UV sterilization to avoid a persistent contamination in our lab. I sterilise pipettes, tips, tubes and water under UV for 20 min. Then I perform my PCR adding everything (primers, dNTPs, water, Mg) but the Taq and DNA and then I sterilise the master mix for 10 min. Then add Taq and DNA. With this protocol I manage to avoid the contamination. The amount of PCR product was a bit lower than without the UV treatment but it was good enough. I never tried to sterilise the Taq but I'm not sure is a good idea. With dNTPs there is not any problem and with primers there is not problems if they don't have several T together (they could form T dimers, that can inhibit the PCR). I send you a paper with some information about UV sterilization (Padua RA, Parrado A, Larghero J, Chomienne C (1999) UV and clean air result in contamination-free PCR. *Leukemia* 13, 1898-1899.) Good luck Javier Montero-Pau Javier Montero Pau Laboratorio de Ecología Evolutiva Institut Cavanilles de Biodiversitat i Biologia Evolutiva Universitat de València AO. 22085 Valencia

I wouldn't expose dNTPs to UV light. UV light excites DNA. In your cells, UV light causes mutations and cancer. We use UV light to "sterilize" things used in PCR because it damages DNA. And dNTPs are the components of DNA, they are also likely to be damaged by UV light. I don't know about the enzymes best.

Hi Claire, I would suggest several things:

Using a negative control (no DNA added) for each PCR will alert you to possible cross contamination. If available, using filter tips will help to minimize cross-contamination. Cleaning your work space and pipettes daily, and making small aliquots (single or a few uses) of your reagents (dNTPs, primers, water, etc) will also help to minimize risk of contamination.

You can order small bottles of double distilled water (if this is not available to you at your institution) for re-suspending primers and for making your master mix (if you order PCR kits, they often come with clean water).

You mentioned sterilizing your Taq and dNTPs and this strikes me as not necessary at all. These two reagents should not be left at room temperature (especially Taq!) for any length of time (I always keep mine in the -20C freezer at all times in an enzyme cooler) and they should arrive free of any DNA (especially free of the DNA you are working with and are concerned with). So exposing them to UV light seems unnecessary.

Good luck! Nikki Freed nicole.freed@env.ethz.ch

Best and safest thing to do is to use separate sets of tips, pipettes, reagents, etc. in different rooms for all pre-PCR reactions. I've heard (and read) it was not good to UV-sterilise PCR tubes, as plastic suffers from it, and I've never UV-sterilised reagents. Title: UV light irradiation of plastic reaction tubes inhibits PCR. Author(s): Burgess, LC; Hall, JO. Source: BIOTECHNIQUES Volume: 27 Issue: 2 Pages: 252-+ Published: AUG 1999 Violeta Muñoz.

Hi Claire, UV sterilizing enzymes will kill them so that is not a good idea. You should try to find a hood somewhere else (i.e. in a lab that does not work on this species or anything related). It is also best if you do the work in a building or part of the building that does not share the same ventilation system. Basically, museum specimens are considered about the same as "ancient DNA" so you really need to use the same sort of precautions. This includes using extraction and PCR blanks to test your reagents, ordering all reagents, gloves etc. separately (and do not take them into the lab where the modern specimens are), and avoiding going into the modern lab before you go to the other lab to work on the museum specimens. It might also be best to do the museum work first. Finally, depending on the age of

the museum specimens, you might need to design your primers such that they amplify short (100-200 bp) fragments. Good luck! Anne

UV treatment of liquid reagents in a hood (with a UV bulb) is not an ideal sterilization method - as I understand it, certain kinds of plastic block UV rays, and UV of this strength can only penetrate in liquid a very short distance - maybe a centimetre at best (imagine how colours change under ocean waters - and that's full-strength solar power!). You're basically just wasting energy and time. And blasting chemicals with bond-breaking rays makes me nervous. For reagent sterilization, 0.2 micron filter units are best - you can use large filter units for larger volumes (250ml+) and syringe filters for smaller volumes. However, I've worked with herbarium specimens also, and with good sterile technique, had no cross-contam problems. Remember that most molecular reagents come pre-sterilized, so re-treating them has more potential to introduce

— / —

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>

---

## Windows bootstrap software

Dear EvolDir Members!

Could anyone suggest me a software for Windows platform with that I can write (by 'hand') the bootstrap values to internal nodes of a phylogram and the branch-length aren't lost? When I did it with TreeView 1.6.6 the branch length were lost even if I asked to save it.

Thanks for your help! Eszter

– Ari, Eszter Scientific research associate ELTE eScience RET, Department of Genetics 1/C Pazmany Peter stny., Budapest, Hungary, H-1117 e-mail: arieszter@gmail.com tel: +3612090555/8691; fax: +3613722641

arieszter@gmail.com

---

## Windows bootstrap software solved

Thank all of you for the helpful suggestions. I solved the problem by text editor and corel draw.

Best wishes, Eszter

—

Dear EvolDir Memebers!

Could anyone suggest me a software for Windows platform with that I can write (by 'hand') the bootstrap values to internal nodes of a phylogram and the branchlength aren't lost? When I did it with TreeView 1.6.6

the branchlength were lost even if I asked to save it.

Thanks for your help! Eszter

– Ari, Eszter Scientific research associate ELTE eScience RET, Department of Genetics 1/C Pazmany Peter stny., Budapest, Hungary, H-1117 e-mail: arieszter@gmail.com tel: +3612090555/8691; fax: +3613722641

arieszter@gmail.com

Ari Eszter <arieszter@gmail.com>

---

## PostDocs

|                                                   |    |                                          |    |
|---------------------------------------------------|----|------------------------------------------|----|
| BangorU MeiofaunaMetagenetics .....               | 55 | UmeaU Evolution at RangeMargins .....    | 64 |
| CardiffU LandscapeGenetics .....                  | 56 | UmeaU PopulationDynamics .....           | 64 |
| CornellU Speciation .....                         | 56 | UMichigan EvolutionaryBiol .....         | 65 |
| EastCarolinaU FishEvolutionaryEcol .....          | 57 | UMichigan GeneByEnvironment .....        | 65 |
| ENS Paris ViabilityAnalysis .....                 | 57 | UNebraska EvolutionaryGenomics .....     | 65 |
| FrenchGuiana RainforestTreeGenetics and Evolution |    | UNebraska MolecularAdaptation .....      | 66 |
| 58                                                |    | UParisSud PhylogeneticLanguage .....     | 66 |
| Grenoble PopulationGenetics .....                 | 59 | UppsalaU EvolutionaryGenomics .....      | 67 |
| HopkinsMarineStation PopulationGenetics .....     | 60 | UppsalaU NorwaySpruceEvolution .....     | 68 |
| IndianaU ReproductiveDiversity .....              | 60 | UTexasAustin DiseaseModeling .....       | 68 |
| MortonArboretum PlantMolPhylogenetics .....       | 60 | UToronto FunctionalMetagenomics .....    | 69 |
| SyracuseU DrosophilaSpermCompetition .....        | 61 | UVigo 2 StatisticalPhylogenomics .....   | 70 |
| UConnecticut ProteinEvolution .....               | 61 | VanderbiltU EarlyMetazoanEvolution ..... | 70 |
| UFlorida MutationRateEvolution .....              | 62 | YaleU MosquitoImmunityEvolution .....    | 71 |
| UKansas QuantGenetics .....                       | 62 |                                          |    |
| UMaryland EukaryoticGenomeEvolution .....         | 63 |                                          |    |

---

## BangorU MeiofaunaMetagenetics

Dear EvolDir

This Autumn, the Molecular Ecology and Fisheries Genetics Laboratory (MEFGL - <http://biology.bangor.ac.uk/research/mefgl/>), School of Biological Sciences, Bangor University, UK will access Natural Environment Research Council (NERC) funding streams that will consolidate research activities

in using 454 ultrasequencing technologies for the analysis and quantification of benthic meiofaunal biodiversity (<http://biology.bangor.ac.uk/%7Ebssa0d/scresearch.htm>). The latter will investigate the relationship between meiofaunal metagenetic community diversity with salinity regimes, biotic and abiotic factors in estuarine ecosystems (<http://biology.bangor.ac.uk/~bssa0d/scresearch.htm>) and would provide an ideal opportunity for linkages with a Marie Curie Action program ([http://ec.europa.eu/research/fp7/understanding/marie-curieinbrief/research-development\\_en.html](http://ec.europa.eu/research/fp7/understanding/marie-curieinbrief/research-development_en.html)) along a related theme. The research platform will enable hypotheses to be

addressed regarding species, functional and phylogenetic diversity in relation to, for example, multi-level biodiversity, ecosystem functioning, environmental change and latitudinal clines.

The Molecular Ecology and Fisheries Genetics Laboratory (MEFGL) is a leading research division within the School of Biological Sciences' (SBS) Molecular Ecology and Evolution Group, one of the largest research areas within the University. A central part of our work is the application of molecular markers such as microsatellites, AFLPs, single nucleotide polymorphisms (SNPs) and sequence data (454 and Sanger) to fundamental evolutionary and ecological questions relating to the origins, levels, distribution and ecological significance of genetic variation in wild populations. The MEFGL, together with other members of the Molecular Ecology & Evolution Group, has recently moved into the purpose-built research suite embedded within the newly built £8 million Environment Centre for Wales (ECW <http://www.ecw.ac.uk/aboutus.html>). The new facility provides open-plan office space for up to 28 postgraduate and postdoctoral researchers, alongside dedicated PCR, sequencing, bioinformatic, and main laboratory facilities.

If you wanted to consider the MEFGL as a research venue to host a Marie Curie (08 closing date of 19 August), or other such Fellowship scheme focusing on meiofaunal metagenetic community diversity, or a related field, please contact Si Creer via the links below.

With best wishes and thanks

Si Creer

– Si Creer Post Doctoral Research Fellow Molecular Ecology and Fisheries Genetics Laboratory School of Biological Sciences University Wales, Bangor Bangor Gwynedd LL57 2UW UK

e-mail: [s.creer@bangor.ac.uk](mailto:s.creer@bangor.ac.uk) Tel: +1248 382302  
 Fax: +1248 371644 Home Page: <http://biology.bangor.ac.uk/~bssa0d/> “Creer,Simon”  
[<s.creer@bangor.ac.uk>](mailto:s.creer@bangor.ac.uk)

---

## CardiffU LandscapeGenetics

Postdoctoral position in molecular ecology/landscape genetics at Cardiff University

A position is available for a Postdoctoral Research Associate in molecular ecology and landscape genetics

with the Biodiversity & Ecological Processes group at Cardiff School of Biosciences.

Funded by a Leverhulme Trust grant, the appointee will work on a research programme carried out in collaboration between Cardiff and Bath University (Prof T. Szekely). The programme of research will involve combining population genetics and landscape modelling, to allow conservation-relevant analysis of four model wetland bird species in Madagascar. The successful candidate will carry out the genetic element of the work using mitochondrial DNA and microsatellite analysis of the four species.

This project provides the successful applicant with experience of conservation-oriented molecular ecology in one of the worlds mega-diverse regions. The successful candidate will have a PhD in a relevant subject area, including experience in microsatellite isolation, optimisation and screening. Experience of landscape genetic analysis would be advantageous.

The position is fixed term for a period of 3 years, available 1 September 2008.

Salary: £28,290 - £33780 per annum (Grade 6).

Informal enquiries and requests for further details can be directed to Prof Mike Bruford at [BrufordMW@Cardiff.ac.uk](mailto:BrufordMW@Cardiff.ac.uk) who can also provide further details on the application procedure.

Closing date for formal applications will be 15 July 2008.

Michael Bruford <[brufordmw@Cardiff.ac.uk](mailto:brufordmw@Cardiff.ac.uk)>

---

## CornellU Speciation

Postdoctoral position in behavioral evolutionary genetics and speciation P.I. : Dr. Kerry Shaw, Cornell University, Ithaca, NY

A postdoctoral position is available to join an NSF-funded project to examine the genetic basis of naturally occurring variation in male signal and female mate preference behavior among closely related species of the Hawaiian cricket genus *Laupala*. While ecologically and morphologically similar, species are easily distinguished by the pulse rates of the male calling song and female acoustic preference. Divergence in acoustic signaling traits is thought to play a large role in the rapid speciation of this genus. Two focal species, *L. paranigra* and *L. kohalensis*, show large differences in the pulse rate of



the male calling song and associated female preference. Biometrical and quantitative trait loci mapping in the focal species indicate that these behaviors are under the genetic control of many loci.

Research Project: The post doc will employ genomic resources to finely map the location of trait and preference loci using hybrid introgression lines and BAC libraries, in order to test alternative hypotheses about the genetic architecture of behavioral evolution and speciation. The successful candidate will be expected to contribute to this collaborative project while developing complementary projects of an independent nature.

Additional background: A comparative phylogenetic framework also exists in which to understand behavioral evolution in this genus. *Laupala* represents a portion of a larger radiation of endemic Hawaiian trigoniine crickets that is conspicuously characterized by frequent speciation and acoustic signaling evolution. In *Laupala*, DNA data suggest that the current radiation began on the oldest island where the genus is presently found (Kauai, 5 mya), and radiated into younger island habitats as those islands appeared within the last 5 million years. These data also show that speciation has occurred both within and between islands and that species ranges are limited to single islands. Communities of *Laupala* occur on all the major Hawaiian Islands and convergent patterns of song evolution among islands, and displaced evolutionary patterns within islands are evident. The two focal species of this study are each endemic to the Big Island of Hawaii and are very closely related. The phylogenetic structure provides a recent evolutionary context in which to study the evolution of genes and behavior.

Requirements: The desired candidate will possess an interest in / experience with a number of bench skills (such as DNA/RNA extraction, PCR, cDNA synthesis, cloning). An interest in the evolution of premating isolation and speciation, and the neurological basis of behavior would be beneficial.

Cornell University has several labs dedicated to the study of evolutionary genetics, speciation genetics, evolutionary basis of behavior and neuroethology. As such, it provides a rich academic environment for those interested in proximate and ultimate causes of behavioral evolution and speciation.

The position can be filled as soon as July 1st 2008 and two years of funding are available. To apply, email a statement of research interests, a curriculum vitae, and the email addresses of three references to Kerry Shaw (KLS4@cornell.edu). Kerry will be at the SSE/SSB/ASN meeting in Minneapolis in June 2008 and would be happy to meet with potential candidates dur-

ing the meeting.

Kerry Shaw <kls4@cornell.edu>

---

## EastCarolinaU FishEvolutionaryEcol

Dear colleagues,

I anticipate having a post-doctoral position available in my laboratory at East Carolina University starting September 08. The position will initially be for one year with possibility of renewal.

Research in my laboratory focuses on fish evolutionary ecology, especially sexual selection (lately emphasizing female ornamental traits and color polymorphisms) and speciation. We work mainly on threespine sticklebacks and the telmatherinid fishes of Sulawesi's Malili lakes. Reprints are available from my website (address will change in the fall): <http://facstaff.uww.edu/~mckinnoj/mckinnon.html> Interested candidates should email me a CV, cover letter and reprints. I will be at the upcoming Evolution meetings in Minneapolis and will be happy to talk with potential post-docs there.

ECU is located in Greenville, NC, a livable and affordable small city situated between the Outer Banks and the Research Triangle. Evolution and Coastal Ecology are two of the principal strengths of the department.

Jeff McKinnon email: [mckinnoj62@yahoo.com](mailto:mckinnoj62@yahoo.com)

[mckinnoj62@yahoo.com](mailto:mckinnoj62@yahoo.com)

---

## ENS Paris ViabilityAnalysis

\*Post-doc in theoretical evolution at ENS Paris\* (CERES-ERTI, Ecology & Evolution Lab UMR 7625)

\*Physiologically structured population models\* \*for viability analysis\*

Second call with new submission deadline: 1 \*September\* 2008

Applications are invited for a one-year postdoctoral position funded by R2DS (<http://www.r2ds.centre-cired.fr/>) to investigate the dynamics of small popu-

lations with plastic life histories, using physiologically structured population models.

**\*Project description\***

Population persistence is notably conditioned by the degree of individual variation in reproductive success, which depends on variation in any part of the life cycle. Yet, the majority of studies that examined population extinction have tended to ignore life history variation and plasticity. Here, we wish to use life history models to inform the dynamics of small populations and ask how plasticity in life history traits influences extinction dynamics. Many aspects of life history can interact with population dynamics and the project concentrates on three of them, namely growth, maturation and survival. The post-doc will explore this issue by developing models that account for variation in life history traits using the theory of physiologically structured populations (PSP). This theory takes into account that physiological development (e.g. growth, maturation) depends on the current state of the environment (e.g., temperature, food and predator densities). In turn, the influence of the population on the environment closes a feedback loop between environment, population and life history. The theory of PSP models is thus particularly well-suited to study the interaction between population dynamics and plastic life history. Small populations are subject to stochastic fluctuation in abundance. The project aims to study the feedback of this variability on life history and the consequences for extinction dynamics. The models will be parameterized with estimates from field and experimental studies undertaken with the common lizard, a species with strong thermal and food plasticity in life history traits.

The post-doc will be based at the Ecology & Evolution Lab (CNRS, UMR 7625) at the Ecole Normale Supérieure (CERES-ERTI) in Paris, where the applicant will work with /David Claessen/ and /Jean-François Le Galliard/. This post-doc project is part of a research network on the dynamics of small populations funded by ANR from 2008 to 2012 and will therefore interact with a larger group of researchers. The post can start on \*October 1st\* or \*November 1st\* 2008 and will run for one year with a possible one year extension by applying to extended funding from the R2DS network in spring 2009. Gross salary will be 2500 EUR per month. The starting date can be postponed in exceptional circumstances.

**\*Candidate profile\***

There are no nationality restrictions and the successful candidate will: (1) Possess a doctoral degree in evolution and/or mathematics, dating no more than 2 years before 1 October 2008, though the last condition may

be negotiated in exceptional circumstances. (2) Not have worked in the hosting lab, nor have prepared his thesis within the hosting lab, except for a return after a period of absence of at least one year. (3) Have strong competence in modeling, with an interest in population dynamics, viability analyses and conservation biology and knowledge of C programming or closely related languages. (4) Personal qualities needed for group work and inter-disciplinary study.

**\*Contact\***

Application: Chantal Cuisinier, tel.: +33 1 44 27 36 89, email: Chantal.Cuisinier@snv.jussieu.fr, postal address: CNRS UMR 7625, Université Paris 6, 7 Quai St Bernard, 75005 Paris

Research project: David Claessen, tel.: +33 1 44 32 27 21, email: david.claessen@ens.fr

**\*How to apply\***

1. Applicants have until \*September\* 1 2008 to send a completed application form available below to the Application contact point. 2. The lab director and a local jury will select one candidate from the application forms and contact the candidates from September 31 2008. 3. The regional office of the CNRS will be responsible for drawing up the contract.

Download a pdf version of the \*Application form\* from <http://www.environnement.ens.fr/postdoc.html> David Claessen <david.claessen@ens.fr>

---

**FrenchGuiana  
RainforestTreeGenetics and  
Evolution**

A two-years post-doc position is open at the Ecological Genetics lab of the "EcoFoG" Joint Research Center, based in Kourou, French Guiana (a French Overseas Department), in the Amazonian forest. Kourou is the town where the European spaceport is located, on the Northern coast of South America. Our lab is fully equipped with all facilities related to molecular biology and genetics, and is only few kilometres away from its study subject - the tropical rainforest - and from giant sea turtles' nesting sites. The proposed job implies collaborations with other labs in France and abroad.

The deadline for applications is July 31, 2008, and the job is supposed to start in September-October 2008, with a salary that depends on the applicant's expe-

rience and that should be minimum 1700 EURO per month.

Please contact me at [ivan.scotti@cirad.fr](mailto:ivan.scotti@cirad.fr) for more information, or visit [http://www.international.inra.fr/-join\\_us/postdoctoral\\_fellows](http://www.international.inra.fr/-join_us/postdoctoral_fellows) Here is the text of the proposal:

#### TREE GENETIC DIVERSITY AND ADAPTATION IN THE GUIANA SHIELD

keywords: population genetics - evolution - forest ecology

In the context of the study of the adaptation of natural populations to global change and of the mechanisms controlling their interactions with the environment, there is a growing interest in the analysis of functional genetic diversity.

Tropical rainforests are among the most diverse ecosystems in the world. The genetic mechanisms of the adaptation of tropical forest trees to their environment may have a major role in the building up of forest communities and in their ability to respond to environmental changes, including anthropogenic pressure and climate change. Nevertheless, these mechanisms are just starting to be elucidated by a three-pronged approach including phylogeographic studies, quantitative genetics, and the characterisation and isolation of genes potentially involved in the response to environmental constraints. Several genes potentially relevant in this context have already been isolated in our laboratory, in particular for functions such as the responses to drought and mechanical stresses; the isolation of genes involved in response to flooding is under way, and development-related genes (wood formation, bud burst) are expected to be isolated soon. In parallel, phylogeographic studies are disclosing the historical patterns of diversity across the Amazonian basin, and experimental quantitative trait studies are being performed in order to break apart the environmental and genetic components of these traits.

The proposed program aims to (i) the cloning of complete cDNA regions from the genes listed above and the isolation of their promoters, (ii) the characterisation of the distribution of their diversity at the population, landscape and phylogeographic scale (iii) the assessment selective pressure at these genes (iv) the identification of concordances and discordances of the distribution of adaptive genetic diversity with historical patterns, as determined by neutral markers, and (v) the identification of concordances and discordances of the distribution of adaptive genetic diversity with ecological trends, as determined by climatic and floristic data. The proposed program will be carried out on a

selected subset of species covering a range of geographical distribution and ecological patterns (*Eperua* spp., *Carapa* spp., *Virola* spp. and *Symphonia* spp.). The sequence data thus obtained will be analysed by methods that take simultaneously into account population divergence, gene flow and selection in order to obtain the combined estimation of all parameters. This study will be backed up by parallel analyses on the distribution of genetic diversity at neutral markers and by experiments of reciprocal transplants among provenances and among environments.

Ivan Scotti INRA - UMR 0745 ECOFOG "Ecologie des Forêts de Guyane" / "Ecology of Guiana Forests" Laboratoire de Génétique écologique / Ecological Genetics Laboratory Campus agronomique, Avenue de France BP 709 - 97387 Kourou CEDEX FRANCE Phone +594 (0)59432-9274, -9285, -9278 Fax +594 (0)59432-4302 MY E-MAIL ADDRESS HAS CHANGED: e-mail: [ivan.scotti@ecofog.gf](mailto:ivan.scotti@ecofog.gf) <<mailto:ivan.scotti@kourou.cirad.fr>>, web: <http://www.ecofog.gf> "Società Italiana di Biologia Evoluzionistica / Italian Society for Evolutionary Biology" <http://www.sibe-iseb.it/> Ivan Scotti <[Ivan.Scotti@ecofog.gf](mailto:Ivan.Scotti@ecofog.gf)>

---

## Grenoble PopulationGenetics

Dear evoldir members,

A call is open for a one-year (possibility of extension pending funding) postdoctoral position in Grenoble, France. The research topics are « Bayesian methods in population genetics with special emphasis on the detection of selection from genome scans ». This postdoctoral position is funded by the Joseph Fourier University (Grenoble) and is part of an ongoing project between two labs: Olivier Francois, TIMC, Faculty of medicine ([olivier.francois@imag.fr](mailto:olivier.francois@imag.fr)) and Oscar Gaggiotti, LECA, Lab Ecologie Alpine ([oscar.gaggiotti@ujf-grenoble.fr](mailto:oscar.gaggiotti@ujf-grenoble.fr)). It should start around september 2008, but the possibility of earlier or later start dates may be discussed with the applicants.

The postdoctoral fellow will be located in one of the two labs, in strong interaction with the people from the other lab which is located in the same city. Applicants should have a solid experience in at least one of the following fields: biostatistics, bioinformatics or population genetics. Application of computer scientists from the field of machine learning is also encouraged. All applicants should send their cv and a list of references

to:

olivier.francois@imag.fr oscar.gaggiotti@ujf-grenoble.fr

Best regards,

Olivier Francois and Oscar Gaggiotti

– Oscar Gaggiotti Professor Equipe Genomique de Populations et Biodiversité LECA UMR CNRS 5553 Université Joseph Fourier BP 53 38041 GRENOBLE France Tel.: 33(0)4 76 51 44 97 Fax: 33(0)4 76 51 42 79 <http://www-leca.ujf-grenoble.fr/membres/-gaggiotti.htm> <http://www-leca.ujf-grenoble.fr/-projets/gaggiottiprojets/IMPBioFr.htm> Oscar Gaggiotti <oscar.gaggiotti@ujf-grenoble.fr>

---

### HopkinsMarineStation PopulationGenetics

Population genetics of west coast marine communities: POSITION AS DOCTORAL RESEARCH FELLOW in biology (molecular ecology) is available in Steve Palumbi's lab at Stanford University's Hopkins Marine Station.

The position is affiliated with a Partnership for the Interdisciplinary Study of Coastal Oceans (PISCO)-funded project exploring the population genetics of a suite of fish and invertebrates along the west coast of the United States. The candidate should have a Ph.D. in biology, molecular biology or related fields. Experience in molecular genetics and/or population dynamic modeling is required. Applications should include a statement summarizing the applicant's scientific work and interest, curriculum vitae and two to three letters of recommendation. The position is available as of September 1, 2008, and applications will be accepted until the position is filled.

Contact Tim Knight at [trknight@stanford.edu](mailto:trknight@stanford.edu) Palumbi lab web site: <http://www.stanford.edu/-group/Palumbi/> [trknight@stanford.edu](mailto:trknight@stanford.edu)

---

### IndianaU ReproductiveDiversity

Indiana University invites applications for a postdoctoral traineeship to be supported by NIH-CHHD via

an NIH T32 training grant entitled, 'Common Themes in Reproductive Diversity.' We offer broadly integrative training in the areas of sexual reproduction and development with a focus on the behavior of animals including humans. Research conducted by participants addresses key questions in the development and expression of sex differences, as well as maternal and paternal effects on morphological, sexual, and social development. Indiana University's excellent support for research and its globally recognized strengths in animal behavior, endocrinology, human sexual health, and evolution of development ensure high quality training.

Traineeships include a competitive salary based on current NIH pay scale commensurate with experience and funds to support research and travel. The successful applicant will help foster collaborations among faculty and serve as a professional model for pre-doctoral trainees. A Ph.D. in biology, psychology, neuroscience, chemistry, gender studies or a related field is required. Candidates are invited to make initial contacts with training faculty. To apply, please visit the following website to find instructions and forms to download: <http://www.indiana.edu/~reprodiv/apply/> Please e-mail your completed application to Linda Summers at [lisummer@indiana.edu](mailto:lisummer@indiana.edu) or (less desired) mail it to 402 N. Park Street, Bloomington, IN 47405. The email subject line should read: CTRD Postdoc-Ketterson. For full consideration, applications should arrive by 1 September 2008, although later applications will be considered. The search will continue until the position is filled. Please note that the traineeship must begin on or before April 2009. Minority applicants are especially encouraged to apply. Trainees must be citizens, non-citizen nationals, or permanent residents of the US. Indiana University is an Equal Opportunity / Affirmative Action Employer.

Ellen Ketterson [ketterso@indiana.edu](mailto:ketterso@indiana.edu)

---

### MortonArboretum PlantMolPhylogenetics

Postdoctoral position in Plant Molecular Phylogenetics / Systematics of Sedges

A postdoctoral research position is available through an NSF-funded Systematics project on the systematics and evolution of chromosome number and genome size in *Carex* subgenus *Vignea* (Cyperaceae). This study provides an excellent opportunity to explore the evolution

of genome structure in a genus with holocentric chromosomes, one that displays a remarkable range of karyotypic diversity. The postdoctoral researcher will work primarily on molecular phylogenetic and cytogenetic aspects of the project, as well as phylogenetic comparative analysis. Responsibilities include field work in North America and China, molecular systematic lab work, chromosome counting, data organization and specimen handling for the project, analysis of molecular and cytogenetic / genome size data, meeting presentations, and manuscript preparation. Candidates are required to have a PhD in plant systematics or related field, with experience in conducting field work and in cytogenetic methods or methods of molecular systematics. Experience or interest in phylogenetic comparative analysis is strongly desired. The researcher will work at The Morton Arboretum with Dr. Andrew L. Hipp (The Morton Arboretum) and Dr. Eric H. Roalson (Washington State University). Information about The Morton Arboretum is available through the Arboretums Web site < <http://www.mortonarb.org/> > and our lab web site < [http://redwood.mortonarb.org/lab\\_pages/hipp](http://redwood.mortonarb.org/lab_pages/hipp) >.

The position is two-year appointment, beginning 1 January 2009 (start date negotiable). Application review begins immediately and continues until the position is filled. To apply, submit via email a curriculum vitae, statement of research interests, and contact information for three references to:

Andrew Hipp, The Morton Arboretum, 4100 Illinois Route 53, Lisle IL 60532-1293 Phone: 630-725-2094; fax: 630-719-2433; e-mail: <[ahipp@mortonarb.org](mailto:ahipp@mortonarb.org)>

Andrew L. Hipp, PhD Plant Systematist and Herbarium Curator The Morton Arboretum 4100 Illinois Route 53 Lisle, IL 60532-1293 [ahipp@mortonarb.org](mailto:ahipp@mortonarb.org) (630) 725-2094 [http://redwood.mortonarb.org/lab\\_pages/hipp](http://redwood.mortonarb.org/lab_pages/hipp) Andrew Hipp <[ahipp@mortonarb.org](mailto:ahipp@mortonarb.org)>

---

## SyracuseU DrosophilaSpermCompetition

We are seeking a Postdoctoral Fellow to join a National Science Foundation supported investigation of mechanisms and genetics of ejaculate-female interactions, sperm competition and postmating/prezygotic reproductive isolation in *Drosophila melanogaster* and related species.

A successful candidate will have a Ph.D. in evolutionary biology, evolutionary genetics, insect reproductive biology or a related field, in addition to a demonstrated history of being a highly creative, motivated and independent scientist. Expertise with dissection and microscopy is advantageous.

Duration of appointment is two years, with second year contingent upon performance during first year. The appointment begins between September 01, 2008 and January 01, 2009, dependent upon the successful candidate's situation.

To apply, please submit by email a CV along with the names and contact information for two references to Scott Pitnick ([sspitnic@syr.edu](mailto:sspitnic@syr.edu)). Deadline for applying is July 15, 2008.

For further information, please visit our websites: <http://biology.syr.edu/pitnick/index.html> <http://biology.syr.edu/belote/index.html> Contact: Scott Pitnick (315-443-5128; [sspitnic@syr.edu](mailto:sspitnic@syr.edu)) John Belote (315-443-3695; [jbelote@syr.edu](mailto:jbelote@syr.edu)) Department of Biology, Syracuse University, Syracuse, NY 13244, USA

Scott Pitnick <[sspitnic@syr.edu](mailto:sspitnic@syr.edu)>

---

## UConnecticut ProteinEvolution

We seek a postdoctoral scientist with laboratory experience in protein expression and functional characterization. The candidate should also have experience in the use of amino acid sequence analyses addressing questions of protein function and evolution. Our NASA-funded project examines the evolution of protein thermostability in the bacterial lineage of Thermotogales. The project also explores the relationship between horizontal acquisition of binding protein-encoding genes and the changes in the binding properties of those proteins. The position will commence no later than Sept. 1, 2008. Applicants must have a Ph.D. at the time of employment. The University of Connecticut, rated first among public universities in New England, is located in northeastern Connecticut with easy access to Boston and New York City. The web page of the Department of Molecular and Cell Biology is <http://mcb.uconn.edu>. Electronic applications should include a curriculum vitae and contact information for three references. Applications should be sent to Dr. Kenneth Noll at [kenneth.noll@uconn.edu](mailto:kenneth.noll@uconn.edu) or Dr. J. Peter Gogarten at [gogarten@uconn.edu](mailto:gogarten@uconn.edu).

-

J. Peter Gogarten Professor of Molecular and Cell Biology University of Connecticut Unit 3125 91 North Eagleville Road Storrs CT 06269-3125 USA

Phone: 860 486 4061 (office) 860 486 1887 (lab)  
 FAX: 860 486 4331 Email: [gogarten@uconn.edu](mailto:gogarten@uconn.edu) www:  
<http://gogarten.uconn.edu/> [jpgogarten@gmail.com](mailto:jpgogarten@gmail.com)

---

## UFlorida MutationRateEvolution

Postdoc / evolution of mutation rate - University of Florida

Applications are invited for a postdoctoral research associate to work on an NIH-funded project on the evolution of mutation rate in the lab of Charles Baer at the University of Florida (<http://www.zoo.ufl.edu/-cbaer/>). The project combines classical mutation-accumulation methods of quantitative genetics with very-high-throughput genome sequencing to investigate several factors potentially underlying variation in the mutation rate, using nematodes in the genus *Caenorhabditis* as a model system. The successful applicant will ideally have some or all of the following skills: *C. elegans* biology, molecular biology, bioinformatics, theoretical population genetics. All applicants will be considered, however, and the only necessary attribute is a commitment to excellent work in an explicitly team-oriented environment. Independent side projects on the part of the postdoc are encouraged and will be supported intellectually and financially if feasible. The initial appointment is for one year, with an additional two years' funding available conditional on satisfactory performance.

Start Date: flexible, but as early as mid-August 2008

Starting Salary: NIH-mandated scale, i competitive benefits, including family health insurance.

Location: Gainesville, Florida, USA. Gainesville is a very pleasant, medium-sized city in north-central Florida with excellent public schools. Outstanding year-round outdoor recreational opportunities abound, as long as they don't involve snow ("This is Florida. No snow, no ice..." - G. Marx).

The University of Florida is an equal-opportunity institution. Members of groups under-represented in the Biological Sciences are especially encouraged to apply.

Applicants please send a cover letter, CV, and contact

information for three references by email to Charles Baer ([cbaer@zoo.ufl.edu](mailto:cbaer@zoo.ufl.edu)). I will be at the SSE meetings in Minneapolis, personal inquiries are welcome!

-

Charles F. Baer Department of Zoology 223 Bartram Hall P. O. Box 118525 University of Florida Gainesville, FL 32611-8525 USA

Phone: 352-392-3550 Fax: 352-392-3704 Email: [cbaer@zoo.ufl.edu](mailto:cbaer@zoo.ufl.edu) web: <http://www.zoo.ufl.edu/-faculty/baer.html> [cbaer@zoo.ufl.edu](mailto:cbaer@zoo.ufl.edu)

---

## UKansas QuantGenetics

Postdoc Position in Quantitative Genetics of Behavior Department of Ecology and Evolutionary Biology University of Kansas

A postdoctoral research associate position is available in Dr. Jennifer Gleason's lab to examine the genetic architecture of *Drosophila* courtship song and cuticular hydrocarbons, two important traits to species recognition, and the genetics of preferences for their traits. The work will use recombinant inbred lines between *D. simulans* and *D. sechellia*. The postdoc will perform behavioral assays, coordinate genotyping of lines, conduct microarray experiments, perform statistical analyses of the resulting data and write journal articles. Specific skills associated with the project include PCR and basic molecular biology skills, behavioral analyses, *Drosophila* culturing, quantitative trait analysis and supervision of undergraduate students working on the project.

Required qualifications are: 1) a PhD. in Biology, Genetics, Evolutionary Biology, or related field. 2) Experience in one of the following areas: molecular biology, quantitative genetics, *Drosophila* genetics, or behavioral genetics. 3) Good statistical, skills as well as verbal and written communication skills demonstrated by materials submitted through the application process, work experience, letters of reference, and/or previous publications.

The position is available for one year, with possible renewal, starting August 1, 2008. To Apply go to: <http://jobs@ku.edu> < [http://jobs@ku.edu](mailto:jobs@ku.edu) > (position #00206817). Attach curriculum vitae and cover letter stating the research and career interests of the applicant. Arrange for 2 reference letters sent to: Dr. Jennifer Gleason, Dept. of Ecology & Evolu-

tionary Biology, Univ. of Kansas, 1200 Sunnyside Avenue, Lawrence, KS 66045-7534, or via email at [jgleason@ku.edu](mailto:jgleason@ku.edu) <<mailto:jgleason@ku.edu>> . Phone: 785-864-5858. Review of applications begins 30 June 2008 and will continue until the position is filled. The University of Kansas is an EO/AA employer.

Dr. Jennifer Gleason Assistant Professor University of Kansas Ecology and Evolutionary Biology 1200 Sunnyside Ave., Haworth Room 6006 Lawrence, KS 66045 785-864-5858 785-864-5321 (FAX) [jgleason@ku.edu](mailto:jgleason@ku.edu) <http://www2.ku.edu/~eeb/faculty/gleason.shtml>

[jgleason@ku.edu](mailto:jgleason@ku.edu) [jgleason@ku.edu](mailto:jgleason@ku.edu)

---

## UMaryland EukaryoticGenomeEvolution

Dear EvoDir members,

The following postdoc ad has now been released. Applications will start being reviewed in mid June and the short-listed applicants will be notified by the end of July. Please forward to potential candidates.

Thanks, Joana

Joana C. Silva, Ph.D. Assistant Professor

University of Maryland School of Medicine Institute for Genome Sciences & Dept Microbiology and Immunology 685 W. Baltimore St., HSF-I Rm 130 Baltimore, MD 21201

[jcsilva@som.umaryland.edu](mailto:jcsilva@som.umaryland.edu) Ph:410.706.6721  
Fax:410.706.6777

### INSTITUTE FOR GENOME SCIENCES

The newly created Institute for Genomes Sciences (IGS) at the University of Maryland, School of Medicine is in a period of rapid expansion with many new appointments anticipated in the next five years. The Institute is led by Claire M. Fraser-Liggett, Ph.D., one of the world's preeminent genome scientists and previous Director and President of the Institute for Genomic Research (TIGR). The Institute for Genome Sciences houses an inter-disciplinary, multi-departmental team of collaborative investigators with a broad spectrum research program related to the genomics of infectious disease agents, human microbial metagenomics, functional genomics, and bioinformatics. The impact of the IGS team on the field of genomics has been substantial, with more than 500 publications during the

past 15 years that have been cited more than 30,000 times.

A POSTDOCTORAL FELLOW position is open in Joana Silva's group at the IGS for an enthusiastic, highly motivated individual interested in studying eukaryotic genome evolution. Potential projects include the evolution of nucleotide composition of genomes, the genomic distribution of substitution rates and the impact of genomic location on nucleotide composition and evolutionary rate. Projects will be mostly computational and are based on the sequenced genomes of over a dozen apicomplexans, including eight Plasmodium, three Theileria and three Cryptosporidium species, the causative agents of malaria, cryptosporidiosis, and theileriosis and East Coast fever, respectively (<http://www.igs.umaryland.edu/~jcsilva>).

The ideal candidate will have a doctoral degree in Genetics, Evolution, Computational Biology or a related field, will be thoroughly familiar with the fields of population genetics, molecular evolution and bioinformatics, and must have documented experience with molecular evolution and phylogeny estimation software (e.g., Paml, HyPhy, DnaSP, Paup, MrBayes, Beast). Programming skills in languages such as C/C++ and Perl, even though not essential, are a plus. A publication record in evolutionary biology is a must. The initial appointment is for one year starting in the Fall 2008 (start date flexible), with possible extension to a second year dependent on performance.

The successful candidate will benefit from a community of very interactive research labs, a large group of bioinformatics programmers and a variety of laboratory, sequencing and computational resources available in a world class genomics institute to support basic, genomic and translational research. To apply, please send a CV, a statement of research interests (include reason for applying to this position; 2 pages maximum) and contact information for three references to [IGS-jobs@som.umaryland.edu](mailto:IGS-jobs@som.umaryland.edu) <<mailto:IGS-jobs@som.umaryland.edu>> . Additional inquiries about the position can be sent to Joana Silva: [jcsilva@som.umaryland.edu](mailto:jcsilva@som.umaryland.edu).

Consideration of candidates will begin upon receipt of applications and will continue until the position is filled. AA/EOE/ADA

[jcsilva@som.umaryland.edu](mailto:jcsilva@som.umaryland.edu)

[jcsilva@som.umaryland.edu](mailto:jcsilva@som.umaryland.edu)

---

## UmeaU Evolution at RangeMargins

A two-year post-doc position is available to study the limits to evolution at range margins. More specifically the research will try to answer when and why adaptations to climate change succeed or fail. The focus will be on genetic variation in populations located at either the range margin or the center of a species distribution. The candidate is expected to analyze genetic variation of populations using DNA-based markers, but the research will also include genetic variation in quantitative characters. Previous experience with molecular methods, evolutionary ecology and quantitative genetics will be considered an advantage.

For more information either consult the web pages of Drs Frank Johansson ([frank.johansson@emg.umu.se](mailto:frank.johansson@emg.umu.se)) and Pär Ingvarsson ([par.ingvarsson@emg.umu.se](mailto:par.ingvarsson@emg.umu.se)) at the Department of Ecology and Environmental Science, Umeå University, [www.emg.umu.se](http://www.emg.umu.se) or contact us by email.

To qualify for the position you should have a PhD degree in ecology, evolutionary biology or equivalent, preferably not more than five years old. The application can be submitted either electronically or in hard-copy form to the address below. Applicants should submit a curriculum vitae, copies of degree certificates, a statement of previous research achievements and teaching merits, a publication list and reprints/copies of published work numbered according to this list, a research plan (maximum 4 pages) and contact information (names, e-mail and postal addresses) of at least two professional references. If you submit the application in hard copy form, two copies of all documents are needed. Note, in order to be considered, applications must include copies of reprints.

NOTE!!! Your complete application, marked with Ref no 315-2174-08, should be sent either electronically (preferred) to:

[jobb@umu.se](mailto:jobb@umu.se)

or by regular mail to:

Registrary Umeå University SE-901 87 Umeå Sweden

To be considered for the position the application must have arrived no later than August 15, 2008.

– Pär K. Ingvarsson Senior Researcher, Swedish Research Council Associate Professor Umeå Plant Sci-

ence Centre Department of Ecology and Environmental Science Umeå University, SE-901 87 Umeå tel. +46-(0)90-786-7414, fax. +46-(0)90-786-6705 web: <http://mendel.emg.umu.se> [pelle@wallace.emg.umu.se](mailto:pelle@wallace.emg.umu.se)

---

## UmeaU PopulationDynamics

Post Doc position in spatial population dynamics, Umeå University, Sweden Ref no 315-2175-08

A post-doc position (2 years) in the project “Spatial heterogeneity, functional responses and predator-prey dynamics” is available.

It is widely believed that spatial heterogeneity stabilizes predator-prey interactions, but the underlying mechanisms are poorly understood. This project focuses on a previously overlooked aspect - the dynamics of the covariance between predator and prey densities. The project involves cooperation with an international group of researchers that contribute with extensive data sets on predator-prey systems. The data involve a diverse set of organisms, including insects, mites, crustaceans, polychaets and mammals. Many of the systems show cycles and complex spatial patterns, e.g., “hide and seek” dynamics.

The project is demanding but will likely yield publications in high ranked journals. A paper that provides a background is found in *Am. Nat.* 167:246-259. For more information about the project, go to < <http://www.emg.umu.se/> > [www.emg.umu.se](http://www.emg.umu.se), or contact Professor Göran Englund, at [goran.englund@emg.umu.se](mailto:goran.englund@emg.umu.se). To qualify for the position you should have a PhD degree or equivalent. The application can be submitted either electronically or in hard-copy form. Applicants should submit a CV, copies of degree certificates, a statement of previous research achievements and teaching merits, a publication list and reprints/copies of published work numbered according to this list, a research plan (maximum 4 pages) and a list of referees, all in two copies if the application is in hard copy form.

The complete application, marked with reference number, should be sent to [jobb@umu.se](mailto:jobb@umu.se) or to the Registrar, Umeå University, SE-901 87 Umeå, Sweden to arrive August 15, 2008 at the latest.

Göran Englund Professor in Animal Ecology Department of Ecology and Environmental Science Umeå Marine Sciences Centre Umeå University, 901 87



Umeå, Sweden Phone: +46 90 786 9728, FAX: +46 90 786 6705 E-mail: Goran.Englund@emg.umu.se  
Homepage: [http://www.emg.umu.se/personal/-goran\\_englund.htm](http://www.emg.umu.se/personal/-goran_englund.htm) goran.englund@emg.umu.se  
goran.englund@emg.umu.se

the Department of Biostatistics ([www.sph.umich.edu/-biostat](http://www.sph.umich.edu/-biostat)) and the Center for Statistical Genetics (csg.sph.umich.edu) at the University of Michigan.

For further details, please contact [szoellne@umich.edu](mailto:szoellne@umich.edu).  
[szoellne@umich.edu](mailto:szoellne@umich.edu)

---

## UMichigan EvolutionaryBiol

The Michigan Society of Fellows invites applications to its postdoctoral fellowship program for recent PhDs in the humanities, arts, sciences, and professions. These three-year positions at the University of Michigan are open to recent PhDs who wish to pursue research opportunities while teaching at a major research university. Eight fellowships are available, with an annual stipend of \$51,500. Four of these fellowships will be awarded in the humanities, with the support of the Andrew W. Mellon Foundation. Applications must be submitted electronically by midnight September 30, 2008. The online application is available at [www.rackham.umich.edu/Faculty/sof.html](http://www.rackham.umich.edu/Faculty/sof.html). Questions may be submitted to [society.of.fellows@umich.edu](mailto:society.of.fellows@umich.edu).

[wittkopp@umich.edu](mailto:wittkopp@umich.edu) [wittkopp@umich.edu](mailto:wittkopp@umich.edu)

---

## UMichigan GeneByEnvironment

University of Michigan

A post-doctoral position is available from September 2008, to work with Sebastian Zollner in collaboration with Noah Rosenberg on Methods for Gene-environment Interaction. We are interested in modeling gene-environment interaction, efficient methods for including environmental covariates in gene mapping and exploring the evolutionary consequences of gene-environment interaction. A possible project involves developing a model to define heritable subtypes of complex disorders such as bipolar disorder by analyzing the joint inheritance of endophenotypes and the clustering of environmental covariates in families. Strong computing skills are essential, and experience with statistical modeling is highly desirable.

The project is funded for three years by the National Institutes of Health. The postdoc will be based in

---

## UNebraska EvolutionaryGenomics

POST-DOCTORAL POSITION in Evolutionary Genomics P.I.: Jay F. Storz, University of Nebraska, Lincoln, NE

A post-doctoral position is available in the Storz lab at the University of Nebraska (<http://www.biosci.unl.edu/labs/storz/index.html>). The NIH-funded research project involves a comparative genomic analysis of globin gene family evolution. Specifically, the goal is to link changes in the size and membership composition of the globin gene families to species differences in hemoglobin function and blood-oxygen transport. The research project addresses questions about the evolution of duplicated genes and multigene families, as well as functional aspects of protein evolution. The work will involve comparative analyses of genome sequences from mammals and other vertebrate groups. The post-doc will have the opportunity to collaborate with a diverse team of researchers with different backgrounds, as related aspects of the same project involve experimental studies of protein function and molecular adaptation.

Ideally, the successful applicant will have experience in bioinformatics, comparative genomics, and molecular phylogenetics, as well as an enthusiasm for integrative evolutionary biology.

If interested, please send a CV, cover letter, and names and contact information for three references. The position could start as early as July, but the start-date is flexible. Funding is available for 3+ years. Salary will be determined by the NIH pay scale and will include full benefits. I will be reviewing applications as they arrive. Please feel free to contact me with any questions ([jstorz2@unl.edu](mailto:jstorz2@unl.edu)).

I will be at the evolution meeting in Minnesota, 20-24 June, and I'd be happy to meet with prospective applicants there.

Jay F. Storz School of Biological Sciences University of Nebraska Lincoln, NE 68588 <http://www.biosci.unl.edu>

www.biosci.unl.edu/labs/storz/index.html Jay F Storz  
<jstorz2@unlnotes.unl.edu>

## UNebraska MolecularAdaptation

POST-DOCTORAL POSITION in Molecular Adaptation P.I.: Jay F. Storz, University of Nebraska, Lincoln, NE

A post-doctoral position is available in the Storz lab at the University of Nebraska (<http://www.biosci.unl.edu/labs/storz/index.html>). The NIH-funded research project involves an experimental investigation of molecular adaptation. Specifically, the goal is to identify mechanisms of hemoglobin adaptation to hypoxia in high-altitude rodents and other vertebrates. An important aspect of the research will involve using a plasmid expression system to generate recombinant hemoglobins for functional and crystallographic studies. The post-doc would be working with myself as well as Dr. Hideaki Moriyama at the University of Nebraska. The post-doc will also work in collaboration with a team of researchers with disparate backgrounds including molecular evolution, molecular population genetics, and comparative functional genomics (Storz lab), as well as structural biology, biophysics, and biochemistry (H. Moriyama lab).

Experience with recombinant DNA methods is essential, and additional training will be provided as needed. Experience with protein purification and methods for analyzing protein structure would be a big plus.

If interested, please send a CV, cover letter, and names and contact information for three references. The position could start as early as July, but the start-date is flexible. Funding is available for 3+ years. Salary will be determined by the NIH pay scale and will include full benefits. I will be reviewing applications as they arrive. Please feel free to contact me with any questions (jstorz2@unl.edu).

I will be at the evolution meeting in Minnesota, 20-24 June, and I'd be happy to meet with prospective applicants there.

Jay F. Storz School of Biological Sciences University of Nebraska Lincoln, NE 68588 Phone: 402/472-1114 E-mail: jstorz2@unl.edu

<http://www.biosci.unl.edu/labs/storz/index.html> Jay F Storz <jstorz2@unlnotes.unl.edu>

## UParisSud PhylogeneticLanguage

We propose a postdoctoral opportunity in the group of Dr. Ch. Froidevaux at the University of Paris-Sud on the following theme: Towards a language to query phylogenetic data

Please send a motivation letter, a resume, and the name of collaborators/advisors able to recommend your application by June 10th, 2008 to Christine Froidevaux (chris@lri.fr) and Sarah Cohen-Boulakia (cohen@lri.fr)

More information is available below and at <http://www.lri.fr/~cohen/phylo.html> \* Advisors Sarah Cohen-Boulakia (Assistant Professor), Christine Froidevaux (Professor) \* Collaborators Bernard Labedan, Olivier Lespinet (Institut de Genetique et de Microbiologie, Universite Paris-Sud, Orsay, France) Val Tannen (University of Pennsylvania, USA) \* Location Bioinformatics group at LRI (Laboratoire de Recherche en Informatique), Universite Paris-Sud, Orsay, France

\* Topic Understanding the relationships between different species may have consequences both at practical level (e.g., history of a pathogen agent involved in a disease), and at fundamental level (e.g., construction of the tree of life: finding the history of all organisms). The study of evolution requires various and numerous pieces of data such as morphological characteristics of a set of specimens or, more importantly, genomic and proteomic sequences of a group of species, functional and structural annotations. For several years now, there has been an avalanche of data available. Combining and integrating masses of phylogenomics data is of paramount importance for better understanding evolution.

\* Background More specifically, this subject is part of two projects, pPOD and Microbiogenomics.

\*\* On the one hand, pPOD is an international project, in which data are collected throughout the world by research groups having distinct interests (specialized on different groups of species). Data collected by those various groups are available in a variety of formats (relational, tabulated files, and so on.).

\*\* On the other hand, partners of the the French project "ANR masses de donnees" Microbiogenomics study evolution by building phylogenetic trees based on families of proteins, part of their data is currently

stored in flat-files format (trees) and within a relational warehouse (sequences, annotations).

In both projects, phylogeneticists need to ask complex questions involving all the data, both produced and consumed by the various steps of the generation and analysis of phylogenetic trees, including the trees themselves or families of trees. Examples of queries include: What are the differences between those two trees? If I modify the alignment by adding gaps, what would be the impact on the final generated tree? or

”Among the available trees, what are the subtrees whose proteins are all involved in a given metabolic pathway? Which are the protein modules appearing in trees in which a given group of species is monophyletic?”

\* Work The aim of this work is to enable various phylogeneticists to make use of all these data in a unified way, in the context of a relational database. One of the main challenges lies in that the relational model does not fit with hierarchical (tree-based) data.

As a first step, queries frequently asked by major pPOD and Microbiogenomics partners should be identified. Queries may be increasingly complex and can be expressed using different kinds of language (relational algebra, SQL and so on). In particular, queries may involve families of trees, comparison and clustering algorithms, and topological features of the trees.

A classification of queries should then be proposed.

The third step would consist in exploring the limitations of current relational standards (latest versions of SQL) to represent phylogenetic data and express queries. This study should provide the building blocks for a more expressive high-level query language.

More information on the pPOD project: <http://phyldata.seas.upenn.edu> More information on the Microbiogenomics project: <http://microbiogenomics.u-psud.fr> More information on the Bioinformatics group at LRI: <http://www.lri.fr/bioinfo>

Sarah Cohen-Boulakia and Christine Froidevaux

Sarah Cohen-Boulakia Assistant Professor University of Paris Sud 11 Computer science department, Bioinformatics group Orsay 91405 cedex France +33 1 69 15 32 16

Sarah Cohen Boulakia <Sarah.Cohen\_Boulakia@lri.fr>

Postdoctoral research fellowship in evolutionary genomics at Uppsala University, Sweden

A postdoctoral fellowship is available at the Department of Evolutionary Biology at Uppsala University. The postdoc is in the research-group of Dr. Hanna Johannesson, and will focus on the evolution of the mating-type chromosome in the filamentous ascomycete *Neurospora tetrasperma*. The fellowship is for one year, with a high likelihood of extension.

Recent studies have revealed that chromosomal regions controlling sexual identity in the fungal kingdom share features with the more complex sex chromosomes of algae, plants and animals. Our group have combined gene divergence data, classical genetics and phylogenetics to show that the mating-type chromosome of *N. tetrasperma* resemble the sex chromosomes in that recombination suppression involved more than one evolutionary event, covers the majority of the chromosome and is flanked by distal regions with obligate crossovers. Now, our group aims at exploring the system further by using a bioinformatics and/or a molecular biology approach. This postdoc project could involve revealing structural or autosomal gene influence on the recombination block, the evolutionary history of the chromosome in different phylogenetic lineages of the species, or whether divergence between the chromosomes is accompanied by differences in gene expression.

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

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

Review of applications will begin immediately and continue until the position is filled.

If you have any questions, please contact [hanna.johannesson@ebc.uu.se](mailto:hanna.johannesson@ebc.uu.se)

To apply, send your CV, including contact information for two references, and a cover letter stating your research interest to:

Dr Hanna Johannesson, Uppsala University, Department of Evolutionary Biology, Norbyvägen 18D, SE-752 36 Uppsala, Sweden,

or by e-mail to [hanna.johannesson@ebc.uu.se](mailto:hanna.johannesson@ebc.uu.se)

[hanna.johannesson@ebc.uu.se](mailto:hanna.johannesson@ebc.uu.se)

[hanna.johannesson@ebc.uu.se](mailto:hanna.johannesson@ebc.uu.se)

---

## UppsalaU NorwaySpruceEvolution

Postdoctoral position in evolutionary genomics One Postdoctoral position will be available at the Program in Evolutionary Functional Genomics in Uppsala with Dr. Martin Lascoux. The successful candidate will work within the framework of the newly funded EU-project Noveltree due to start in June. Within this project, our group, together with the group of Michele Morgante at the University of Udine (Italy), will focus on the development of genomic resources for Norway spruce (*Picea abies*) and the use of these in evolutionary genomics and tree breeding. We are also part of the Evoltree network of Excellence and there will be many opportunities to cooperate with other groups in Europe and abroad. The successful candidate will be hired for a period of 2 years and could start as early as July 2008.

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

For more information, please contact:

Dr Martin Lascoux

Program in Evolutionary Functional Genomics

Evolutionary Biology Centre

[Martin.Lascoux@ebc.uu.se](mailto:Martin.Lascoux@ebc.uu.se) Phone: +46-18-4716416  
Fax: +46-18-4716424

The position is open to anyone with a PhD with experience from and interest in one or several of the following areas: plant molecular biology, bioinformatics, population genetics, breeding, evolutionary biology or related subjects. Documented work with large scale DNA sequencing and genotyping will be considered a merit.

Interested parties should send a statement of interest, and a detailed CV including contact information for two references to Martin Lascoux, Program in Evolutionary Functional Genomics, Evolutionary Biology Centre, Uppsala University, Norbyvägen 18 D 752 36 UPPSALA, Sweden; fax +46-(0)18-471 6424 no later than the June 20, 2008. An application by fax or e-mail must be followed by a letter containing the original documents, at the latest 10 days after application deadline.

Martin Lascoux Program in Evolutionary Functional Genomics EGS/EBC, Uppsala University Norbyvägen 18D 75236 Uppsala Sweden Tel +46 (0) 18 471 64 16  
Fax +46 (0) 18 471 64 24

[martin.Lascoux <Martin.Lascoux@ebc.uu.se>](mailto:martin.Lascoux@ebc.uu.se)

---

## UTexasAustin DiseaseModeling

POSTDOCTORAL POSITION: MATHEMATICAL DESIGN OF CANADIAN AND AMERICAN INFLUENZA INTERVENTION STRATEGIES

One postdoctoral position in biostatistics and mathematical modeling is currently available to be spent jointly at the Section of Integrative Biology at the University of Texas at Austin and the British Columbia Centre for Disease Control (BCCDC) in Vancouver, BC. This position is supported by a grant from the Canadian Institutes of Health Research (CIHR).

Open: until August 2008

Length: anticipated for two years (one year at the University of Texas at Austin followed by one year at the BCCDC)

Contacts: - Lauren Ancel Meyers Section of Integrative Biology University of Texas at Austin 1 University Station C0930 Austin, TX 78712  
Ph: 512-471-4950, Fax: 512-471-3878 URL: <http://cluster3.biosci.utexas.edu/research/meyers/> Email: [laurenmeyers@mail.utexas.edu](mailto:laurenmeyers@mail.utexas.edu)

- Babak Pourbohloul, BCCDC,

Babak.Pourbohloul@bccdc.ca

Location: University of Texas at Austin in Austin, Texas; British Columbia Centre for Disease Control in Vancouver, BC.

Project: Evaluation of Ontario's Universal Influenza Immunization Program

In July 2000, Ontario initiated the world's first large-scale universal influenza immunization program (UIIP) to provide free influenza vaccines for the entire population aged 6 months or older. We aim to evaluate Ontario's UIIP in relation to targeted influenza immunization programs (TIIP) that exist in other provinces in Canada.

This proposal combines six components using a variety of approaches to address several objectives. The postdoctoral researcher will be involved in the mathematical modeling and data analysis component which aims to: a) to build demographic-specific contact network models for the cities of Toronto, Vancouver and Halifax, b) to estimate transmissibility of different influenza strains using morbidity data in conjunction with the network models constructed for each city; c) to compare currently-used urban vaccination strategies assuming various degrees of vaccine efficacy, coverage, and cross-immunity for each city; and d) to determine the coverage necessary for each strategy to achieve herd immunity for the population as a whole as well as the most vulnerable segments of the population.

Job description: The postdoctoral researcher will be involved in multiple aspects of the project, in collaboration with epidemiologists, infectious disease specialists, public health officials, mathematical modelers and statisticians from the University of Texas at Austin, the British Columbia Centre for Disease Control and several other Canadian public health and medical institutions. He/ she will contribute to the analysis of epidemiological data, the development of new mathematical modeling, and the application of statistics and modeling to evaluating and designing optimal influenza intervention plans. The postdoctoral researcher will be expected to prepare and publish research papers in the peer-reviewed literature. He/she will be based at both the University of Texas at Austin and the British Columbia Centre for Disease Control in Vancouver, BC; ideally the person will spend one year in Austin followed by one year in Vancouver, with occasional visits to the other site. This position is for two years, with a starting date between September and December 2008.

Educational qualifications: A PhD in one of the following areas is required: biostatistics, epidemiology, demography, statistics, mathematics, physics or a re-

lated quantitative discipline. Prior research experience in the one or more of the following areas is desirable: epidemiology of infectious diseases, mathematical modeling, and statistical analysis of complex data.

Other requirements: We are seeking applicants who are able to work independently and as part of a multidisciplinary research team, and have the flexibility to travel between research sites.

Salary: The salary will be approximately US\$45,000 to US\$60,000 per annum, commensurate with training and experience. Full benefits will be included, and funds to support position-related travel.

To apply: Please contact Lauren Ancel Meyers (laurenmeyers@mail.utexas.edu) and Babak Pourbohloul (Babak.Pourbohloul@bccdc.ca) to inquire about or apply for the position. To apply, please submit a CV, a brief statement describing your interest in the position and relevant qualifications and at least three letters of reference.

More information: For more information about the Meyers group and the Section of Integrative Biology at the University of Texas at Austin, please visit:

<http://cluster3.biosci.utexas.edu/research/meyers/>  
<http://www.biosci.utexas.edu/IB/>

— / —

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>

---

## UToronto FunctionalMetagenomics

Postdoctoral Fellowship in Functional Metagenomics  
PI: Dr. David Guttman, University of Toronto, Canada

We are seeking a postdoctoral fellow with both molecular biology and bioinformatics experience to pursue a cutting-edge project in the functional metagenomics of lung infections. This five year project supported by the National Sanitarium Association aims to study the transcriptional profile and dynamics of whole pulmonary bacterial communities during respiratory tract infections, and in response to antibiotic treatment. The candidate will generate digital gene expression data on an Illumina Solexa Genome Analyzer GAI, the latest in next-generation genome analysis platforms. This study will provide unprecedented insights into gene and

species interactions important in antibiotic response and resistance in the human microbiome.

The candidate must have extensive wet bench experience with DNA and RNA manipulation. They should also be comfortable with bioinformatic methods for the analysis of transcriptome data. Some experience with database management and bioinformatic scripting (e.g. PERL) is strongly preferred.

The project is a collaboration between Drs. David Guttman (Cell & Systems Biology, University of Toronto), David Hwang (Pathology, Toronto General Hospital), and Elizabeth Tullis (Respirology, St. Michael's Hospital). Work will be carried out in the Guttman laboratory, where there are numerous opportunities for interaction among the students, post-docs, faculty, and staff in the Departments of Cell & Systems Biology ([www.csb.utoronto.ca](http://www.csb.utoronto.ca)), Ecology and Evolutionary Biology ([www.eeb.utoronto.ca](http://www.eeb.utoronto.ca)), and Centre for the Analysis of Genome Evolution & Function ([www.cagef.utoronto.ca](http://www.cagef.utoronto.ca)). Toronto is a vibrant and multicultural city, with a tremendous quality of life.

The position is available immediate.

Candidates should send a letter of interest, CV, and three letters of reference to:

David Guttman Department of Cell & Systems Biology University of Toronto 25 Willcocks St Toronto, ON M5S3B2 CANADA

David S. Guttman Ph.D. Associate Professor Canada Research Chair in Comparative Genomics Director, Centre for the Analysis of Genome Evolution & Function Department of Cell & Systems Biology Department of Ecology & Evolutionary Biology University of Toronto 25 Willcocks St. Toronto, ON M5S 3B2 Canada

416 978-6865 ph-office 416 946-7121 ph-lab  
416 978-5878 fax david.guttman@utoronto.ca  
labs.csb.utoronto.ca/guttman [www.cagef.utoronto.ca](http://www.cagef.utoronto.ca)  
david.guttman@utoronto.ca  
david.guttman@utoronto.ca

search Council (ERC) on models of genome evolution and phylogenomics in David Posada's lab at the University of Vigo, Spain (<http://darwin.uvigo.es>).

Initial appointments will be made for one year, with a possible extension to up to three years. Gross salary including benefits will be around 25-30 kEuros, commensurate with experience. Starting date is negotiable.

**REQUIREMENTS:** Candidates should have a doctoral degree in Statistics, Mathematics, Computer Science, Biology, or related fields. Both positions are computationally oriented, and excellent programming skills are essential, especially in Perl, C and C++. Familiarity with parallel and distributed computing environments is convenient. Strong communication and teamwork abilities are key.

For one position the ideal candidate would have in addition demonstrable experience in the development of likelihood and MCMC Bayesian methods. Familiarity with evolutionary biology would be very convenient.

For the other position the ideal candidate would have in addition a very strong background in evolutionary genomics. Advanced statistical skills would be a plus.

**APPLICATION:** Please send a letter of interest, C.V., and the names and contact details of two referees to David Posada, indicating <sup>3</sup>postdoctoral position in statistical phylogenomics<sup>2</sup> in the subject of the email. Questions and requests for more information should be directed at the same address. Review of applications will begin immediately, and continue until the positions are filled.

– David Posada Facultad de Biología Campus Universitario 36310 Vigo Spain

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

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

---

## VanderbiltU EarlyMetazoanEvolution

---

### UVigo 2 StatisticalPhylogenomics

2 postdoctoral positions in Statistical Phylogenomics University of Vigo, Spain

**DESCRIPTION:** Two postdoctoral positions are available to work in a project funded by the European Re-

3-YEAR POSTDOC ON EARLY METAZOAN EVOLUTION / ROKAS LAB AT VANDERBILT UNIVERSITY

A postdoctoral position studying early metazoan phylogeny, and the origin and early evolution of the genetic toolkit for metazoan development is available in

the Rokas lab at Vanderbilt University. This position will involve the generation of transcriptome data from a variety of early-branching metazoan phyla, the evolutionary and functional characterization of genes and domains participating in metazoan development, as well as comparative analysis of existing genomic data from a variety of animal phyla.

Funds are currently available to support this position for up to three years through the Searle Scholars Program (<http://www.searlescholars.net/people/-2008/rokas.html>). Applicants interested in and qualified for applying for additional postdoctoral funding will be given preference. Applicants should have a strong background in phylogenetics, protein evolution and/or comparative genomics. Basic computer programming skills and familiarity with the UNIX/Linux system, as well as with basic molecular biology bench work are desirable.

To apply, please send your CV, a statement of research interests, and contact information for three references to: [antonis.rokas@vanderbilt.edu](mailto:antonis.rokas@vanderbilt.edu)

Informal inquiries are encouraged. Review of applications will begin immediately and continue until the position is filled. For more information about the Department of Biological Sciences and Vanderbilt University, please visit: <http://sitemason.vanderbilt.edu/biosci/-index> Information on the Rokas lab can be found at: <http://people.vanderbilt.edu/~antonis.rokas/> – Antonis Rokas Department of Biological Sciences Vanderbilt University VU Station B 351634, Nashville, TN 37235 Email: [antonis.rokas@Vanderbilt.Edu](mailto:antonis.rokas@Vanderbilt.Edu) Tel: +1-615-936-3892 Fax: +1-615-343-6707 –

[antonis.rokas@vanderbilt.edu](mailto:antonis.rokas@vanderbilt.edu)

#### Post-doctoral Position in Evolution of Anti-malarial Immune Genes

A post-doctoral position is available in the laboratory of Jeffrey Powell in the Department of Ecology and Evolutionary Biology at Yale University, effective August 1st 2008 or as early as possible.

As part of the effort to develop a malaria-resistant transgenic mosquito, much attention has been devoted to identifying immune genes that play a role in the defense of Anopheles mosquitoes against malaria. Numerous genes have been identified that are up-regulated in response to Plasmodium infection, or whose suppression modifies Plasmodium infection intensity. In an effort to identify those genes that play a primary role in the Plasmodium defense of the mosquito and whose effects are specific to malaria, the Powell lab is investigating the population genetics of anti-malarial candidate genes in several groups of African malaria vectors.

This work is based on the observation that Plasmodium and Anopheles show clear signs of co-evolution. By studying the genetic variation in the candidate genes in natural populations of malaria vectors and their non-transmitting siblings, we can identify genes that show evidence of adaptation in malaria vectors, but not in the closely related species that do not transmit Plasmodium.

For more information please contact Jeffrey Powell.

To apply please send C.V. and cover letter to:

email: [Jeffrey.powell@yale.edu](mailto:Jeffrey.powell@yale.edu)

phone: 1 203 432 3887

[michel.slotman@yale.edu](mailto:michel.slotman@yale.edu) [michel.slotman@yale.edu](mailto:michel.slotman@yale.edu)

---

**YaleU MosquitoImmunityEvolution**

---

**WorkshopsCourses**

|                                                   |    |                                             |    |
|---------------------------------------------------|----|---------------------------------------------|----|
| Budapest ComputationalBiology Sep8-12 .....       | 72 | UManchester CommunityGenetics Sep9-10 ..... | 73 |
| Porto Portugal ConservationGenetics Sep9-15 ..... | 72 |                                             |    |

---

## Budapest ComputationalBiology Sep8-12

### Topics in Computational Biology

This is a one week course (8-12.9.2008) taught by Istvan Miklos and Jotun Hein in Budapest, Hungary. It is aimed a researchers/students with a strong quantitative background (mathematics, physics, statistics, computer science,) that wants an overview of computational biology with a wish to do research in the area. Each day is devoted to a topic. Each day has 2 90 minutes lectures, 1 90 minutes computer practical and ends with a 90 minute presentation/criticism/discussion of two projects one practical (data analysis) and one theoretical. Examples of projects can be found at <http://www.stats.ox.ac.uk/genome/projects>, the set of projects will be expanded before September. Preparation of the project discussion will take 4-8 hours preparation. Beyond this the course should be self-contained.

Day 0 Evening: Prepare projects

Day 1: Molecular Evolution Lecture: Models of Sequence Evolution and Statistical Alignment Lecture: Molecular Evolution & Comparative Genomics Practical: Molecular Evolution Student Activity: 2 Projects

Evening: Prepare projects

Day 2: Population Biology and Mapping Lecture: Population Genetics and Gene Genealogies Lecture: Inferring Recombination Histories Practical: DNA Sequence Analysis Student Activity: 2 Projects

Evening: Prepare projects

Day 3: Integrative Genomics Lecture: Models and Inference for Integrative Genomics – Lecture: Data and Results in Integrative Genomics – Practical: Integrative Data Analysis Student Activity: 2 Projects

Evening: Prepare projects

Day 4: Comparative Biology Lecture: Models for comparative biology: Networks, Structures and Shapes - Lecture: Progress and Open Problems in Comparative Biology – Practical: Networks, Structures and Shapes Student Activity: 2 Projects

Evening: Prepare projects

Day 5: Systems Biology Lecture: Models in Cellular Biology - Lecture: Progress in Systems Biology - Practical: Dynamic Network Inference Student Activity: 2 Projects

The 5 days course should give an overview of computational biology at present and outline problems suited for research projects. If you are interested in attending send an email to Jotun Hein [hein@stats.ox.ac.uk](mailto:hein@stats.ox.ac.uk) and Istvan Miklos [miklos@stats.ox.ac.uk](mailto:miklos@stats.ox.ac.uk) with a CV and description of your research interest. The attendee list will be finalized August 1st. There will be computer practical<sup>1</sup>s, but you must bring your own laptop.

Jotun Hein <[hein@stats.ox.ac.uk](mailto:hein@stats.ox.ac.uk)>

---

## Porto Portugal ConservationGenetics Sep9-15

\*\*\*\*\* Second Call

Many people have been asking for an application period extension, we decide to postpone the application deadline to 15 July \*\*\*\*\* 3rd Conservation Genetics Data Analysis Course Recent Approaches for Estimation of Population Size, Structure, Gene flow, Landscape Genetics, Selection Detection & Bioinformatics 9 - 15 September, 2008, Porto, Portugal Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genetics of natural and managed populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg propor-



tions and gametic disequilibrium. Participation will be limited to 20 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students at the end of their degree program). Deadline for application is 15 July, 2008

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyzes together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

Instructors: Fred Allendorf, University of Montana, USA Mark Beaumont, University of Reading, England Oscar Gaggiotti, University Joseph Fourier in Grenoble, France Gordon Luikart, CIBIO, Portugal & University of Montana Christian Schlötterer, Veterinary University of Vienna, Austria Albano Beja-Pereira, CIBIO, Portugal Mike Schwartz, US Forest Service, Missoula, USA David Tallmon, University of Alaska, Juneau, USA Robin Waples, Northwest Fisheries Science Center of the National Marine Fisheries Service, USA Miguel Angel Toro, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Spain Gilles GUILLOT, Department of Applied Mathematics INRA, France.

Location: \*The course will be held in the facilities at CIBIO (Center for Investigation of Biodiversity and Genetic Resources; <http://cibio.up.pt/> ) on the Campus for Agricultural Sciences in the rural village of Vairão, just north of Porto, and a few kilometres from the Atlantic coast and the airport. Vairão is an ancient village whose origins can be traced back to the Roman Period (the Roman village Valeriani). Application and cost: \*For detailed information see <http://popgen.eu/-congen2008/> . Accommodations and meals are included in the registration fee. Cost: 1,000 euros per person will cover all meals, lodging, transportation to and from the airport.

conservation genetics course  
<congen@mail.icav.up.pt>

---

## UManchester CommunityGenetics Sep9-10

Other: Community Genetics Workshop - Manchester - Sept 08 - 2nd call

Second call European Community Genetics workshop 9-10th September 2008, Manchester, UK.

This is a second call for a two day workshop on Community Genetics supported by The Genetics Society. The workshop is aimed at European-based researchers and will be held at the University of Manchester 9-10th September 2008. The aim of the workshop is to bring together ecologists and evolutionary biologists from Europe to discuss current and future research in the emerging field of Community Genetics. The meeting will be a mixture of invited talks and discussions. The following speakers are confirmed:

Prof. J. Antonovics (The University of Virginia)  
Prof. A. Gatehouse (Newcastle University) Prof. P. Grime (The University of Sheffield) Dr. G. Iason (The Macaulay Institute) S. Zytynska (The University of Manchester) Dr. J. Ferrari (The University of Oxford) Dr. R. Preziosi (The University of Manchester) Dr. D. Shuker (The University of Edinburgh) Dr. F. Vavre (Université de Lyon) Dr. J. Wolf (The University of Manchester)

If you are interested in attending or would like further information please contact Jennifer Rowntree by July 31st via email at [jennifer.rowntree@manchester.ac.uk](mailto:jennifer.rowntree@manchester.ac.uk)

We look forward to hearing from you.

Jennifer Rowntree, Richard Preziosi (University of Manchester), Dave Shuker (University of Edinburgh)

Dr Jennifer Rowntree Preziosi Lab Faculty of Life Sciences University of Manchester Smith Building Oxford Road Manchester M13 9PT

[jennifer.rowntree@manchester.ac.uk](mailto:jennifer.rowntree@manchester.ac.uk)

<http://www.preziosilab.org>  
<http://personalpages.manchester.ac.uk/staff/-Richard.Preziosi/jennyindex.html>

<http://personalpages.manchester.ac.uk/staff/-Jennifer.Rowntree/jennyindex.html>

Rowntree Jennifer  
<[jennifer.rowntree@manchester.ac.uk](mailto:jennifer.rowntree@manchester.ac.uk)>

## Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

## Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L<sup>A</sup>T<sub>E</sub>X do not try to embed L<sup>A</sup>T<sub>E</sub>X or T<sub>E</sub>X in your message (or other formats) since my program will strip these from the message.