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# E v o l D i r

February 1, 2004

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

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## Forward

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

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

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### Atlanta SEEC2004 Mar5-7 2

**\*\*Please Distribute Widely\*\*** **\*\*Apologies for Cross Postings\*\***

#### THIRD CALL FOR ABSTRACTS

SEEC 2004 SOUTHEASTERN ECOLOGY AND EVOLUTION CONFERENCE GEORGIA INSTITUTE OF TECHNOLOGY ATLANTA, GEORGIA 5-7 MARCH 2004 <<http://www.biology.gatech.edu/-SEEC/SEEC.html>><http://www.biology.gatech.edu/-SEEC/SEEC.html> FREE REGISTRATION AND ABSTRACT SUBMISSION REGISTRATION AND ABSTRACT SUBMITTAL DEADLINE: 31 JANUARY 2004

We invite all graduate, undergraduate, and post-doctoral researchers studying in the environmental sciences to submit abstracts for either oral or poster presentations at the Southeastern Ecology and Evolution Conference (SEEC) to be held March 5-7, 2004, at the Georgia Institute of Technology in Atlanta, Georgia. Keynote speaker will be Dr. Mark Hay, Teasley Professor of Environmental Sciences at the Georgia Institute of Technology.

SEEC is a professional meeting intended for students in the environmental sciences to present their research to their colleagues in a comfortable, fun, and low stress environment. Such events are designed to encourage new friendships within our field and to share newly developed research ideas for feedback. While we ex-

pect most SEEC participants to be from the Southeast, we encourage and welcome all interested individuals to submit abstracts and/or attend. Thus far, we have almost 50 registrants from 30 schools in 13 states and 2 countries. Don't miss out, because it is guaranteed to be blast ... or your registration fees back :)

To encourage attendance, registration is FREE and covers meeting attendance, two continental breakfasts, snacks, coffee, a t-shirt, and \$100 cash awards for the best oral and poster presentations. The registration and abstract submission deadline is January 31, 2004, and may be completed at the following web site:

Registration: <<http://www.prism.gatech.edu/~aw181/SEEC/Registration.htm>><http://www.prism.gatech.edu/~aw181/SEEC/Registration.htm> We look forward to seeing you at the Georgia Institute of Technology for the 1st Annual Southeastern Ecology and Evolution Conference this March!

For more information, go to <<http://www.biology.gatech.edu/SEEC/SEEC.html>><http://www.biology.gatech.edu/SEEC/SEEC.html> or email Alan Wilson at [alan.wilson@biology.gatech.edu](mailto:alan.wilson@biology.gatech.edu)

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### Boston ArtificialLife Sep12-15

Dear colleagues,

It is my great pleasure to be involved in the organization of the 'simulation and synthesis of living systems' conference to be held here in Boston next year. Personally, I have enjoyed tremendous benefits from opportunities for cross-disciplinary work between evolutionary biology and evolutionary computation/artificial life and I am happy to invite you to participate in this exchange in the upcoming conference.

Richard Watson.

#### Call for Papers ARTIFICIAL LIFE IX

The Ninth International Conference on the Simulation and Synthesis of Living Systems

Boston, USA, 12-15 September 2004

ELECTRONIC SUBMISSION DEADLINE: JAN 30th 2004

<http://www.alife9.org>

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Artificial life is the interdisciplinary enterprise investigating the fundamental properties of living systems through the simulation and synthesis of life-like processes in artificial media. The Artificial Life IX conference will showcase the best current work in this area of research, highlight promising new avenues of investigation, provide leading edge workshops, and present top keynote speakers. All authors of conference papers are encouraged to explain how their work sheds light on the fundamental properties of living systems and makes progress on important open questions. Paper submissions (6 pages single spaced) are welcome in all areas of the field, including:

- \* Origin of life, self-organization, self-replication, artificial chemistries
- \* Development and differentiation
- \* Evolutionary and adaptive dynamics, evolutionary games, coevolution
- \* Communication, cooperation and collective behavior
- \* Simulation and synthesis tools and methodologies
- \* Mathematical and philosophical foundations and implications of ALife
- \* Applications of ALife technologies
- \* Robots and agents, evolutionary robotics
- \* New and creative syntheses in ALife

For a full list of topics see: <http://www.alife9.org/cfp.htm> Both oral and poster presentations will be published in a single volume by MIT Press. ALife 9 will also include a series of workshops and tutorials, which you are invited to propose. The conference web page, [www.alife9.org](http://www.alife9.org), will provide the most current information about the meeting and venue.

Conference Chair: Dr. Jordan Pollack (Brandeis University) Program Committee Co-Chairs: Dr. Mark Bedau (Reed College), Dr. Phil Husbands (Sussex Uni-

versity), Dr. Takashi Ikegami (University of Tokyo), Dr. Richard Watson (Harvard University)

Conference Secretariat: Ms. Myrna Fox (Brandeis University)

Questions, concerns, and inquiries see <http://www.alife9.org/contact.htm>, or email [secy@alife9.org](mailto:secy@alife9.org), or phone (781) 736-2700.

Richard A. Watson lab: 617 495 1568 [rwatson@oeb.harvard.edu](mailto:rwatson@oeb.harvard.edu) [www.oeb.harvard.edu/faculty/wakeley/richard](http://www.oeb.harvard.edu/faculty/wakeley/richard)

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## California Astrobiology Mar28-Apr1

It is with great pleasure and anticipation that we announce the call for abstracts for Astrobiology Science Conference 2004. The meeting is the third to be held at NASA Ames Research Center in Moffett Field, California, and will take place 28 March to 1 April 2004. The meeting will consist of invited plenaries, contributed talks, posters, and topical sessions such as the Ethics of Exploration and Astrobiology and the Press. The language of the conference will be English, but one session will be conducted in Spanish.

To submit an abstract, please go to <http://abscicon2004.arc.nasa.gov/main2.html>, download the word file, and submit as directed. All abstracts will be reviewed by the Science Organizing Committee for suitability and quality. Each abstract will then be selected for a contributed oral presentation or poster. Occasionally a contributed abstract is deemed so outstanding that the author is asked to give a short plenary. In the past several abstracts have been rejected because the material was not suitable, so please follow the directions carefully. A prize will be awarded to the first 10 abstracts submitted.

The categories for abstracts are: Astrobiology Missions Biogeochemistry Detection and Characterization of Extrasolar Planets Earth History Earth Science including remote sensing Environment & Evolution Europa Extreme Environments Global Change Habitable Planets Humans in an Astrobiological Context Mars Origin of Life/Prebiotic Chemistry Outreach/Education Search for life beyond Earth (microbes to SETI) Technology in support of Astrobiology Science Terrestrial life beyond Earth (includes gravity studies) Other

In addition to one of the above categories, and abstract can be designated for consideration at the NAI Student

Poster Contest if a lead author is a student.

The deadline for abstracts is January 22, 2004.

On behalf of the Science Organizing Committee and the Local Organizing Committee, we eagerly anticipate your participation in "AbSciCon 2004". We anticipate over 800 participants ranging from scientists to educators to students and the press, and can guarantee a stimulating and exciting few days.

Lynn J. Rothschild Chair, Science Organizing Committee Astrobiology Science Conference 2004

– Lynn J. Rothschild, Ph.D., F.L.S. Mail Stop 239-20  
NASA Ames Research Center Moffett Field, CA 94035-1000

650.604.6525

Lynn Rothschild <Lynn.J.Rothschild@nasa.gov>

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## Cambridge StatMolBiol Mar22-23

MASAMB-XIV: 14th Annual Meeting on Mathematical and Statistical Aspects of Molecular Biology at the Isaac Newton Institute for Mathematical Sciences, Cambridge

Monday 22nd March - Tuesday 23rd March, 2004

Scientific Organisers: Nick Goldman, EBI-EMBL, Hinxton, Cambridge (goldman@ebi.ac.uk) Wally Gilks, MRC Biostatistics Unit, Cambridge (wally.gilks@mrc-bsu.cam.ac.uk)

Bioinformatics and statistical genetics, twin themes of the long-running series of annual MASAMB meetings, have gained huge impetus from large-scale genome sequencing projects and development of high-throughput biological assay systems, including gene-expression microarrays. These immense data resources, and the underlying complexities of molecular and cell biology, provide exciting research opportunities for numerate scientists.

With typically around 60-80 participants from mathematics, statistics, computer science, bioinformatics, biology and related fields, the MASAMB meetings provide an intimate setting for exchange of ideas in methodological and applied research. Research students and scientists newly entering the field of genomic research are particularly welcome.

The meeting will contain approximately 12 half-hour talks selected from participants' submissions, plus a

poster session.

The cost of attendance at the meeting, including dinner on the Monday evening, will be:

£120 (full residential) or £90 (without accommodation),

or for full-time students:

£90 (full residential) or £60 (without accommodation).

This will be the only mailing of this notice! Please inform your colleagues of this notice!

If you would like to attend the meeting, please complete the on-line registration application form at <http://www.newton.cam.ac.uk/events/masamb/> \*\*\* by 31 December 2003 at the latest ! \*\*\*

(apologies for the late posting). Further information will only be sent to registered applicants. Accommodation will be quite limited for this meeting, and it is important that we get accurate estimates of numbers attending as soon as possible.

Further information on the meeting will also be posted, as it becomes available, at <http://www.ebi.ac.uk/goldman-srv/masamb>. This site also contains information on past MASAMB meetings.

For questions on the scientific content of the meeting, please contact one of the organisers, above. On administrative matters, please contact:

Tracey Andrew (t.andrew@newton.cam.ac.uk) Isaac Newton Institute for Mathematical Sciences, 20 Clarkson Road, Cambridge CB3 0EH, UK

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## ColoradoStateU SSB GradSymp Jun26-30

We are seeking proposals from graduate student or beginning post-doctoral researchers to participate in a symposium entitled "Regulatory genes and the evolution of plant phenotype" that will be held at the Society for the Study of Evolution meetings at Colorado State University, June 26-30, 2004. This symposium will explore the impact of plant regulatory gene evolution on phenotypic change in model systems, in natural populations, and at the macroevolutionary level. The symposium has been designed to emphasize the research of young investigators in this rapidly emerging area of inquiry, but will also feature presentations by a few well-established scientists. One speaking

slot in the symposium will be filled from among the applicants. The selected speaker will give a 15-30 minute talk during the symposium and will be eligible to receive reimbursements for travel and registration expenses up to \$700. Although all relevant proposals will be considered, special consideration will be given to empirical or theoretical studies of regulatory gene evolution in natural plant populations. To apply, please email a research abstract, CV, and contact information for two references (able to comment on the applicant's speaking ability) to Pat Reeves ([reevesp@lamar.colostate.edu](mailto:reevesp@lamar.colostate.edu)). The deadline for proposals is March 1, 2004. Applicants will be notified by March 15 whether they have been selected for the position. More information on the symposium can be obtained at <http://lamar.colostate.edu/~reevesp/evolution2004.html> <<http://lamar.colostate.edu/~reevesp/evolution2004.html>> . Please direct any questions regarding this opportunity to the members of the organizing committee: Chris Richards ([crichard@lamar.colostate.edu](mailto:crichard@lamar.colostate.edu)), David Baum ([dbaum@wisc.edu](mailto:dbaum@wisc.edu)), and Pat Reeves ([reevesp@lamar.colostate.edu](mailto:reevesp@lamar.colostate.edu)).

This message has been posted to the EvoDir and PDE newsgroups. I apologize for any duplicate mailings you might have received.

[reevesp@lamar.colostate.edu](mailto:reevesp@lamar.colostate.edu)

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## Denmark SocialEvol Sept2-6

### INTEGRATED STUDIES OF SOCIAL EVOLUTION

Helsing, Denmark

2-6 September 2004

The closing symposium of the EU research-training network INSECTS (Integrated Studies of the Economy of Insect Societies) will be a focal point for European Social Insect research, which will build on the links that have been established within and across disciplines studying social evolution throughout the life of the network.

The scientific program will include several plenary sessions with invited speakers from outside the network (Those confirmed so far are Eric Bonabeau and Stuart West), as well as the network group leaders (Koos Boomsma, Johan Billen, Jürgen Heinze, Bert Hölldobler, Graeme Jones, Laurent Keller, Pekka Pamilo, Francis Ratnieks, Paul Schmid-Hempel, Lotta

Sundström and Stefano Turillazzi). There will also be talks by the INSECTS postdocs as well as open slots for contributed talks. Open poster sessions will also feature prominently in the meeting.

The symposium will be held at the LO-skolen, a residential conference centre in the historic town of Helsing(or Elsinor, as Shakespeare called it in Hamlet), 50km North of Copenhagen. The conference venue is within walking distance of Kronborg castle, and provides easy access to the Louisiana museum of modern art, the picturesque north coast of Zealand and the cosmopolitan delights of Copenhagen.

The cost of the meeting will be approximately DKK 4400 (ca. GBP 400, EUR 600, USD 600), which will cover all accommodation and meal costs as well as registration, conference materials, the conference banquet and a half-day excursion to the royal castles of Fredriksborg and Fredensborg.

Dates for your diary:

1 March 2004 Registration via the symposium web site opens

1 June 2004 Closing date for registration

2 -6 September 2004 The symposium

The symposium web site, including an outline program of the meeting, and a printable PDF version of this announcement, can be found at:

<http://www.zi.ku.dk/eunet/helsingor/> More details of the INSECTS network can be found at:

<http://www.zi.ku.dk/eunet/> If you would like to receive priority information on the symposium, please consider belonging to the INSECTSmail mailing list, which you can do by simply sending an e-mail message to [INSECTS@zi.ku.dk](mailto:INSECTS@zi.ku.dk) asking to join.

[DRNash@zi.ku.dk](mailto:DRNash@zi.ku.dk)

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## EugeneOR GeneRegulation Mar12-14

Symposium Announcement:

THE EVOLUTION OF GENE REGULATION March 12-14, 2004 at the University of Oregon

Fourth annual symposium on Evolution, Development and Genomics sponsored by the joint NSF-IGERT training of the University of Oregon and Indiana Uni-

versity.

Conference details available at <http://evodevo.uoregon.edu> The goal in of this symposium is to reach across fields to foster discussion of emerging issues related to the detection, functional significance, and evolutionary consequences of gene regulation and regulatory regions.

Plenary lecture: John Postlethwait, University of Oregon Introduction and Overview: Patrick Phillips, University of Oregon

Invited Speakers:

Duccio Cavalieri, Harvard University "Evolution of regulatory networks in natural populations of *S. cerevisiae*"

Manolis Dermitzakis, University of Geneva (soon at the Sanger Institute) "Dissecting regulatory variation and evolution in the human genome"

John Finnerty, Boston University "Surprising complexity in the genomic regulatory systems of cnidarians."

Michael Freeling, UC Berkeley "The evolution of regulatory complexity in higher plants"

Veronica Hineman, Cal Tech "Developmental gene regulatory network architecture across 500 MYA of echinoderm evolution"

Thom Kaufman, Indiana University "A comparison of segmentation and limb development in long and short germband insects. Is *Oncopeltus* the new *Drosophila*?"

Mike Levine, UC Berkeley "Whole-genome analysis of *Drosophila* gastrulation"

Michael Ludwig, University of Chicago "Enhancer evolution"

Simon Malcomber, Univ. Missouri, Saint Louis "Heterogeneous expression patterns and separate roles of *SEPALLATA* genes in grasses (*Poaceae*)"

Steve Proulx, University of Oregon: "Evolution of regulatory specificity"

Trisha Wittcopp, Cornell University: "The genetic basis of divergent gene expression in *Drosophila*: cis and trans"

Logistics:

The symposium will begin on the evening of March 12 with a reception at 6 pm and the plenary lecture at 7:30 pm. The symposium will end on the morning of March 14 at 11 am with a brunch. The symposium will be held at the Valley River Inn in Eugene, Oregon, right on the Willamette River, near the University of Oregon.

Note: Registration materials should be available by

Jan. 21.

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

## Glasgow ISMB Jul31-Aug4 2

Call for Posters - ISMB/ECCB2004

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Due date: Monday, April 19, 2004 12:00 BST Details and submission form available here: [http://www.iscb.org/ismbeccb2004/poster\\_call.html](http://www.iscb.org/ismbeccb2004/poster_call.html) The International Society for Computational Biology (ISCB) is pleased to invite you to participate in the 12th International Conference on Intelligent Systems for Molecular Biology (ISMB) and the Third European Conference on Computational Biology (ECCB)ISMB/ECCB 2004 ([www.iscb.org/ismbeccb2004](http://www.iscb.org/ismbeccb2004)) to be held in Glasgow, Scotland, UK July 31-August 4, 2004.

We invite you to consider presenting a poster. Cash prizes donated by SGI will be awarded to the top 10 best posters. Poster presentations describing original research in the following areas are welcome:

-Systems Biology -Genome and Proteome Annotation -Comparative and Functional Genomics -Structural Biology -Phylogeny and Evolution -Predictive Methods -Algorithms -Statistics -Data and Text Mining, Visualisation and Integration -Ontologies and e-Biology -Databases and LIMS -Microarrays and Proteomics -New Frontiers

Before submitting a poster abstract, please note the following:

All abstracts must be submitted via our web site by the abstract deadline: Monday 19th April at 12:00 BST - You must submit two versions of your poster abstract: a 50-word abstract that will be printed in the conference program, and a one-page abstract (1000 words) to be posted on the conference web site. -At least one of the poster authors must be present at the conference. -Posters are intended to convey a scientific result and are not advertisements for commercial software packages. When you submit your poster you will



be asked to check a box confirming that this is the case for your poster. We will be providing a separate space for commercial posters in the exhibition area. See Industry Posters for more details. [http://www.iscb.org/-ismbeccb2004/sponsor\\_ops5.html](http://www.iscb.org/-ismbeccb2004/sponsor_ops5.html) -Space for posters is limited and, although we will make every effort to accommodate all groups who wish to present a poster, we might not be able to accept all poster submissions. Submit your poster abstract well before the deadline to ensure acceptance. -Presenters of accepted posters will be notified by 3 May 2004. -The size of the poster space is: Height: 170 cm, Width: 90 cm. Fasteners will be provided at the site, please DO NOT bring tape, tacks or pins. -Owing to lack of space, we regret that we will not be able to offer tables for laptop computer demos this year. If you would like to demonstrate your software, we strongly encourage you to submit an application for a software demo. [http://www.iscb.org/-ismbeccb2004/np\\_demos.html](http://www.iscb.org/-ismbeccb2004/np_demos.html) -There is a maximum of one poster per presenting author.

Guidelines for preparing your poster for presentation: [http://www.iscb.org/ismbeccb2004/-poster\\_guidelines.html](http://www.iscb.org/ismbeccb2004/-poster_guidelines.html) All questions pertaining to the ISMB/ECCB 2004 poster session should be directed to: posters04@ismbconf.org

ISMB/ECCB Keynote speakers

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Eric Green, National Human Genome Research Institute Leroy Hood, Institute for Systems Biology Matthias Mann, University of Southern Denmark Denis Noble, University of Oxford Svante Paabo, Max Planck Institute for Evolutionary Anthropology Anna Tramontano, University of Rom "La Sapienza"

ISMB/ECCB Steering Committee Members

=====

David Gilbert (co-chair), University of Glasgow, Scotland, UK Janet Thornton (co-chair), EMBL-European Bioinformatics Institute, Cambridge, UK Philip Bourne, University of California, San Diego, USA Thomas Lengauer, Max-Planck Institute for Informatics, Saarbruecken, Germany David Moss, Birkbeck College, London, UK Mark Ragan, University of Queensland, Brisbane, Australia Shoba Ranganathan, Macquarie University, Sydney, Australia Hershel Safer, Weizmann Institute of Science, Rehovot, Israel Marie-France Sagot, Inria Rhone-Alpes, Villeurbanne, France Anna Tramontano, University of Rome "La Sapienza," Italy

ISMB/ECCB Program Committee Members

=====

Janet Thornton (Chair), European Bioinformatics Institute, Cambridge, UK Ying Xu, University of Geor-

gia, Athens, GA, USA Gene Myers, University of California, Berkeley, CA, USA Des Higgins, University College Dublin, Ireland Martin Vingron, Max Planck Institute for Molecular Genetics, Berlin, Germany John Quackenbush, The Institute for Genomic Research, Rockville, MD, USA Michal Linial, The Hebrew University, Jerusalem, Israel Michael Gribskov, University of California, San Diego, CA, USA R. Sowdhamini, Indian Institute of Science, Bangalore, India Burkhard Rost, Columbia University, New York, NY, USA Minoru Kanehisa, Kyoto University, Japan

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

## JAX Maine EvolNeurogenetics

JAX Neurogenetics Conference V June 9 - 12, 2004 The Jackson Laboratory Bar Harbor, Maine

This meeting provides a forum for researchers and students who work in areas of neurobiology that impact directly upon or use the laboratory mouse as a genetic model system. The laboratory mouse is widely considered the premiere experimental organism for genetic studies that have implications, often direct, for human neurological disorders. The Fifth workshop continues the tradition of bringing students and established investigators with varying expertise and experience together to discuss their research findings, identify areas of common research interest and develop future directions.

Session Topics: Complex traits of neurological disease Mouse mutant resources and mutagenesis programs Genetic mediation of pain Reverse and forward genetics approaches to mouse models of eye disease Mouse models of human genetic diseases: matches and misses Protein misfolding in neurodegenerative disease

Scientific Organizer: Wayne N. Frankel, Ph.D., The Jackson Laboratory

For additional information, please access the web page at: [http://www.jax.org/courses/2004/-2004\\_neurogenetics\\_conference.html](http://www.jax.org/courses/2004/-2004_neurogenetics_conference.html)

Karen Grant Course Coordinator The Jackson Laboratory 600 Main Street Bar Harbor, Maine 04609-1500 Phone: 207-288-6263 Fax: 207-288-6080 E-mail: [kgk@jax.org](mailto:kgk@jax.org) web address: <http://www.jax.org/courses>

Office Hours: 7:00 am - 3:00 pm Monday - Friday  
 Office Hours: 7:00 am - 3:00 pm Monday - Friday

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### Marseille EvolBiol Sep22-24

The 8th Evolutionary Biology Meeting at Marseille, will take place this year from september 22nd to september 24th.

The presentations will include : systematics, biodiversity, comparative genomics and post-genomics (at all the taxonomic levels), gene duplication and evolution, functional phylogenesis, paleontology, concept of evolution. For more information Please visit <http://evolution.luminy.univ-mrs.fr> Best regards

Pierre Pontarotti

Phylogenomics Laboratory

Université d'Aix Marseille I Centre St Charles  
 3 Place Victor Hugo 13331 Marseille Cedex  
 3 33491106489 <http://www.up.univ-mrs.fr/evol>  
 Pierre.Pontarotti@up.univ-mrs.fr

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### RoscoffFrance HostParasite Sep4-8

Meeting : "Evolutionary ecology of host-parasite relationships" Roscoff (France), September 4-8, 2004

The Department of Life Sciences of the French C.N.R.S. (Centre National de la Recherche Scientifique) organizes a series of meetings entitled the "Jacques Monod Conferences" each year, on topics involving the status of recent progress in the different fields within fundamental biology and their applications to biotechnology, health or agronomy.

We are please to advertise for a conference in 2004 on "Evolutionary ecology of host-parasite relationships". This conference will held at Roscoff, France on September 4-8, 2004.

The goal of this conference is to stress innovative researches in 3 main topics: on the different ways parasites exploit their hosts; on the epidemiology and population genetics of parasitic infections; on the evolution of virulence, resistance and host immunity. In all cases,

we will try to bridge the gap between theory and empirical works.

Invited speakers are the following: Marie-Charlotte Anstett (Montpellier, France), Janis Antonovics (Charlottesville, USA), Sebastian Bonhoeffer (Zürich, Switzerland), Troy Day (Kingston, Canada), Alison Dunn (Leeds, United Kingdom), Dieter Ebert (Fribourg, Switzerland), Sylvain Gandon (Montpellier, France), Bryan Grenfell (Cambridge, UK), Michael Hochberg (Montpellier, France), Peter Hudson (Pennsylvania State University, USA), Gregory Hurst (London, UK), Jacob Koella (Paris, France), Marc-Henri Lebrun (Lyon, France), Bruce Levin (Atlanta, USA), Curt Lively (Bloomington, USA), Yannis Michalakis (Montpellier, France), Manfred Milinski (Plön, Germany), Nancy Moran (Tucson, USA), Serge Morand (Montferrier-sur-Lez, France), Dustin Penn (Vienna, Austria), Robert Poulin (Dunedin, New Zealand), Andrew Read (Edinburgh, Scotland), Thierry Rigaud (Dijon, France), Paul Schmid-Hempel (Zürich, Switzerland), Mike Siva-Jothy (Sheffield, UK), Pierre Sonigo (Paris, France), Gabriele Sorci (Paris, France), Marcel Tanner (Basel, Switzerland), André Théron (Perpignan, France).

Registration fee, including accommodation, food, and coffee breaks are 360 Euros for PhD Students ; 500 Euros for other participants How to Apply ? The total number of participants is limited to 100 and all participants are expected to attend for the whole duration of the conference. Selection is made on the basis of the affinity of potential participants with the topics of the conference. Scientists and PhD Students interested in the meeting should send the following informations to T. Rigaud ([thierry.rigaud@u-bourgogne.fr](mailto:thierry.rigaud@u-bourgogne.fr)): a 1 page curriculum vitae; the list of their main publications for the 3 last years; the abstract of their presentation (talk or poster). The deadline for application is May 15, 2004. Among participants, a restricted number (due to little time available) will be selected for oral presentation. Others will present their studies on posters, during poster sessions where a lot of time will be keep to discussion. See also the web site <http://www.cnrs.fr/-SDV/Actions/cjm.html> or contact the organizers.

The organizers : Thierry Rigaud (Dijon, France, [thierry.rigaud@u-bourgogne.fr](mailto:thierry.rigaud@u-bourgogne.fr)) & Dieter Ebert (Fribourg, Switzerland, [dieter.ebert@unifr.ch](mailto:dieter.ebert@unifr.ch)).

Thierry Rigaud Université de Bourgogne UMR 5561 Biogéosciences Equipe Ecologie Evolutive 6 boulevard Gabriel 21000 Dijon [thierry.rigaud@u-bourgogne.fr](mailto:thierry.rigaud@u-bourgogne.fr) Tel: +33 (0) 3 80 39 39 45 Fax: +33 (0) 3 80 39 62 31



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## UNotreDame MEEC Mar5-7 2

Final call for papers -

24th Annual Midwest Ecology and Evolution Conference, University of Notre Dame March 5th-7th, 2004

The graduate students in the Department of Biological Sciences at the University of Notre Dame would like to invite graduate students and post-doctoral associates from the Midwestern United States to submit abstracts for oral and poster presentations at the 24th Annual Midwest Ecology and Evolution Conference (MEEC).

This year, MEEC will be held on the campus of The University of Notre Dame, in South Bend, Indiana from March 5-7, 2004. Keynote speaker will be Dr. Michael Rosenzweig, professor of ecology and evolutionary biology at the University of Arizona.

In addition to contributed sessions on topics in ecology and evolution, invited and contributed papers will be considered for two special symposia: (1) Conservation Issues in the Midwest, and (2) Conceptual Innovations in Ecology and Evolution. Papers presented at these symposia will be considered for publication in a special issue of the American Midland Naturalist. MEEC provides an opportunity for graduate students and post-docs to present their research in a relatively informal environment and is a great way to meet other ecology and evolutionary scientists in the Midwest eco-region.

Deadline for submission of abstracts is January 31th, 2004. Registration fee is \$40.

For more information, go to <http://meec2004.org> or email drake.4@nd.edu.

Hattie Dambroski <hdambros@nd.edu>

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## UNotreDame MMEC Mar5-7

2nd Call for papers -

24th Annual Midwest Ecology and Evolution Conference, University of Notre Dame March 5th-7th, 2004

The graduate students in the Department of Biological Sciences at the University of Notre Dame would

like to invite graduate students and post-doctoral associates from the Midwestern United States to submit abstracts for oral and poster presentations at the 24th Annual Midwest Ecology and Evolution Conference (MEEC). This year, MEEC will be held on the campus of The University of Notre Dame, in South Bend, Indiana from March 5-7, 2004. Keynote speaker will be Dr. Michael Rosenzweig, professor of ecology and evolutionary biology at the University of Arizona. In addition to contributed sessions on topics in ecology and evolution, invited and contributed papers will be considered for two special symposia: (1) Conservation Issues in the Midwest, and (2) Conceptual Innovations in Ecology and Evolution. Papers presented at these symposia will be considered for publication in a special issue of the American Midland Naturalist. MEEC provides an opportunity for graduate students and post-docs to present their research in a relatively informal environment and is a great way to meet other ecology and evolutionary scientists in the Midwest eco-region.

Deadline for submission of abstracts is January 31th, 2004. Registration fee is \$40.

For more information, go to <http://meec2004.org> or email drake.4@nd.edu.

Hattie Dambroski <hdambros@nd.edu>

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## UWarwick GeneticsSociety Mar14-16

The UK Genetics Society spring meeting (14 - 16 March 2004, University of Warwick) includes some evolutionary topics, which may interest Evoldir members. The programme can be seen at

<http://www.genetics.org.uk/>

The GENETICS SOCIETY BALFOUR LECTURE will be by Gilean McVean, Oxford, UK

There are places for contributed talks in the session on Balanced polymorphic systems which includes the following three invited talks:

Self incompatibility in flowering plants Mikkel Schierup, Aarhus, Denmark MHC polymorphisms in non-human animals Scott Edwards, Cambridge, USA Balancing selection in malaria parasites David Conway, London, UK and in the session on The evolution of repetitive DNAs

Mobile elements and primate genomic diversity Mark Batzer, Louisiana, USA Mechanisms of L1 transposi-

tion John Moran, Ann Arbor, USA Transposable elements in genomes Andrew Flavell –

Professor Deborah Charlesworth Institute of Cell, Animal and Population Biology University of Edinburgh

Ashworth Lab. King's Buildings, W. Mains Rd., Edinburgh EH9 3JT, UK Tel: (+44)(0)131 650 5751 Fax: (+44)(0)131 650 6564

Deborah Charlesworth <Deborah.Charlesworth@ed.ac.uk>

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Fabra 08003 BARCELONA Phone: 00 34 93 5422841  
E-mail: francesc.calafell@upf.edu

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### Barcelona MolEvol

One PhD grant is available starting as soon as possible in the area of Theoretical molecular evolution and Bioinformatics, at the Unitat de Biologia Evolutiva of the Universitat Pompeu Fabra (Barcelona, Spain)

The research group that the successful candidate will join has several lines of research dealing with genomic variation at both the intraspecific and interspecific levels in hominids. The PhD will be involved in the study of variation of Linkage Disequilibrium patterns across the genome and across populations.

Candidates should have a Bachelor's degree (or equivalent) in Biology, Physics, Mathematics or similar. Last year students will be considered. Motivated and potentially competitive applicants should send a short letter of interest and CV to:

Francesc Calafell Unitat de Biologia Evolutiva Facultat de Ciències de la Salut i de la Vida Universitat Pompeu

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### GeorgiaSouthernU PlantInvasiveness

I am seeking undergraduates interested in pursuing graduate studies at the Masters level. The goal of this NSF-funded project is to study the ecological and genetic basis of invasiveness in plants. The research involves a collaboration with Doug Taylor (University of Virginia) and uses a combination of approaches (e.g. molecular phylogenetics, field work) for exploring the biology of *Silene latifolia* in both its native (Europe) and introduced (North America) ranges. The Department of Biology (<http://www.bio.gasou.edu>) at Georgia Southern University has active graduate and research programs in ecology and evolutionary biology. The university is located in Statesboro, a pleasant city of 25,000 and only 45 minutes from the beaches

of Savannah. And while many are shoveling snow today in various corners of North America, the daffodils are blooming in Statesboro! So please pass this information to any potentially interested undergrads. For more information please contact Lorne Wolfe (wolfe@gasou.edu) (<http://www.bio.gasou.edu/wolfe>). – Dr. Lorne Wolfe Department of Biology P.O. Box 8042 Georgia Southern University Statesboro, Georgia. 30460.

wolfe@georgiasouthern.edu Phone: 912-681-0848 Fax: 912-681-0845 <http://www.bio.gasou.edu/wolfe>

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## IIASA Austria Evolution

### SUMMER PROJECT STIPENDS FOR YOUNG SCIENTISTS AT THE INTERNATIONAL INSTITUTE FOR APPLIED SYSTEMS ANALYSIS

Funding is offered for young scientists interested in collaborative research in

Population Ecology Evolutionary Ecology Spatial Ecology Fisheries Science

As in previous years, Ph.D. students can apply for participation in the Young Scientists Summer Program (YSSP), hosted - from June 1 to August 31, 2004 - by the International Institute for Applied Systems Analysis (IIASA), Laxenburg, Austria. Training is based on close interaction with the advising senior scientists, and typically leads to a publication in an international journal, and, where applicable, to a chapter in a candidate's Ph.D. thesis. In general, IIASA's summer program offers exceptional opportunities for acquiring experience in an international research environment. The Institute is located in the former summer palace of the Habsburgs, ca. 10 km south of Vienna.

Young scientists from Austria, China, Egypt, Estonia, Finland, Germany, Japan, the Netherlands, Norway, Poland, Russia, Sweden, and the USA are eligible for personal stipends providing full funding. For students from other countries, travel and accommodation stipends can be arranged on a case-by-case basis.

While successful applicants will usually pursue a Ph.D. program at their home institutions, exceptions for master students and young postdocs are certainly possible. Projects relating to any of the nine areas described under "Research Activities" on [www.iiasa.ac.at/Research/ADN](http://www.iiasa.ac.at/Research/ADN) are eligible. Chances of success are increased when candidates informally dis-

cuss, prior to their application, specific research interests and plans with the project leader of the Adaptive Dynamics Network, Dr Ulf Dieckmann (dieckmann@iiasa.ac.at).

Review of applications will commence immediately. To receive full consideration, online applications should be completed before January 22, 2004 (after that date, please apply by sending an email to Ulf Dieckmann).

Some useful links: + [www.iiasa.ac.at/Research/ADN](http://www.iiasa.ac.at/Research/ADN) Information about the Adaptive Dynamics Network + [www.iiasa.ac.at/YSSP](http://www.iiasa.ac.at/YSSP) Details about the summer program, and online application + [www.iiasa.ac.at/Research/ADN/Students.html](http://www.iiasa.ac.at/Research/ADN/Students.html) Examples of successful student projects + [www.iiasa.ac.at](http://www.iiasa.ac.at) General information about IIASA

Ulf Dieckmann Phone +43 2236 807 386 Project Leader +43 2236 807 275 (secretary) Adaptive Dynamics Network +43 2236 807 231 (secretary) International Institute Fax +43 2236 71313 for Applied Systems Analysis Email dieckmann@iiasa.ac.at A-2361 Laxenburg Web [www.iiasa.ac.at/Research/ADN](http://www.iiasa.ac.at/Research/ADN) Austria [www.iiasa.ac.at/~dieckman](http://www.iiasa.ac.at/~dieckman)

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## Muenster ParasiteHostEvol

PhD position on parasite-host evolution in Muenster, Germany

We invite applications for

1 PhD position

at the Institute for Animal Evolution and Ecology in Muenster, Germany; financed through the German Science Foundation.

Subject of the project: Impact of parasites on host evolution in the nematode *Caenorhabditis elegans*. Contents: Employment of selection experiments (experimental evolution under controlled conditions) in order to characterise the influence of parasites on the evolution of phenotypic traits (host resistance, survival ability, reproductive rate) and molecular traits (resistance genes). Techniques include fitness assays, microsatellite analysis to determine outcrossing rates, and gene expression analysis with the help of microarrays and Northern blotting. The PhD project is part of a larger research project, in which *C. elegans* is used as a model host to study the evolution of parasite-host interactions and which includes a second PhD project (see

recent job announcement). Further information is available on our homepage: <http://www.uni-muenster.de/-biologie.evoeco/evolbio/>.

Requirements: Degree in Biology (BA, BSc, MA, MSc, or equivalent degree); good knowledge of molecular techniques (PCR, DNA Sequencing, etc.) and statistics; ideally already knowledge concerning work with *C. elegans*, analysis of microarrays or mathematical models of parasite-host co-evolution.

Deadline for applications: 1st March 2004. Start of position: as soon as possible, at the latest: 1st May 2004. The position is currently available for 2 years, and thereafter, it can be extended for another year.

In case of equivalent qualifications, disabled people are preferentially employed. We also specifically encourage applications from women.

Applications should include CV, 1-2 reprints of publications (if available), and names and emails of 2 referees. They should be sent preferentially by email to Dr. Hinrich Schulenburg, [hschulen@uni-muenster.de](mailto:hschulen@uni-muenster.de), or conventional mail: Institute for Animal Evolution and Ecology, Hüfferstr. 1, 48149 Münster; Germany

Dr. Hinrich Schulenburg Department of Evolutionary Biology Institute for Animal Evolution and Ecology Westphalian Wilhelms-University Hüfferstr. 1 48149 Muenster Germany Tel.: +49-251-8321019 or -8324664 Fax: +49-251-8324668 e-mail: [hschulen@uni-muenster.de](mailto:hschulen@uni-muenster.de) <http://www.uni-muenster.de/biologie.evoeco/evolbio/>

Hinrich Schulenburg <[hschulen@uni-muenster.de](mailto:hschulen@uni-muenster.de)>

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### Munich MolEvol

A PhD student position is available in the laboratory of John Parsch at the University of Munich (LMU). The position is part of a project funded by the German Science Foundation (DFG) to study the molecular evolution of reproductive genes in *Drosophila*. The work will include both experimental and bioinformatic approaches to studying DNA sequence evolution and sex-biased gene expression. The position will be paid as BatIIa/2 according to the German pay scale, which is approximately 19,500 Euro (24,000 \$US) per year depending on age and experience. Requirements are a master's degree (or equivalent) in biology and a strong interest in molecular evolution and population genetics. The University of Munich has a strong, interactive

group in evolutionary biology, including theoreticians and experimentalists working on both plant and animal systems. We have a very international group and the everyday working language is English. Beginning August 2004, our department will be housed in a new, state-of-the-art BioCenter on the University of Munich High-Tech campus. More information is available on the web at:

<http://www.zi.biologie.uni-muenchen.de/institute/zi-abtln/evolutionsbiologie> Interested candidates should send a statement of interest and curriculum vitae per email to:

[parsch@zi.biologie.uni-muenchen.de](mailto:parsch@zi.biologie.uni-muenchen.de)

Prof. Dr. John Parsch Department of Biology II University of Munich Luisenstr. 14 80333 Munich Germany

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### OxfordU BacterialVariation

This position is open to all nationalities, thus providing a route for both EU and non-EU citizens to obtain a doctorate in the UK.

Research Assistant, analysis of spatial patterns of genetic variation in pathogenic bacteria

Academic-Related Research Staff Grade 1B. Salary in Range £18,265- £20,311 (UK sterling).

Applications are invited for a three year position, funded by the Wellcome Trust. It is anticipated that the appointee will register for a doctoral degree with the University of Oxford. This position provides an opportunity for someone with a degree in a mathematical or biological subject to perform research in a rapidly developing area of genetics.

Pathogenic bacteria remain a potent threat to human health, killing millions worldwide each year. Extensive DNA sequence datasets are now becoming available for a wide range of pathogens, allowing us to more accurately reconstruct the history of each species and its interaction with the human host, and to characterise the dynamics of transmission. The appointee will develop novel mathematical and statistical methods for analyzing patterns of spatial variation, which, depending on the species in question, reflect evolutionary processes taking place on timescales of weeks, years or even millennia. As well as addressing challenging methodological issues, an important goal of the research is to develop practical methods of data analysis, with the

goal of informing public health interventions.

The Peter Medawar Building ([www.medawar.ox.ac.uk](http://www.medawar.ox.ac.uk)) houses multidisciplinary teams of scientists involved in the collection, analysis and interpretation of sequence data from pathogens, as well as a world leading mathematical genetics and bioinformatics group. The wider Oxford environment also includes experts on viral evolution, epidemiology, tropical medicine and spatial statistics, amongst other disciplines.

Candidates should have, or be expecting to soon receive, a good bachelors degree in a mathematically or biologically related subject. Knowledge in some of the following specific subject areas would be an advantage, but are not essential for candidates committed to moving into the field: (1) population genetics (2) programming in C or C++ (3) modern computationally-intensive statistical methods (4) bacterial sequence typing.

Further particulars are available from <http://www.stats.ox.ac.uk>. Potential applicants are encouraged to contact Daniel Falush ([falush@stats.ox.ac.uk](mailto:falush@stats.ox.ac.uk)). Applications, comprising a Curriculum Vitae and the names of at least two academic referees should be submitted to Mrs Sue Wood, Department of Statistics, 1 South Parks Road, Oxford OX1 3TG or emailed to [wood@stats.ox.ac.uk](mailto:wood@stats.ox.ac.uk) (acceptable provided a hard copy follows by post) before February 6th 2004. Please quote AM-04-001 on all correspondence.

[falush@stats.ox.ac.uk](mailto:falush@stats.ox.ac.uk)

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## QueensU MathEvolEcol

### Graduate Student Positions in Mathematical Evolution Ecology

Applications are sought from outstanding students interested in doctoral research in mathematical evolutionary ecology in the labs of Dr. Peter Taylor and/or Dr. Troy Day. Potential research projects include epidemiological modeling (including the evolution of virulence and host/parasite interactions), the evolution of senescence, multilevel selection and kin selection, the evolutionary consequences of genetic and/or sexual conflict, and the effects of spatial population structure on evolutionary dynamics. Successful applicants will be free to conduct research in any of these or other related areas of interest. For more information on research topics see: [www.mast.queensu.ca/~tday](http://www.mast.queensu.ca/~tday) and

[www.mast.queensu.ca/~tday](http://www.mast.queensu.ca/~tday) Information about the Department of Mathematics and Statistics and Queen's University can be found at [www.mast.queensu.ca](http://www.mast.queensu.ca) and [www.queensu.ca](http://www.queensu.ca) respectively.

To apply, send a current CV and statement of research interests Dr. Troy Day, Dept. of Mathematics and Statistics, Queen's University, Kingston, ON, K7L 3N6, Canada (email applications are also acceptable; send to [tday@mast.queensu.ca](mailto:tday@mast.queensu.ca)). Applications should be post-marked by Feb. 28, 2004.

- Troy Day Departments of Mathematics & Biology Jeffery Hall Queen's University Kingston, ON, K7L 3N6, Canada [tday@mast.queensu.ca](mailto:tday@mast.queensu.ca) Phone: 613-533-2431 Fax: 613-533-2964 <http://www.mast.queensu.ca/~tday/> <http://www.mast.queensu.ca/~tday/>

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## UAlberta EvolGenetics

Graduate Student Research Opportunities at the University of Alberta.

I am seeking highly motivated students interested in pursuing graduate study at either the MSc or Phd level in the fields of Molecular Ecology and Evolutionary Genetics in the Department of Biological Sciences at the University of Alberta (<http://www.biology.ualberta.ca/programs/-graduate/prospective/>) to start in Sept 2004 or Jan 2005. Research in my lab is focussed on studying the maintenance and adaptive significance of molecular and quantitative genetic variation in wild populations using molecular markers, particularly microsatellites, as primary tools.

### Projects

Research projects typically involve close collaboration with field biologists and ecologists (for examples see <http://www.sheffield.ac.uk/aps/-staffdavidcoltman.html>). The following are some potential topics that could form the basis of graduate student project work, but I would also encourage potential applicants to suggest other ideas.

- Population structure and evolutionary history of North American mountain goats (in collaboration with Steve Cote, University of Laval) - Genetic basis of maternal performance in Sable Island grey seals (in collaboration with Don Bowen, Department of Fisheries and Oceans) - Mapping QTL and candidate genes associated with horn growth and life-history variation



in bighorn sheep (in collaboration with Marco Festa-Bianchet, University of Sherbrooke) - Molecular evolution of prion genes in Holarctic ruminants - Genetic structure of northern carnivore populations (in collaboration with Andrew Derocher, University of Alberta)

The Department of Biological Sciences has a core lab fully equipped for molecular genetic analyses with state-of-the-art automated DNA sequencing apparatus (<http://www.biology.ualberta.ca/facilities>).

Funding and Application details:

Potential applicants (see Admission Requirements via <http://www.biology.ualberta.ca/programs/-graduate/prospective>) are encouraged to contact me directly to discuss their interests and suitability (d.coltman@sheffield.ac.uk). A variety of sources of funding for some international (U.S., U.K, Australia or New Zealand) as well as Canadian students with high academic standing are available for 2004 (follow links on <http://www.biology.ualberta.ca/programs/-graduate/prospective>).

\*\*\*Completed applications requiring funding should be submitted to the department no later than March 1, 2004\*\*\*\*

Students holding an NSERC PGS are also entitled to the Walter H. Johns Graduate Fellowship, which covers tuition and fees, plus approximately \$700 each year that recipient holds the NSERC. The current approximate value/year is \$4,322. They also receive a Faculty of Science Graduate Entrance Scholarship worth \$2,000 in Year 1.

Contact details

Until July 1, 2004

Dr. David W. Coltman Department of Animal and Plant Sciences University of Sheffield Sheffield UK S10 2TN Tel: +44 (0)114 222 0117 Fax: +44 (0)114 222 0002 Email: d.coltman@sheffield.ac.uk

After July 1:

Dr. David W. Coltman Associate Professor Department of Biological Sciences CW 405, Biological Sciences Centre University of Alberta Edmonton, Alberta Canada T6G 2E9

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## UCollegeLondon BiolComplexity

10 studentships are available for a 4 year MRes/Phd in

Theoretical and Experimental Approaches to understanding Biological Complexity, at University College London, commencing September 2004.

For more information please look at the departmental website for CoMPLEX (Centre for mathematics and Physics in the Life Sciences and Experimental Biology). The address is:

<http://www.ucl.ac.uk/complex> Centre for Mathematics and Physics in the Life Sciences and Experimental Biology (CoMPLEX) University College London Wolfson Hse (2nd Floor) 4 Stephenson Way London NW1 2HE

tel: 020 7679 5033 internal 25033 email: CoMPLEX@ucl.ac.uk CoMPLEX website: <http://www.ucl.ac.uk/CoMPLEX> contact: Hugh McCready

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## UDurham EvolGenet

Two new PhD studentships at the School of Biological and Biomedical Sciences, University of Durham for UK citizens:

Male-mediated gene flow in the southern elephant seal and killer whale; consequences for the evolution of population structure.

&

Extra-pair paternities and genomic correlates to lifetime reproductive success in the tawny owl

for further details see:

<http://www.dur.ac.uk/a.r.hoelzel/-megwebpageStud04.htm>

A. Rus Hoelzel  
a.r.hoelzel@durham.ac.uk

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## UGreifswald BirdPhylogenetics

Stellenausschreibung

An der Vogelwarte Hiddensee des Zoologischen Instituts der Universität Greifswald ist zum nächstmöglichen Zeitpunkt eine Stelle als nicht vollbeschäftigte/r (50 v.H.)

wissenschaftliche/r Mitarbeiter/in

(20 Wochenstunden)

zu besetzen. Die Einstellung erfolgt befristet zunächst für die Dauer von drei Jahren, eine Verlängerung um weitere drei Jahre im Rahmen der HRG-Befristungsgrenzen ist beabsichtigt.

Die Vergütung erfolgt nach BAT-O IIa.

Dienort ist Kloster/Hiddensee. Eine Wohnmöglichkeit (zur Miete) ist vorhanden.

Voraussetzungen: abgeschlossenes Hochschulstudium der Biologie; Interesse an molekularbiologischen Arbeiten und phylogenetischen Fragestellungen; Erfahrung mit gängigen molekulargenetischen Labormethoden (PCR, DNA-Sequenzierung) und phylogenetischen Analyseverfahren.

Aufgaben: Untersuchungen zur Stammesgeschichte und Populationsgenetik der Vögel anhand von DNA-Sequenzen und anderen molekularen Markern. Mitarbeit in der Lehre (2 SWS). Die Bearbeitung eines Promotionsvorhabens ist erwünscht.

Bewerbungskosten werden vom Land Mecklenburg-Vorpommern nicht übernommen. Bewerbungen mit den üblichen Unterlagen werden bis zum 31.1.2004 erbeten an

Prof. Dr. A.J. Helbig

Vogelwarte Hiddensee

Zum Hochland 17

D-18565 Kloster

(helbig@uni-greifswald.de)

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Ph.D. or post-doc position

Applications are invited for a Ph.D. or post-doctoral position (50% BAT IIa Ost) at the Vogelwarte Hiddensee, Institute of Zoology, University of Greifswald, to be filled as soon as possible. The contract will run for 3 years and can be extended up to six years. Place of work is Kloster on the island of Hiddensee, Mecklenburg Vorpommern.

The successful candidate is expected to work on molecular phylogenetics or population genetics of birds and will assist in teaching a molecular phylogenetics course. Requirements: Diploma or Master's degree in Biology, fluency in German language. Closing date for applications: 31 Jan. 2004. Please send application with CV and names and email addresses of two referees to

Prof. Dr. A.J. Helbig

Vogelwarte Hiddensee

Zum Hochland 17

D-18565 Kloster, Germany

(helbig@uni-greifswald.de)

Prof. Dr. Andreas J. Helbig Vogelwarte Hiddensee University of Greifswald D-18565 Kloster Germany Tel (49)-38300-212 FAX (49)-38300-50441 [www.vogelwarte.uni-greifswald.de](http://www.vogelwarte.uni-greifswald.de) "Andreas J. Helbig" <helbig@mail.uni-greifswald.de>

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## UHamburg LandSnailRadiations

Ph.D. position

At the Zoological Museum of the University Hamburg, a Ph.D. position (BAT IIa/2) is to be filled as soon as possible. The contract will run for 2 years and might be extended. The candidate will cooperate in a project about land snail radiations in the context of the DFG program "Radiations - Origins of Biological Diversity". The project includes field work, molecular genetic as well as morphological investigations and phylogenetic and biogeographical analysis. Experience with molecular genetic methods (PCR, DNA Sequenzierung) is desirable, but not necessary. Requirements: Diploma or Master's degree in Biology, fluency in German language. Closing date for applications: 1 March 2004. Please send application with CV to

Dr. Bernhard Hausdorf Zoologisches Museum der Universität Hamburg Martin-Luther-King-Platz 3 20146 Hamburg Tel. 040/428382284 email [hausdorf@zoologie.uni-hamburg.de](mailto:hausdorf@zoologie.uni-hamburg.de)

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## UIIdaho KenaiBlackBear

MS Student Opportunity Kenai Peninsula Black Bear Genetics Project University of Idaho

We are currently recruiting a MS student to conduct genetic research on Kenai Peninsula black bears. Our research project will evaluate genetic diversity and genetic structure of black bears on the Kenai Peninsula using mitochondrial DNA sequence analysis and nuclear DNA microsatellite analysis. The graduate student will be involved in the field collection of samples

in Alaska under the supervision of Ian Martin and the generation and analysis of the genetic data at the University of Idaho under the supervision of Dr. Lisette Waits. The graduate position will be available starting May 2004 when the field project will be initiated and the student will start classes in Aug 2004. Funding: Graduate student stipend of \$14,164/yr for 2 1/2 years with an out-of-state tuition waiver.

Desired qualifications: BS degree in biological sciences or related field, field and/or laboratory experience

To apply: Please send an application letter, resume, GRE scores (general test required, subject test optional), college transcripts, and 2 letters of recommendation to Dr. Lisette Waits, Department of Fish and Wildlife, University of Idaho, PO Box 441136, Moscow ID 83844-1146 or by email [lwaits@uidaho.edu](mailto:lwaits@uidaho.edu). Applications will be evaluated as they are received..application deadline Feb 26th.

– Lisette Waits, PHD Associate Professor Fish and Wildlife Resources University of Idaho PO Box 441136 Moscow, ID 83844-1136 Phone: (208) 885 7823 Fax: (208) 885 9080 [lwaits@uidaho.edu](mailto:lwaits@uidaho.edu) <http://www.uidaho.edu/cfwr/fishwild/lwaits.htm>

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## UK CEH

CEH NERC FUNDED PhD Studentships 2004 For full list of projects please see: <http://www.ceh.ac.uk/news/studentships.htm>

Applications are invited from graduates or final year students who have, or expect to have a First or Upper Second Class Honours Degree in a relevant subject, for a wide range of projects available throughout our UK sites. The start date will be October 2004. Full funding is restricted to UK students studying in England, Scotland or Wales.

For more information please click on the project titles. CEH will award a total of approximately 15 studentships from this list of projects. The supervisor of the projects can be contacted by email for further information.

For more information regarding the deadline dates for application, please contact the appropriate CEH supervisor.

To apply for one of the awards, please send a CV and the names of two academic referees to the first named

CEH supervisor.

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## U Lausanne HostParasiteInteractions

One or two (depending on funding) PhD positions are available to study host-parasite interactions and evolution of immune defences at the Department of Ecology and Evolution at the University of Lausanne (Switzerland).

The research will focus on host parasite interactions as a selective force in birds, bats and voles, with special attention to the relationships between immune responses and life history traits, as well as the evolution of parasite specialization and specificity.

One of the positions involves the teaching of practical (mostly in French) to undergraduate students

Deadline for application: February 15th

Please send a CV, a summary of experience, research interests and contact details of two referees to Philippe Christe, Dpt of Ecology and Evolution, University of Lausanne, BB, Ch-1015 Lausanne [philippe.christe@iezea.unil.ch](mailto:philippe.christe@iezea.unil.ch)

Further informations: <http://www.unil.ch/izea/people/pchriste.html> <http://www2.unil.ch/izea/index.html>

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## UMarylandBaltimoreCounty Aging

Genetics of Aging - Ph.D. Research Assistant ? UMBC, Dr. Jeff Leips Graduate students sought who are interested in the quantitative and molecular genetics of aging using *Drosophila melanogaster* as a model system. Opportunities available to work on NIH or NSF funded projects involving identification and characterization of genes contributing to natural variation in the age-related decline of various fitness components. Opportunities are also available to develop independent research interests in related areas of study. Students that have strong interests or experience in life-history evolution, evolutionary ecology, quantitative and evolutionary genetics are especially encouraged to apply. Graduate stipends start at \$19,000. Interested students should send a letter of interest and CV to:

Jeff Leips leips@umbc.edu Department of Biological Sciences University of Maryland Baltimore County 1000 Hilltop Circle Baltimore, MD 21250 410-455-2238 (phone) 410-455-3875 (fax) <http://www.umbc.edu/biosci/Faculty/leips.html> Jeff Leips <leips@umbc.edu>

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## UOtago AllelicVariation

PhD SCHOLARSHIP IN ZOOLOGY  
DEPARTMENT OF ZOOLOGY, UNIVERSITY OF OTAGO DUNEDIN, NEW ZEALAND

Applications are invited from suitably qualified students for one PhD scholarship to work under the supervision of Associate Professor Hamish G. Spencer. The scholarship is funded by the Marsden Fund and is available immediately for three years.

The research project entitled "Why are there so many kinds of alleles? Frequency-dependent selection and genetic variability" will involve mathematical analysis and computer simulations of models of frequency-dependent selection, in an investigation of how genetic variation may be maintained in natural populations. There will be some scope for the student to develop a project that meets her/his interests, as long as it remains within the framework of the research program. Candidates should have interests and/or experience in either population genetics or mathematical modelling. Most importantly, candidates should be highly motivated and enthusiastic about this sort of research.

PhD applicants must have been awarded the degree of BSc(Hons) or MSc (or equivalent) before taking up the scholarship. The emolument is NZ\$20,000 per annum for 3 years. There is an additional NZ\$4,000 per year to cover tuition fees at the level paid by New Zealand, Australian, French and German citizens (citizens of other countries would need further support), and some money available in the final year for thesis preparation costs.

Specific enquiries may be made to Associate Professor Hamish G. Spencer, Tel +64-3-479-7981, Fax +64-3-479-7584 or email [h.spencer@otago.ac.nz](mailto:h.spencer@otago.ac.nz)

### METHOD OF APPLICATION

Applicants should send a cover letter stating briefly why they are interested in this scholarship, together with the names, addresses, fax numbers and e-mail of 2-3 referees. Candidates should also include a curriculum vitae.

These documents should be sent to Associate Professor Hamish G. Spencer, Department of Zoology, University of Otago, P.O. Box 56, Dunedin, New Zealand (FAX: +64-3-479-7584; email: [h.spencer@otago.ac.nz](mailto:h.spencer@otago.ac.nz)).

Further details regarding the University and how to apply for admission in postgraduate programs can be found at our homepage at <http://www.otago.ac.nz>

Assoc. Prof. Hamish G. Spencer Phone: +64-3-479 7981 Department of Zoology Fax: +64-3-479 7584 University of Otago Email: [h.spencer@otago.ac.nz](mailto:h.spencer@otago.ac.nz) P.O. Box 56 <http://www.otago.ac.nz/zoology/staff/-academic/spencer.html> Dunedin, New Zealand Courier: 340 Great King Street, Dunedin

Allan Wilson Centre for Molecular Ecology and Evolution: <http://awcmee.massey.ac.nz/> <http://-awcmee.massey.ac.nz/>

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## UUtah NYBotanicalGarden Solanum monograph

Graduate fellowships.

Three graduate student fellowships, two at the University of Utah and one at the New York Botanical Garden, are available on an internationally collaborative project to produce a global monograph of the genus *Solanum* (Solanaceae). The project is one of four Planetary Biodiversity Inventory programs funded by NSF in collaboration with the ALL Species Foundation. *Solanum* includes between 1000 and 2000 species and is one of the largest genera of angiosperms. Students will pursue Ph.D. projects on groups within *Solanum*, culminating in synthetic treatments encompassing monographic taxonomy of the selected species groups; field work for the collection of herbarium, seed and silica gel samples; molecular phylogenetic analyses; and presentation of data in electronic format. Substantial interaction is expected with students and scientists at the four primary institutions (University of Utah, University of Wisconsin-Madison, the New York Botanical Garden, and the Natural History Museum, London) as well as with other national and international collaborators on this project. Candidates should be enrolled in a Ph.D. program. All three positions are available beginning in August 2004 and extendable for up to five years. It is likely that students will be supported from a mixture of research funds and teaching assistantships.

For the positions at the University of Utah: Students

will be primarily advised by Lynn Bohs. Contact Dr. Bohs for more information about the project or potential thesis topics:

Lynn Bohs Department of Biology 257 South 1400 East University of Utah Salt Lake City, UT 84112 USA E-mail: bohs@biology.utah.edu Phone: (801) 585-0380

Information on the Biology Department at the University of Utah is available at [www.biology.utah.edu](http://www.biology.utah.edu) Information about the application process, admission requirements, and deadlines is available at [www.biology.utah.edu/grads.php](http://www.biology.utah.edu/grads.php)

For the position at the New York Botanical Garden: Students will be primarily advised by Michael Nee and will be enrolled at one of the academic institutions in the New York City area; partner schools are listed on the NYBG website. Contact Dr. Nee for more information about the project or potential thesis topics:

Michael Nee New York Botanical Garden Bronx, NY 10458-5126 USA E-mail: mnee@nybg.org Phone: (718) 220-6504

Information on graduate studies at the New York Botanical Garden is available at <http://sciweb.nybg.org/science2/GraduateStudies.asp>

Lynn Bohs Department of Biology 257 South 1400 East University of Utah Salt Lake City, UT 84112 (801) 585-0380

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## UtahStateU GreatSaltLake Ecosystem

The College of Natural Resources at Utah State University is seeking qualified applicants for up to five PhD fellowships to be awarded annually. Fellows will work with faculty supervisors on aspects of a large, collaborative project designed to understand the science and management of the Greater Salt Lake Watershed and Ecosystem. Fellows will be admitted into one of three academic departments: Aquatic, Watershed and Earth Resources; Environment and Society; or Forest, Range, and Wildlife Sciences. Fellowships are awarded for a four-year duration, contingent upon annual progress toward completion of degree requirements. Fellowship awards are \$20,000 per year plus \$12,000 for in-state and out-of-state tuition. For a list of projects, cooperating investigators, eligibility, and application instructions please visit <http://www.cnr.usu.edu> and follow the link for 2004-2005 S.J. and Jessie E. Quinney PhD

Fellowships.

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## VanderbiltU EcolEvol 2

Re-posting: \*\*\* review of applications begins January 15 \*\*\*

### GRADUATE STUDIES IN ECOLOGY AND EVOLUTION AT VANDERBILT

Dear colleagues and prospective students,

The Department of Biological Sciences at Vanderbilt University seeks interested and highly motivated graduate students to join a group of laboratories with complementary research interests focusing on ecological and genetic mechanisms of evolutionary diversification. Ongoing research investigates all stages of evolutionary diversification (population structure, reproductive isolation, speciation, phylogenetic radiation) and several fundamental ecological processes (adaptation, ecological specialization, symbiosis, social interactions).

Our group occupies a new (2002) building complete with DNA sequencing facility, abundant environmentally controlled rooms, and an adjoining state-of-the-art greenhouse. Vanderbilt researchers enjoy the participation of excellent undergraduates and the resources of a thriving medical center on a beautiful campus in the heart of Nashville, a friendly and inexpensive city situated amidst the lush rolling hills of biologically diverse middle Tennessee. Graduate students receive generous stipends and are trained in a highly interactive inter-lab community.

Ecology & Evolution faculty, research interests include:

Patrick Abbot ([abbot@uts.cc.texas.edu](mailto:abbot@uts.cc.texas.edu)) social evolution, symbioses, molecular evolutionary genetics in insects and microbes

John Burke ([john.m.burke@vanderbilt.edu](mailto:john.m.burke@vanderbilt.edu)) genetic basis of adaptation and speciation in plants

Dan Funk ([daniel.j.funk@vanderbilt.edu](mailto:daniel.j.funk@vanderbilt.edu)) ecological specialization and speciation, phylogenetics in herbivorous insects

Manuel Leal ([manuel.leal@vanderbilt.edu](mailto:manuel.leal@vanderbilt.edu)) animal communication and mate choice, predator-prey interactions, and sensory ecology in lizard

Dave McCauley ([david.e.mccauley@vanderbilt.edu](mailto:david.e.mccauley@vanderbilt.edu)) population biology, population structure, local adaptation in plants and insects



For further information on research and graduate study at Vanderbilt, please consult our departmental web page at: <http://sitemason.vanderbilt.edu/biosci>. Spe-

cific questions can be directed to any of the above faculty.

Daniel Funk <daniel.j.funk@vanderbilt.edu>

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### Barcelona Bioinformatics

The Spanish National Genotyping Center (NGC) seeks one senior and one junior bioinformaticists. The senior bioinformatician is required to initiate and lead, acting as Project Manager, the development and implementation of the database and data analysis tools necessary for the NGC's high-throughput SNP genotyping operation. Candidates should have a PhD and expertise in Bioinformatics and Genomics. Other requirements are strong programming skills (C++, Java, Perl or other languages will be considered) and experience in database construction (working knowledge of SQL). Experience in extant genomics-oriented software, particularly health- and population-oriented tools is desired.

The junior bioinformatician will be mainly involved in programming tasks for the aforementioned project. Candidates should have a degree in scientific areas and strong programming skills. Experience in bioinformatics is highly desirable.

Salaries will be commensurate to experience. Contracts will have one year duration, with the possibility of extensions according to performance and needs.

Please contact Francesc Calafell (francesc.calafell@upf.edu) or Arcadi Navarro (arcadi.navarro@upf.edu) Unitat de Biologia Evolutiva Facultat de Ciències de la Salut i de la Vida Universitat Pompeu Fabra 08003 BARCELONA Phone: 00 34 93 5422841 arcadi.navarro@upf.edu

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### BostonU TechPosition

A position is currently available in the Department of Biology at Boston University. The job description follows. The position includes opportunities for collaborative research and is an excellent opportunity for those interested in molecular ecology and/or molecular systematics and evolution to gain additional research experience. Starting salary is ~\$28K. Interested persons can apply at the link below. Questions about the position can be directed to Michael Sorenson at msoren@bu.edu

1304/K183 - DNA SEQUENCER LAB MANAGER, COLLEGE OF ARTS AND SCIENCES, BIOLOGY, GRADE 72 Oversee the operation and use of a shared molecular biology laboratory whose primary function will be DNA sequencing. Operate an Applied Biosystems 3100 automated DNA sequencer and train faculty

and students in its use. Engage in independent and collaborate research in fields such as molecular evolution and population genetics. Requires: B.A./B.S. or equivalent in biology, biochemistry, or related discipline and two years of related experience. This position is grant-funded. (Kelley A. Ferretti)

[http://www2.openhire.com/onlinejobs/jobs/-submit.cfm?fuseaction=dspjob& id#& jobid9562& company\\_id509& source=O NLINE& JobOwner9914& level=levelid2& levelid2B71& parent=Charles%20River%20Campus%3B%3B%3BProfessional%2FAdministrative& startflag=3& CFID%4789 67& CFTOKEN820162](http://www2.openhire.com/onlinejobs/jobs/-submit.cfm?fuseaction=dspjob& id#& jobid9562& company_id509& source=O NLINE& JobOwner9914& level=levelid2& levelid2B71& parent=Charles%20River%20Campus%3B%3B%3BProfessional%2FAdministrative)

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

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

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## CityUNewYork LabTech

### LAB RESEARCH TECHNICIAN - PART TIME

Research in Molecular Evolution & Genetics at the Center for Study of Gene Structure & Function / Dept. of Anthropology, Hunter College, City University of New York, 695 Park Ave, NY, NY 10021.

#### Duties and Responsibilities:

Assist in research projects under the supervision of faculty member whose work focuses on the molecular evolution of malaria adaptation in primates. Responsibilities include DNA extraction, gene cloning, PCR, electrophoresis, DNA sequence analysis, computer-based management of DNA sequence data, and assessment of lab inventory.

#### Qualifications:

B.A. / B.S. degree & 2 years experience or Master's degree and 1 year experience. Knowledge of molecular genetics and PCR . Computing proficiency on Mac and Windows. A background in molecular evolution and computer networking is a plus.

#### Salary:

Salary: \$12,500 - 16,000 [HALF TIME/20 hrs week] + fringe benefits including medical plan and dental plan. EO/AA/ADA Employer.

Please e-mail PDF versions of your CV and cover letter to Michael E. Steiper, Ph.D, Department of Anthropology, Hunter College, msteiper@hunter.cuny.edu.

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## Denmark SpatialModelling

### Senior researcher/researcher - spatial modelling

The National Environmental Research Institute (NERI), Department of Arctic Environment (AE), invites applications for a 3-year position as a full time senior researcher/researcher to work with spatial modelling of animal populations

AE conducts research and monitoring of animal populations, their ecology and reactions to anthropogenic activities and climate, both in the Arctic and in Denmark (in Denmark sea mammals only). We study spatial and temporal distribution of animals in relation to biotic and abiotic conditions by use of e.g., surveys (from ship and airplane) and satellite tracking. We work with both marine and terrestrial ecosystems.

AE wants to improve its expertise in spatial modelling of the relationship between environmental and human induced variables and the distribution of animal populations and, ultimately, their population dynamics. We are particularly interested in improving our predictive skills with regard to how species will respond to major environmental changes, such as climate change, oil spills, disturbance, shooting and hyper-eutrophication.

Applicants must have substantial analytical skills and expertise in spatial modelling, including coupling of models and GIS (ArcView and ArcInfo). Qualifications include a Ph.D. (or equivalent). Experience with programming is important. The successful candidate will play a central role in a team of scientists with expertises in population biology, bio-statistics, GIS and satellite image interpretation. The ability to work in a team is essential.

Place of work: Roskilde, Denmark.

Wages and the conditions of employment will be stated according to current agreements and structure of positions for scientific staff with research tasks at Danish sector research institutions. The duration of employment will be for 3 years (however, with a possibility of extension).

Enquiries about the position may be made to head of the Department of Arctic Environment, Dr. Jesper Madsen (phone +45 46301940, e-mail jm@dnu.dk).

Closing date for the position is 18 February 2004.

The application, marked "013/101-0131" and including your CV, should be submitted in four copies to:

National Environmental Research Institute Frederiksborgvej 399 P.O.Box 358 DK-4000 Roskilde Denmark

"Madsen, Jesper" <jm@DMU.dk>

period.

Sarah Cohen Romberg Tiburon Center for Environmental Studies and the Biology Department San Francisco State University 3152 Paradise Drive Tiburon, CA 94920

sarahcoh@sfsu.edu phone 415-338-3750 (office)/415-338-3754 (lab) <http://rtc.sfsu.edu/>

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## SanFranciscoStateU ResearchTech

Research technician position in a marine molecular ecology and evolution lab A position is available in a new lab at San Francisco State University (<<http://www.sfsu.edu/~biology/>><http://www.sfsu.edu/~biology/>) and the Romberg Tiburon Center for Environmental Studies (<<http://rtc.sfsu.edu/>><http://rtc.sfsu.edu/>). Two major projects are: 1) immunogenetic (MHC) variation in natural populations of killifish and associated issues on MHC genomic architecture and population genetic variation at other loci, and 2) connections between populations of marine invertebrates. Duties will consist of routine molecular lab procedures (including, but not limited to, nucleic acid extraction, PCR, cloning, and sequencing) and data manipulation and analysis (e.g., sequence alignments, phylogenetic, and population genetic analysis). General lab maintenance (e.g., ordering, keeping track of supplies, collection maintenance) and assistance in training new lab members will also be expected. Minimum qualifications are an undergraduate college degree and additional work experience, as well as good organizational and communication skills. Candidates interested in this position or the lab (see Cohen, under <<http://www.sfsu.edu/%7ebiology/pages/gpages/-frameset.html>><http://www.sfsu.edu/%7ebiology/-pages/gpages/frameset.html>), should contact Sarah Cohen, preferably by email (sarahcoh@sfsu.edu) or at: Dr. Sarah Cohen, Biology Department, San Francisco State University, 1600 Holloway Avenue, San Francisco, CA 94132, USA. AA/EOE/ADA. To apply, please send material to two places: To Sarah Cohen (email preferred): a cover letter stating why you are interested in the job and a CV. To officially apply to the university, please send a CV to the following address: Include JOB#7727.39 and your social security number with your application. Send resume to: San Francisco State University, Human Resources, 1600 Holloway Ave., ADM 252, San Francisco, California 94132. No email, no faxes. The position is currently open until Feb. 2 or until filled. And, there is funding in place to extend the position beyond the listed time

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## TexasStateU EvolQuantEcol

DEPARTMENT OF BIOLOGY TEXAS STATE UNIVERSITY-SAN MARCOS

(Quantitative Ecologist)

The Department of Biology invites applications for a tenure-track position in Quantitative Ecology, including but not limited to, studies of Population, Community, or Ecosystem Processes; Modeling, Mathematical Ecology and Demography. Individuals whose research program emphasizes development and testing of models/theory and who can contribute to our Ph.D. Program in Aquatic Resources are especially welcome. The individual is expected to establish an extramurally funded research program, train graduate students, and teach at the undergraduate and graduate level. Applicants should submit a cover letter with names and contact information of three references, curriculum vitae, copies of up to five publications, and statements of research and teaching interests to Francis L. Rose, Chair, Biology Department, Texas State University-San Marcos, TX 78666. Review of applications begins on March 1st, 2004 and continues until a successful candidate is found. Please visit <http://www.bio.txstate.edu> for a full description of the position and the Department's Programs and Faculty. Texas State University is an Equal Opportunity employer.

Chris Nice <ccnice@txstate.edu>

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## UCBerkeley ArthropodBiodiversity

The University of California, Berkeley, Department of Environmental Science, Policy, and Management, Division of Insect Biology is conducting a search for a

tenure-track Assistant Professor in Arthropod Biodiversity. The deadline date for applications is March 1, 2004. A copy of the advertisement is attached as well as pasted in this email below.

ASSISTANT PROFESSOR ARTHROPOD BIODIVERSITY University of California, Berkeley

The University of California, Berkeley, invites applications for a tenure-track Assistant Professor in arthropod biodiversity with concurrent appointment in the Agricultural Experiment Station. The successful applicant will be expected to establish an active research program in any area of biodiversity science, including, but not limited to the use of systematic and ecological approaches to understand arthropod biodiversity and conservation. This position will be an annual nine-month appointment, with salary and step within rank dependent on experience, qualifications, and budgetary approval. The position will be available July 1, 2004.

Applicants must have earned a doctoral degree in a field appropriate for the study of arthropod biodiversity, and will be expected to develop a vigorous externally funded research program, direct student research, and contribute to both undergraduate and graduate instruction. Responsibilities will include the development of courses in biodiversity and/or conservation biology, and significant interactions with the Essig Museum of Entomology, which is part of a strong consortium of natural history museums at the University of California at Berkeley

Interested persons should apply by submitting a résumé, statement of research interests, list of publications, and three letters of reference to:

Chair of Arthropod Biodiversity Search Committee  
University of California Department of Environmental Science, Policy, and Management (ESPM) Division of Insect Biology 201 Wellman Hall Berkeley, CA 94720-3112

The closing date for applications is March 1, 2004.

The University of California is an Equal Opportunity/Affirmative Action Employer

Penny Hines Academic Personnel Analyst University of California ESPM: Insect Biology

phines@nature.berkeley.edu

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**UCDavis EvolBehaviorist**

ANIMAL BEHAVIORIST, UNIVERSITY OF CALIFORNIA, DAVIS – The Division of Biological Sciences, University of California, Davis invites applications and nominations for a position in the Section of Evolution and Ecology at the tenure-track ASSISTANT PROFESSOR level. Candidates must have a Ph.D. (or equivalent) in the biological sciences or related fields, and are expected to have a strong record of research in animal behavior, preferably on topics related to ecological and evolutionary issues. Teaching responsibilities may include an undergraduate course in introductory biology, evolution, or ecology, and specialized courses in animal behavior. Applicants should send copies of (1) a curriculum vitae, (2) a description of current and projected research, (3) a summary of teaching interests and experience, (4) no more than 5 publications (paper only); and have three letters of recommendation (electronic preferred) sent to: Chair, Animal Behavior Search Committee, Section of Evolution and Ecology, University of California, One Shields Avenue, Davis, CA 95616-8755; bashaneyfelt@ucdavis.edu. Closing Date: Open until filled, but all application materials, including letters of recommendation, must be received by March 1, 2004 to assure full consideration. The University of California is an Equal Opportunity/ Affirmative Action Employer with a strong institutional commitment to the development of a climate that supports equality of opportunity and respect for differences.

Judy Stamps <jastamps@ucdavis.edu>

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### **UFlorida ConservationGenetics**

CONSERVATION GENETICS UNIVERSITY OF FLORIDA

Applications are invited for a 12-month, tenure-accruing faculty position at the Assistant Professor level. This will be a joint appointment in the Departments of Fisheries and Aquatic Sciences and Wildlife Ecology and Conservation (WEC), with tenure accruing in WEC. A Ph.D. in a relevant biological discipline is required and expertise in a broad range of vertebrate taxa, including fish, is preferred. The successful applicant will be expected to develop a vigorous research program (60%) and teach graduate and undergraduate courses in genetics applied to wildlife conservation and fisheries management (40%). Applicants should submit their curriculum vitae, a statement of their professional goals and teaching philosophy, and three letters of recommendation by 1 March 2004 to: Chair, Search Com-

mittee, Department of Fisheries and Aquatic Sciences, University of Florida, 7922 NW 71st Street, Gainesville, FL 32653. A full description of this position may be viewed at: <http://personnel.ifas.ufl.edu/StatePositionDescription/915420.htm> An Equal Opportunity, Equal Access, Affirmative Action Institution

Marta L. Wayne PO Box 118525 Department of Zoology University of Florida Gainesville, FL 32611-8525 Vox: 352-392-9925 Fax: 352-392-3704 Web: <http://www.zoo.ufl.edu/mlwayne>

“Marta L. Wayne” <mlwayne@zoo.ufl.edu>

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## UFlorida ConservationGenetics 2

\*\*\*Sorry for repeat posting; error in website address in previous email\*\*\*

### CONSERVATION GENETICS UNIVERSITY OF FLORIDA

Applications are invited for a 12-month, tenure-accruing faculty position at the Assistant Professor level. This will be a joint appointment in the Departments of Fisheries and Aquatic Sciences and Wildlife Ecology and Conservation (WEC), with tenure accruing in WEC. A Ph.D. in a relevant biological discipline is required and expertise in a broad range of vertebrate taxa, including fish, is preferred. The successful applicant will be expected to develop a vigorous research program (60%) and teach graduate and undergraduate courses in genetics applied to wildlife conservation and fisheries management (40%). Applicants should submit their curriculum vitae, a statement of their professional goals and teaching philosophy, and three letters of recommendation by 1 March 2004 to: Chair, Search Committee, Department of Fisheries and Aquatic Sciences, University of Florida, 7922 NW 71st Street, Gainesville, FL 32653. A full description of this position may be viewed at: <http://personnel.ifas.ufl.edu/StatePositionDescriptions/915420.htm> An Equal Opportunity, Equal Access, Affirmative Action Institution

Marta L. Wayne PO Box 118525 Department of Zoology University of Florida Gainesville, FL 32611-8525 Vox: 352-392-9925 Fax: 352-392-3704 Web: <http://www.zoo.ufl.edu/mlwayne> “Marta L. Wayne” <mlwayne@zoo.ufl.edu>

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## UGeorgia ResearchTech

Job: Research tech, evolutionary genetics

A full-time research technician III position is available immediately at the University of Georgia in a lab working on various evolutionary genetic questions using *Drosophila*. The position is for a minimum of 2 years.

The ideal candidate will be a detail-oriented person with good communication skills, the ability to work independently and as part of a team, and someone with previous biology research experience.

The working conditions, intellectual atmosphere, and facilities in Genetics at Georgia are excellent. Athens is a lovely and inexpensive place in which to live with all of the advantages and culture of a 200-year-old university town. See the Department of Genetics web site at <http://www.genetics.uga.edu>. Review of applicants will begin immediately and will continue until the position is filled. Interested persons should send (by e-mail) a resume/CV (with GPA), a statement of current interests and future plans, and the names and contact information of 2 references to: Daniel Promislow, Department of Genetics, University of Georgia [promislow@uga.edu](mailto:promislow@uga.edu)

Daniel Promislow <promislow@uga.edu>

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## UHawaii EvolMarineScience

ASSISTANT PROFESSOR OF MARINE SCIENCE (coral biologist/ geneticist), position number 86483, College of Arts and Sciences, general funds, pending available funding, full-time, tenure-track, nine-month appointment to begin August 2004. The University reserves the right to hire at another rank when the selected candidate is qualified for that rank. Duties: Teach undergraduate and MS level graduate courses, including: undergraduate Marine Biology lecture and lab, Coral Biology/ Ecology, Molecular Marine Biology/ Ecology, a graduate course in Nearshore Monitoring and Analysis, and courses in the applicant's specialty; participate in summer courses for additional compensation; conduct research and publish results



on coral biology/ genetics, mentor undergraduate and graduate student research, seek extramural research funding; advise students; participate in departmental, community and University service. Minimum Qualifications: Ph.D. from an accredited college or university in a biological or oceanographic discipline, research experience in coral biology with relevant publications, demonstrated expertise in teaching at the university level. Desirable Qualifications: Record of extramural funding, expertise in molecular genetic techniques. Salary: Competitive. To Apply: Submit letter of application, vita, and three letters of reference by email or hard copy to Dr. Marta deMaintenon, Marine Science, University of Hawai'i at Hilo, 200 W. Kawili St., Hilo, HI, 96720-4091. Electronic submissions may be submitted to demainte@hawaii.edu. Inquires: Dr. Marta deMaintenon, 808-933-3902, email demainte@hawaii.edu. Application Deadline: Mailed applications postmarked no later than February 20, 2004, electronic applications received by February 20, 2004. UH Hilo is an EEO/AA Employer D/M/V/W.

"Susan I. Jarvi" <jarvi@hawaii.edu>

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## UTennessee CompBiol

As seen in the 16 January issue of Science:

### Position Advertisement

ASSISTANT/ASSOCIATE PROFESSOR in Bioinformatics or Computational Biology. The Joint Institute for Computational Sciences at the University of Tennessee and the Oak Ridge National Laboratory seeks to fill a tenure-track position in the area of bioinformatics/computational biology to begin August 2004. Applications from individuals whose research focuses on the use of high-end computers to understand the molecular mechanisms of evolutionary processes, to predict protein structure and interactions, or to analyze ge-

netic and proteomic data to identify and characterize metabolic, regulatory and other networks important for understanding biological function towards developing in silico models of cell behavior would be especially welcome to complement existing strengths within the Biology Division at the University of Tennessee and the newly formed Computational Biology Institute at the Oak Ridge National Lab, but applications from outstanding individuals in all areas will be considered.

Required qualifications for the position include a Ph.D. and relevant postdoctoral experience, evidence of significant scientific productivity, and a commitment to an integrated program of teaching and research. The successful candidate will be qualified for appointment in one of the following departments represented in the Division of Biology: Microbiology, Ecology and Evolutionary Biology, or Biochemistry, Cell, and Molecular Biology. Interested candidates should submit a resume and a description of proposed research program. Applicants should also arrange for at least three letters of reference to be submitted. Review of applications will begin upon receipt and will continue until the position is filled.

All application materials should be sent to the address below or to [compbiosearch@jics.utk.edu](mailto:compbiosearch@jics.utk.edu) <<http://aaas.sciencecareers.org/texis/-apply?id@06ace24a04a20&lookidas&to=-compbiosearch@jics.utk.edu>>

Bioinformatics/Computational Biology Search Committee Joint Institute for Computational Sciences University of Tennessee-Oak Ridge National Laboratory P. O. Box 2008 Oak Ridge National Laboratory Oak Ridge, TN 37831-6008

Sergey Gavrilets, Professor Department of Ecology and Evolutionary Biology Department of Mathematics University of Tennessee Knoxville, TN 37996

phone: (865) 974-8136 fax: (865) 974-3067 e-mail: [sergey@tiem.utk.edu](mailto:sergey@tiem.utk.edu) web: [www.tiem.utk.edu/~gavrila](http://www.tiem.utk.edu/~gavrila)

sergey <[sergey@tiem.utk.edu](mailto:sergey@tiem.utk.edu)>

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### AMOVA question

Happy New Year! I have a question about analysis of molecular variance based on microsatellite data.

We are working on the analysis of a microsatellite data set collected from different populations of a eusocial sweat bee in southern Greece. Eventually, the analysis will also include specimens from other parts of the Mediterranean. We would like to do an analysis of molecular variance aimed at partitioning out the genetic variance at the following levels:

1. among countries (e.g. France vs Germany vs Greece)
2. among regions within these countries
3. among subpopulations within regions
4. among families within subpopulations
5. among individuals within families

The problem is that as far as I can tell, available models for AMOVA only can be used for a sampling protocol with three levels (e.g. individuals randomly sampled from different subpopulations within populations). For instance, this is how Arlequin treats data. I have searched various databases and inquired of various authors to find out if AMOVA models have been derived for data sets like ours, but have found none.

My question is, am I correct that more complicated, multilevel models have not been derived? Or if they have, could somebody steer me in the right direction? A colleague and I intend to derive the models if this has not been done previously, but we don't want to reinvent the wheel.

Yours sincerely,

Miriam H. Richards Dept. Biological Sciences Brock University St. Catharines, ON L2S 3A1 Email: Miriam.Richards@brocku.ca

Miriam Richards <miriam.richards@brocku.ca>

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### Any workshops

Hello all,

I am looking for workshops, courses, etc. to be offered in 2004 in statistical genetics, population genetics, conservation genetics, or a similar field. I participated in the Summer Institute at NC State last summer, and know of a few other opportunities, but they can sometimes be difficult to find out about. If anyone knows of such workshops (classroom or laboratory-based), could you please email me at emily@fnr.purdue.edu? I will then compile a list and distribute to the group.

Thanks, Emily

Emily Latch Ph.D. Candidate, wildlife genetics Dept. of Forestry and Natural Resources 195 Marsteller St. Purdue University West Lafayette, IN 47907 (765) 496-6868 emily@fnr.purdue.edu

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### Arlequin

Dear all,

I am trying to analyze my mtDNA sequences by using Arlequin, but I have some troubles with the proyect. I have followed the guide, but when I try to run the program there is an error message telling that it is unable to read the data because it can't find the identifier. I've tried to write the haplotypes in different ways but the message is always the same. Can anyone help me to solve this problem?

Thanks in advanced

Beatriz López Lab. Genética U. Autónoma de Madrid  
España e-mail: blopez@abulafia.ciencias.uchile.cl  
beatriz.lasala@yahoo.es

Este mensaje fue enviado usando IMP sobre Debian GNU/Linux.

Beatriz Lopez <blopez@abulafia.ciencias.uchile.cl>

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### CNN evolution poll

Today a CNN poll confirms what educators and researchers - and by far the majority of Americans' perspective that evolution is at the core of any meaningful biological sciences curriculum.

See the poll today at [www.cnn.com](http://www.cnn.com) at of 9:18 this morning:

Should the word "evolution" be removed from Georgia's science curriculum?

Yes 15% 1869 votes

No 85% 10867 votes

Total: 12736 votes

Spread the good word!!!

Cheers,

Jim Lyons-Weiler <http://bioinformatics.upmc.edu>

"Lyons-Weiler, James" <lyonsweilerj@upmc.edu>

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### Calonectris micros

Dear Evoldir Members,

Does anyone out there know of any published or unpublished work on development of microsatellite markers in *Calonectris diomedea* (corys shearwater) or the next related species? I need it for my master. Thanks in advance for your help

Linda Weber

<lweber@ix.urz.uni-heidelberg.de>

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### Dobzhansky Prize correction

PLEASE NOTE:

The announcement published in the journal *Evolution* is incorrect. Below is the correct announcement for the application for the 2004 Dobzhansky Prize. It is important that ALL APPLICATIONS, INCLUDING LETTERS OF REFERENCE, MUST BE SUBMITTED AS PDF FILES.

Allen Moore

Applications for the 2004 Theodosius Dobzhansky Prize

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

**Eligibility** The candidate must have a Ph.D. (or equivalent) awarded no earlier than June 2001 and no later than February 2004, and must be actively involved in research in the field of evolutionary biology. There are no other restrictions. Applicants do not have to be members of the Society for the Study of Evolution, but such membership is encouraged.

**Nomination/Application.**- Candidates may apply directly or may be nominated by someone else. Established researchers are encouraged to nominate outstanding young scientists who may be unaware of the existence and prestige of this prize. Each candidacy must be supported by the following materials prepared by the candidate, and submitted by either the nominating scientist or the candidate: (1) a curriculum vitae, (2) a summary of research accomplishments, (3) a statement of research plans for the next several years, (4) copies of three recent publications, (5) names and addresses of three referees (including the nominating

scientist where applicable) who have sent supporting letters. PLEASE NOTE THAT LETTERS OF REFERENCE ARE SENT SEPARATELY, but no application will be considered without these letters.

All application/nomination materials must be sent as PDF e-mail attachments. No file type other than PDF will be accepted. The deadline for receipt of all materials, including letters of reference, is February 15, 2004. All materials should be sent via e-mail as PDF attachments to the secretary of SSE (Allen J. Moore):

allen.j.moore@man.ac.uk

Award.- The Dobzhansky Prize is accompanied by a check for U.S. \$5000, and will be awarded at the annual meeting of the Society for the Study of Evolution in Fort Collins, CO, USA, 26 June - 30 June, 2004. The recipient is expected to be present to receive the award, and to give an oral presentation about his/her research. To facilitate attendance, the SSE provides funds to cover the costs of conference registration, accommodations during the conference, and expenses for travel to and from the conference. The recipient will be notified of the award by early May 2003.

Allen J. Moore Professor of Evolutionary Biology School of Biological Sciences 3.614 Stopford Building University of Manchester Oxford Road Manchester M13 9PT UK

phone: +44 (0)161-275-7221 (office) +44 (0)161-275-7401 (laboratory) fax: +44 (0)161-275-3938

<http://www.sbs.man.ac.uk/staff/user.asp?id=817&item=Research> Allen.J.Moore@man.ac.uk

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## Fagus DNA AFLP

Dear Evoldir members,

I would be grateful for any help or advice with the following.

I am intending to investigate beech (*Fagus sylvatica*) trees using AFLPs. Owing to the location of study populations it is most likely that I will have to extract DNA from silica gel-dried leaves rather than fresh.

Obviously, I would prefer to find the quickest and highest throughput method of getting clean DNA. I've used various extraction protocols in previous work but would like to know if anyone has had any success with using kits to extract and purify from dried leaf samples or a favourite protocol for this situation.

Also, does anyone know of any groups that are currently working with AFLPs in beech?

Many thanks in advance,

Alistair Jump

Dr. A.S. Jump

Centre de Recerca Ecològica i Aplicacions Forestals (CREAF) Edifici C, Universitat Autònoma de Barcelona E-08193 BELLATERRA (Barcelona) Spain

0034 935813345 (Office) 0034 675445719 (Fieldwork) 0034 935814151 (Fax)

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## Figure copyright

Dear Evoldir Members,

I'm interested in to use the follow picture (<http://www.hcnet.usp.br/ipq/revista/DNA.gif>) in a publication, however I couldn't remember were I got it but I would like to request to the author of this art authorization for the use of the picture.

Did someone know the source of this picture?

Thanks in advance,

Pedro. <pedson@usp.br>

Pedro Edson Moreira Guimaraes The Laboratory of Neuroscience LIM-27 Department & Institute of Psychiatry R. Dr. Ovidio Pires de Campos n785 3o andar 05403-010 Sao Paulo SP Brazil Voice: +55-11-3069-7283 Fax: +55-11-852 4851 [www.hcnetusp.br/ipq/neuroscience/index.html](http://www.hcnetusp.br/ipq/neuroscience/index.html)

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## Genetic analysis

dear and reputable members of the evoldir,

to a 90% approximation cells are machines to synthesize and degrade ribosomes. to a 99% approximation cells are machines to express and degrade the products of highly expressed genes. even the nuclear membrane appears to be little more than a passive pump to export from the nucleus rRNAs bound to ribosomal subunits and to keep fully assembled ribosomes outside the nucleus. and yet for most of us who have done empirical

molecular-biology work, ribosomal proteins and rRNAs are rather nuisances that hamper our attempts to study truly interesting (sic) genes and gene products. this is probably due to epistemological biases created by the limits that history imposed on genetic analysis, e.g. by the biased nature of the phenotypes early geneticists were compelled to study in order to understand heredity, phenotypes that acquired afterwards a unjustified legitimacy as phenotypes tout court becoming more and more studied and ending up shaping in an illegitimate way our view of cells as biomachines. importantly, this has resulted in a remarkable neglect of the overwhelming functional and thus cyto-architectural, cyto-metabolic, and evolutionary centrality of those cellular functions that require extremely high levels of gene expression and gene-product turnover. below are some thoughts about aging as it can be envisioned when one attempts to look at the cell without the deforming optics that genetic analysis has compelled most of us to adopt unwittingly. and further below is a coda with re-imaginings of sex, the germ line, the nucleus, somatic mutation, etc.

feedback welcome :)

best to you all

marcos

//// transcription-associated mutation and aging  
 //////////////////////////////////

1) transcription is well-known to be mutagenic to the gene being transcribed and to its immediate surroundings (point mutations, rearrangements, etc), and an impressive DNA repair machinery is mobilized around the transcription bubble. 2) to a 90% approximation cells are machines to express the genes whose products are necessary to carry out transcription, translation, and orderly protein and RNA degradation. In fact, the bulk of transcription, translation, and protein/RNA degradation in the cell is directed at synthesizing and degrading ribosomal-protein mRNAs, ribosomal RNAs (rRNAs), ribosomal proteins, and the RNAs and proteins needed for transcription and protein/RNA degradation. 3) therefore most transcription-associated mutations that manage to evade the surveillance of transcription-associated repair must alter the primary-structure of the above highly transcribed genes. 4) these genes should therefore accumulate mutations over the active life of a cell. 5) the accuracy and speed of transcription, translation, and protein/RNA degradation and possibly the containment of transcription-associated mutagenicity (if the involved genes are highly expressed), depend on the primary-structural integrity of these highly transcribed genes, genes that non-surprisingly are very con-

served phylogenetically. 6) the accumulation of mutations in these genes must reduce progressively the accuracy and speed of transcription, translation, and protein/RNA degradation in the cell, and may increase transcription-associated mutagenicity. 7) in particular, mutations in these highly transcribed genes must also impair the speed and accuracy of the transcription and translation of these genes themselves altering additionally epigenetically the primary structure of the gene products expressed by the mutated genes. 8) over the years the speed and accuracy of transcription, translation, and protein/RNA degradation, and possibly the containment of transcription-associated mutagenicity, should worsen inexorably compromising quantitatively and qualitatively the steady-state transcriptome and proteome.

hence

9) aging is likely to be due to a progressive accumulation of mutations in the crucially important genes whose products carry out transcription, translation, protein/RNA degradation, and, possibly, contain transcription-associated mutagenicity, mutations caused by the huge transcription rates of these genes. 10) such mutations should impair the above functions not only directly, by modifying the primary structure of these genes and thus altering the intrinsic capability of the involved gene products to function correctly, but also indirectly, by decreasing the accuracy and the speed of the transcription and translation of these genes themselves, mutated or not, which would alter their gene products additionally compounding their loss of functionality. 11) aging may not require that most genes mutate over time since the transcription-associated mutations that massively expressed genes are expected to accumulate, should suffice. 12) indeed such mutations must be much more frequent than any others and

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

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**Georgia K12**

Hi All,

Recently the Georgia Department of Education released drafts for new K-12 science standards for public schools.



These standards were based on the excellent AAAS project 2061 benchmarks, but intentionally removed many of the central ideas of modern science like common descent, human origins, the mere mention of “evolution,” the age of the earth, plate tectonics (mostly), the Big Bang, and human reproduction. The standards can be reviewed at <http://www.glc.k12.ga.us/spotlight/gps2.htm>. (That site also allows for comments.)

More information, including links to the AAAS benchmarks, can be found at <http://www.georgiascience.org>. There is an online petition to encourage GADOE to incorporate the entirety of the AAAS project 2061 benchmarks.

<http://www.petitiononline.com/gasci04/> Please sign and pass the link around. You don't have to be a Georgia resident to sign.

Reed A. Cartwright Phone: (706) 542-1455 Graduate Student Fax: (706) 542-3910 University of Georgia <http://www.rufus.ws> Department of Genetics C212 Life Sciences Bldg Athens, GA 30602-7223

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## Grass Carp MolGenet

Hello everyone I am carrying out project: Genetic variation of grass carp broodstocks in Vietnam. If you have any grass carp paper (mtDNA and nDNA) please sent to me. I will give you full acknowledgements or co-authors. Cheers

Binh Thai Master Student School of Ecology and Environment Deakin University Warrnambool VIC 3280 AUSTRALIA Tel: 61.3.55633569, 61.3.55615831 Mob: 0408038242 [http://www.deakin.edu.au/sch\\_ecol\\_env/-research/mol.ecol.bio/home.htm](http://www.deakin.edu.au/sch_ecol_env/-research/mol.ecol.bio/home.htm)

Binh Thai <tbt@deakin.edu.au>

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## Gyny levels in ants

Subject: gyny-levels and colony sizes in several ant species

Dear colleagues, I am working on a comparative study on life history aspects in ants and would like to have

information on the primary mono-/polygyny and/or mean colony size of the different species hereafter. This information can in many cases not be found in the (accessible) literature, either because the references are so old as to not be included in the on-line databases or because the data have not yet been published. I would therefore very much appreciate it if you should have any information on gyny-levels and colony size in the species listed below and would most kindly be prepared to let me include unpublished data in my study. All due reference and acknowledgement would naturally be given. Cryptopone gilva Gnamptogenys simplicoides Vollenhovia emeryi Strumigenys manga Melissotarsus insularis Camponotus lateralis Camponotus pilicornis Formica gagates Formica selysi Lasius carniolicus Lasius flavus Crematogaster scutellaris Leptothorax unifasciatus Manica rubida Myrmica rubra Myrmica sabuleti Solenopsis fugax Tetramorium caespitum Pachycondyla villosa Plectroctena subterranea

–  
mathieu.molet@ens.fr

Laboratoire d'Ecologie Université Paris 6 - Pierre et Marie Curie 7 quai Saint-Bernard 75005 Paris FRANCE

batiment A, 7ème étage, pièce 713 tel: 01.44.27.26.94 mobile: 06.70.20.29.38

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## IGE

2004: MEEGID VII and the year of Infection, Genetics and Evolution

Dear readers,

It is my pleasure to wish you a very happy and scientifically productive year 2004. This New Year will see the arrival of the 7th session of our international meeting “Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases” (MEEGID VII). The MEEGID meetings were launched in 1996 under the auspices of the Centers for Disease Control and Prevention (CDC) in Atlanta, the Institut de Recherche pour le Développement (IRD; the French governmental agency for applied research in developing countries), and the Centre National de la Recherche Scientifique (CNRS; the French governmental agency for basic research). The MEEGID meetings have been the forum that matured the unique scientific concept of Infection, Genetics and Evolution: integrating lines of research deal-

ing with genetics, genomics and evolutionary biology of hosts, pathogens and vectors to disrupt the unwelcome compartmentalization that hinders the development of this field of research. This scope makes the uniqueness of the MEEGID congresses and of *Infection, Genetics and Evolution*. The sole meetings and journal where you can find communications on human genetics, as well as on mosquito vector morphometry and *Mycobacterium tuberculosis* phylogenetics; that welcomes works on bacteria as well as viruses, fungi and parasites; that encourages general methodological approaches together with specialized research. The goal is no less than the founding a new scientific discipline and a new scientific community. MEEGID VI, July 2002, Pasteur Institute, Paris (France) was quite successful. MEEGID VII will be the session of maturity. It will be hosted in very favorable conditions. The venue will be Valencia (Spain), one of the most dynamic cities of a country with ambitions to play a major role in the great Europe of 25. MEEGID VII (19-24th July 2004) has been purposely organized in tight synchronization with the 9th European Multicolloquium of Parasitology (EMOP IX; <http://www.uv.es/emop9/>), a large meeting of several thousand participants. The principal EMOP IX organizer, and local organizer of MEEGID VII, will be Professor Santiago Mas Coma, the receiving editor of *Infection, Genetics and Evolution* for Spain. MEEGID VII will take advantage of the logistics and resources of EMOP IX, thus saving much effort. Many sessions will be organized in common, and reduced registration fees will be offered to those who register for both congresses. Many parasitologists who constitute the usual EMOP audience will be attracted by the specialized sessions of MEEGID VII, and in turn, the usual MEEGID attendees will have the opportunity to learn from other fields, such as, clinical research or field epidemiology, leading to a productive cross-fertilization of ideas. As for the Paris meeting, MEEGID VII will be definitely focused on debates, with the new formula of “express debates” (a single talk of 20 minutes on a hot topic, followed by a free discussion of 40 minutes). Students will be exempted from registration fees for MEEGID VII, and will benefit from reduced fees if they attend both MEEGID VII and EMOP IX. A specific student symposium will be organized, with students acting as chairs. Three awards will be given in the framework of MEEGID VII: best communication by a student, best communication by a scientist from the developing world on a problem specifically relevant to their part of the world, and best communication “all categories”.

This year will see also the ranking of our journal by the Institute for Scientific Information (ISI). Launched in 2001, *Infection, Genetics and Evolution* (of which the

14th issue is presently being compiled) is published now at a rhythm of 6 issues per year. It follows and promotes the latest developments in our field, with for example 2 papers recently published on the molecular evolution of the SARS virus. Its evaluation by the National Library of Medicine (Washington) has been excellent (ranked 3.5 for a maximum of 4.0; “very good”), which led to its coverage (starting from the 1st issue) by Medline and Index Medicus. The visibility and traceability of the papers published in *Infection, Genetics and Evolution* is therefore excellent. However, many authors still are reluctant to send papers to the journal, due to the lack of an official ISI impact index, the new religious mantra of many scientists. The impact index is useful and informative, although many have recently underlined its biases. However, for a new journal it is a kind of vicious circle and a major challenge. How to attract major contributions when their authors would be able to publish them in well-established stars? How to encourage young beginners to submit when a non-ranked new journal will be much less relevant for their curriculum vitae? Our journal is

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

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## KentStateU TeachingFellowProgram

Teaching Fellows in Biological Sciences-Kent State University

We currently have opportunities for individuals to serve as Teaching Fellows as they pursue their doctoral degree in Biological Sciences. The Teaching Fellow program integrates research and education. Each participant will conduct their dissertation research under the guidance of a member of our graduate faculty in physiology, ecology or evolutionary biology. Teaching Fellows will have additional training and opportunities in education at the university level beyond that of our graduate teaching assistants including lecturing in classes of various types, classroom observations and mentoring, and helping guide undergraduate research projects. These fellowships are designed for students who intend to seek faculty positions at colleges or universities that value teaching skills. Details about the department and our faculty can be found at [www.kent.edu/biology](http://www.kent.edu/biology). Re-

quirements for admission to our graduate program and for application for a teaching fellowship include: an undergraduate GPA of 3.0 and, if applicable, a graduate GPA of 3.25, results of the GRE general test, and TOEFL scores at the 600 level or higher for international applicants. The stipend is \$16,000 per year (12 months) and there is an accompanying tuition scholarship. Students accepted into the program will also be considered for a Biological Sciences Award of up to \$1000 that may be renewable. If you are interested in applying, please contact Pat Williams at our Graduate Studies office at: Graduate Studies Office, Department of Biological Sciences, Kent State University, Kent, OH 44242, (330) 672-2819, e mail: pwilliam@kent.edu

aschwarz@kent.edu

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### Lice Taxonomy

Hi, Are there any people out there who who might want to get involved in an interesting project involving molecular systematics of lice? See below. If so, contact Jack Mortensen. Mike

Michael Blouin Dept. Zoology, 3029 Cordley Hall Oregon State University Corvallis, OR 97331-2914 Tel. 541-737-2362 Fax. M. Blouin: 503-714-9907 Fax. Dept. Zoology: 541-737-0501 blouinm@science.oregonstate.edu <http://oregonstate.edu/~blouinm/index.htm> > — Original Message —

From: <Jack.A.Mortenson@aphis.usda.gov> To: <blouinm@science.oregonstate.edu> Sent: Wednesday, December 17, 2003 10:40 AM Subject: lice taxonomy question

Mike, I haven't run into you in a few years. Hope you are still going strong n Zoology. I have a genetics question for you.

I am investigating a lice problem in Oregon deer. It appears that the deer in western Oregon have an exotic lice on them and most likely the reason for the hair-loss syndrome seen over the last few years. I am working with a morphological taxonomist for biting lice and he can identify the enus, subgenus, but is relatively certain this is an undescribed species. I would like to follow up on the identification of this lice with a enetic comparison to confirm genus and species.

Would you be able to do this type of work, or would you be able to point me in the right direction. I realize

it would take some samples of knowns and unknowns to do this work. These are available.

Best Regards,

Jack Mortenson, DVM, MS Epidemiologist USDA, Veterinary Services 530 Center St NE, Suite 335 Salem, OR 97301 503-399-5703

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### M13 primer reponses

As promised here is a collection of the main comments that I received for my query through EvoDir concerning the use of universal primer tails to fluorescently label microsatellites. Many people wrote to learn more about the technique as a way to reduce costs. I got many responses from people who have used this technique, and I thank them for sharing their experiences with me. Their names are excluded to shelter them from e-mail inundations! Thanks to all for your comments, advice, and encouragement! Alexis

The basic technique is described in a number of articles, but my primary sources were: Schuelke, M (2000) An economic method for the fluorescent labeling of PCR fragments. *Nature Biotechnology* 18: 233-234

Oetting et al (1995) Linkage analysis with multiplexed short tandem repeat polymorphisms using infrared fluorescence and M13 tailed primers. *Genomics* 30 (3): 450-458

There is also a new book out on PCR including a chapter by M. Scheulke. *PCR Technology: Current Innovations* by Thomas Weissensteiner(Editor), Thomas Weissensteiner, Hugh G. Griffin (Editor), Annette M. Griffin (Editor), ISBN 0849311845

As a quick summary there is a mixed review of the technique for large numbers of samples and multiplexing many loci - for some people it works very well, but for others it has not worked when multiplexing. Nearly everyone seems to agree that it is exceedingly useful for identifying useful microsatellites from a genomic library - i.e. finding how polymorphic they are and their lengths for planning multiplexing. This is primarily due to the cost involved when dealing with fluorescently labeled primers such as are required for an ABI3100. The problems people experienced were primarily in PCR, where the two step binding process complicated optimization for many people, especially when multiplexing more than 3 loci. Few had any problems multiplexing the fragment analysis when PCRs were done separately

or when a small number of loci were multiplexed in PCR. Too many similar sized fragments with different dyes did cause problems moving through the capillary for some people. A number of authors suggested that for efficiency's sake, the technique was great for identifying useful loci and determining their size, but that then using labeled specific primers was much more efficient for a large number of individuals, both in terms of time and money (optimization and PCR).

Specific tips and tricks: M13 is not the only universal tail - authors point out that there are a number of others:

M13 Forward (-29) 5' -CACGACGTTGTAACGAC -3' M13 Reverse 5' -GGATAACAATTCACACAGG -3' T3 Promoter 5' - AATTAACCTCACTAAAG -3' T7 Promoter 5' - TAATACGACTCACTATAGGG -3' SP6 Promoter 5' -GATTTAGGTGACACTATAG -3' And you can find more information about these from: [www.licor.com](http://www.licor.com) This can also be coupled with different fluorescent labels. Furthermore, one respondent suggested that these tails have similar melting points, so they can potentially multiplex quite well if labeled with different colors (or if there is a sufficient size difference between loci).

Someone who has had success with multiplexing 6 loci in PCR suggests using a QIAgen multiplexing kit (cat# 206143) which despite being recommended for 50ul reactions works well with 15ul reactions. This also seems to space the loci apart a bit more than normal making similar sized loci easier to tell apart!

Extending the cycling time may also help (1 min denature, 1 minute anneal, 1.5 minute extension).

Making your own size standard is both economical and very helpful to multiplexing since it can allow packing in more loci into one run.

Fluorescently labeled UTPs (fUTP) works on some machines - this means you don't need to buy the labeled primers. The problem is figuring out which matrix on the sequencer works best in reading it. Blue fUTPs worked on ABI 377.

HotStar Taq helps a great deal when multiplexing PCR. It seems to reduce accidental binding between primers.

Alexis Chaine <[chaine@biology.ucsc.edu](mailto:chaine@biology.ucsc.edu)>

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## MDE more evol

## INCREASED EMPHASIS ON THE MOLECULAR EVOLUTION IN THE JOURNAL

### JEZ-Part B: Molecular and Developmental Evolution

While maintaining its commitment to publishing papers from all disciplines contributing to Developmental Evolution, four recent appointments to the editorial board signal an increased emphasis on molecular evolution of developmental genes and molecular phylogenetics. The new appointees are:

Toby Kellog (Missouri State University) Sudhir Kumar (Arizona State University) Mark Martindale (University of Hawaii) Michael Purugganan (University of North Carolina)

All have a strong track record in molecular evolution of developmental genes and will foster submissions in this area.

MDE is an independent part of the Journal of Experimental Zoology, called

Journal of Experimental Zoology Part B: Molecular and Developmental Evolution,

and is published in six issues per year by John Wiley & Sons, Inc.

Currently, the average time to decision is 1.8 months and the time to publication is 3.6 months. Online publication precedes the print edition. MDE is indexed in all major databases independently of the JEZ-Part A.

In addition to speedy publication, we offer our authors one free color page per article.

Please visit our web page at

<http://www.interscience.wiley.com/journal/mde> for further information.

Online manuscript submission is available at:

<http://jez-wiley.manuscriptcentral.com/>

[gunter.wagner@yale.edu](mailto:gunter.wagner@yale.edu)

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## Marine genetic markers

Apologies for cross postings

Dear members

A few years ago (1997) our group posted a query regarding the use of molecular genetic markers in marine fishery management and received some useful responses. We are now compiling a review and need more up to

date information on their use. We are particularly interested in cases where genetic data has influenced a management plan for a particular stock or species. Are you or a colleague using genetics for fisheries and if so for what sort of application? Any help would be greatly appreciated, even if its only a reference to a website, organisation or, of course published materials.

Many thanks Helen

Dr Helen Wilcock Department of Biological Sciences  
Cottingham Road University of Hull Hull HU6 7RX  
U.K. 01482 465542/465536 h.r.wilcock@hull.ac.uk

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## NEON NatIEcolObsNet

NEON - National Ecological Observatory Network - NSF Funding (Other) Through a series of workshops, reports, and planning activities the research community determined that the National Ecological Observatory Network (NEON) should be the new tool: a continent-wide research platform, composed of networked state-of-the-art analytical and communication technologies. NEON will create new collaborative environments, support multi-and inter-disciplinary research, stimulate innovative approaches to information management, develop human capital, and facilitate the integration of research and education across a wide range of the biological, geophysical, engineering and social sciences.

The Directorate for Biological Sciences of the National Science Foundation announces its intention to support the establishment of a NEON Coordinating Consortium (NCC), which will provide the scientific leadership, administration, community participation, and overall governance of NEON and include a NEON Project Office. The latter will initially plan and coordinate activities for NEON, while, ultimately, it will be responsible for the construction and daily management of NEON.

Identification of the goals of NEON must include evolutionary perspective in order for this activity to have its broadest and most effective application. Therefore, involvement of evolutionary biologists at all levels of NEON is exceptionally important as this major funding and research effort gets underway.

The announcement for the NCC competition can be found at <http://www.nsf.gov/pubsys/ods/getpub.cfm?nsf04549>. General inquiries regarding this program should be made to: \* Elizabeth R. Blood, Program Director, Directorate for Biological

Sciences, Division of Biological Infrastructure, 615 N, telephone: (703) 292-8470, email: [eblood@nsf.gov](mailto:eblood@nsf.gov) <<mailto:eblood@nsf.gov>>

“Courtney, Mark W.” <[mcourtne@nsf.gov](mailto:mcourtne@nsf.gov)>

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## Phylogeny markers

hello

I search molecular markers for study phylogeny relationship in the Genus *Viola* (section *Melanium*). In a recent study, the ITS and PCR-RFLP don't be enough polymorph to evaluate the phylogeny relationship. Is this someone know others markers relevant to do this study?

thank you very much for your help

[bizoux.jp@fsagx.ac.be](mailto:bizoux.jp@fsagx.ac.be)

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## Senecioneae material

Subject: A request for Senecioneae material

Dear colleagues,

Joachim Kadereit, Bertil Nordenstam, Linda Watson, and Pieter Pelter have recently started up a project that aims to resolve the intergeneric molecular phylogeny of the tribe Senecioneae (Asteraceae). Initially Joachim Kadereit and Bertil Nordenstam will focus on the Old World representatives of this tribe and Linda Watson and Pieter Pelter will study the New World taxa.

We now ask you to help us to obtain a taxon sampling that covers all (ca. 140) genera in Senecioneae and most subgenera and sections of large genera in this tribe including of course *Senecio*. We are especially interested in obtaining material of type species of the genera in Senecioneae and the various sections of *Senecio*.

You can help us in various ways. For instance by:

- 1) sending us tissue/DNA samples or well preserved herbarium specimens of Senecioneae, 2) providing us with a list of fresh Senecioneae material present in your institute or private collection, or by 3) sending us the contact information of people that might be able to help us.



Material or information can be sent to Pelsers (New World) or Kadereit (Old World).

Please contact any of us if you wish to receive a list of New World or Old World Senecioneae genera or additional information. Of course, we will acknowledge your help and will keep you informed about the progress of this project.

Thanks for your help,

Pieter B. Pelsers Department of Botany, Miami University, 316 Pearson Hall, Oxford OH 45056, USA e-mail: Pelserspb@muohio.edu

Prof. Dr. Joachim Kadereit Institut für Spezielle Botanik und Botanischer Garten, Johannes Gutenberg-Universität Mainz, 55099 Mainz, Germany e-mail: kadereit@mail.uni-mainz.de

Linda E. Watson, Assoc. Professor and Chair Department of Botany, Miami University, 316 Pearson Hall, Oxford OH 45056, USA e-mail: watsonle@muohio.edu

Bertil Nordenstam, Professor emeritus Department of Phanerogamic Botany, Swedish Museum of Natural History, Box 50007, SE-104 05 Stockholm, Sweden e-mail: bertil.nordenstam@nrm.se

Pieter Pelsers <pelserspb@muohio.edu>

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## SocSystBiol Graduate Award

2004 Society of Systematic Biologists Awards for Graduate Student Research

DEADLINE: February 15, 2004

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

and \$2000. Up to six awards will be made.

For full details, please see the web site:

<http://systbiol.org/info/gradaward.html> All application materials should be sent electronically to <sedwards@oeb.harvard.edu> and are due no later than February 15, 2004.

“Scott V. Edwards” <sedwards@fas.harvard.edu>

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## Software DataMonkey PositiveSelection

DATAMONKEY: DETECTING SELECTION ON INDIVIDUAL AMINO ACID SITES

Interested in looking for positive selection in sequence data? Like maximum likelihood, but tired of waiting? Worried about synonymous variation in your dataset? Worry no more!

We are proud to announce the launch of DataMonkey (<http://www.datamonkey.org>), a web-based interface to HyPhy (<http://www.hyphy.org>), a multi-platform, free phylogenetic analysis program.

Our first tool to be made available is a heavily modified and efficiently implemented version of the method of Suzuki and Gojobori (Molecular Biology And Evolution, 1999, 16:1315-1328), which detects positive and negative selection on individual amino acid sites. In brief, the method involves counting the number of non-synonymous and synonymous substitutions that have occurred at each site over its evolutionary history, based on a maximum likelihood ancestral reconstruction obtained using a codon-based substitution model.

Features include:

- \* Fast turnaround of results, e.g. 100 sequences, 100 codons each will run in < 1 minute.
- \* Import of NEXUS, PHYLIP and FASTA formats, with two methods for handling ambiguous codons.
- \* Use of a large number of genetic codes.
- \* Choice of using a user-specified phylogeny or generation of a neighbor-joining tree.
- \* Choice of any underlying reversible nucleotide model, with maximum likelihood estimation of parameters.
- \* Choice of user-supplied or estimated global dN/dS.
- \* Generation of HTML and CSV reports.
- \* User-customizable plots of nonsynonymous and synonymous rate variation.

Currently, analyses are restricted to 100 sequences/ 10 000 codons, but this restriction may be lifted depend-

ing upon level of interest and availability of computer resources.

A preprint describing the method is available on the DataMonkey website. A suite of other approaches to detect positive selection, which take uncertainty in ancestral reconstruction into account, are also described within the preprint, and are implemented within the current build of HyPhy. This research was supported by the National Institutes of Health (grant numbers 5 R01 AI47745 and 5 U01 AI43638 Supp), the University of California Universitywide AIDS Research Program (grant number IS02-SD-701), and by a University of California, San Diego Center for AIDS Research/NIAID Developmental Award to S.D.W.F. (grant no. 2 P30 AI36214).

Sergei L. Kosakovsky Pond & Simon D.W. Frost

“Speed, it seems to me, provides the one genuinely modern pleasure.” Aldous Huxley. “Speed is good only when wisdom leads the way.” from ‘Around The World In 80 Days’, during the film’s prologue (1956).

Department of Pathology University of California, San Diego Antiviral Research Center 150 W. Washington St., Suite 100 San Diego, CA 92103 USA

method 10) New Predefined Genetic Codes.

... and other more features

SYSTEM REQUIREMENTS IBM-Compatible PC Windows 98, NT, 2000, XP Macintosh PowerMac with VirtualPC software emulator Linux using WMWare or Wine emulators.

INPUT Data Files NBRF/PIR MEGA (interleaved and sequential formats) NEXUS (interleaved and sequential formats) FASTA PHYLIP (interleaved and sequential formats)

OUTPUT Windows with text, tables and graphs

AVAILABILITY For academic uses, DnaSP is distributed free of charge.

MORE INFORMATION <http://www.ub.es/dnasp>

REFERENCE Rozas, J., Sánchez-DelBarrio, J. C., Messeguer, X. and Rozas, R. (2003). DnaSP, DNA polymorphism analyses by the coalescent and other methods. *Bioinformatics* 19: 2496-2497.

Julio Rozas

Julio Rozas Departament de Genetica Facultat de Biologia Universitat de Barcelona Diagonal 645 Barcelona 08071 Spain Tel: (34) 93 402 1495 Fax: (34) 93 411 0969 <http://www.ub.es/molevol/julio> <http://www.ub.es/dnasp> <http://www.ub.es/molevol/jrozas@ub.edu>

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## Software DnaSP v4

Announcing DnaSP version 4.0 DnaSP, DNA Sequence Polymorphism, Software J. Rozas, J. C. Sánchez-DelBarrio, X. Messeguer, R. Rozas

DnaSP, DNA Sequence Polymorphism, is a software package for PC-Windows that performs extensive population genetics analyses from DNA sequence data.

MAIN NEW FEATURES IN version 4.0 1) New Interface 2) Possibility to define set of sequences. Store that information in NEXUS files. Analysis in set of sequences 3) Increase the length of the DNA sequence to be analyzed (until ~5 Mb) 4) Extensive Coalescent Simulation analyses 5) Estimation of Gene Flow between and among populations 6) Testing for Genetic Differentiation (Permutation test) 7) Analysis of preferred and unpreferred synonymous codons. Possibility to define synonymous codon preference tables. Store codon preferences information in NEXUS files 8) Estimation of new test statistics (Fay and Wu’s H; Rozas et al.’s ZZ; Ramos-Onsins and Rozas R2; and more). Analysis of Fay and Wu’s H by sliding window 9) Analysis of Pi(a)/Pi(s) and Ka/Ks ratios by the sliding window

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## Software IBD v1 5

The software “IBD” for analyzing (genetic) isolation by (geographic) distance has been updated to version 1.5.

IBD is a fast, simple and specialized package for Mac and Windows that will analyze 1) raw data from diploid/codominant marker data sets (e.g., allozymes, microsatellites) 2) geographic and genetic distance matrices that have been derived using any method

- Like other packages, IBD will test for a statistical association between the distance and geographic matrices using a Mantel Test.

- IBD will also determine the STRENGTH of this relationship by regressing all pairwise genetic similarity values against their corresponding geographic distances, using Reduced Major Axis (RMA) regression.

- Confidence intervals for the regression statistics are calculated using a number of different approaches, some

of which account for the nonindependence of data points.

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Improvements since version 1.2 include:

- A summary of the results is saved in a tab-delimited text file. - Input files can be in matrix format, pairwise lists, or raw data. - The genetic distances M (Slatkin) and  $F/(1-F)$  (Rousset) are calculated from raw data. - Partial Mantel tests can be used to assess partial correlations between genetic distance and two additional matrices.

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IBD is available as shareware from: <http://www.bio.sdsu.edu/pub/andy/IBD.html> A previous version of the software is documented in: Bohonak, A. J. 2002. IBD (Isolation By Distance): A program for analyses of isolation by distance. *Journal of Heredity* 93: 154-155.

and in a manual available with the download.

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Andrew J. Bohonak

Assistant Professor San Diego State University Department of Biology 5500 Campanile Drive San Diego, CA 92182-4614

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Phone: 619-594-0414 Fax: 619-594-5676 Email: bohonak@sciences.sdsu.edu Web: <http://www.bio.sdsu.edu/pub/andy/index.html> Office: 212 Life Science North

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## Spider micros

Does anyone have microsatellites (or know of a reference for microsatellites) for the spiny orb weaver spider (*Micrathena gracilis*). Thank you for your help. Ron Woodruff -

R. C. Woodruff Distinguished Research Professor Editor, GENETICA Department of Biological Sciences Corner Merry and N. College Life Sciences Building Bowling Green State University Bowling Green, Ohio 43403 Telephone: 419-372-0376 Fax: 419-372-2024 email: rwoodru@bgnet.bgsu.edu

Ron Woodruff <rwoodru@bgnet.bgsu.edu>

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## Taxa diversity

I'm getting some revisions done on a paper and I need to find some software that will help me correct my between species estimates of divergence for within-taxa diversity (as in Edwards and Beerli, 2000). Does anyone know of a good software package that can help me out with this? PC-based preferably. Also, able to correct HKY85 distances.

Thanks in advance for the help.

David

David A. Ray, Ph.D. Department of Biological Sciences Louisiana State University 202 Life Sciences Building Baton Rouge, LA 70803

Phone: 225-578-7104 Fax: 225-578-7105 E-mail: daray@lsu.edu <http://batzerlab.lsu.edu/davidweb/-david.htm>

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## UCollegeLondon Wolbachia volunteer

We are studying Wolbachia induced sex ratio distortion in the butterfly *Hypolimnys bolina*, and are looking for a volunteer to help collect and breed *Hypolimnys* butterflies in S.E. Asia for a period of four to eight weeks in spring/summer 2004.

The volunteer would be working alongside a graduate student in the field. We are keen to find a committed individual, with independence, who is prepared to work in basic facilities in tropical field conditions. Excellent basic health and fitness is therefore a prerequisite. Fieldwork experience and a biological/ecological background, would also be welcome. We are happy to contribute towards the fare to S.E. Asia, and also with daily living expenses during the visit.

Please write, with details of background and experience, to Greg Hurst (g.hurst@ucl.ac.uk).

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## Used sequencers

Dear EvoDir Members, I am about to buy used capillary automatic genetic analyser with programs both for sequencing and fragment analysis (STRs). The problem is that I don't have much money but still wish to buy a machine capable to analyse at least 96 samples daily (as far as I know ABl 310 is much slower). I wish to know your opinions about: - which device would be good for STRs but also well-suited to sequencing? - where I should look for used lab equipment? Maybe some of you want to earn that "easy" money ;) - what properties of used stuff are most crucial for it's factual value?

Kind regards

Maciek Konopinski

(Polish PS. polskie oferty sa bardzo mile widziane)

- Institute of Nature Conservation Al. Mickiewicza 33, 31-120 Krakow, POLAND tel. +48-12-6322221 or 6322755 ext. 102, fax. 6322432

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## WGHill award

Bill Hill has been recognized by the British government for his many contributions to quantitative genetics. That he is to receive an OBE (Order of the British Empire) was announced in the 2004 New Year Honours list.

His email address is [w.g.hill@ed.ac.uk](mailto:w.g.hill@ed.ac.uk)

"Bruce S. Weir" <[weir@stat.ncsu.edu](mailto:weir@stat.ncsu.edu)>

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## mtDNA recombination answers

Dear all,

A long time ago, I posted a query regarding how mtDNA recombination would affect the coalescent time

of neutral mutation (would it make mitochondrial Eve younger or older?). I tried to post the answers in the past, but it seems that there was a problem. I am posting it again, because a lot of you got in contact with me asking for the answers.

The topic generated a lot of interest, and I have included a summary of the responses below.

I would like to thank you for sending me your opinions. I think that for this subject it is very difficult to come to a conclusion.

Regards,

Anastasios Tsaousis

— Paper by Shirup and Hein (2001 or 2002) indicates that the coalescent time would be greater. Basically recombination takes the most recent common ancestor and places it in two separate portions of the phylogeny such that these two new ancestors have to have a MRCA even further back in the tree.

Francis Villablanca, Ph.D. — I would like to take this opportunity to suggest a recent paper that appeared in the journal of mathematical biology: "Conditional ancestral times and related properties of an extant mutant at a locus A given the number of segregating sites at a linked locus B." It just might be of interest to you in regard to your question to the EvoDir.

Dr. Paul F. Slade — It should make it older, as it essentially increases the  $N_e$ . There are several good papers out there that discuss this in detail.

Dr. Tina M. Hambuch — It would depend. Recombination with male mtDNA would lead to an underestimate of Eve's age. However, the assumption of a coalescent model would produce younger ages. See Hagelberg, Trends in Genetics, 2003, 19:84-90. Dr. Connie J. Mulligan — Recombination lowers the variance in the time to most recent common ancestor, it does not effect the mean time. Thus, if there is recombination in the mtDNA, the expected time to MRCA is unchanged, but the variance in that estimate is likely to be lower (i.e. the estimate is likely to be better). All this is in the absence of natural selection. If we assume that selection exists, all bets are off.

David J. Cutler, Ph. D. — The short answer is that the genealogy will vary along the sequence, so that there is no single most recent common ancestor for the sequence as a whole. The distribution of the neutral coalescent at single sites will be uninfluenced by recombination, but the genealogies at different sites will represent correlated draws from this distribution. As for biased estimation of coalescent times using recombinant sequences, that will depend on the estimator used. One

discussion of these matters is given in the following reference: Schierup, MH and Hein, J. 2000. Consequences of recombination on traditional phylogenetic analysis. *Genetics* 156: 879-891. In general, the estimators are complicated non-linear functionals of the data so that analytical results are very difficult to obtain. However, it is relatively easy to simulate sequences using a coalescent process with recombination and then numerically determine the bias for any particular estimator. A complicating issue is that population structure can either mask or enhance the effects of recombination on the apparent phylogeny. For example, if the rate of coalescence within populations is much greater than the migration rate between populations, then the tree may decompose into well-defined nets corresponding to distinct populations. Provided that there is a unique ancestral population, the effect of recombination on estimates of the time to the most recent common ancestor will be limited to recombination events which occur in the basal portion of the genealogy. If the coalescent time is dominated by the time required for all of the sequences to have ancestors in this one population, then the bias due

to recombination will be reduced relative to the panmictic case. Of course, one can also construct scenarios in which the bias is greater than would be expected under panmixis. Dr. Jay Taylor — If there is recombination mitochondrial Eve does not exist, but of course Eve, our most recent common ancestor does. Recombination will mean that we have underestimated the age of Eve - see attached paper in which this is explained in some detail.

Dr. A.C. Eyre-Walker

— Mikkel Schierup has done some work on the effect of ignoring recombination in HIV: [http://www.birc.dk/Publications/Articles/Schierup\\_2002a.pdf](http://www.birc.dk/Publications/Articles/Schierup_2002a.pdf) This suggests that ignoring recombination will tend to cause an overestimation of the date of MRCA.

Dr. Andrew Rambaut —

— / —

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

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## PostDocs

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## Atlanta SocialInsects

### POSTDOCTORAL POSITION IN SOCIAL INSECT BIOLOGY

A full-time Postdoctoral Research position is available to pursue a variety of potential studies in social insect biology. Candidates with interests in social insect genomics, population structure, hybridization, development, behavior, or evolution are encouraged to apply.

Position is available immediately and the starting date is flexible. Funding is for at least two years and starting salary will be commensurate with experience. Applicants should have a Ph.D. in genetics, genomics, behavior, entomology, evolution or a related field and have demonstrated research excellence.

Interested applicants should send CV, names and e-mail addresses for three references, and a one-page letter of interest including a proposed start date to michael.goodisman@biology.gatech.edu. Alternatively, applications can be sent to Michael A D Goodisman, Assistant Professor, School of Biology, The Georgia Institute of Technology, 310 Ferst Drive, Atlanta, GA 30332-0230, United States. For additional information visit <http://www.biology.gatech.edu/professors/goodisman.html> or send an e-mail to the application address.

Michael A D Goodisman Assistant Professor School of Biology The Georgia Institute of Technology Cherry Emerson Bldg A110 310 Ferst Drive Atlanta, GA 30332-0230 United States

webpage: <http://www.biology.gatech.edu/professors/goodisman.html> email:  
michael.goodisman@biology.gatech.edu office: 404-385-6311 lab: 404-385-6312 fax: 404-894-0519

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## Barcelona HumanGenomics

Human Genomics Postdoc in Barcelona

A 3-year postdoctoral position in human evolutionary genomics is available immediately in the Evolutionary Biology Group in the Universitat Pompeu Fabra in Barcelona, Spain.

This position is associated with a collaborative project

to examine the role of segmental duplications in neurodevelopmental, neurological and behavioral disorders and involves the study of a wide variety of evolutionary questions concerning genome duplications and chromosomal rearrangements.

Candidates should have a PhD and, ideally, some post-doctoral experience in population genomics. A strong background in molecular biology and molecular evolution techniques is required. We are looking for a highly motivated individual who is willing to join a research group that studies genomic variation at both the intraspecific and interspecific levels in hominids. The group is based in the PRBB (Biomedical Research Park of Barcelona, <http://www.prbb.org/>), where opportunities for scientific interaction are plentiful.

Motivated and potentially competitive applicants should send a short letter of interest and CV to the address below.

Dr. Arcadi Navarro Unitat de Biologia Evolutiva Departament de Ciències Experimentals i de la Salut Universitat Pompeu Fabra Doctor Aiguader 80 08003 Barcelona, Spain Phone: 00 34 93 5422841 Fax: 00 34 93 5422802 E-mail: arcadi.navarro@upf.edu

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## DalhousieU ProtistPhylogenetics

### POST DOCTORAL POSITION: PROTIST PHYLOGENETICS

A two-year post-doctoral position in the phylogenetics and molecular evolution of protistan eukaryotes is available immediately, at Dalhousie University, Canada. The successful applicant will work on collaborative research involving the laboratories of Alastair Simpson (Dept. Biology) and Andrew Roger (Dept. Biochemistry), through the Canadian Institute for Advanced Research (CIAR) Program in Evolutionary Biology. See below for some relevant publications.

Applicants will need extensive research experience with laboratory molecular biology and with molecular phylogenetics, as well as an established professional interest in protozoa/protists. They will have a strong publication record in international journals.

The successful applicant will have the opportunity to interact with world-class phylogenomicists and bioinformaticians at Dalhousie University involved in the CIAR Program and Genome Atlantic. Dalhousie University is the premier research university in maritime

Canada, and was judged the best institution outside the US for postdoctoral researchers in a recent survey (The Scientist magazine).

Please send a C.V. and contact details for two references to:

Alastair Simpson Department of Biology, Dalhousie University, Halifax, B3H 4J1, N.S., Canada Fax: 1 902 494 3736 Email: [asimpo2@dal.ca](mailto:asimpo2@dal.ca).

by Feb 6th. 2004

Some Relevant Publications:

SIMPSON, A.G.B. and ROGER, A.J. (2004) Protein phylogenies robustly resolve the deep-level relationships within Euglenozoa. *Molecular Phylogenetics and Evolution* 30: 201-212

SIMPSON, A.G.B. MacQuarrie, E.K., and ROGER, A.J. (2002) Early origin of canonical introns. *Nature* 419: 270

SIMPSON, A.G.B. and ROGER, A.J. (2002) Eukaryotic evolution: Getting to the root of the problem. *Current Biology* 12: 691-693.

SIMPSON, A.G.B., ROGER A.J. et al. (2002) Evolutionary history of early diverging eukaryotes: The excavate taxon *Carpediemonas* is closely related to *Giardia*. *Molecular Biology and Evolution* 19: 1782-1791.

Baldauf, S.L., ROGER, A.J., Wenk-Siefert, I and Doolittle, W.F. (2000) A kingdom level phylogeny of eukaryotes based on combined protein data. *Science* 290, 972-977.

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Alastair G.B. Simpson, PhD Assistant Professor, Department of Biology, Dalhousie University Canadian Institute for Advanced Research (Program in Evolutionary Biology)

Department of Biology Life Sciences Centre, 1355 Oxford St, Halifax, Nova Scotia, B3H 4J1, Canada

Phone: 902 494 1247 (Country code 1) Fax: 902 494 3736 (Country code 1) Email: [asimpo2@dal.ca](mailto:asimpo2@dal.ca)

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[asimpo2 <asimpo2@dal.ca>](mailto:asimpo2@dal.ca)

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**DalhousieU StatEvolBioinformatics**

Postdoctoral position in statistical and evolutionary

bioinformatics/phylogenetics.

We are seeking a postdoctoral candidate with training and/or experience in statistical/mathematical modeling to join a collaborative group at Dalhousie University in Halifax, Nova Scotia funded by Genome Atlantic, one of five Genome centres in Canada and sponsored by the Canadian Institute for Advanced Research, Program in Evolutionary Biology. The postdoctoral position would be funded for 2 years, starting in March 2004, with the possibility of an additional year, at a salary commensurate with qualifications and experience.

The successful candidate would join ongoing research projects in the general areas of modeling genome and proteome evolution at the most ancient levels of divergence (i.e. at the prokaryotic/eukaryotic split). Specific interests include developing phylogenetic methods and software tools that incorporate lateral gene transfer as a process, more accurate models of protein evolution that account for covarion, rate-shift and 3D structural effects and site-specific amino acid frequencies, developing methods for phylogenetic inference from multiple gene sets and developing methods for estimating confidence intervals for phylogenies.

Candidates with strong programming skills and a background in statistical modeling, statistical genetics or molecular systematics are desired. The successful candidate will be situated in the Mathematics and Statistics Department but will have the opportunity to work closely with a vibrant collaborative group of statisticians, genomicists, and bioinformaticians from the Department of Mathematics and Statistics (Ed Susko and Chris Field), Department of Biochemistry and Molecular Biology (Andrew Roger and W. Ford Doolittle) Department of Biology (Joe Bielawski) and the Faculty of Computer Science at Dalhousie University (Christian Blouin).

A flavour of the research interests of the group can be gleaned from the following publications:

Susko, E., Field, C., Blouin, C. and Roger, A.J. (2003). Estimation of rates-across-sites distributions in phylogenetic substitution models. *Systematic Biology*, 52, 594-603.

Inagaki, Y., Blouin, C., Susko, E. and Roger A.J. (2003). Assessing functional divergence of EF-1alpha and its paralogues in eukaryotes and archaeobacteria. *Nucleic Acids Research*, 31, 4227-4237.

Susko, E. (2003). Confidence regions and hypothesis tests for topologies using generalized least squares. *Molecular Biology and Evolution*, 20:862-868.

Blouin, C., Boucher, Y and Roger, A.J. (2003) Inferring

functional constraints and divergence in protein families using 3D mapping of phylogenetic information. *Nucl. Acids Research* 31:790-797

Susko E., Inagaki, Y., Field, C., Holder, M.E. and Roger, A.J. (2002) Testing for differences in rates-across-sites distributions in phylogenetic subtrees *Mol. Biol. Evol.* 19:1514-1523

Archibald, J.M. and Roger, A.J. (2002) Gene conversion and the evolution of euryarchaeal chaperonins: a maximum likelihood-based method for detecting conflicting phylogenetic signals. *J Mol Evol.* 55:232-245

Interested candidates should send letter of application, a CV (including a list of publications) and a list of references to the address below.

Dr. Edward Susko Department of Mathematics and Statistics Chase Building Dalhousie University Halifax, Nova Scotia B3H 3J5 susko@mathstat.dal.ca

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### FSUJena PlantEvoDevo

POSTDOC POSITION at the GENETICS CHAIR, FSU JENA, GERMANY (two years with the possibility for prolongation)

The candidate should have a phd degree in biology or a related field and a strong interest in basic research in evolutionary developmental biology of plants. Research experience in molecular biological techniques is essential, a background in plant molecular biology, bioinformatics, evolutionary or developmental biology is preferable.

Our group studies the connection between the evolution of MADS box genes and the origin of evolutionary novelties in plants (see Winter et al. 1999, *PNAS* 96:7342-7347; Theissen et al., 2000, *Plant. Mol. Biol.* 42, 115-149). Current research topics focus on the function of MADS box genes in phylogenetically informative taxa, the evolution of MADS protein interactions and the evolutionary role of floral homeotic mutants.

The position is obliged with undergraduate teaching in the range of approx. 4 hours per week. The vacancy is available from 1 April 2004 onwards; candidates will be considered until the position is filled. Knowledge of German language would be an advantage.

Requests and complete application documents to: Prof. Guenter Theissen; FSU Jena, Lehrstuhl für Genetik, Philosophenweg 12, D-07743 Jena; Tel.

+49-3641-949550 <http://www2.uni-jena.de/biologie/-genetik/index.htm>

Kerstin Kaufmann <kerstin.kaufmann@uni-jena.de>

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### FloridaStateU FlyWings

Postdoc: Relationship of variation to evolution in fly wings A Postdoctoral Research position is available in David Houle's laboratory at Florida State University to study the relationship between mutational, genetic and among species variation, using wings of flies in the family Drosophilidae as a model system. Applicants should have interests in large issues such as the relationship between genotype and phenotype, between structure and function, and the role of constraints in evolution. Successful applicants will have expertise in one or more of the following areas: developmental genetics, quantitative genetics, multivariate statistics or population/evolutionary genetics. In addition, programming expertise would be very welcome. The position is available immediately, although it could start as late as summer 2004. Funding is for up to three years with a salary of \$28,000-\$30,000 per year depending on experience. For more detail on the fly wing system, see <<http://http://www.biomedcentral.com/1471-2148/3/25>>Houle<<http://http://www.biomedcentral.com/1471-2148/3/25>> et al. 2003 *BMC Evolutionary Biology* 3:25. For more information about the Houle lab, see <http://bio.fsu.edu/~dhoule/>. To apply, contact David Houle (dhoule@bio.fsu.edu) with a letter detailing your expertise and interest in the position, a Curriculum Vitae and the names of three references that we may contact.

Florida State University has a dynamic and expanding group of 20 ecologists and evolutionary biologists, including recent hires Dave Swofford, Gavin Naylor and Peter Beerli. The atmosphere is both collegial and interactive. For more information, see the Ecology and Evolution group's web site . Tallahassee is a great place to live because of its modest size, warm weather, and the many opportunities the surrounding area offers for outdoor recreation.

Technician. Thomas Hansen and David Houle are seeking to hire a technician to run a large set of artificial selection experiments using *Drosophila melanogaster* wings as a model system. The person hired will be expected to care for fly stocks, manage the undergraduate assistants involved with this project, and to curate

the data produced in the experiment. Consequently the following would be helpful (although not required): experience with *Drosophila* maintenance and genetics, experience managing part-time employees, and experience with computers. The position is available Feb. 1, 2004. Salary will be between \$20,000 and \$24,000, depending on experience, and will continue for up to three years. The ideas behind this project can be discerned in the Hansen and Houle paper available from the Houle website; the experimental system is described in the BMC Evolutionary Biology paper linked above. To apply, contact David Houle (dhoule@bio.fsu.edu) with a letter detailing your expertise and interest in the position, a Curriculum Vitae and the names of three references that may be contacted concerning past work experience.

David Houle

Phone: 850-645-0388 FAX: 850-644-9829 <http://bio.fsu.edu/~dhoule/> Department of Biological Science Florida State University Tallahassee, FL 32306-1100

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## Granada ParasiticChromosomes

Dear colleagues,

My research group is looking for a post-doctoral candidate who has recently (within the last 3 years) finished his/her (PhD) thesis, and who is interested in applying for a Juan de la Cierva postdoctoral grant to join our project BOS2003-06635 entitled Parasitic chromosomes: cellular effects and molecular changes associated to the genetic conflict with A chromosomes. If funded, the grant provides support for 3 years, with a salary of approximately 24000 per annum. The main task of this project will be the development of molecular markers in the grasshopper *Eyprepocnemis plorans*, followed by their use in the detection of loci in the standard chromosomes which might be associated with resistance to parasitic chromosomes. Interested people should contact Juan Pedro M. Camacho (e-mail: [jpmcamac@ugr.es](mailto:jpmcamac@ugr.es)), and should provide both CV and a description of their research experience. Best wishes,

Juan Pedro M. Camacho Departamento de Genética Universidad de Granada 18071 Granada Spain E-mail: [jpmcamac@ugr.es](mailto:jpmcamac@ugr.es) web: <http://www.ugr.es/~cvi165/> <http://darwin.ugr.es/bpo>

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## HarvardU SpeciationGenetics

Postdoctoral in speciation genetics

Applications are invited for a postdoctoral position in molecular evolution in the laboratory of Daniel L. Hartl at Harvard University (<http://www.oeb.harvard.edu/~hartl/lab/>). We are particularly interested in applicants with strong experience in molecular genetics, especially in *Drosophila*, augmented by some experience in bioinformatics. The successful candidate will join a group led by Dr. Yun Tao working on the identification and characterization of genes associated with reproductive isolation between *Drosophila simulans* and *D. mauritiana* [PNAS 98: 13183-13188 (2001); Genetics 164: 1383-1397 (2003); Genetics 164: 1399-1418 (2003) and Evolution 57: 2580-2598 (2003)]. This group has developed an efficient method for identifying the relevant genes and has already identified two. Our goal is to identify additional genes implicated in reproductive isolation and to carry out a functional analysis of these genes. Candidates should email their CV and names of three references to Daniel L. Hartl ([dhartl@oeb.harvard.edu](mailto:dhartl@oeb.harvard.edu)). Harvard University is an equal opportunity/affirmative action employer.

Daniel Hartl <[dhartl@oeb.harvard.edu](mailto:dhartl@oeb.harvard.edu)>

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## IndianaU Acacia

Postdoctoral Position - Pollination Biology of African Acacias

A 2-4-year position is available to study the effect of competition for pollination on anther dehiscence time in East African acacia tree communities. Tentative starting date for the position is 1 May 2004. Application should be received by 14 February 2004.

The research will include analyses of phenotypic selection, mating systems, and pollen gene flow, as well as experiments into competition through pollinator preference and heterospecific pollen transfer. The project will be conducted within the context of ongoing studies by several collaborators into community-level pollination ecology, pollination webs, and ant/pollinator

interactions. Significant opportunities will exist for the development of independent projects and for the mentoring of undergraduate researchers. The position will be based at the PI's home institution (Indiana University South Bend), but 4-6 months of each year will be spent in Kenya (Mpala Research Centre - see [www.nasm.edu/ceps/mpala/main.html](http://www.nasm.edu/ceps/mpala/main.html)).

Candidates must have a strong background in ecological and evolutionary field research and must be able to work independently in Kenya for extended periods each year. Research experience in molecular biological techniques is also highly desirable. To apply, send a letter of application, a CV, and a list of 3 references to Andrew Schnabel ([aschnabe@iusb.edu](mailto:aschnabe@iusb.edu)), Department of Biological Sciences, Indiana University South Bend, South Bend, IN 46634.

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### IndianaU Acacias

#### POSTDOCTORAL POSITION – POLLINATION BIOLOGY OF AFRICAN ACACIAS

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Candidates must have a strong background in ecological and evolutionary field research and be able to work independently in Kenya for extended periods each year. Research experience in molecular biological techniques is also highly desirable. To apply, send a letter of application, a CV, and contact information for 2 references to Andrew Schnabel ([aschnabe@iusb.edu](mailto:aschnabe@iusb.edu)), Department of Biological Sciences, Indiana University South Bend,

South Bend, IN 46634. – Andrew Schnabel Associate Professor of Ecology and Evolution Department of Biological Sciences Indiana University South Bend South Bend IN 46634-7111 574-237-4413 (office) 574-237-6589 (FAX) [aschnabe@iusb.edu](mailto:aschnabe@iusb.edu) [aschnabe@iusb.edu](mailto:aschnabe@iusb.edu)

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### IndianaU IntronEvol

#### POSTDOCTORAL POSITION – EVOLUTION OF INTRONS

A three-year position is available to perform bioinformatic studies on issues related to the evolution of introns in the protein-coding genes of eukaryotes. Drawing largely from the information in whole-genome sequences, the various projects will include studies of the rate of birth and loss of introns in discrete phylogenetic lineages, the mechanisms of intron birth, the evolution of the components of the spliceosome, and the evolution of various transcript-processing mechanisms such as the exon-junction complex and nonsense-mediated decay. Candidates must have a strong background in bioinformatic methodology, and good familiarity with molecular biology and evolution is highly desirable. Mathematical and/or statistical skills would also be helpful. The position will be held in a lab that is currently investigating a wide range of issues in genome evolution at the empirical and theoretical levels. If interested, please contact: Michael Lynch ([mlynch@bio.indiana.edu](mailto:mlynch@bio.indiana.edu)), Department of Biology, Indiana University, Bloomington, IN 47405.

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 Michael Lynch [mlynch@bio.indiana.edu](mailto:mlynch@bio.indiana.edu) Dept. of Biology Phone: 812-855-7384 Indiana University FAX: 812-855-6705 Bloomington, IN 47405

Lab Research: <http://www.bio.indiana.edu/facultyresearch/faculty/Lynch.html> IU Biology: <http://www.bio.indiana.edu/> NSF Training Grant in Evolution, Development, and Genomics: <http://evodevo.uoregon.edu/> Daphnia Genome Consortium: <http://daphnia.cgb.indiana.edu/>

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### MonashU ClimaticStress



Dear EvolDir member,

If you, or any of your students/colleagues, are interested in the following position we are happy to supply further details.

**POSTDOCTORAL POSITION** Molecular population and quantitative genetics: identifying genes underlying adaptive responses to climatic stress

Centre for Environmental Stress and Adaptation Research Monash University and La Trobe University

The Centre for Environmental Stress and Adaptation Research (CESAR) is a prestigious Special Research Centre, funded by the Australian Research Committee, examining the ways that organisms adapt to environmental stresses. The climatic adaptation program of CESAR currently requires a molecular population biologist with experience in microsatellites and other DNA markers to undertake experiments aimed at isolating genes involved in climatic stress resistance in natural populations using *Drosophila* as a model system. The research is aimed at identifying genes contributing to differences between temperate and tropical natural populations using a combination of clinal analysis, candidate gene identification, QLT mapping in selected lines and microarraying. This is an excellent opportunity to join a well resourced and world leading research team that is helping to understand the ways organisms can evolve to cope with global climatic change.

For further details, please contact Assoc. Prof. Steve McKechnie (61 3 9905 3863; [stephen.mckechnie@sci.monash.edu.au](mailto:stephen.mckechnie@sci.monash.edu.au)) or Prof Ary Hoffmann 61 3 9479 2769; [A.Hoffmann@latrobe.edu.au](mailto:A.Hoffmann@latrobe.edu.au)). Expressions of interest/applications by the end of February please.

Cheers, Steve [stephen.mckechnie@sci.monash.edu.au](mailto:stephen.mckechnie@sci.monash.edu.au)  
[stephen.mckechnie@sci.monash.edu.au](mailto:stephen.mckechnie@sci.monash.edu.au)

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## NCStateU FlyMolSyst

Postdoctoral Position

Molecular Systematics of Flies

A postdoctoral position is available in the lab of Brian Wiegmann to study molecular phylogenetics of the insect order Diptera as part of a National Science Foundation funded Assembling the Tree of Life project. The successful candidate will contribute to large-scale DNA sequencing efforts and will conduct phylogenetic and

molecular evolutionary analyses to assess higher-level evolutionary relationships among flies. Experience in insect molecular systematics is desirable. The position duration is 2 years.

The position requires a person with a Ph.D. in entomology, biology, zoology or other related field. Desired qualifications would include laboratory experience in molecular systematics. Experience and previous publication record using phylogenetic and molecular evolutionary analyses of sequence data are desired. This position can begin as early as March 1, 2004, but can be delayed for the right person.

Send a letter of application, statement of research interests, curriculum vitae, and names of three references to:

Brian M. Wiegmann Department of Entomology Box 7613 North Carolina State University Raleigh NC 27695  
email: [bwiegman@unity.ncsu.edu](mailto:bwiegman@unity.ncsu.edu)

Deadline for applications: February 20, 2004.

AA/EOE. ADA Accommodations: Dr. Brian Wiegmann [brian\\_wiegmann@ncsu.edu](mailto:brian_wiegmann@ncsu.edu) 919-515-1653. In addition, NC State welcomes all persons without regard to sexual orientation.

Brian M. Wiegmann Associate Professor Department of Entomology Box 7613 North Carolina State University Raleigh NC 27695

phone: 919-515-1653 fax: 919-515-7746 email: [bwiegman@unity.ncsu.edu](mailto:bwiegman@unity.ncsu.edu)

Wiegmann <[bwiegman@unity.ncsu.edu](mailto:bwiegman@unity.ncsu.edu)>

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## OhioStateU ConservationGenetics

Postdoctoral Fellowship in Conservation Genetics in the lab of Dr. H. Lisle Gibbs, Department of Evolution, Ecology and Organismal Biology, Ohio State University. I am seeking a highly motivated student with a demonstrated ability to work independently for a lab-based project that will use microsatellite DNA markers to determine the stock identity of harvested samples of Canada Geese from Ohio. This position, funded by the Ohio Department of Natural Resources, is initially for one year with strong likelihood of renewal for an additional year pending satisfactory performance and availability of funding. Start date of position is 1 July 2004 or as soon after as possible. Salary is competitive and includes full benefits. Candidates must have prior

experience with DNA-based genetic analysis including experience in using a wide range of software packages for data analyses. They must also be willing to work closely with ODNR personnel to coordinate sample collection and analyses and direct lab technicians in the collection of data. Individual will join an active lab group pursuing a variety of research projects in the area of conservation genetics/molecular ecology (see <http://www.biosci.ohio-state.edu/~eeob/faculty/gibbs.html>). Applicants should send a letter of interest including a description of research experience, CV and contact information for 3 references to Dr. H. LISLE GIBBS, Department of Evolution, Ecology and Organismal Biology, 318 W. 12th Ave. Ohio State University, Columbus OH 43210-1293 (EM: gibbs.128@osu.edu; PH: 614 688 3861). Review of applicants will begin 1 April 2004 and will continue until a suitable candidate is identified. – H. Lisle Gibbs Associate Professor Department of Evolution, Ecology and Organismal Biology Ohio State University 300 Aronoff Laboratory 318 W. 12th Ave. Columbus, OH 43210-1293

Tel: 614-688-3861, Fax: 614-292-2030 email: gibbs.128@osu.edu <http://www.biosci.ohio-state.edu/~eeob/gibbs/index.html>

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## PIMS MathSciences

PIMS Postdoctoral Fellowships, Call for Nominations.

The Pacific Institute for the Mathematical Sciences (PIMS) invites applications for Postdoctoral Fellowships from outstanding young researchers in the mathematical sciences for the year 2004-2005. Applicants must be nominated by one or more scientists affiliated with PIMS or by a Department (or Departments) affiliated with PIMS. The fellowships are intended to supplement support made available through such a sponsor. The Institute expects to support up to 20 fellowships tenable at any of its Canadian member universities: Simon Fraser University, the University of Alberta, the University of British Columbia, the University of Calgary, and the University of Victoria, as well as the affiliated universities: the University of Northern British Columbia and the University of Lethbridge. For the 2004-2005 competition, the amount of the award is \$20,000 and the sponsor(s) is (are) required to provide additional funds to finance a minimum stipend of \$40,000 (including benefits). Award decisions are made by the PIMS PDF Review Panel based on excellence of the candidate, potential for participation in PIMS pro-

grams and potential for involvement with PIMS partners. PIMS Postdoctoral Fellows will be expected to participate in all PIMS activities related to the Fellow's area of expertise and will be encouraged to spend time at other sites. To ensure that PIMS Postdoctoral Fellows are able to participate fully in Institute activities, they may not teach more than one single-term course per year. Applicants must have a Ph.D. or equivalent (or expect to receive a Ph.D. by December 31 2004) and must have received their Ph.D. after January 1, 2001. The fellowship may be taken up at any time between April 1, 2004 and January 1, 2005. The fellowship is for one year and is renewable for a maximum of one additional year. Applications should include curriculum vitae, statement of research interests, three letters of reference (including one from a sponsoring scientist), and statement of anticipated support from the sponsor. Nominations must be received by February 6, 2004.

For further information please see the Web page at <http://www.pims.math.ca/opportunities/pdf.html>

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## QueensU MathEvolEcol

3 yr Coleman Postdoctoral Fellowship in Mathematical Evolutionary Ecology.

Applications are sought from outstanding researchers for a 3year position as a Coleman Postdoctoral Fellow in mathematical evolutionary ecology in the labs of Dr. Peter Taylor and/or Dr. Troy Day. Potential research projects include epidemiological modeling (including the evolution of virulence and host/parasite interactions), the evolution of senescence, multilevel selection and kin selection, the evolutionary consequences of genetic and/or sexual conflict, and the effects of spatial population structure on evolutionary dynamics. Successful applicants will be free to conduct research in any of these or other related areas of interest. For more information on research topics see: [www.mast.queensu.ca/~tday](http://www.mast.queensu.ca/~tday) and [www.mast.queensu.ca/~peter](http://www.mast.queensu.ca/~peter). Information about the Department of Mathematics and Statistics and Queen's University can be found at [www.mast.queensu.ca](http://www.mast.queensu.ca) and [www.mast.queensu.ca](http://www.mast.queensu.ca) respectively.

To apply, send a current CV and statement of research interests Dr. Troy Day, Dept. of Mathematics and Statistics, Queen's University, Kingston, ON, K7L 3N6, Canada (email applications are also acceptable; send to [tday@mast.queensu.ca](mailto:tday@mast.queensu.ca)). Applications

should be postmarked by Feb. 28, 2004. – Troy Day  
 Departments of Mathematics & Biology Jeffery Hall  
 Queen's University Kingston, ON, K7L 3N6, Canada  
 tday@mast.queensu.ca Phone: 613-533-2431 Fax: 613-  
 533-2964 <http://www.mast.queensu.ca/~tday/> <http://www.mast.queensu.ca/~tday/>

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### RiceU EvolBiol

EVOLUTIONARY BIOLOGIST. The Ecology and Evolutionary Biology Department at Rice University (<http://www.ruf.rice.edu/~eeb/> <<http://www.ruf.rice.edu/%7Eeeb/>>) seeks to fill a HUXLEY POSTDOCTORAL /TEACHING FELLOWSHIP. This is a 2-year appointment for a recent Ph.D. for research and teaching. The teaching component is expected to be one upper-level undergraduate course per year. Preference will be given to candidates who will work collaboratively with the other faculty in the department. Applications, including curriculum vitae, a summary of research interests, and three letters of reference, should be sent to: Huxley Fellowship Search Committee, Department of Ecology and Evolutionary Biology MS-170, Rice University, P.O. Box 1892, Houston TX 77251 - 1892. Review of applications will commence on January 30, 2004. Rice University is an Equal Opportunity/Affirmative Action Employer. \*\*\*

– Lisa Marie Meffert Department of Ecology and Evolutionary Biology Rice University - MS 170 P.O. Box 1892 Houston, TX 77251-1892

Phone: 713-348-2564 (office) 713-348-2569 (lab) Fax: 713-348-5232 E-mail: [lmeffert@rice.edu](mailto:lmeffert@rice.edu)

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### Spain MolEvol

Postdoctoral position in Spain: models of protein evolution in mitochondrial genomes

A two-year postdoctoral position is available to work in the statistical selection of models of protein evolution and in the study of mitochondrial protein evolution in vertebrates, with David Posada (University of Vigo, Spain) and Rafael Zardoya (National Museum of Natural Sciences, Spain).

This position is funded by the BBVA Foundation (Spain). The ideal starting date would be between April and September 2004. The successful candidate will work between Vigo and Madrid. Salary, including benefits, will be 24,000 – 30,000 EUR, commensurate with experience. Information about our labs can be found in <http://darwin.uvigo.es> (D. Posada) and <http://161.111.10.54/investigacion/bbe-zardoya/primer.htm> (R. Zardoya).

Ideal candidates will have strong programming skills (Java, Perl, C++, C) and a background in mathematical statistics. Some background and experience in bioinformatics and/or evolutionary biology is highly desirable. We seek individuals who are independent and motivated.

Deadline for applications is March 31. These should include a CV, a letter of intent, and contact information for two referees, and should be sent to David Posada <[dposada@uvigo.es](mailto:dposada@uvigo.es)> and Rafael Zardoya <[rafaz@mncn.csic.es](mailto:rafaz@mncn.csic.es)>.

Best wishes,

David.

– David Posada Departamento de Bioquímica, Genética e Inmunología Facultad de Ciencias Universidad de Vigo Vigo 36200, 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)

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### StonyBrook EvolEcol

As part of establishing a new laboratory at SUNY-Stony Brook beginning in August 2004, I am looking for a post-doctoral associate to work on open-ended projects concerning plant evolutionary ecology. The appointment will be for two years, starting during the summer or early fall of 2004. The research project can be agreed upon with the chosen candidate, but preference will be given to projects concerning natural selection and/or quantitative genetic constraints on plant adaptation.

For more information about the lab, see [www.genotypebyenvironment.org](http://www.genotypebyenvironment.org). For more on Stony Brook's Ecology & Evolution department, see <http://life.bio.sunysb.edu/ee/> The town of Stony Brook is a small community located on the north central shore of Long Island. The area is wooded, with a gently rolling topography. To the west, downtown

Manhattan is 90 minutes away by car or commuter train; the two eastern Forks of Long Island are about 90 minutes (Orient Point) and two hour's (Montauk Point) drive in the opposite direction. Bridgeport, Connecticut, is a little over an hour away by ferry across Long Island Sound.

If interested, please contact Massimo Pigliucci at [pi@genotypebyenvironment.org](mailto:pi@genotypebyenvironment.org).

~~~ Massimo Pigliucci, Professor Exec. VP, Society for the Study of Evolution Depts. of Botany and of Ecology & Evol. Biology University of Tennessee, Knoxville, TN 37996-1100 phone 865-974-6221, fax 2258

[www.genotypebyenvironment.org](http://www.genotypebyenvironment.org) "All observation must be for or against some view if it is to be of any service." -Charles Darwin -Charles Darwin

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## UAngers Dispersal

Postdoctoral Research Assistant - Laboratory of Animal Ecology, University of Angers (France).

Influence of environmental stability and predictability on the evolution of dispersal and mating strategies in hydrosystems.

There is an opportunity of a 12-month post-doctoral position (EU 6th Framework) in the laboratory of animal ecology in Angers (France). Evolutionary ecology of vertebrates (amphibians, birds, mustelids) in hydrosystems is the main research topic of the laboratory (<http://sciences.univ-angers.fr/-ecologie/animalecology.html>). We are looking for a researcher with experience in the field of modelling the evolution of life history traits. The project aims at building a predictive model on the evolution of alternative mating strategies (monogamy, polygyny, polyandry) in relation to environmental stability and predictability. The work has to take into account hydrosystem specificities and to provide explicit theoretical predictions which can be tested empirically or experimentally on vertebrates. The candidate is fully part of the application. The funding of the final project is conditional to acceptance by the university scientific committee. The deadline for candidate application is February 5th 2004. The position starts in September 2004. The position is applicable to all EU members but French. The applicant should have not been resident in France for the last 3 years. Please send a CV and a list of publications by e-mail only.

Contact: Pr. Thierry LODE Laboratoire d'Ecologie Animale Faculté des Sciences Université d'Angers Campus de Belle-Beille 2 bd Lavoisier F-49045 Angers France e-mail: [thierry.lode@univ-angers.fr](mailto:thierry.lode@univ-angers.fr)

Jean Secondi <[jean.secondi@univ-angers.fr](mailto:jean.secondi@univ-angers.fr)>

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## UArizona InsectEvolution

Research Associate Center for Insect Science University of Arizona

Postdoctoral Excellence in Research and Teaching (PERT) offers up to three years of support to outstanding candidates seeking advanced research training in insect science and preparation for the additional demands of an academic career. PERT trainees may select from among over thirty-five faculty research mentors representing a broad range of insect science disciplines: genetics, biochemistry, neurobiology, ecology, evolutionary biology, molecular/cellular biology, entomology, physiology and behavior. Funded through the NIH, the starting salary will be based on the NIH NRSA scale for years of postdoctoral experience, with an annual allowance of \$5,000 for research supplies and \$1,000 for travel. Each trainee will have exclusive use of a laptop computer. Applicants must have a Ph.D. in a related field and must be U.S. citizens or permanent residents. Applicants should have no more than four previous years of postdoctoral experience. Additional information about the Center for Insect Science and the PERT program is available at <http://cis.arl.arizona.edu/PERT>. To apply, please submit a letter of application that includes a statement explaining how the PERT program will assist the applicant in his/her career goals, a CV, three letters of reference, a two to three page research proposal developed with the intended CIS research mentor describing the project to be undertaken during the training period, and a letter of support from the intended CIS research mentor to: PERT, Center for Insect Science, P.O. Box 210106, University of Arizona, Tucson, AZ 85721-0106. Review of applications will begin February 27, 2004 for appointments beginning August 1, 2004 and will continue until positions are filled. The University of Arizona is an EEO/AA Employer -M/W/D/V. Please contact Teresa Kudrna, [tkudrna@email.arizona.edu](mailto:tkudrna@email.arizona.edu), 520-621-4923, for further information.

Teresa Kudrna Administrative Assistant Center for Insect Science University of Arizona 1007 E. Lowell Street

P.O. Box 210106 Tucson, AZ 85721-0106 (520) 621-4923  
 FAX: (520) 621-2590

58th Street Chicago, IL 60637 Ph. (773)834-1037  
 FAX (773)834-0505 Ph. (773)834-5239 (lab) Ph.  
 (773)834-5304 (Tamiko Charley, assistant) <http://www.genes.uchicago.edu>

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## UChicago EvolutionaryDrugs

Postdoctoral position in computational genomics at the University of Chicago

An NIH-funded postdoctoral position is available immediately in the Departments of Human Genetics and Medicine at the University of Chicago to work on the analysis of large-scale re-sequencing data of genes involved in drug response. Possible projects will include the development of new methods or the use of existing methods to predict polymorphic variants that affect gene function. The information arising from these projects will be used to design more powerful studies aimed at elucidating the role of common and rare variants in drug response. The postdoctoral fellow will be part of a multi-institutional research group working on the pharmacogenetics of anti-cancer agents (<http://www.pharmacogenetics.org>), which involves frequent interactions with a broad range of scientists with expertise in human genetics, bioinformatics, clinical pharmacology, and molecular pharmacology.

Experience in molecular genetics is expected and programming experience in at least one language is highly desirable. Experience in working with genome databases, and/or bioinformatics tools is also desirable.

The Departments of Human Genetics and Medicine at the University of Chicago provide a stimulating and interactive environment with several labs interested in diverse aspects of human variation, statistical and computational genetics, cancer genetics and clinical pharmacology. The postdoctoral fellow will work jointly with Drs. Anna Di Rienzo and Mark Ratain.

Review of applications will begin immediately and continue until a suitable candidate is found. For additional information, contact Dr. Anna Di Rienzo (773-8341037; [dirienzo@genetics.uchicago.edu](mailto:dirienzo@genetics.uchicago.edu)). Applicants should send a curriculum vitae, a one-page letter describing their prior research experience, current interests and goals, and should provide names and contact information of three references to: Dr. Anna Di Rienzo Department of Human Genetics CLSC507F 920 E. 58th Street Chicago, IL 60637

– Anna Di Rienzo Department of Human Genetics University of Chicago CLSC 507F 920 E.

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## UCincinnati EvolBiol

Two NSF-funded postdoctoral positions in EVOLUTIONARY GENETICS are available at the University of Cincinnati. We seek highly motivated evolutionary biologists with a broad conceptual foundation to study evolutionary processes in animal populations. The successful candidates will join an expanding group of interactive faculty, students and postdocs in ecology, evolution and behavior (<http://www.biology.uc.edu/>).

1) COMPARATIVE LANDSCAPE GENETICS. This project involves testing components of dispersal and speciation models in Darwin's finches. The approach is to compare multilocus molecular genetic variation among populations and species to infer evolutionary processes. Good quantitative skills are essential, and experience with molecular laboratory methods will be considered a strength. Specific skills of coalescent modeling, genotyping ancient DNA, phylogeographic analysis, or comparisons among molecular markers will be considered advantageous. Position available March 1, 2004. Contact: Ken Petren ([ken.petren@uc.edu](mailto:ken.petren@uc.edu)).

2) EVOLUTION OF PARASITE RESISTANCE. The research will test for costs of genetically-based resistance against parasitism in the *Drosophila-Macrocheles* mite system, in the context of understanding the role of life-history tradeoffs in the maintenance of genetic variation for fitness in natural populations. Emphasis will be placed on testing for pleiotropic costs under variable stress conditions to which the host organism is known to be exposed in its natural Sonoran Desert habitat. Knowledge of quantitative genetics, experimental design and statistics is desired. Position available September 1, 2004. Contact: Michal Polak ([polakm@email.uc.edu](mailto:polakm@email.uc.edu)).

The successful candidates will be expected to work independently and will have the opportunity to develop their own research project. These positions are available for a full year with the possibility of renewal. Salary will be commensurate with experience. Inquiries may be directed to the contacts above. Please send by email a CV, list of publications, a brief description of past and future research interests, and the names and



contact information for two referees, before March 1, 2004. (Applications may also be mailed to Ken Petren or Michal Polak, Department of Biological Sciences, University of Cincinnati, Cincinnati, OH 45221-0006). The University of Cincinnati is an Affirmative Action/Equal Opportunity Employer.

Kenneth Petren Department of Biological Sciences University of Cincinnati Cincinnati, OH 45221-0006

ph: 513-556-9719 fx: 513-556-5299 email: ken.petren@uc.edu web: <http://www.biology.uc.edu/~faculty/petren/index.html>

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## UCollegeLondon MatingGifts

BBSRC-funded Post-Doctoral Research Fellow Department of Biology University College London

The mating 'gifts' of *D. melanogaster* males: functions and fitness effects of male seminal fluid accessory gland proteins.

A full-time BBSRC funded post-doctoral position is available for 36 months in the fruit-fly laboratory of Dr Tracey Chapman in the Department of Biology at University College London (<http://www.ucl.ac.uk/~ucbhtoc/tc1.html>). The seminal fluid proteins of male fruit flies have striking effects on female behaviour and physiology. For example, they can reduce female sexual receptivity, increase egg laying and contribute significantly to success in sperm competition. Seminal fluid proteins are also implicated in mediating conflicts of interests between males and females over reproductive decisions (e.g. Chapman et al. 1995 *Nature* 373, 241-244). The genes encoding seminal fluid proteins can show extraordinarily rapid evolutionary change. In this project we will study the function of seminal fluid proteins implicated in important fitness traits. We will use RNA interference to knock down specific seminal fluid protein levels in males (e.g. Chapman et al. 2003 *PNAS*, 100, 9923-9928). The research will involve the construction, verification and testing of transgenic strains of fruit flies. The candidate should therefore have experience in general molecular biology and flywork. Experience in constructing transgenic strains is highly desirable. The state-of-the-art fruit fly facility is situated in the thriving research environment of the recently refurbished Centre for Evolutionary Genomics. Starting salary is 20,311 GBP per annum pro-rata (22,445 GBP including London Allowance).

To apply and for further information, please send a covering letter and a CV with the names and contact details of 3 referees to Tracey Chapman ([t.chapman@ucl.ac.uk](mailto:t.chapman@ucl.ac.uk)) Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT. Tel:020 7679 4393 Fax:020 7679 7096. Applications by email are preferred. The closing date is Friday Feb 27th 2004.

Tracey Chapman <[t.chapman@ucl.ac.uk](mailto:t.chapman@ucl.ac.uk)>

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## UEastAnglia TreeGeneticDiversity

POSTDOCTORAL RESEARCH FELLOWSHIP  
School of Biological Sciences, University of East Anglia  
Genetic Diversity in Refugial Trees

A postdoctoral position is available from April 2004 for a period of 3 years in a UK NERC funded joint project between UEA Norwich and University of Leeds. This project seeks to combine recent fossil pollen results in Greece and the Balkans, with genetic studies using DNA sequence analysis of trees from refugial and non refugial sites. The oak and hornbeam are chosen as exemplars of temperate species with good fossil records. Informative chloroplast DNA regions will be identified and sequenced using state of the art facilities in Biology and adjacent John Innes Centre. The large dataset will be analysed by modern computer-based methods that take full advantage of the sequence information. These analyses will allow us to test hypotheses concerning the structure and dynamics of refugial areas, and their role in colonizing non-refugial areas in the Balkans and Europe. In Norwich we seek a postdoctoral researcher competent in generating and analysing the molecular data, and to be involved in the field collection of samples and the interpretation of results. Comparison with palaeobotanical information will be done in conjunction with Dr Chronis Tzedakis, University of Leeds.

Salary will be £20,311 per annum (under review).

Further details of the project can be obtained from Professor Godfrey Hewitt, e-mail: [g.hewitt@uea.ac.uk](mailto:g.hewitt@uea.ac.uk), or Dr Brent Emerson, e-mail: [b.emerson@uea.ac.uk](mailto:b.emerson@uea.ac.uk) Information about the School can be found at: [www.uea.ac.uk/bio/](http://www.uea.ac.uk/bio/) An application form should be obtained from the Personnel Office, University of East Anglia, Norwich, NR4 7TJ (Internet: <http://www.uea.ac.uk/personnel/jobs/> or e-mail: [personnel@uea.ac.uk](mailto:personnel@uea.ac.uk) or answer phone: 01603 593493), to be

returned by 7th March 2004. Please quote reference RA25.

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

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## UHouston Bioinformatics

Postdoctoral positions in Data Analysis/Bioinformatics with emphasis on Molecular Evolution

Postdoctoral positions are available immediately to work on large-scale molecular data analyses and development of bioinformatic tools and databases. There is considerable freedom in the choice of research topics, although evolutionary and comparative genomics, as well as phylogenetics and phylogenomics are of particular interest. Some experience with computer programming, statistics or data analysis is required. Some background and experience in molecular & evolutionary biology is desirable. We seek individuals who are independent and motivated.

Applications (including a CV, a research statement, and contact information of three references) should be submitted to Dan Graur at dgraur@uh.edu

The University of Houston is an Equal Opportunity/Affirmative Action employer. Minorities, women, veterans, and persons with disabilities are encouraged to apply.

Dan Graur Department of Biology and Biochemistry University of Houston Houston, TX 77204-5001

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## ULeeds SelfishDNA

The University of Leeds FACULTY OF BIOLOGICAL SCIENCES School of Biology

Research Fellow

female mating frequency and selfish genetic elements

A NERC funded post is available from 1 April 2004 for a fixed term of up to 3 years to investigate the importance of a selfish genetic element - X-linked meiotic drive - in the evolution of polyandry using the fruit fly model *Drosophila pseudoobscura*. With a PhD in a relevant subject area, you will have a strong background in evolutionary genetics and/or sexual selection. Experience of molecular genetics and *Drosophila* work would be an advantage. A full current UK driving licence is essential.

Salary: Research 1A (£18,265 - £20,311 p.a. pay award pending) according to qualifications and relevant experience.

Informal enquiries to Dr Nina Wedell: N.Wedell@leeds.ac.uk <mailto:N.Wedell@leeds.ac.uk>

Application forms and further enquiries may be obtained from <http://www.notes2.leeds.ac.uk/jobs/-unijob.nsf/Jobs> or Mrs Gill Partridge, School of Biology, Miall Building, University of Leeds, Leeds LS2 9JT; email: bgyjobs@leeds.ac.uk

Job Ref: 026231 Closing date: 19 February 2004

The University of Leeds promotes an equal opportunities policy.

Gill Partridge <G.M.Partridge@leeds.ac.uk>

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## ULeiden EvolAnimalEcol

/The Institute of Biology/ is part of the Faculty of Natural Sciences of Leiden University. The Institute teaches and studies biology at all levels of organization from molecule to community. The approach is both fundamental and applied (see <http://www.bio.leidenuniv.nl/>) In the institute seeks candidates for the following vacancy:

\*Post-doctoral position in Evolutionary Animal Ecology/Genetics at the Institute of Biology at Leiden University\*

/Task:/ Research and Teaching in Evolutionary Animal Ecology. The research of the group focuses in particular on the study of adaptation in behaviour, physiology and life-history characters of insects and fish. Teaching is at all levels and includes all aspects of Animal Ecology.

/Profile of the ideal candidate/

The ideal candidate has proven to be a successful and productive scientist, by publishing in high-ranking ecological & evolutionary journals. He/She has a profound interest in evolutionary ecology and is a skilful researcher. The selected candidate will collaborate in a team with behavioural ecologists and population biologists. His/Her research will be in the fields of evolutionary ecology and genetics and will study how natural, sexual and kin-selection operates under different ecological regimes and how this affects the genetics of life history, behavioural and physiological traits. We are particularly interested in candidates who can apply molecular techniques to coevolution between parasites, insect parasitoids and their host such as arms races and the evolution of virulence. The selected candidate Will work at the Institute of Biology Leiden and is willing to develop active collaboration with colleagues of other teams within the IBL and scientists in other institutions of Leiden University. Is an enthusiastic and inspiring teacher, who motivates his students for evolutionary ecology & genetics. Takes a fair share of the work in administration and organization of the Section/Institute Has a proven capability to obtain external funding for research projects Is able to initiate and maintain international collaborations

The suitable candidate will be appointed on Post-Doctoral position, which conditionally can lead to a tenure position.

Information: Prof. Dr. J.J.M. van Alphen Section of Animal Ecology Institute of Biology Leiden P.O Box 9516 2300 RA Leiden Tel 31 71 5274992 E-mail: [alphen@rulsfb.leidenuniv.nl](mailto:alphen@rulsfb.leidenuniv.nl)

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### ULeipzig HumanPopGenet

A postdoctoral position in human population genetics is available in the group of Prof. Dr. Mark Stoneking at the Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany. We are looking for someone to assist with data analysis and to address, via analytical methods and/or simulations, questions that arise in using molecular genetic analyses to investigate human population history, detect the signature of recent selection on the human genome, etc. See our website (<http://www.eva.mpg.de/genetics>) for further details concerning the ongoing projects in the department. Applicants should have a Ph.D. in a relevant field and a strong

background in population genetics or other quantitative science. The position is available from March 1, 2004, for an initial period of one year, renewable for up to five years. Send inquiries and application materials (CV, list of publications, and names of three references) to Mark Stoneking ([stoneking@eva.mpg.de](mailto:stoneking@eva.mpg.de)).

NOTE NEW STREET ADDRESS AND PHONE NUMBERS!

Dr. Mark Stoneking Max Planck Institute for Evolutionary Anthropology Deutscher Platz 6 D-04103 Leipzig Germany Phone: +49-341-3550-502 FAX: +49-341-3550-555 Secretary: +49-341-3550-504 e-mail: [stoneking@eva.mpg.de](mailto:stoneking@eva.mpg.de) <http://www.eva.mpg.de/genetics/>

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### UMichigan MolEvol

Post-doctoral position at the Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, Michigan.

I am seeking a post-doctoral candidate to work on open-ended projects investigating the molecular evolution of conotoxins of the marine gastropod genus *Conus*. The exact nature of the research project will be agreed upon with the successful candidate. The position will be funded for one-year and can commence in the fall or winter of 2004. The ideal candidate should be well versed in molecular techniques as well as analyses of molecular evolution.

If interested, please contact Tom Duda at [tf-duda@u.washington.edu](mailto:tf-duda@u.washington.edu).

The University of Michigan is a nondiscriminatory, affirmative action employer.

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### UQueensland Eukaryotic Genomics

POSTDOCTORAL POSITION AVAILABLE EVOLUTION OF EUKARYOTIC GENOMES

Institute for Molecular Bioscience The University of Queensland Brisbane, Australia

A postdoctoral Research Associateship in comparative eukaryotic genomics will be available from May 2004

within the Australian Research Council (ARC) Centre in Bioinformatics, based at the Institute for Molecular Bioscience, University of Queensland.

The successful applicant will work closely with Professor Mark Ragan and will take primary responsibility for extending to eukaryotic (including mammalian) genomes the automated identification, alignment and phylogenetic analysis of orthologous genomic regions. Applicants must have strong programming skills, and be fully conversant with likelihood-based phylogenetic inference. Experience with eukaryotic genomes and gene structure, relational databases and high-performance computing would be highly beneficial.

Highly motivated applicants who have (or will soon receive) a PhD or equivalent degree in a relevant field (bioinformatics, genomics, mathematics, molecular biology) are encouraged to send a covering letter, CV, and contact information for three academic referees to [m.ragan@imb.uq.edu.au](mailto:m.ragan@imb.uq.edu.au).

The Institute for Molecular Bioscience brings together more than 400 researchers in fundamental mammalian cell and molecular biology, developmental biology, structural biology, biological chemistry, genomics, proteomics, computational biology and bioinformatics. Together with more than 200 researchers from CSIRO Livestock Industries and Plant Industry, IMB is based in the new A\$ 105M Queensland Biosciences Precinct, the largest bioscience research initiative in the Southern Hemisphere. IMB researchers enjoy superb infrastructure including high-performance computing and database infrastructure under a research alliance with IBM.

The ARC Centre in Bioinformatics is a new initiative of the Australian Research Council. The Centre aims to understand the mammalian cell as a complex system of molecular networks. It brings together researchers at four Australian universities as well as overseas in algorithmics, statistics, machine learning, pattern discovery, mathematical modelling and simulation, 3-D visualisation, advanced databases, and high-throughput experimental validation.

For more information please contact Mark Ragan.

Mark A. Ragan, Professor and Head Division of Genomics & Computational Biology The Institute for Molecular Bioscience The University of Queensland Brisbane, Qld 4072 Australia

and Director, ARC Centre in Bioinformatics

tel +61-7-3346-2616 [m.ragan@imb.uq.edu.au](mailto:m.ragan@imb.uq.edu.au) <http://www.imb.uq.edu.au> Personal assistant: Ms Lanna

Wong tel +61-7-3346-2617 fax +61-7-3346-2101 [l.wong@imb.uq.edu.au](mailto:l.wong@imb.uq.edu.au)

Mark Ragan <[m.ragan@imb.uq.edu.au](mailto:m.ragan@imb.uq.edu.au)>

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## Vienna MouseChemicalSignals

POST-DOCTORAL POSITION: behavioral and evolutionary ecology Konrad Lorenz Institute of Comparative Ethology, Vienna, Austria

Dr. Dustin Penn is searching for a postdoctoral scientist to begin collaborative work on chemical signals in house mice. Only applicants with a strong background in behavioral ecology or sensory biology \* preferably chemical communication \* will be considered for this position. Experience in working with house mice or molecular genetic techniques is highly desirable. The position is for 2 years. Salary is competitive and depends upon experience. Appointments include healthcare benefits and research/travel allowance. Review of applications begins immediately and will continue until the position is filled. The starting date is flexible, though March 2004 is optimal. Persons with excellent English communication skills are preferable, and German would be useful (the Institute operates bilingually, and English is widely spoken in Vienna, which allows non-German speaking researchers to integrate easily).

The Konrad Lorenz Institute is located in the Vienna Woods, on the outskirts of Vienna, and provides a stimulating scientific environment with a number of research groups focusing on behavioral and evolutionary ecology (see <http://www.oeaw.ac.at/klivv/>).

To apply, send (1) CV, (2) copies of recent publications (3 maximum), (3) a statement of research interests, (4) letters of reference from three individuals by e-mail (or regular mail, see address below) to Dr. Sabine Fischer.

Dr. Sabine Fischer Konrad Lorenz Institute Austrian Academy of Sciences Savoyenstrasse 1a A-1160 Vienna, Austria Phone: +43-1-515 81-2761 FAX: +43-1-515 81-2800 E-mail: [s.fischer@klivv.oeaw.ac.at](mailto:s.fischer@klivv.oeaw.ac.at)

Sabine Fischer <[S.Fischer@klivv.oeaw.ac.at](mailto:S.Fischer@klivv.oeaw.ac.at)>

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## WalnutCreek MicrobeGenomics

Postdoc position Comparative community genomics of the gut microbiota. DOE Joint Genome Institute

An NIH-funded postdoctoral position is available to study the diverse microbial community that inhabits the gastrointestinal tract, specifically that of humans and mice. This community has important roles in host physiology, is rich in ecological interactions, and has potential for providing clues to the evolution of commensalism and pathogenicity. Some specific objectives of the project include understanding the diversity within the gut, the main differences between commensals and their pathogenic relatives, and the paths of horizontal gene exchange within the gastrointestinal environment. We are looking for a postdoctoral researcher to participate in all aspects of the project, such as production and screening of BAC libraries, and comparative sequence analyses of the obtained sequences. Applicants should have skills in evolutionary genetics, genomics, computational biology or microbiology. Programming abilities a plus.

The person will be based in the Evolutionary Genomics Department of the DOE Joint Genome Institute (<http://www.jgi.doe.gov/programs/comparative/>), but will also have the opportunity to interact with the laboratory of Howard Ochman at the University of Arizona at Tucson. The DOE Joint Genome Institute, established on January 1, 1997, is a consortium of scientists, engineers and support staff from the U.S. Department of Energy's Lawrence Berkeley, Lawrence Livermore and Los Alamos National Laboratories, and is located in Walnut Creek, a nice community approximately 25 miles from San Francisco and 20 miles from Berkeley, with easy access to many locations in the Bay Area.

Please send inquiries and applications to Pilar Francino at [mpfrancino@lbl.gov](mailto:mpfrancino@lbl.gov). Applications should include a cover letter describing your research interests, a CV and

names of three references. – M. Pilar Francino, Ph. D. Research Scientist Genomics Division, Lawrence Berkeley National Lab and Evolutionary Genomics Department, DOE Joint Genome Institute 2800 Mitchell Drive Walnut Creek, CA 94598

phone: (925) 296-5872 fax: (925) 296-5666 e-mail: [mpfrancino@lbl.gov](mailto:mpfrancino@lbl.gov) e-mail: [mpfrancino@lbl.gov](mailto:mpfrancino@lbl.gov)

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### YaleU MosquitoEvolGenet

**POSTDOCTORAL POSITION IN ANOPHELES/AEDES EVOLUTIONARY GENETICS AT YALE** A postdoctoral position is available to work on a evolutionary genetics of mosquitoes on a parasitology training grant in the research group headed by Jeffrey Powell and Adalgisa Caccone at Yale. Much of our recent work is with malaria vectors (Anopheles), but we are in the planning stages of moving into *Aedes aegypti* with an eye to dengue. So someone interested in either malaria or dengue vectors would be appropriate. The candidate will be selected on the basis of laboratory/field expertise and research productivity. The application is simple: a CV, a brief description of research interests and three letters of recommendation. The hang-up is this is due by January 31st, 2004. If interested, please contact ASAP Jeffrey Powell at [Jeffrey.powell@yale.edu](mailto:Jeffrey.powell@yale.edu) or Gisella Caccone at [Adalgisa.caccone@yale.edu](mailto:Adalgisa.caccone@yale.edu) –

– Gisella Caccone YIBS-Molecular Systematics and Conservation Genetics Lab. ESC 140 Yale University 21 Sachem St., New Haven, CT, 06520-205105 USA Tel 203-432-5259 Fax 203-432-7394 Fax 203-432-7394

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## WorkshopsCourses

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## BodegaBay ApplPhylogenetics May2-11

UC Davis WORKSHOP IN APPLIED PHYLOGENETICS at Bodega Marine Laboratory, Bodega Bay, California May 2-7, 2004 with a special supplementary course on Supertree Construction May 9-11, 2004 sponsored by the Center for Biosystematics, Bodega Marine Laboratory, and Center for Population Biology, University of California, Davis Introduction. Phylogenetic methods have revolutionized modern systematics and become indispensable tools in evolution, ecology and comparative biology, playing an increasingly important role in analyses of biological data at levels of organization ranging from molecules to ecosystems. The construction of phylogenetic trees is becoming a methodology that is well-defined, with broad agreement on the central issues and questions. A nearly standard set of topics is now taught as part of the curriculum at many colleges and universities. On the other hand, applications of phylogenetic methods to interesting problems outside of systematics is an area of special excitement, innovation, and controversy, and perspectives vary widely.

In May, 2004, for the fifth year, we will teach a workshop for graduate students interested in applying phylogenetic methods to diverse topics in biology. The one-week course will be an intensive exploration of problems to which modern phylogenetic tools are being applied, including topics in biogeography, ecology, conservation biology, phylogenomics, functional morphology, macroevolution, speciation, and character evolution. The course leads off with recent advances in phylogenetic methodology, and then turns to methods and tools that can be brought to bear to address these "applied" issues in the context of a given phylogeny.

This year we will also teach a special three day supplementary workshop on supertree construction—the assembly of large trees from collections of smaller ones. Supertree methods are an increasingly important tool in phylogenetics and comparative biology. We will examine currently available methods and software tools and examine supertree construction critically from several perspectives. Instructors in this part of the course include several individuals who have developed new supertree methods, supertree software or both.

The course will be held entirely at Bodega Marine Lab on the Northern California coast, which has newly renovated facilities, including extensive computing resources and on-site housing. The course format will involve equal parts of lecture, discussion, and training in software and internet tools. One afternoon during the week will be left free for field trips to local natural areas.

Specific Topics to be Covered in the first week

Finding, evaluating and interpreting phylogenetic trees; phylogenetic databases Recent advances in tree reconstruction: Bayesian inference; stochastic optimization strategies; divide-and-conquer methods Analysis of character evolution—theory: parsimony, likelihood and Bayesian approaches; null models and statistical testing Analysis of character evolution—form and function of complex character systems Phylogenetic biogeography and phylogeography; coalescent methods for inferring migration rates and patterns Phylogenetic comparative methods Phylogenetic perspectives on biodiversity and conservation biology Data mining of sequence databases for phylogenetic analysis Estimation of divergence times from sequence data

Instructors for the main workshop. Dr. Michael Sanderson, UC Davis Dr. Peter Wainwright, UC Davis Dr. Tom Near, University of Tennessee Dr. Amy Driskell, UC Davis Dr. Charles Nunn, UC Davis Dr. Campbell Webb, UC Davis Dr. Gordon Burleigh, UC Davis Dr. Shelley McMahon, UC Davis

Instructors for the supertree workshop. Dr. Michael Sanderson, UC Davis, USA Dr. Rod Page, University of Glasgow, UK Dr. Mike Steel, University of Canterbury, New Zealand Dr. Olaf Bininda-Emonds, Technical University of Munich, Germany Dr. Oliver Eulenstein, Iowa State University, USA Dr. David Fernandez-Baca, Iowa State University, USA

Prerequisites. Students should have some familiarity with phylogenetic methods through previous coursework. Some experience with PAUP, PHYLIP, or other programs for phylogeny reconstruction will be > assumed.

Admission and Fees. Students will be admitted based on academic qualifications and appropriateness of research interests. The course fee is \$350 for students taking only the one-week course and \$475 for those students wishing to stay for the supertree workshop. This includes room and board at BML for duration of the course. UC Davis students may take the course for

credit and can apply for a partial waiver of this fee.

Application Deadline. Applications are due February 27, 2003 and are available from the workshop website

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

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## BonnGermany Gender Apr21-25

### SECOND ANNOUNCEMENT

Workshop on *G e n d e r t r a n s i t i o n s* from hermaphroditism to gonochorism and back Wed 21 - Sun 25 April 2004, Haus Humboldtstein (near Bonn, Germany)

Goal To discuss the three main aspects of transitions in gender expression: (1) The selective forces that favour and stabilise a particular mode of gender expression (2) The genetic mechanisms that underlie gender expression (3) Destabilising factors and mechanisms that can lead to a transition in gender expression

The emphasis will be on animals, but botanists who work in this field are strongly invited to participate.

Programme Arrival on Wednesday with welcome drink, followed by three days with 18 contributed and 6 invited talks, leaving plenty of time for informal discussion and evening activities. Final party on Saturday night and departure on Sunday. Poster presentation is possible (e.g. if required by your funding agency).

Invited speakers Peter Klinkhamer (sex allocation in plants, Leiden) John R. Pannell (gender expression in plants, Oxford) Mikael Puurtinen (gender expression versus mating rates, Jyvaskyla) Leo W. Beukeboom (sex determination, Groningen)

Venue A small, cosy conference centre in a superb location South of Bonn, high on the West bank of the Rhine valley, with beautiful views and the opportunity to walk in the surrounding forests. [www.haus-humboldtstein.de](http://www.haus-humboldtstein.de) (in German). Easy to reach by train from the international airports Frankfurt & Duesseldorf.

Accommodation Full board, including coffee breaks, ca. 300 EURO per person. Room for 34-53 people, depending on single or double occupancy of the rooms.

Daytime participants (excluding bedroom and breakfast, including coffee breaks, lunch and dinner) pay ca. 30 per day when registered in advance.

Registration We are still taking registrations - the next deadline is 14 February. Later registration is possible, but without a guarantee that a contribution can be made. Please send your interest to participate to [doberenz@uni-muenster.de](mailto:doberenz@uni-muenster.de) with transitions in the subject line. In addition to contact details, your email should include a brief abstract that describes your possible contribution to the meeting as well as a few lines on what your interests are. We shall let you know as soon as possible whether your application was accepted for an oral presentation.

Web site <http://www.uni-muenster.de/Biologie.EvoEco/Evolbio/gender/frameset.htm>

Organisers Nils Anthes and Nico Michiels, Evolutionary Biology, University Muenster, Huefferstrasse 1, D-48149 Muenster, Germany. [michiels@uni-muenster.de](mailto:michiels@uni-muenster.de) (for information, not for registration).

Related pre-announcement If you cannot attend our workshop, note that the 2005 meeting of the Society of Integrative and Comparative Biology (SICB) (Jan 4-8, San Diego, California) will feature a workshop on Sexual Selection & Mating Systems in Hermaphrodites organised by Janet L. Leonard (UCSC). Bookmark <http://www.sicb.org/index.php3> for details (to appear later this year).

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Prof. Dr. Nico K. Michiels Institute of Animal Evolution and Ecology Westphalian Wilhelms-University Muenster Huefferstrasse 1, D-48149 Muenster, Germany

Tel. +49 (0)251 83 24661 Mobile +49 (0)170 4758003 Fax. +49 (0)251 83 24668

[michiels@uni-muenster.de](mailto:michiels@uni-muenster.de) <http://www.uni-muenster.de/Biologie.EvoEco/Evolbio/>

Nico Michiels <[michiels@uni-muenster.de](mailto:michiels@uni-muenster.de)>

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## EvolPopGenet list

EvoDir members,

I have compiled the list of workshops and courses based on information I received. Hopefully this helps, and maybe I'll see you at one of these courses!

Emily

Emily K. Latch Ph.D. candidate, Wildlife Genetics Dept. of Forestry and Natural Resources Purdue University West Lafayette, IN 47907 emily@fnr.purdue.edu

1) Title: Recent Advances in Conservation Genetics

Offered by: the American Genetic Association, the Laboratory of Genomic Diversity/National Cancer Institute, and the Smithsonian Institution's Conservation and Research Center

Location: Front Royal, Virginia, USA

Date: August 2004

Cost: \$2000 (food and lodging included)

Information: <http://home.ncifcrf.gov/ccr/lgd/geneticcourse/index4.htm> 2) Title: Workshop on Molecular Evolution

Offered by: Marine Biological Laboratory

Location: Woods Hole, Massachusetts, USA

Date: July 25 - August 6, 2004 (August 6 - 13 for extended topics session)

Cost: \$1500 (+\$750 for extended topics session) (food and lodging included)

Information: <http://workshop.molecularevolution.org/> 3) Title: Intensive Course in Molecular Systematics

Offered by: The University of Reading

Location: Reading, United Kingdom

Date: March 23 - April 2, 2004

Cost: £550 (lunch included)

Information: <http://www.plantsci.rdg.ac.uk/molecularcourse.htm> 4) Title: First Baikal Workshop on Evolutionary Biology: "Tracing Environmental Changes in Genetic Diversity of Contemporary Faunas"

Offered by: Limnological Institute, Siberian Branch Russian Academy of Sciences

Location: Irkutsk, Siberia, Russia

Date: September 6-11, 2004

Cost: 400 Euro (includes tours and banquets)

Information: <http://lin.irk.ru/1BWEB/> 5) Title: Phylogenies and Genealogies from DNA: Reconstruction and Applications

Offered by: Special Center for Research in Taxonomy, Phylogeny, and Molecular Ecology

Location: Barcelona, Spain

Date: July 6-16, 2004

Cost: 350 Euro

Information: <http://www.ub.es/certfem/filogen2004.html> <<http://www.ub.es/certfem/filogen2003.html>>

\*\*\*This course is taught entirely in Spanish - the info given is translated to the best of my ability, but I make no guarantees :-)

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## RiodeJaneiro Complexity Nov

Workshop on Complexity and Philosophy Co-hosted by: Federal university of Rio de Janeiro Institute for the Study of Coherence and Emergence Cathedra for the Study of Complexity (Instituto de Filosofia de La Habana) Calling Notice November 2004, Rio de Janeiro (exact dates to be determined shortly) Call for Participants I am writing to you today to inform you about the upcoming two-day Complexity and Philosophy workshop to be held this November (2004) in Rio de Janeiro and hosted by the Institute for the Study of Coherence and Emergence (<http://www.isce.edu>), U.F.R.J. (Federal university of Rio de Janeiro), and the Cathedra for the Study of Complexity (Instituto de Filosofia de La Habana). The aim of this meeting is to explore the philosophical implications of the fledgling science of complex systems. This workshop complements the 2nd Biennial International Seminar on the Philosophical, Epistemological and Methodological Implications of Complexity Theory that was held in Havana, Cuba, January 2004. The larger international seminar provides a forum to discuss complexity and philosophy-related issues in general, whereas the aim of the smaller workshop event is to consider specific issues at a greater length with more time made available for discussion rather than presentation. The location for the workshop event is expected to change location each time it is held. In 2002 the event was held in Norwood (just outside Boston) in the US. This time we are pleased to announce that the next event will be held in Rio de Janeiro, with the very generous assistance of the Federal university of Rio de Janeiro. Call for Papers Potential attendees are encouraged to submit papers on the following topics: Status, limits and legitimacy of knowledge regarding complex systems Relationship between linear and nonlinear philosophies Complexity-based ethics Frameworks for the analysis of complex systems Complex limits to 'theories of everything' Complexity and the social sciences Complex-

ity and globalization Complexity and human subjectivity All paper submissions will be considered for publication in the international journal *Emergence: Complexity and Organization* (depending upon suitability), and/or publication in an edited book of papers to be published by IAP Press as part of ISCE's Managing the Complex Book Series. Selected papers from the previous event have appeared in *Nonlinear Dynamics, Psychology and the Life Sciences*, and this journal may again prove to be a publishing avenue for selected papers. All papers will be considered for publication even if time cannot be found for the papers to be presented at the conference itself (the emergent properties of such an event and the organiser's hope to focus on discussion/dialogue rather than a standard presentation format may at times dictate the proceedings). Provisional Timetable Please let Caroline Richardson (complexity-workshop@isce.edu) know of your interest in attending this event as soon as possible. Attendance at the event will be strictly limited to 30 so as to encourage genuine dialogue amongst participants - selection of attendees will be determined simply on a first come first serve basis. A block of 30 rooms will be reserved for the event and a reduced room rate (that includes breakfast) will be negotiated. Final details concerning hotel rates will be made available in the next month or so. Extended abstracts of at least 1000 words to be submitted to Dr. Kurt Richardson (kurt@kurtrichardson.com) by end of July, 2004. The decision by the academic board (which will comprise members of I.S.C.E.'s fellowship) to encourage submission of a full paper - to be no longer than 5000 words - will occur by end of August, 2004. Full papers to be submitted by end of October, 2004. The decision as to what papers will be published and in what form will occur shortly after the closing of the conference. It is hoped that participants will play an integral role in the development of the event timetable before and during the event. The exact cost of registration will be determined shortly, but fees are expected to be around US\$300. As well as administrative and location costs, fees will also cover lunch during the event as well as a Brazilian-style dinner event at the close of the second day. Participants will be responsible for their own hotel costs. If you would like to attend the workshop please send an email to Caroline Richardson (complexityworkshop@isce.edu) with the following information: Name, academic affiliation and status if any, address, phone, fax, and email. Caroline will contact you for further information re hotel confirmation and payment of workshop fees. If you have any questions at all please do not hesitate to contact Kurt or Caroline (complexityworkshop@isce.edu).

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## Smithsonian ConsGenetics Aug16-27

American Genetic Association Laboratory of Genomic Diversity - National Cancer Institute The Smithsonian Institution<sup>1</sup>'s Conservation & Research Center announce a course

<sup>3</sup>RECENT ADVANCES IN CONSERVATION GENETICS<sup>2</sup>

August 16-27, 2004

At the Smithsonian Institution's Conservation & Research Center in Front Royal, Virginia, outside Washington, DC, the AGA and the LGD are presenting a 10-day intensive course in methods, interpretation, and applications of molecular genetic analyses for conservation of endangered species. This course will be taught by scientists with expertise and a variety of personal experiences in this important field. Participants will learn how to develop and interpret a wide range of genetic data.

**COURSE DIRECTOR:** Stephen J. O'Brien, Chief, Laboratory of Genomic Diversity, National Cancer Institute-Frederick, MD, USA

**TOPICS include:** Sample collection and processing PCR-based technologies for polymorphism detection Genetic analysis: bioinformatics and the use of molecular genetic databases estimating relative genetic diversity with gene markers phylogenetic algorithms: their use and interpretation phylogeography subspecies and population substructure demographic and genetic simulation modeling of small populations kinship and paternity assessment Host-pathogen interactions Conservation management applications

**TUITION:** US \$2,000 (includes housing, all meals, and airport transfers) **Deadline for receipt of applications:** March 15, 2004. Admission is competitive; participants will be limited to 24. Limited financial aid is available.

**VISIT THE WEB PAGE:**

<http://lgd.nci.nih.gov> - select "Courses - Conservation Genetics

or contact:

Ms. Jan Martenson, Course Coordinator, e-mail: noah-scr@ncifcrf.gov NCI-Frederick, P.O. Box B Frederick, MD 21702-1201 Phone: 301/846-7513 FAX: 301/846-6327



Al Roca <roca@ncifcrf.gov>

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## UFlorida MolecularMarkers Mar1-5

Molecular Markers Workshop March 1-5, 2004. Early registration deadline February 10, 2004. Register at [www.biotech.ufl.edu/WorkshopsCourses](http://www.biotech.ufl.edu/WorkshopsCourses) or contact Teresa Benton at 352-392-8408 University of Florida-Interdisciplinary Center for Biotechnology Research Education and Training Core Laboratory offer a hands-on workshop:

Microsatellites are a powerful class of genetic markers used in a variety of molecular studies such as determining fine scale population structure, parentage, and individual identification. The genomes of most eukaryotes contain thousands of loci containing short nucleotide sequence motifs tandemly repeated many times, such as (CT/GA)<sub>n</sub>. The repeat units tend to be highly polymorphic, and several loci taken together produce a genetic fingerprint that is consistent and unchanging from one individual to the next. While readily used and analyzed, it is generally necessary to develop a new set of markers for each species, as there tends to be little crossover between species unless fairly closely related.

Developing a microsatellite library can be a long and troublesome task, especially for those with limited molecular background. This workshop will take participants through the steps used to build an enriched microsatellite library using DNA from their species of interest using a variety of molecular techniques such as restriction enzyme digestion, ligation, PCR, and several screening protocols to find loci containing polymorphic repeat motifs. Participants will also learn about primer design and statistical analyses.

Sharon Norton Scientific Research Manager University of Florida ICBR- Education and Training Core Laboratory PO Box 100156 Gainesville, FL 32610 (352) 846-1337

Sharon Norton <norton@biotech.ufl.edu>

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## UVirginia EvolBiol

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MOUNTAIN LAKE BIOLOGICAL STATION  
[www.mlbs.org](http://www.mlbs.org) 2004 Summer Courses and REU Opportunities

The Mountain Lake Biological Station (University of Virginia) announces credit courses in field biology, and paid research opportunities for undergraduates. We offer students hands-on experience and training in a wide variety of biological field studies. Join us for an exciting and unforgettable summer in a first-class field biology teaching and research environment. Scholarships and financial aid are available.

Courses: [www.mlbs.org/courses.html](http://www.mlbs.org/courses.html) 1) MYCOLOGY May 31 - June 25. An introduction to the biology of fungi, with emphasis on field identification and current experimental methods used to study fungal genetics, ecology and evolution. 2) FIELD GEOLOGY May 31 - June 25. Designed for undergraduates interested in geology or ecology. 3) CONSERVATION BIOLOGY June 28 - July 23. An introduction to the concepts and field methods used to address issues in conservation of communities and endangered populations. 4) PLANT BIODIVERSITY AND CONSERVATION June 28 - July 23. The extraordinary diversity of the Southern Appalachians will serve as a backdrop to explore the world of plants. 5) ECOLOGY OF AMPHIBIANS July 26 - August 6. Course will introduce students to the diverse amphibian fauna of the Southern Appalachian Mountains, a world hot-spot for salamander diversity.

NSF-funded Research Experience for Undergraduates (REU) program: [www.mlbs.org/REU.html](http://www.mlbs.org/REU.html) We match undergraduate students with visiting scientists for 10 weeks of advanced, independent research on a project of the student's own design. REU positions come with a stipend of \$3,500 and pay all room and board expenses (pending final NSF approval). Deadline for receipt of applications is March 1. Minority students are especially encouraged to apply.

Our field station is located on a mountaintop in southwestern Virginia and is home to a lively research, teaching and social community. For details on these programs, full course descriptions, application material, and a list of research areas see our web page:

[www.mlbs.org](http://www.mlbs.org) You can also contact us by email, mail, fax or phone:

Mountain Lake Biological Station University of Virginia  
238 Gilmer Hall, PO Box 400327 Charlottesville VA  
22904-4327 mlbs@virginia.edu tel: 434-982-5486 fax:  
434-982-5626

Eric S. Nagy, Ph.D. Associate Director, Mountain Lake



Biological Station Assistant Professor, Department of Biology University of Virginia, 238 Gilmer Hall, P.O. Box 400327 Charlottesville, VA 22904-4327 USA 434-982-5486 office (540-626-5227 summer) 434-982-5626 fax (540-626-5229 summer) 434-906-3122 cell <mailto:enagy@virginia.edu>enagy@virginia.edu

Mountain Lake Biological Station: <<http://www.mlbs.org/>>mlbs.org Organization of Biological Field Stations: <<http://www.obfs.org/>>obfs.org Organization of Biological Field Stations: <<http://www.obfs.org/>>obfs.org

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## Instructions

Instructions: To be added to the EvoDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvoDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvoDir direct them to the email [evoldir@evol.biology.McMaster.CA](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as 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 one of the keywords “Conference, Grad, Job, Other:, Postdoc, Workshop” and then the message stands a better chance of being correctly parsed.

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. So 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.