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# E v o l D i r

October 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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## Conferences

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### HatfieldUK EvolLanguage Apr12-15

Call for Papers:

Second International Symposium on the Emergence and Evolution of Linguistic Communication (EELC'05) at the AISB'05 Convention 12-15 April 2005, Hatfield UK

Programme Chairs:

Angelo Cangelosi, University of Plymouth, UK (Chair)  
 Chrystopher L. Nehaniv, University of Herfordshire, UK (Co-Chair)

Invited Speakers:

Luc Steels (AI Lab Vrije Universiteit Brussel, Belgium)  
 Alison Wray\* (Cardiff University, Wales) W. Tecumseh Fitch\* (University of St. Andrews, Scotland) (\* = pending confirmation)

Scope of the Symposium

The renewed scientific interest in the emergence and evolution of linguistic communication has become one of the most important research issues in Artificial Intelligence and Cognitive Science. The EELC'05 Symposium will focus on the latest empirical and modelling research on the evolutionary factors that affect the acquisition, self-organization and origins of linguistic communication systems and their precursors. This considers both language-specific abilities (e.g. speech, semantics and syntax) and other cognitive, sensorimotor and social abilities (e.g. category learning, action and embodiment, social networks). Key questions relate to the

the emergence of: symbol grounding; deixis, gesture, and reference; predication; negation; syntactic categories; and compositionality; among other issues in the context of embodied, social interaction and evolution. This is a field characterized by a highly interdisciplinary and multi-methodological approach. It benefits from the contribution of researchers from wide ranging disciplines such as linguistics, psychology, neuroscience, anthropology and computer science. The methodologies adopted cover a wide range of approaches, from animal and human experiments, to brain studies and to computational and robotic modelling of linguistic behaviour. For example, computational models of language evolution and emergence involve artificial intelligence methods (e.g. artificial neural networks, evolutionary computation, rule-based systems) and techniques for the simulation of behaviour (artificial life, multi-agent systems, adaptive behaviour and robotics). The symposium will create the opportunity for the many of most influential in the field to present their latest research and to discuss the agenda for future studies.

The use of computational models for simulating the evolution of language has been one of the main contributors to the renewed interest in language evolution research. In fact, up to 10 years ago, very few researchers were directly interested in the origins and evolution of language and publications on new language evolution studies were uncommon. This was partly the result of the famous ban in the 19th century by the Société Linguistique de Paris on research and publication on language origins to quell rampant, unfounded speculation on the topic. The development of the first language evolution models in the early 90s permitted to deal with some of the main difficulties in such a scientific field. Theories of language origins and evolution not only were difficult to test empirically but they

tended to be stated in vague and general terms and were unable to generate detailed empirical predictions. This has been partially due to the problem of the objective scarcity of empirical evidence. It is this very problematic aspect of the study of language evolution which computer simulations can help us to overcome. Computer simulations are theories of the empirical phenomena that are simulated (Cangelosi & Parisi 2002). Simulations are a novel way to express theories in science. They are scientific theories expressed as computer programs. The program incorporates a set of hypotheses on the causes, mechanisms, and processes underlying the simulated phenomena and, when the program runs in the computer, the results of the simulations are the empirical predictions derived from the theory incorporated in the simulation. All this contributes to the development of a new approach to the study of the origins and evolution of language.

The EELC Symposium Series

Following on from the success of the First International Workshop on the Emergence and Evolution of Linguistic Communication in Japan 2004, and the Evolution of Language conferences. This symposium will be held 14-15 April 2005 at the University of Hertfordshire, de Havilland Campus, Hatfield, just outside London. It will be part of the AISB-2005 convention 12-15 April 2005, whose overall theme is "Social Intelligence and Interaction in Animals, Robots and Agents". EELC'04 was the First International Workshop on the Emergence and Evolution of

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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>

## Marseille 9thEvolBiol Sept21-23

The 9th evolutionary biology meeting at marseille will take place in 2005 the September 21st, 22nd and 23rd information will be soon available at <http://www.up.univ-mrs.fr/evol/congres/> All the best Pierre – EA 3781 EGEE Evolution Génome Environnement Université de Provence 3 place V Hugo 13331 Marseille cedex 3 0491106489 <http://www.up.univ-mrs.fr/evol/egee@up.univ-mrs.fr>

## Munich BiolSystems Oct7-8

CALL FOR POSTER PRESENTATIONS: PLEASE REGISTER UNTIL 25 SEPTEMBER 2004

Complex Stochastic Systems  
in Biology and Medicine

Munich, 7-8 October, 2004

<http://www.stat.uni-muenchen.de/sfb386/workshop/css2004/> While registration of contributed talks is closed we are now cordially inviting \*poster contributions\*.

This meeting aims to bring together state-of-the-art researchers working, e.g., on methods for

\* graphical models and multiple time series, \* inference of high-dimensional models, and \* dynamics of complex systems

with focus on application areas such as

\* genetic networks, \* gene expression analysis, and \* systems biology.

Experimental researchers working in these fields are also highly welcome.

Please register for presenting a poster and for participation until FRIDAY 25 SEPTEMBER 2004.

For further information please visit the conference web page (s.o.) where you will also find all contact details.

FEES

Students: free Postdocs: 25 EUR Senior scientists: 50 EUR Industry: 100 EUR

PRELIMINARY PROGRAM OF INVITED AND CONTRIBUTED TALKS

Thursday 7 October —————

9:50 Welcome 10:00 MIKE WEST (Durham, US) "Sparsity, stochastic search and visualisation in high-dimensional graphical models: applications in gene expressions association studies" 10:50 ANJA WILLE (Zurich, CH) "Graphical Gaussian modeling for genetic regulatory network inference" 11:20 Coffee break 11:40 JEAN-PHILIPPE VERT (FONTAINEBLEAU, FR) "Analysis and inference of gene networks from genomic data" 12:30 FLORIAN MARKOWETZ (Berlin, DE) "Gene networks from RNA interence data" 13:00 Lunch break 15:00 LORENZ WERNISCH (London,

UK) “Graphical modeling of nonlinear dependencies in gene networks” 15:50 MARCO GRZEGORCZYK (Dortmund, DE) “Determination of interacting genes in kidney tissues using Bayesian networks” 16:20 Coffee and cake break 16:40 HAIJUN ZHOU (Potsdam, DE) “Brownian walks on networks and the community structure of the budding yeast protein-protein interaction network” 17:10 CLAUDIA RANGEL (Los Angeles, US) “Linear dynamical systems modeling of genetic regulatory networks” 18:00 Break 19:30 Conference dinner

Friday 8 October

9:40 LINDA PETZOLD (Santa Barbara, US) “Multi-scale simulation of biochemical networks” 10:30 BARBEL FINKENSTADT (Warwick, UK) “Parameter estimation for simplified stochastic models of gene regulatory networks” 11:00 Coffee break 11:20 ANNE-METTE HEIN (London, UK) “BGX: a fully Bayesian gene expression index for Affymetrix GeneChip data” 12:10 CHRIS HOLMES (Oxford, UK) “Bayesian co-clustering and the analysis of gene expression time profiles under multiple treatments” 13:00 Lunch break 15:00 ERWIN FREY (Berlin, DE) “Collective Phenomena in intracellular processes” 15:50 MARTIN FALCKE (Berlin, DE) “Fluctuations create structures in intracellular Ca<sup>2+</sup> dynamics” 16:20 Coffee and cake break 16:40 JOHANNES MULLER (Garching, DE) “Quorum sensing and diffusion sensing” 17:10 ANTON WAKOLBINGER (Frankfurt, DE) “The coalescent and some of its ramifications” 18:00 Farewell

SCIENTIFIC COMMITTEE

Leonhard Held, Barabara Hellriegel, Ludwig Fahrmeir, Eduardo Mendoza, Wolfgang Stephan, Korbinian Strimmer, Gerhard Winkler, Ralf Zimmer.

SFB 386: “Statistical Analysis of Discrete Structures” MSBF: “Munich Systems Biology Forum” (<http://www.sysbio-muenchen.de>)

korbinian.strimmer@lmu.de

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## NHMLondon Barcoding Feb6-9

International Conference for the Barcoding of Life

On behalf of the Consortium for the Barcoding of Life (CBOL) the Natural History Museum, London (NHM) is hosting the first International Conference for the Barcoding of Life on Sunday 6th - Wednesday 9th February

2005 in NHM’s Flett Theatre, South Kensington, London.

This conference will be focused on advancing the theoretical and practical issues in DNA barcoding. It aims to review and advance the state-of-the-art, expand the worldwide community interested in ‘barcoding’, and harmonize research efforts.

If you would like further details log on to: <http://www.nhm.ac.uk/science/BOL/> r.cowan@rbgkew.org.uk

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## RoyalSocLondon EvolOfDomestication Nov19

The Genetics Society Autumn Meeting

Friday 19th November, 2004, The Royal Society, London

A walk from the wild side: the genetics of domestication of livestock and crops

The livestock and crop species currently used by humans around the world are remarkably distinct from the wild animals and plants from which they are derived. This divergence occurred much faster than “natural evolution”. How did this happen, what genes were involved, and what changes might we expect in the future? What will be the relative contributions of traditional breeding and genetic engineering? This meeting will assemble a panel of expert speakers to answer the questions “what happened during domestication?” and “what can we expect next?”.

For further details and online registration please visit: [https://www.kcchosting.co.uk/~genetics/-autumn2004\\_form.htm](https://www.kcchosting.co.uk/~genetics/-autumn2004_form.htm) Student members of the Genetics Society can apply for travel grants.

**SPEAKERS** Maize Domestication/functional genomics Ed Buckler, Cornell University <http://www.maizegenetics.net/people/buckler.htm> Molecular genetics of modern maize breeding Scott Tingey, DuPont Agricultural Products

Domestication, genetic diversity in cattle Dan Bradley, Trinity College [http://www.tcd.ie/Genetics/-staff/Dan\\_Bradley.html](http://www.tcd.ie/Genetics/-staff/Dan_Bradley.html) Identification of mutations underlying phenotypic changes in domestic animals Leif Andersson, Uppsala University <http://www.imbim.uu.se/forskning/anderssonresearch.html>

The genetics of dog domestication Robert Wayne,

UCLA, <http://www.ioe.ucla.edu/faculty/RWayne.htm>

Bioarchaeology of domestication Alan Cooper, University of Oxford <http://evolve.zoo.ox.ac.uk/-people.html?id=coopera> Re-domestication of tomato wild species Dani Zamir, The Hebrew University of Jerusalem

GENETICS SOCIETY MENDEL LECTURE Arabidopsis as a model system to accelerate domestication and crop improvement Chris Somerville, Carnegie Institution [http://carnegiedpb.stanford.edu/research/-research\\_csomerville.php](http://carnegiedpb.stanford.edu/research/-research_csomerville.php)

Scientific Programme [http://www.genetics.org.uk/-?page=autumn\\_2004\\_programme](http://www.genetics.org.uk/-?page=autumn_2004_programme)

#### ORGANISERS

HELEN SANG (ROSLIN INSTITUTE)

[helen.sang@bbsrc.ac.uk](mailto:helen.sang@bbsrc.ac.uk)

JONATHAN JONES (THE SAINSBURY LABORATORY)

[jonathan.jones@sainsbury-laboratory.ac.uk](mailto:jonathan.jones@sainsbury-laboratory.ac.uk)

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### ToulouseU OrchidSystematics

The scientific program of the Symposium NEW PERSPECTIVES ON THE SYSTEMATICS & ECOLOGY OF ORCHIDS at Toulouse University is now online and can be found on <http://www.ladybio.ups-tlse.fr/-Orchid-Symposium> "SCHEDULE".

Speakers include: Mark W. Chase; Luc Gignord; Michael Fay; Lauren Gardiner; Pavel Kindlmann; Melissa McCormick; Claire Micheneau; Anneke Padolina; David L. Roberts; Qazi Sadruddin; Bertrand Schatz; Marc André Selosse; T. Julou; J.-C. Abadie; Ann Smithson; Thomas Tully, Timo Van der Niet; Analisa Daniela Abele; Donata Cafasso; Donata Pellegrino; Philipp M Schlüter; Errol Véla; Nicolas J. Vereecken...

Registration is open and you can download the form at "REGISTRATION" Information on accommodations, and travel can also be found on the Web site

Laure Civeyrel,

For further information you can contact Laure Civeyrel on [npseo@cict.fr](mailto:npseo@cict.fr) tel +33 (0)561 55 67 50 fax +33 (0)561 55 61 96 web <http://www.ladybio.ups-tlse.fr/Orchid-Symposium> orchid symposium <[npseo@cict.fr](mailto:npseo@cict.fr)>

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### TuftsU NEMEB Nov6

NEMEB 2004

The 15th annual meeting of the New England Molecular Evolutionary Biologists will convene November 6, 2004 at Tufts University in Massachusetts.

This is an opportunity to meet other molecular evolutionary biologists and to present and discuss ideas from a wide range of empirical and theoretical topics.

The meeting is open to all scientists from any geographic region and research from around the world. NEMEB serves as an excellent place for graduate students to present their work and their participation is highly encouraged.

Please spread the word and mark the date on your calendar.

We are building a web site at <http://www.tufts.edu/-vet/richlab/nemeb/> We will post another announcement to evoldir when it is time to register.

Yours truly, Stephen Rich and Ned Young, Meeting organizers

e-mail: [Ned.Young@tufts.edu](mailto:Ned.Young@tufts.edu) 508-887-4540

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### UCIrvine SystematicsOriginsOfSpecies Dec16-18

Dear Colleague:

This is to invite you to attend a National Academy of Sciences Sackler Colloquium on Systematics and the Origin of Species. On Ernst Mayr's 100th Anniversary, to be held December 16-18, 2004 at the Beckman Center of the National Academies of Sciences and Engineering in Irvine, California. The following information, and Preliminary Program and Registration Forms, can be accessed at the NAS web site. <http://www4.nationalacademies.org/nas/-nashome.nsf/urllinks/NAS-58MTTC?OpenDocument> The Colloquium will celebrate the 100th birthday of the eminent evolutionist Ernst Mayr and the 62nd an-

niversary of the publication of his Systematics and the Origin of Species (1942), one of the four books often considered as the foundations of the modern theory of evolution. The Colloquium will explore the main topics in Mayr's book and examine the same (and related) issues in the light of current science, although the focus will be on speciation, rather than on systematics.

Attendance at the Colloquium is limited to 250 registered individuals. To facilitate the participation of younger scientists, we request that you extend this invitation to interested graduate students and postdocs. The NAS has provided funds to supplement the expenses of participating graduate students and postdocs up to \$100 for hotel costs and \$150 for air travel. A maximum of 100 awards will be granted, with priority based exclusively on the order in which requests (accompanied by the registration fee) are received. Notification of the award will be made shortly after receiving the application but the awards will be paid after the Colloquium, upon documentation of qualifying expenses. The Travel/Hotel Award Form is attached.

Registrations will be accepted only when the registration fee is included and in the order in which they are received. The registration fee is \$350, which includes the cost of meals, reception, and banquet. However, an early registration fee of \$250 (also including meals, reception, and banquet) is available to those posting their registration by November 1, 2004. And, a reduced all-inclusive registration fee of \$100 is offered to Graduate Students and Postdocs who register by November 1st. A block of hotel rooms has been reserved at the Hyatt Newporter Resort at a discount rate of \$106, plus tax, for a single or a double. Hotel reservations must be made when registering (see Registration Form for more information). Hotel reservations must be made by November 24, 2004. Please do not call the hotel directly for room reservations, as they can only accept reservations through the NAS. Shuttle bus service between the hotel and the Beckman Center will be provided free of charge at specified times.

Sincerely, Francisco J. Ayala for the Colloquium Organizing Committee, Jody Hey, Walter M. Fitch, and Francisco J. Ayala

Program - <http://www4.nationalacademies.org/nas/nashome.nsf/2bcd43d2a04ce99085256b87005a8c7b/-bcb31cf4edcd064085256e8d006c951c?OpenDocument>

Registration Form - <http://www4.nationalacademies.org/nas/nashome.nsf/2bcd43d2a04ce99085256b87005a8c7b/-f1ee04265ae74dfe85256e12007a9f29?OpenDocument>

Graduate Student/Postdoc Grant Application - <http://www4.nationalacademies.org/nas/>

[nashome.nsf/2bcd43d2a04ce99085256b87005a8c7b/-353e9df463de94aa85256a4200694d47?OpenDocument](http://www4.nationalacademies.org/nas/nashome.nsf/2bcd43d2a04ce99085256b87005a8c7b/-353e9df463de94aa85256a4200694d47?OpenDocument)

Hotel and Travel Information - <http://www4.nationalacademies.org/nas/nashome.nsf/2bcd43d2a04ce99085256b87005a8c7b/-74dfe23960b1c0c485256eed0070aa9b?OpenDocument>

Francisco J. Ayala 2001 National Medal of Science Laureate University Professor Donald Bren Professor of Biological Sciences University of California, Irvine Department of Ecology and Evolutionary Biology 321 Steinhaus Hall Irvine, CA 92697-2525, USA tel: +1-949-824-8293 fax: +1-949-824-2474 [fjayala@uci.edu](mailto:fjayala@uci.edu) [http://www.faculty.uci.edu/profile.cfm?faculty\\_id=-2134](http://www.faculty.uci.edu/profile.cfm?faculty_id=-2134)

"Francisco J. Ayala" <[fjayala@UCI.EDU](mailto:fjayala@UCI.EDU)>

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## ULausanne EvolGenomics Oct7-8

The program of the Lausanne Ecological and Evolutionary Genomics meeting Oct 7-8 2004 is available at the following link

<http://www.3eme-cycle.ch/biologie/pages/joint.html>

The meeting is free and open to everybody

Sincerely, Laurent Keller

Laurent Keller Department of Ecology and Evolution BB University of Lausanne 1015 lausanne Switzerland [Laurent.Keller@ie-zea.unil.ch](mailto:Laurent.Keller@ie-zea.unil.ch) <http://www.unil.ch/dee/page6763.html>

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## UReading PopGenetics Dec15-17

The 38th annual meeting of the Population Genetics Group will be held at the University of Reading, hosted by the School of Animal and Microbial Sciences.

All registration is web-based and details can be found at

<http://www.rubic.rdg.ac.uk/~pgg> \*\*\*\*\*

PopGroup is an informal meeting which brings together scientists working in population genetics and evolutionary biology, mainly, but by no means exclusively, from the United Kingdom and other European countries. All areas of evolutionary biology are

covered. See <http://www.lifesci.sussex.ac.uk/CSE/-popgroup/programme.pdf> for the programme of the previous meeting.

This year there will be three plenary talks, given by Rasmus Nielsen, Steve Oliver, and Sara Via. There will be three parallel sessions at other times and a poster session. Talks will be allocated on a first-come-first-served basis. The conference will start on the evening of Tuesday December 14th, with the first talk at 9am on the Wednesday, and run through to lunchtime on Friday December 17th.

Reading lies a half-hour train journey on the line be-

tween London and Oxford. It is also about an hour's coach journey from Heathrow Airport. All the conference facilities are on campus and within easy walking distance of each other. Reading is easily accessible by rail, road and air (see travel information and maps).

– Mark A. Beaumont, School of Animal and Microbial Sciences, University of Reading, Whiteknights, P.O. Box 228, Reading RG6 6AJ, UK

Tel 0118 378 7707 Fax 0118 931 0180 Email: [m.a.beaumont@reading.ac.uk](mailto:m.a.beaumont@reading.ac.uk) WWW: <http://www.rubic.rdg.ac.uk/~mab/>

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## GradStudentPositions

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### Lisbon FishEvol

The Department of Animal Biology (Faculty of Sciences - University of Lisbon) has a 10 month Graduate Student Research Grant, immediately available in the frame of the FCT/FEDER project "Genetic structure and evolutionary potential of the a hybridogenetic Iberian fish: a study with molecular markers". The successful candidate will have a Graduation in Biology, with research interests in population genetic structure or related topics and experience with microsatellites and/or sequencing. Furthermore a very good English background and a strong commitment to timely publication of results will be essential.

Informal inquiries may be made to Prof Manuela Coelho at the email address: [mmcoelho@fc.ul.pt](mailto:mmcoelho@fc.ul.pt). Ap-

plication is by CV with details of one referee to the same address.

The deadline for applications is the 30h September 2004.

Please note this grant is available only to Portuguese citizens. Thank you for your attention,

Manuela Coelho (Associate Professor) [mmcoelho@fc.ul.pt](mailto:mmcoelho@fc.ul.pt) Faculdade de Ciências da Universidade de Lisboa 1749-016 Lisboa tel. 217500000 ext. 24319 fax. 217500028.

Maria Manuela Coelho <[mmcoelho@fc.ul.pt](mailto:mmcoelho@fc.ul.pt)>

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### MNHNParis Evol

RESEARCH ASSISTANT and Professor, MNHN, Paris,

If you are interested by position of researchers at the MNHN of Paris (Maîtres de conférences and Professors) you must know that the procedure is rather long and that one needs first of all is registered on a list of qualification, without knowing the positions which will be opened.

Thus I remind to you that the procedure of inscription on the lists of qualification to the functions of Professors and Maîtres de conférences of the Muséum National d'Histoire Naturelle is open since September 10 and until October 19, 2004 on Internet site of the Ministère de l'Éducation Nationale, <http://www.education.gouv.fr>, heading "les enseignants du supérieur" then Antares. (sorry but all is in French in the website!).

I invite all the researchers potentially interested to be registered on this list. About mid of December who are registered now will receive a letter which will require of them to send a file (CV + 2 to 5 publications+ ) to two reviewers. Those which will be accepted could be candidates on the positions which will be published between 2005 and 2009.

Jean-Noël LABAT MUSEUM NATIONAL D'HISTOIRE NATURELLE Département de Systématique et Evolution USM 602 \ UMS 2700 CNRS 16 Rue Buffon CASE POSTALE N 39 75231 PARIS CEDEX 05 FRANCE

tél: 00 33 (0)1 40 79 33 81 fax: 00 33 (0)1 40 79 33 42  
mail: labat@mnhn.fr

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### MaxPlanckInst ZebraFish

Two PhD positions are available at the Max Planck Institute for Ornithology in Seewiesen (near Munich, Germany) starting around December 2004 to study the evolutionary significance of variation in sexual personality traits in a captive zebra finch population.

We seek highly motivated individuals who share our fascination with the diversity of personalities found in animals and who have a background or strong interest in some of the following fields: behavioural ecology, evolution, ethology, psychology, quantitative genetics, and endocrinology. The positions are funded by the DFG in the framework of a newly established Emmy-Noether Research Group "Individual differences in sexual behaviour: proximate mechanisms and adaptive value".

We study the inheritance and fitness consequences of individual differences in male sex drive and aggressiveness as well as female promiscuity and mating preferences. We use a quantitative genetic approach (animal models) to disentangle the different sources (additive genetic, maternal, rearing environment) potentially causing the variation in sexual personality traits. We will also obtain measures of lifetime reproductive success under aviary conditions to test for frequency-dependent selection of personality types and for the adaptive significance of maternal programming of offspring personalities.

The work will involve: breeding and cross-fostering zebra finches, behavioural testing and analysis of videos (using "The Observer"), observation of birds in aviaries, parentage analysis (using microsatellite markers), and quantitative genetic analyses (using "REML-VCE"). However, enthusiasm, reliability and commitment will be more important than experience in those tasks listed. The two PhD students will be expected to work independently as well as contributing to the research of the group.

Initial appointment will be for two years with a possible extension for a further two years subject to research progress. Payment is based on the German BAT IIa/2 federal public service scale. The Max Planck Society is an equal opportunity employer and encourages disabled persons to apply. It also aims at increasing the number of women in fields where they are underrepresented, and therefore encourages them to apply.

Applications should include a concise statement of research interests and work experiences relevant to the project, curriculum vitae and contact details for 2-3 academic references. Please send your application as a single file (Word-doc or pdf) before October 8, 2004 (but late applications may be considered) to <<mailto:forstmeier@orn.mpg.de>> forstmeier@orn.mpg.de. For further information please do not hesitate to contact Wolfgang Forstmeier at: forstmeier@orn.mpg.de.

Max Planck Institute for Ornithology Postfach 15 64 82305 Starnberg (Seewiesen), Germany

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### MichiganStateU SturgeonEvol

Graduate Research Assistantship

Assessment of simulated lake sturgeon supplementation



in Michigan drainages of the Great Lakes

A graduate research assistantship is available at either the PhD or Masters level to study the effects of alternative supplementation strategies on recruitment and genetic diversity of lake sturgeon. The student will join a long-term collaborative study between Michigan State University, the Michigan Department of Natural Resources, and Sturgeon for Tomorrow being conducted on the Black River in the northern lower peninsula of Michigan. Research would include both field and laboratory components. Field work would include capture of adults, collection of gametes and larvae at different life history stages using multiple sampling techniques, assessment of sources of mortality, telemetry, and stream-side rearing of juveniles. Laboratory studies would involve use of molecular and quantitative genetic analyses to assess the effects of the lake sturgeon mating system, stage-based mortality, and of different simulated supplementation strategies on genetic diversity and population levels of coancestry and inbreeding. The successful candidate would start the spring semester (1 January) 2005 or when a suitable candidate is found. Send resume, letter of research interests and contact information for 3 references to: Kim Scribner, PhD, Departments of Fisheries & Wildlife and Zoology, Michigan State University, 13 Natural Resources Building, East Lansing, MI 48824-1222, Tel: (517)-353-3288, e-mail: <mailto:scribne3@msu.edu>scribne3@msu.edu

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## Munich FuncMorphology

Munich, Germany: PhD-position in Physiology / Functional Morphology

We invite applications for 1 PhD position in a DFG financed research project Living at the Extremes Feeding and Fasting, Resting and Exercise in the Arctic. The project will be located at the Department of Biology II of the Ludwig-Maximilians-University, Munich, Germany

The project aims to characterize morphological and physiological plasticity in working Greenland sled dogs. Because they experience extreme seasonal fluctuations in environmental temperature, coupled with changes in food intake and activity levels, these dogs are a good model for studies of plasticity. We will use non-invasive repeated measurements on the same dogs over several years, of oxygen consumption, heart rate, food intake and fecal and urinary output, to estimating whole-

body metabolic rate and energy balance. We will assess seasonal and exercise-related changes in muscle and intestine size using B-image ultrasonography, and cardiac output using Doppler-ultrasonography. Endoscopic biopsies will enable us to monitor concomitant changes in stomach and intestine mucosal ultrastructure. Percutaneous muscle biopsies will provide material for fiber type characterization, quantification of intramuscular lipid stores and enzyme activities, and muscle capillarity. We will use external data loggers to measure heart rate and peripheral arterial oxygen saturation continuously in dogs exercising in the field, while recording running speed and elevation profiles using a global positioning system. Fieldwork will be conducted in Germany and at the Danish Arctic Station at Qeqertarsuaq, on Disko Island off the southwestern coast of Greenland.

The project will be jointly supervised by Prof. Dr. Matthias Starck, Department of Biology II, Ludwig-Maximilians University, and Dr. Sue Jackson, Department of Botany and Zoology, University of Stellenbosch, South Africa.

Requirements: Degree in Biology (MA, MSc, or equivalent degree); good knowledge of physiological and histochemical techniques and statistics; excellent English language skills.

Deadline for applications: 15 Oct. 2004. The position is available for 2 years.

In case of equivalent qualifications, disabled people are preferentially employed.

Application: Send CV, pdfs of publications (if available), and email details of 2 referees by email to J. Matthias Starck (starck@uni-muenchen.de)

Prof. Dr. J. Matthias Starck Department of Biology II University of Munich (LMU) Großhaderner Str. 2 D-82152 Planegg-Martinsried Germany

phone: ++49-89-218074134 fax: ++49-89-21809974134 email: starck@uni-muenchen.de

“J. Matthias Starck” <starck@uni-muenchen.de>

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## UBern Cichlids

Two PhD positions in Ecological Genetics of Speciation and Hybridization in African cichlid fish

Two 3-years PhD projects are available in the research group of Ole Seehausen in both the Aquatic Ecology

section of the Institute of Zoology, University of Bern, Switzerland and the Limnological Research Centre of the EAWAG, Kastanienbaum, Switzerland, to investigate using African cichlid fish, (a) the role of different types of selection during speciation-with-geneflow, (b) the role of hybridization in generating adaptive novelty. One of the least well understood problems in evolutionary biology and biodiversity research is why some organisms have undergone massive speciation and adaptive diversification in very short time, whereas many others, often closely related and superficially similar, have not. Variation in the propensity to speciation with geneflow, driven by ecological processes that exert disruptive or diversifying selection is now receiving a lot of attention, and an intensive debate centres on possible causes of disruptive selection during such speciation. Diverging mating preferences are assumed in many of the models, and in most speciation scenarios for cichlids. However, it is unclear whether such divergence of mating preferences is recruited by selection resulting from competition for ecological resources or by selection resulting from competition for mating opportunities, followed by ecological character displacement.

One PhD project ('speciation project') will aim at developing experimental tests of predictions made by alternative speciation models with regard to the emergence of gene associations and genetic linkage groups comprising alternative sets of genes. We will use hybridizing morphs or incipient species of Lake Victoria cichlids to (i) subject different classes of traits to tests of disruptive selection, and (ii) to identify chromosomal linkage groups containing "speciation traits" by association scans with AFLP markers.

Another unresolved problem associated with the rapid emergence of adaptive diversity is the source of genetic variation that endows some lineages with unusually high rates of phenotypic evolution. One idea is that hybridization in novel environments between genetically well differentiated lineages endows resulting hybrid populations with large variation in quantitative traits that allow them subsequently to radiate in response to diversifying selection. The second PhD project ('hybridisation project') will use experimental ecological genetics to test predictions of this hypothesis. This involves experimental quantification of morphological diversity generated by interspecific hybridization and experimental parameterisation of endogenous and ecological hybrid fitness and functional hybrid diversity in relation to genomic and ecological distinctiveness of parental species. We will work with cichlid fish species that we have recently identified as likely ancestors of several African radiations.

We are looking for enthusiastic, dedicated students with

a master's degree or equivalent (e.g. Diplom) in Biology and background in evolutionary theory and population genetics or quantitative morphometrics. The speciation project will involve a large amount of work in our molecular laboratory, extracting DNA, PCR, fragment separation on automated sequencers, genetic data analysis, but considerable amounts of morphometric and ecological work, fieldwork on Lake Victoria, and possibly experimental fish breeding too. The hybridization project involves breeding and hybridization experiments in our new purpose built fish house on Lake Lucerne, quantification of shape using geometric morphometrics, quantification of colour and behaviour, molecular genetic work using AFLPs, and some fieldwork to collect cichlids. Some experience in the generation and analysis of molecular genetic data will be required for the speciation project, and will be advantageous for the hybridization project too. Experience with quantitative morphometric data analysis and quantitative genetics will be advantageous, as will be experience with handling and maintaining life fish. The successful applicants will be able to work independently, as well as in small teams. They will collaborate closely with postdoctoral researchers in our research group. Further, they will interact with the large community of population biologists, ecologists and geneticists at the Institute of Zoology (<http://www.zoology.unibe.ch/index.php>) and the population and system ecologists at the Limnological Research Centre ([http://www.eawag.ch/research\\_e/kastanienbaum/e\\_index.html](http://www.eawag.ch/research_e/kastanienbaum/e_index.html)). Besides research, PhD students are expected to contribute to undergraduate teaching and supervision (teaching load not exceeding 10 percent of working time). Salaries will be according to Swiss National Science

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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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## UHawaii Manoa BioControl

We are looking for a Ph.D. candidate to work on:

Ecological and genetic change in a biological control agent following introduction to a new region.

(PI's: Russell H. Messing, Mark G. Wright, Ania M. Wiczorek, George Roderick)

Summary: Classical biological control has the potential to mitigate invasive arthropod problems in agroecosystems, reduce insecticide use, and provide greater crop security by combating exotic pests. However, there is a large gap in our understanding of the ecological and genetic changes that occur in natural enemies AFTER they are released in a new environment. The potential risk to non-target species inherent in these changes makes it increasingly difficult to practice biocontrol in an efficient and timely manner. In this project we propose to analyze the behavioral, ecological, and genetic changes, that have taken place in an introduced parasitoid that has been established in Hawaii for ~100 years. *Diachasmimorpha tryoni* was imported early last century from Australia to control the Mediterranean fruit fly, *Ceratitis capitata*, one of the most economically important crop pests in the world, and an enormous threat to U.S. agriculture. The parasitoid became well established on all major Hawaiian islands, contributed significantly to medfly control, but was later documented to attack a non-target beneficial species, the lantana gall fly (*Eutreta xanthochaeta*). The basis for this host-shift and the changes that occurred due to random genetic drift and natural selection have never been examined. We will use a combination of modern genetic (microsatellite DNA and mitochondrial DNA), statistical techniques and behavioral analyses to examine phenotypic and genetic differentiation of parasitoid populations on a variety of spatial scales, including comparisons of original (source) and introduced populations; populations separated on different islands; laboratory and field cohorts; and populations reproducing in nature on target- and non-target hosts. In so doing we will increase our understanding of post-colonization genetic change. The results will be important not only for the practice of biological control, but also for understanding changes in invasive arthropod species. Finally, the project will break new ground in methodology for more robust long-term risk assessment. To our knowledge, this will be the first study to examine directly genetic change in a biological control agent associated with a shift to a non-target species.

A 50% GRA with benefits and tuition waiver applies. Please contact Mark G. Wright, Email [markwrig@hawaii.edu](mailto:markwrig@hawaii.edu)

Mark G. Wright Ph.D. Department of Plant & Environmental Protection Sciences University of Hawaii at Manoa Tel: 808 956-7670

<http://www.ctahr.hawaii.edu/peps/> <http://www2.hawaii.edu/~markwrig> "Mark G. Wright" <[markwrig@hawaii.edu](mailto:markwrig@hawaii.edu)>

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## ULausanne GrassEvolGenomics

### PhD position in Grass Evolutionary Genomics

A 3-years PhD project is available in the Department of Ecology and Evolution, Institute of Biology, University of Lausanne, Switzerland. The goals of this project are to bring insights about evolution of C4 photosynthesis in grasses. The C4 photosynthesis is an important adaptive trait of plants growing in warm conditions. This character has independently appeared in several families and probably independently in several grass subfamilies. The project will focus on the evolution of the gene family encoding Phosphoenolpyruvate carboxylases (PEPCs) in grasses, and particularly on the gene encoding the C4 isoform (ppc-C4). The occurrence of positive events, convergent evolution and gradual selection in C4 characteristics of the ppc-C4 enzyme during the diversification of the grass family will be tested. A broad sample of species representative of both the different grass sub-families and the different photosynthetic pathways will be used. Ppc-C4 sequence data covering gene regions containing codons under selection will be generated for phylogenetic analyses and to detect positive selection. The ppc-C4 gene structure is expected to have been deeply modified during grass diversification in relation to the C4 photosynthesis expression, and the organization of gene parts (such as promoter or intron) and the gene transcription of ppc-C4 will be analyzed in a few species and several genotypes to investigate the evolutionary significance of these re-organizations on the gene expression.

We are looking for an enthusiastic student with a master's degree or equivalent in Biology and background in phylogenetics and molecular genetics. The project will involve a large amount of work in our molecular laboratory (PCR, cloning, phylogenetic data analysis, gene transcription analysis). The applicant will have the opportunity to interact with our collaborators at Kew Gardens (London) and University of Dublin, Trinity College. Several stays and meetings at Kew Gardens and Dublin are anticipated. Salaries will be according to Swiss National Science Foundation (SNF) salary schemes.

Closing date is the 15th of October 2004. Starting date could be as soon as the 1st of November 2004 and should be no later than the 1st of January 2005. Please send a CV, comprising a summary of past re-

search experience and contact details of two referees, and a motivation letter by email to G. Besnard (Guillaume.Besnard@ie-bsg.unil.ch).

Guillaume BESNARD Department of Ecology and Evolution Institute of Biology University of Lausanne CH-1018 Lausanne, Switzerland Tel 0041 21 692 4244 <mailto:Guillaume.Besnard@ie-bsg.unil.ch> Guillaume.Besnard@ie-bsg.unil.ch  
[http://www.unil.ch/dee/page7203\\_fr.html](http://www.unil.ch/dee/page7203_fr.html)  
 Guillaume.Besnard@ie-bsg.unil.ch

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### UOttawa ExptEvol

Graduate student positions in experimental evolution are currently available. Possible projects include, but are not limited to:

1. Distribution of fitness effects among new mutations;
2. Ecology and genetics of diversification in a model adaptive radiation;
3. Evolution of ecological patterns of diversity in model food webs.

Interested candidates should contact Rees Kassen (rees.kassen@uottawa.ca) for details. See also the University of Ottawa website ([www.uottawa.ca](http://www.uottawa.ca)) and the Centre for Advanced Research in Environmental Genomics website ([www.careg.uottawa.ca](http://www.careg.uottawa.ca)) for details.

rkassen@uottawa.ca

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### UWashington ComparativeEvol

NSF-funded Graduate Research Assistanship in Social Insect Neuroethology: A three year, half-time (summer and one academic quarter/year) graduate research assistanship is available in my lab for research on brain and behavioral plasticity in tropical eusocial paper wasps (Hymenoptera: Vespidae). Teaching assistant support is guaranteed for the rest of the year. Research support includes salary and benefits, and travel and living expenses associated with annual field research in Costa Rica, Central America. Field work is conducted in cloud forest habitat in the Monteverde area (<http://www.monteverdeinfo.com/>).

The project includes developmental and experimental studies of targeted brain regions (mushroom bodies) and their functional role in behavioral differences among wasp workers. The project is comparative in approach: we will be performing similar studies on species with simple and relatively complex societies, in order to assess how brain/behavior relationships have evolved along with changes on social complexity. Main methods include field observations/behavioral data collection, and neuroanatomical and stereological analyses of brain morphology, including brain region volumes and neuronal complexity.

Students interested in pursuing a PhD in Animal Behavior can enter my lab at the University of Washington (Seattle) by applying to either the Psychology Department (<http://web.psych.washington.edu/graduate/>) or the Biology Department (<http://depts.washington.edu/biology/graduate.htm>) For more information contact Prof. Sean O'Donnell at sodonnel@u.washington.edu tel. (206) 543-2315.

See my web page for more information: <http://faculty.washington.edu/sodonnell/> Sean O'Donnell Associate Professor Psychology (Animal Behavior) Box 351525 University of Washington Seattle, WA 98195 USA

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### UZurich PlantMolSyst

RESEARCH ASSISTANTSHIPS IN PLANT MOLECULAR SYSTEMATICS/BIOGEOGRAPHY AT THE UNIVERSITY OF ZURICH

POSITION DESCRIPTION: Applications are open for two 3-yr Ph.D. assistantships (or one Ph.D. and one post-doctoral assistantship) in the general research area of plant molecular systematics/biogeography. This international collaborative project, funded by the Swiss National Science Foundation, is entitled: "Dating the origins of plants endemic to the Corso-Sardinian microplate: A window on the biogeography of the western Mediterranean basin" and focuses on seven genera that include species endemic to Corsica and Sardinia. REQUIREMENTS: Demonstrated experience in field collecting, molecular techniques, phylogenetic and molecular dating analysis, and/or ancestral area reconstruction is highly desirable. Excellent knowledge of the English language, written and oral, required. Familiarity with additional European languages would be useful for field work in the Mediterranean and living

in Switzerland. FACILITIES: The Institute for Plant Systematics of the University of Zurich offers excellent research facilities in an international and stimulating academic environment. Located in the heart of Europe, Zurich offers all the cultural opportunities of a major European city in close proximity to the Alps. HOW TO APPLY: Send the following to Prof. Elena Conti, Institute for Systematic Botany, Zollikerstrasse 107, 8008, Zurich, Switzerland (Ph: 0041-1-634 8424; Fax: 0041-1-634 8403; email: ContiElena@access.unizh.ch): I) a one- to two-page application letter addressing, but not limited to the following questions: a) why are you interested in this position? b) What are your career goals?; II) your detailed curriculum vitae, including a list of field collecting, molecular, analytical, and linguistic skills, presentations at scientific meetings, and publications (if applicable); III) a copy of your undergraduate and graduate academic record; IV) two letters (Ph.D. applicants) or three letters (post-doctoral applicants) from your academic advisors addressing i) your intellectual and academic skills, ii) your dedication to science, and iii) your ability to work cooperatively in a team. DEADLINE FOR APPLICATION: October 30, 2004. Positions will remain open until suitable candidates are found. STARTING DATE: Between Jan. 1 and March 1, 2005. –

Elena Conti, Associate Professor University of Zuerich Institute for Systematic Botany, Zollikerstrasse 107, 8008 Zuerich, SWITZERLAND Ph: 0041 1 634 8424 Fax: 0041 1 634 84 03 email: ContiElena@access.unizh.ch <http://www.systbot.unizh.ch/-institut/personen/professoren/conti.htm>

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### UmeaU EvolEcol

A PhD student position at the Department of Ecology and Environmental Science at Umeå University, Sweden.

A PhD student position in ecology (Ref no 313-2739-04)

The PhD position is focused on advancing our understanding of the development of intra-cohort size variation in fish populations in particular and in size-structured populations in general to increase our ability to predict recruitment variation in exploited populations like fish populations. The project will involve a combination of field studies, field and laboratory experiments and size-structured modeling. Aspects to be addressed are the origin of size variation and the devel-

opment of size variation over ontogeny.

Applications in 2 copies should include a short description of your research interests and why you are interested in the position, list of qualifications, attested copies of certificates from higher education and copies of publications including Bachelors/Masters thesis . Further information can be obtained from professor Lennart Persson <lennart.persson@eg.umu.se>. Applications, quoting appropriate reg.no. 313-2739-04, are sent to Umeå University, The Registrar, SE-901 87, Umeå, Sweden, and should arrive no later than September 30, 2004.

Professor Lennart Persson Department of Ecology and Environmental Science Umeå university SE-901 87 Umeå SWEDEN

Phone +46-90-7866316 Fax +46-90-7866705 E mail Lennart.Persson@eg.umu.se [http://www.eg.umu.se/-sve/forskning/akv\\_eko.html](http://www.eg.umu.se/-sve/forskning/akv_eko.html)

Lennart Persson <lennart.persson@eg.umu.se>

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### WashingtonU Biodiversity

Dear Colleague,

The graduate program in Evolution, Ecology, and Population Biology at Washington University in St. Louis is seeking interested and highly motivated graduate students to join a group of laboratories with research interests focusing on the study of the generation and maintenance of biodiversity including studies on: systematics and phylogenetics; behavioral, population and community ecology; population genetics, speciation, macroevolution and macroecology; evolution and development, and the role of biodiversity in ecosystem functioning.

As part of the Division of Biology and Biomedical Sciences ( <http://dbbs.wustl.edu>) our program provides students with the opportunity to conduct research rotations in a wide variety of laboratory atmospheres. Resources outside of the university include the Missouri Botanical Garden, the St. Louis Zoo, and Washington University's biological Tyson research station. Weekly student seminars provide students with frequent opportunities to discuss their own ideas and research, and frequent departmental seminars and visiting scientists give students access to the leading researchers.

A listing of the EEPB faculty and their research interests are included in this mailing.

Each student receives a generous stipend (\$22,000 for 2004-2005), tuition remission and health/disability coverage. Optional group dental coverage is also available. Students are encouraged to apply for nationally competitive fellowships. Students who obtain competitive external funding for at least three years and paying at least 75% of the DBBS stipend may receive an enhanced stipend of \$5,000. The enhanced stipend will continue, as long as he/she remains in academic good standing. Some additional stipulations apply to these awards.

We are deeply committed to creating a diverse program, and ask that you keep us in mind in your interactions with underrepresented student groups (e.g., women, minorities).

We would appreciate your help in making your students aware of exciting graduate opportunities at Washington University in St. Louis. Interested students are encouraged to access our website at ([http://-](http://www.biology.wustl.edu/EEPB/evolbiology.php)

[www.biology.wustl.edu/EEPB/evolbiology.php](http://www.biology.wustl.edu/EEPB/evolbiology.php)). Application to the program is free, and applications are available via the internet (<http://dbbs.wustl.edu/>). You may call the Division of Biology and Biomedical Sciences at (800) 852-9074 for additional application questions.

Thank you for helping make undergraduates at your institution aware of the opportunities at Washington University.

Sincerely,

Jonathan Losos, Ph.D Program Director Evolution, Ecology, and Population Biology

Dana Sterbenz Graduate Student Coordinator Washington University Division of Biology and Biomedical Sciences 660 S. Euclid Ave Box 8226 St. Louis, MO 63110 Medical School office (314) 362-4806 Main Campus office (314) 935-4201 Admissions (800) 852-9074

[sterbenzd@dbbs.wustl.edu](mailto:sterbenzd@dbbs.wustl.edu)

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## AmherstCollege GenomicBiology

The Department of Biology at Amherst College invites applications for a tenure-track position at the Assistant Professor level in some aspect of genomic biology. Areas of interest include, but are not limited to, comparative or functional genomics, protein structure and interactions, and metabolic relations. We especially desire candidates having an experimental research program that can involve undergraduate biology majors. Teaching duties include participation in a team-taught, introductory course that covers genetics, cellular, and molecular biology and includes a lab component, and two upper-level courses in the candidate's area, one with lab. A Ph.D. in biological sciences is required, and postdoctoral experience is expected. Send curriculum vitae and a statement of research and teaching interests to Genomic Biologist Search Committee, Department of Biology, Amherst College, P.O. Box 5000, Amherst, MA 01002 -5000. Have three letters of recommendation sent separately. Review of applications will begin October 18, 2004, and continue until the position has been filled. Further information on the department can be found at [www.amherst.edu/~biology](http://www.amherst.edu/~biology). Ethan Clotfelter Genomic biology Amherst College, USA

Ethan Clotfelter <edclotfelter@amherst.edu>

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## ClemsonU EvolPlantEcol

Faculty positions in Plant Ecology, Invertebrate Biology, Cell Biology and Pathogenic Microbiology

The Department of Biological Sciences at Clemson University invites applications for four tenure-track positions at the Assistant Professor level to support the continuing development of emphasis areas in biomedicine, biotechnology and sustainable environment. Exceptional candidates of higher rank may be considered. We

are seeking broadly educated biologists who can interact with other faculty having diverse interests ranging from cell and molecular biology through organismal biology to ecology and evolution. Research may be in any area(s) of the specialty. Successful candidates will be expected to establish research programs of national distinction and be inspiring teachers. Postdoctoral experience is required. Primary teaching responsibilities will be an undergraduate course for majors and graduate course(s) in one's specialty.

Applications should include a resume, up to three reprints, a statement of current and planned research, a statement of teaching interests and philosophy, and three letters of recommendation sent by the applicant's references. Applications and letters of recommendation should be sent to: Ms. Vicky Freeman, Search Committees, Department of Biological Sciences, Clemson University, Clemson, SC 29634-0314. (Letters and envelopes should clearly indicate the position sought, e.g. "Cell Biology".) Electronic applications and letters of recommendation may be sent to Ms. Freeman at: [vfrmn@clemson.edu](mailto:vfrmn@clemson.edu). (Include the name of the position followed by "Search Committee" on the subject line.) Completed applications should arrive by October 15, 2004.

Brief descriptions of the four positions are listed below. Additional information on Departmental resources and the research interests of faculty may be obtained at our departmental website: [www.clemson.edu/biosc](http://www.clemson.edu/biosc). Plant ecology. We seek a broadly trained botanist with expertise in plant ecology. Areas of specialization include (but are not limited to) global change, restoration ecology and physiological ecology. Primary teaching responsibilities include a large undergraduate course in plant biology and a graduate level course in a specialty area.

Invertebrate Biology. We seek a broadly trained invertebrate biologist who uses modern (e.g. cell, molecular, modeling) techniques in his/her research. The research specialty is open, but individuals with interests in behavior, evolution, development, comparative immunology or comparative physiology would complement existing strengths. Primary teaching responsibilities include a large undergraduate course in invertebrate biology and a graduate level course in a specialty area. This individual would also serve as a campus-wide re-

source to those faculty and students using or studying invertebrate systems.

**Cell Biology.** We seek individuals who use innovative approaches to study fundamental problems in cell biology in plant, animal, or microbial systems. Applicants using state-of-the-art molecular and cellular techniques and a strong interest in imaging as applied to a topical problem in cell biology are encouraged to apply. The specific area of research is open, but should be one that is competitive for NIH funding. Primary teaching responsibilities include a large enrollment undergraduate cell biology course and a graduate level course in a specialty area. This individual would be expected to serve as a resource to other researchers within and outside the department who use cells or cellular techniques in their research.

**Pathogenic Microbiology.** We seek a broadly trained microbiologist who, in keeping with other strengths in the department and on campus, studies problems involving interactions among organisms such as food safety, bacterial biofilms, biosecurity issues, microbial community dynamics, or induction of synergistic or opportunistic infection. Primary teaching responsibilities include an upper level pathogenic microbiology course which is required of all microbiology majors and a graduate level course in a specialty area.

Clemson University is an Equal Opportunity/ Affirmative Action Employer. Women and minority candidates are encouraged to apply

– Dr. Timothy P. Spira Professor, Department of Biological Sciences 132 Long Hall Clemson University Clemson, SC 29634-0314

864-656-1424 (Voice) 864-656-0435 (FAX) [stimoth@clemson.edu](mailto:stimoth@clemson.edu)

Timothy Spira <[stimoth@CLEMSON.EDU](mailto:stimoth@CLEMSON.EDU)>

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### CollegeWilliamMary EvolDevo

#### FACULTY POSITION IN DEVELOPMENTAL BIOLOGY

The College of William and Mary's Department of Biology invites applicants for a tenure track position at the ASSISTANT PROFESSOR level in developmental biology. In particular, candidates with an interest in "evo-devo" or developmental genetics are encouraged to apply. The successful candidate will be expected to

establish and maintain an extramurally funded research program involving both undergraduate and master's degree students. Teaching responsibilities include an upper division course in developmental biology and another course in the candidate's area of expertise. Candidates must demonstrate the potential and motivation to achieve excellence in teaching. Previous experience teaching undergraduate courses would be viewed favorably, and postdoctoral research experience is expected. A competitive start-up package is available. Review begins November 1, 2004, and will continue until an appointment is made. Submit a letter of application, curriculum vitae, statements of research plans and teaching philosophy, and three letters of reference to Developmental Biology Search Committee, Department of Biology, The College of William and Mary, P. O. Box 8795, Williamsburg, VA 23187-8795. Information on the college may be obtained at <http://www.wm.edu/>. The College is an EEO/AA employer.

Dr John Swaddle Biology Department College of William and Mary Williamsburg, VA 23187-8795 Tel. 757.221.2231 Fax. 757.221.6483 <http://fsweb.wm.edu/~jpswad>

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### CollegeWilliamMary PlantEvolution

#### PLANT PHYSIOLOGY/PLANT DEVELOPMENT POSITION

The Department of Biology of the College of William and Mary (a state-supported university, and our nation's second oldest institution of higher learning) announces its search for a tenure track ASSISTANT PROFESSOR in PLANT PHYSIOLOGY or PLANT DEVELOPMENT. The Department offers a moderate teaching load (one course a semester) in an environment that encourages high quality research. We are looking for a person with a strong background in botanical sciences; one who can excite undergraduate and graduate students about the scope and significance of research in plant biology from organismal to molecular levels. The candidate is expected to incorporate very bright and highly motivated students into their research program.

Teaching responsibilities are a plant physiology course with laboratory, the lecture portion of a large course in general botany (250 students, mostly biology majors) to be taught in alternate years, and another course in the area of the candidate's expertise to alternate with general botany. Laboratories to accompany the lectures



in the general botany course will be organized, coordinated, and taught by another faculty member and a corps of graduate students in consultation with the new faculty member. Candidates must possess skills in communicating with and motivating undergraduates and masters-level graduate students in both large and small courses, and must demonstrate the potential and motivation to achieve excellence in teaching. The first year's teaching load is negotiable.

We are searching for a person who can interact with other biologists from the organismal to the molecular biology level, and motivate students to learn about plants. The successful candidate will be a Teacher/scholar: an accomplished teacher who can maintain an active research program involving both undergraduate and graduate students, and secure extramural funding to support that research. We offer a competitive start-up package. Our Department members (24 tenure track positions, 5 research faculty) have productive research programs, often with students as co-authors of publications. Our faculty have been very successful in obtaining outside funding for their research programs (e.g., NSF, NIH, HHMI, NASA, and other federal, state, and private agencies including 8 NSF CAREER or equivalent awards since 1994). Further information about our faculty and their research activities can be obtained at <http://www.wm.edu/biology>. We would appreciate it if you would distribute this notice to other laboratories in plant physiology/plant development and to any recent Ph.D. or Post-doctoral students who might be appropriate for our position.

Review begins October 1, 2004, and will continue until an appointment is made. Interested candidates should submit a letter of application, curriculum vitae, statements of research plans and teaching philosophy, a list of courses relevant to the botanical sciences taken and taught, and three letters of reference to Plant Physiology Search Committee, Department of Biology, The College of William and Mary, P. O. Box 8795, Williamsburg, VA 23187-8795. The College is an EEO/AA employer.

George W. Gilchrist Email #1: [gwgilc@wm.edu](mailto:gwgilc@wm.edu)  
Department of Biology, Box 8795 Email #2:  
[kitesci@cox.net](mailto:kitesci@cox.net) College of William & Mary Phone:  
(757) 221-7751 Williamsburg, VA 23187-8795 Fax:  
(757) 221-6483 <http://gwgilc.people.wm.edu/>

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## Finland FishQuantGenet

Hi,

MTT Agrifood Research Finland seeks

Research Scientist

To participate a research project developing breeding scheme for farmed European whitefish (*Coregonus lavaretus*). A three-year project includes estimation of genetic parameters (heritabilities and genetic correlations) and economic values for production, quality and feed utilisation traits. The breeding scheme will be optimised based on the economic and genetic information.

The successful candidate will join in the Biometrical Genetics team at MTT Animal Breeding. MTT Animal Breeding is a highly productive, international and interdisciplinary section focusing on quantitative genetics, molecular genetics, biodiversity and reproductive biology of farm animals and farmed fish. The Biometrical Genetics team is an internationally recognized group developing breeding schemes for farm animals and fish, and methods for breeding value estimation, and studying quantitative genetics of production, quality and health traits in animals. The team has close intellectual ties to other top-quality research groups in Europe and North-America and to industrial breeding organisations. The team consists of 11 researchers. For further information see [www.mtt.fi/english/](http://www.mtt.fi/english/) or contact Dr. Antti Kause (email: [Antti.Kause@mtt.fi](mailto:Antti.Kause@mtt.fi); work tel: +358-3-41883608).

The successful candidate should have either have PhD or MSc. Salary will be agreed based on qualifications. The candidate should have interest in developing expertises in the field of biology and genetics of farmed fish, animal breeding, biometrics and scientific writing. Strong guidance in these fields will be provided.

The three-year position will start 3 January or as agreed between the parties. The position is located in Jokioinen, in SW Finland.

Please send your application with a subtitle 'c/o Asko Mäki-Tanila' before 4 October 2004 to: MTT Agrifood Research Finland, Kirjaamo, 31600 Jokioinen, Finland, or to [kirjaamo@mtt.fi](mailto:kirjaamo@mtt.fi).

MTT Agrifood Research Finland is a research institute acting under the Ministry of Agriculture and Forestry in Finland. MTT has 900 employees. Our research

fields are biology, technology and economy.

Antti Kause

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 Antti Kause MTT Agrifood Research Finland Animal  
 Production Research Animal Breeding 31600  
 Jokioinen Finland work tel: 358-3-41883608 work  
 fax: 358-3-41883618 email: Antti.Kause@mtt.fi <http://www.mtt.fi/english/>  
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### GreatLakesWaterInst EvolBiolResTech

Research Specialist position is available in the laboratory of Dr. Rebecca Klaper at the Great Lakes WATER Institute to assist in research to develop genomic indicators of ecological adaptations and environmental health of species within the Great Lakes. Individual will be responsible for assisting in field collections of fish and invertebrates, animal cultures, RNA and protein extractions, plasmid preparation, QPCR and general laboratory management.

Qualification: B.S. in biology, molecular biology or ecology/environmental science with at least two years of experience using molecular techniques described above (M.S. preferred). Ability to do field work and laboratory work with an attention to detail.

The Great Lakes WATER Institute is located in beautiful Milwaukee, Wisconsin on the shores of Lake Michigan. The Great Lakes WATER Institute provides a focal point for research, education and outreach in the state of Wisconsin, aimed at a thorough understanding of the Great Lakes and other aquatic and environmental resources. The WATER Institute is associated with the University of Wisconsin-Milwaukee which serves more than 23,000 students, including 4,000 graduate students. Milwaukee is known for its many summer festivals and other cultural options including museums, an active music scene, and wonderful food. Home to the Milwaukee Brewers and the Wave. Milwaukee is also in close proximity to several other Midwestern cities including Chicago and Madison and to many natural areas available for skiing, biking, fishing hunting etc.

This is a 12-month appointment with possibility of extension. Salary will be range 2 (dependent upon qualifications) with excellent fringe benefits.

Deadline is October 10, 2004. To apply please send let-

ter of application outlining qualification and interests as well as a resume and contact information for three references to Rebecca Klaper at rklaper@uwm.edu.

For full description of position please see: [www.uwm.edu/Dept/GLWI/pos/res\\_spec\\_200409.html](http://www.uwm.edu/Dept/GLWI/pos/res_spec_200409.html)  
 rklaper@uwm.edu

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### HaverfordCollege EvolBiol

Haverford College seeks an evolutionary biologist with a cellular and molecular perspective for a new tenure-track position beginning Fall 2005. The successful candidate will contribute to a vibrant, interdisciplinary, liberal arts curriculum and receive teaching credit for maintaining an active research program engaging undergraduate students. Applications are especially welcome from scholars applying evolutionary and/or computational approaches to areas in plant biology, developmental biology, the emergence and diversity of life, or comparative genomic analyses. At least two years of post-doctoral research experience required. Send letter of application, c.v., statements of research plans and teaching interests, and three current letters of reference by October 18, 2004 to: Merleen MacDonald, Search Secretary, Haverford College, 370 Lancaster Avenue, Haverford, PA 19041-1392. Questions to Jennifer Punt, Dept. Chair (jpunt@haverford.edu). Haverford College (<http://www.haverford.edu>) is an Equal Opportunity/Affirmative Action Employer and is committed to diversifying its faculty and enriching its curriculum. –

Jenni Punt Associate Professor and Chair, Biology Haverford College 370 W. Lancaster Ave. Haverford, PA 19041

TEL: 610-896-1304 FAX: 610-896-4963 e-mail: jpunt@haverford.edu

<http://www.haverford.edu/biology/Punt/punt.html>  
<http://www.haverford.edu/biology/Punt/punt.html>

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### IowaStateU EvolTheory

Department of Ecology, Evolution, and Organismal Biology Iowa State University

Faculty Position: Ecological/Evolutionary Theory

The Department of Ecology, Evolution, and Organismal Biology (EEOB) at Iowa State University seeks a tenure-track assistant professor developing theory relevant to ecological and/or evolutionary processes. EEOB ([www.eeob.iastate.edu](http://www.eeob.iastate.edu)) comprises 32 faculty who use integrative approaches that bridge disciplines and span multiple levels of biological organization. The successful candidate is expected to develop a nationally recognized research program and contribute to undergraduate and graduate teaching. Applicants must have a Ph.D. in ecology, evolution, or related field and demonstrate excellent research and teaching potential. Applicants should submit a curriculum vitae, statements of research/teaching interests, and selected reprints and have three letters of recommendation sent to Dr. Kirk Moloney (<<mailto:kmoloney@iastate.edu>>[kmoloney@iastate.edu](mailto:kmoloney@iastate.edu)), Search Committee Chair, EEOB Department, Iowa State University, Ames, IA 50011-1020 by October 25, 2004 to guarantee consideration. ISU is an EO/AA employer. Women and members of minority groups are encouraged to apply.

Dean C. Adams Assistant Professor Department of Ecology, Evolution, and Organismal Biology Department of Statistics Iowa State University Ames, IA 50011 tel: (515) 294-3834 fax: (515) 294-8457 web: <http://www.public.iastate.edu/~dcadams>

Dean Adams <[dcadams@iastate.edu](mailto:dcadams@iastate.edu)>

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### LehighU EvoEcol

Dear Colleagues:

The Department of Earth and Environmental Sciences has an opening at the assistant professor level for an ecologist with expertise in natural or anthropogenically induced environmental change. We are particularly interested in individuals whose research integrates issues in conservation ecology or biodiversity with alteration of ecosystem structure and function. We expect the successful applicant to develop a vigorous, externally funded research program, teach undergraduate courses in areas such as conservation ecology or biodiversity, statistics, and graduate courses in their specialty to complement our curriculum, and to mentor Ph.D., M.S., and undergraduate students. This position is the one of several new hires in Earth and Environmental Sciences, engineering, and the social sciences expected to participate in a university wide, multidis-

ciplinary initiative focusing on the environment.

To receive full consideration, applicants should submit by November 15th a letter of application, curriculum vitae, statement of research and teaching interests, up to 3 reprints, and the names of three referees to: Donald Morris, Search Committee Chair, Department of Earth and Environmental Sciences, 31 Williams Drive, Lehigh University, Bethlehem, PA 18015. For further information contact Donald Morris ([dpm2@lehigh.edu](mailto:dpm2@lehigh.edu)) or see the EES Department web page at: <http://www.ees.lehigh.edu/>

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### LouisianaStateU QuantGenetics

#### QUANTITATIVE GENETICS

The Department of Biological Sciences at Louisiana State University invites applications for a tenure-track position in the area of quantitative genetics, broadly defined. While we anticipate hiring at the Assistant Professor level, candidates at higher academic ranks are also encouraged to apply. We are especially interested in those whose research interests bridge departmental strengths in ecology and evolution. A Ph.D. or equivalent degree in a biological science or related field is required; post-doctoral experience is preferred. The successful candidate will be expected to develop a strong, extramurally funded research program and contribute to teaching and advising at the graduate and undergraduate levels. Review of applications will begin November 15, 2004, and will continue until a suitable candidate is identified. Send curriculum vitae (including e-mail address), statements of research and teaching interests, three letters of recommendation, and no more than three representative publications to: Dr. Michael Hellberg, Chair, Quantitative Genetics Search, Department of Biological Sciences, Louisiana State University, 202 Life Sciences Bldg., Baton Rouge, LA 70803 U.S.A. Ref. Log #0169. Additional information about the LSU Department of Biological Sciences is available at: <http://www.biology.lsu.edu> .

LSU is an Equal Opportunity/Equal Access Employer.

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### MaxPlanckInst EvoEcol

## Avian Behavioural / Evolutionary Ecologist

Applications are invited for a 5-year research position at the Max Planck Institute for Ornithology at the Radolfzell location, starting February 2005. We are looking for a highly motivated scientist who is interested in developing a research program that links studies of migration and breeding ecology. Priority will be given to projects that complement research done at Seewiesen. Current research there focuses on reproductive behaviour, including timing of reproduction, hormonal control of sexual behaviour, effects of inbreeding, the evolution of song and plumage colour, the neuroendocrine control of song, mate choice, sperm competition, promiscuity, and avian personalities.

The Max Planck Society is an independent, non-profit organization that promotes research in its own institutes. We offer a highly stimulating, international environment, outstanding research facilities (both locally and at Seewiesen) including unique aviary facilities, access to molecular and endocrinological laboratories, access to a long-term ringing scheme and superb logistic support. The working language is English. There are no teaching obligations, but the institute has an active PhD program via connections to the Universities of Konstanz and Munich.

For further information, please contact Prof. Dr. Bart Kempenaers ([b.kempenaers@orn.mpg.de](mailto:b.kempenaers@orn.mpg.de)), or visit <http://www.ornithol.mpg.de> Candidates should send a curriculum vitae, a statement of research interests and scientific goals, and the names and addresses of three referees to the address below. To ensure full consideration, applications should arrive before 1 December 2004. Short-listed candidates will be invited to Radolfzell in January 2005 for a symposium at which they have the opportunity to present their work.

Applications should be addressed to:

Ms. Heike Gorny-Leimpeters Max Planck Institute for Ornithology Postfach 1564 D-82305 Starnberg-Seewiesen, Germany Phone: +49-(0)8157-932-232 E-mail: [gorny@orn.mpg.de](mailto:gorny@orn.mpg.de) Fax: +49-(0)8157-932-400

The Max Planck Society is an equal opportunity employer and encourages disabled persons to apply. It also aims at increasing the number of female staff members in fields where they are underrepresented, and therefore encourages women to apply.

[b.kempenaers@orn.mpg.de](mailto:b.kempenaers@orn.mpg.de)

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**MaxPlanckInstOrnithology**  
**AvianEvolGenetics**

## Behavioural Geneticist / Molecular Ecologist

A full-time scientist position is available at the Max Planck Institute for Ornithology to work in the newly established research group Behavioural Ecology and Evolutionary Genetics. We are looking for a highly motivated scientist who is interested in developing a research program in avian evolutionary genetics, in close collaboration with behavioural ecologists. The candidate should be willing to invest in developing genetic tools to study behaviour and sexually selected ornaments of birds. We are particularly interested in the study of reproductive behaviour, including timing of reproduction, effects of inbreeding, mate choice, the evolution of promiscuity, and avian personalities.

We offer a highly stimulating, international environment, outstanding research facilities including new laboratories and aviary facilities, and superb logistic support. The working language in our group is English. The position does not include teaching, but teaching is encouraged via existing contacts and collaboration with the University of Munich (LMU).

The starting date is January 01, 2005. The position is initially for five years, with an option to become permanent.

The salary will be according to German public service rules (BAT) including social security benefits.

The Max Planck Society is an equal opportunity employer and encourages disabled persons to apply. It also aims at increasing the number of female staff members in fields where they are underrepresented, and therefore encourages women to apply.

Candidates should send a statement of research interests and a curriculum vitae to the address below. To ensure full consideration, applications should arrive before November 01, 2004.

Prof. Dr. Bart Kempenaers Director Max Planck Institute for Ornithology Postfach 15 64 D-82305 Starnberg (Seewiesen) Germany

E-mail: [b.kempenaers@orn.mpg.de](mailto:b.kempenaers@orn.mpg.de) Phone: +49-(0)8157-932-334 or -232 Fax: +49-(0)8157-932-400

Bart kempenaers <[b.kempenaers@orn.mpg.de](mailto:b.kempenaers@orn.mpg.de)>

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## MiamiU Bioinformatics

Miami University, Oxford, Ohio Department of Botany Bioinformatics

Applications are invited for a tenure-track Assistant Professorship, beginning August 2005 on the Oxford campus, to join a broadly based department committed to educational and scholarly excellence, faculty/student diversity, and international preeminence as a comprehensive botanical program. We seek a plant biologist with expertise in bioinformatics with strong computer and programming skills. Research areas may include (but are not limited to): genomics, functional genomics, proteomics, gene expression, or systems biology/modeling. Ph.D. in botany/closely related discipline and commitment to teacher-scholar excellence required. Postdoctoral experience is preferred. Candidates will teach courses from introductory to graduate level, develop a vigorous, extramurally-funded research program, mentor student research, and perform service to the University. Participation in the interdisciplinary graduate program in Molecular Biology, as appropriate, is expected.

Miami University is ranked among the top national public universities. The Oxford campus, 32 miles NW of Cincinnati, has over 16,000 students. The Botany Department (17 full-time/3 affiliate faculty, 32 graduate/60 undergraduate students) offers B.S./A.B. through Ph.D. degrees in Botany and an M.A.T. in Biological Science. The Turrell Herbarium, Electron Microscopy Facility, Ecology Research Center, and Center for Bioinformatics and Functional Genomics offer research support (see [www.muohio.edu/botany](http://www.muohio.edu/botany) for additional information). Applications (curriculum vitae; teaching statement including experience, interests, and philosophy; statement of research goals and experience; 3 reprints) and 3 reference letters should be sent to: Dr. Linda E. Watson, Chair, (indicate Bioinformatics Search), Department of Botany, Miami University, Oxford, OH 45056 fax (513) 529-4243. Screening begins 15 November 2004. Miami University is an equal opportunity affirmative action employer.

Linda Watson <[watsonle@muohio.edu](mailto:watsonle@muohio.edu)>

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## MiamiU EvolBiology

Miami University, Oxford, Ohio Department of Botany Evolutionary Biology

Applications are invited for a tenure-track Assistant Professorship, beginning August 2005 on the Oxford campus, to join a broadly based department committed to educational and scholarly excellence, faculty/student diversity, and international preeminence as a comprehensive botanical program. We are seeking candidates with expertise in the evolutionary biology of plants, fungi, or protists. Applications are encouraged from scientists who are investigating evolutionary questions at the molecular, cellular, or organismal level. Ph.D. in botany/closely related discipline and commitment to teacher-scholar excellence required. Postdoctoral experience is preferred. Candidates will teach courses from introductory to graduate level, develop a vigorous, extramurally-funded research program, mentor student research, and perform service to the University. Participation in interdisciplinary graduate programs in Ecology and/or Molecular Biology, as appropriate, is expected.

Miami University is ranked among the top national public universities. The Oxford campus, 32 miles NW of Cincinnati, has over 16,000 students. The Botany Department (17 full-time/3 affiliate faculty, 32 graduate/60 undergraduate students) offers B.S./A.B. through Ph.D. degrees in Botany and an M.A.T. in Biological Science. The Turrell Herbarium, Electron Microscopy Facility, Ecology Research Center, and Center for Bioinformatics and Functional Genomics offer research support (see [www.muohio.edu/botany](http://www.muohio.edu/botany) for additional information). Applications (curriculum vitae; teaching statement including experience, interests, and philosophy; statement of research goals and experience; 3 reprints) and 3 reference letters should be sent to: Dr. Linda E. Watson, Chair, (indicate Evolutionary Biology Search), Department of Botany, Miami University, Oxford, OH 45056 fax (513) 529-4243. Screening begins 15 November 2004. Miami University is an equal opportunity affirmative action employer.

Linda Watson <[watsonle@muohio.edu](mailto:watsonle@muohio.edu)>

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## MichiganStateU EvolutionaryEcol

Four Faculty Positions in Ecology W.K. Kellogg Biological Station - Michigan State University

Michigan State University's W.K. Kellogg Biological Station (KBS), internationally recognized for research and education in ecology, evolutionary biology, and sustainable agriculture, invites applications for the positions of Director and three additional tenure-stream faculty. Successful candidates will become part of a 10-member faculty committed to the discovery and application of fundamental ecological knowledge in complex landscapes.

Director of KBS

We seek a dynamic and interactive individual with broad interests in ecology, excellent research credentials and leadership abilities, and a demonstrated interest in field stations to be the next Director of KBS. This position carries programmatic responsibilities for research, education, and outreach programs that utilize the outstanding facilities of the Station. The position is expected to be filled at the rank of Full Professor in any area of ecology, evolutionary biology, agriculture, or natural resources.

Aquatic Ecology

This position is open to all areas of aquatic ecology. We are looking for an individual with broad conceptual interests and strong quantitative skills, and in particular for applicants working at the population or community level and who have an appreciation for the interactions among ecological, evolutionary, and behavioral processes. This position will be filled at the Assistant or Associate Professor level.

Microbial Ecology

We are looking for a field-oriented microbial ecologist with research interests in the interplay between microbial populations and communities and the processes and interactions they mediate in aquatic and terrestrial habitats. This position will be filled at the Assistant Professor level.

Agronomy / Cropping Systems Ecology

We seek an agronomic innovator committed to improving row-crop ecosystems by incorporating ecological and management knowledge in novel ways, and with broad interests in soil and plant ecology and manage-

ment. This position will be filled at the Assistant or Associate Professor level.

More information about the Kellogg Biological Station and these positions, including application procedures, can be found at [www.kbs.msu.edu](http://www.kbs.msu.edu). Applications will be reviewed beginning November 1 (Director, Aquatic, and Microbial Ecology positions) or November 15 (Cropping Systems position).

Michigan State University is an Equal Opportunity / Affirmative Action Institution

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## NewYorkU ComparativeFuncGenomics

To appear soon in Nature, Science and Cell:

NEW YORK UNIVERSITY Faculty Positions Department of Biology Center for Comparative Functional Genomics

As part of a multi-year hiring plan, New York University's Center for Comparative Functional Genomics in the Department of Biology invites applications for multiple faculty positions (rank open) to begin September 1, 2005, or as negotiated, subject to budgetary and administrative approval. Candidates using experimental and/or computational methods and working at the interface of biological mechanisms, evolution, and genomics/bioinformatics are especially encouraged to apply. Candidates will be expected to have or develop active, externally funded research programs and to participate in the department's teaching activities at both the undergraduate and graduate levels. The department offers an outstanding and collegial research environment with a strong molecular genetic and developmental focus, as well as active collaborations with other programs within the university, including bioinformatics, computational biology, and genomic consortia initiatives with New York institutions. Application letter with research statement, curriculum vitae, and three letters of reference should be sent to: Chair of the Search Committee, Department of Biology, New York University, 1009 Silver Center, 100 Washington Square East, New York, N.Y. 10003. Selection of initial candidates will begin November 1, 2004, and proceed on a rolling basis thereafter. NYU is an Equal Opportunity/Affirmative Action Employer.

Mark L. Siegal email: [mark.siegal@nyu.edu](mailto:mark.siegal@nyu.edu) <http://www.nyu.edu/fas/dept/biology/faculty/siegal/>

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## PennState EvoAnthro

The College of Liberal Arts at Penn State invites applications for the position of

HEAD of the Department of Anthropology

to be filled at tenured professor rank effective August 1, 2005. Applicants should have scholarly credentials commensurate with such rank at major research-intensive institutions, an active scientific research program, familiarity with the nature of university research in the natural sciences, and administrative experience or interests. The Department of Anthropology is structured around an emphasis on archaeology, bioanthropology and their integration, with a strong commitment to field and laboratory research. Theoretical perspectives of the department are materialist and evolutionary, with substantive emphasis on genetic, developmental, and evolutionary aspects of complex phenotypes, biomedical genetics, paleontology, population sciences, human ecology, and the evolution of complex societies and of social complexity. The successful candidate will lead a department that, though small, has a distinguished history, with multiple faculty members and graduates achieving honors such as membership in US and international academies of science and MacArthur fellowships. We seek a new generation of leadership to use opportunities for development here to implement creative objectives for the future of anthropology, evolutionary sciences, and/or their connections. Review of applications will begin October 15th, 2004 and will continue until the position is filled. Send letter of applications, c.v., and the names of three references to: Ms. Karen Connelly, Administrative Assistant, Anthropology Headship Search Committee, 111 Sparks Building, The Pennsylvania State University, University Park, PA 16802. Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

For information about the Department, see <http://www.anthro.psu.edu/> Kenneth M Weiss Dept of Anthropology Penn State University 409 Carpenter Bldg University Park, PA 16802-3404

phone: 814.865.0989 fax: 814.863.1474 email: kenweiss@psu.edu (my old ID of kmw4@psu.edu still works) lab web page: [http://www.anthro.psu.edu/-weiss\\_lab/index.html](http://www.anthro.psu.edu/-weiss_lab/index.html) Ken Weiss <kenweiss@psu.edu>

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## PortlandStateU EvoBiol

Expansion of the Department of Biology at Portland State University continues this year with the addition of faculty members in the areas of plant systematics, plant physiology, genetics, and microbial physiology/ecology. We expect to continue to add new faculty for the next three to five years to build on our thematic strengths in ecology and evolutionary biology, environmental genomics, conservation biology, extremophile biology, physiology and behavior, and science education. We are particularly interested in applications from individuals whose interests and research activities span one or more of the above areas. More information about the department can be found on our web site: <http://www.bio.pdx.edu/>. Following is a copy of the text from an ad for the four positions we plan to fill this year that will appear in an upcoming edition of Science.

The Department of Biology at Portland State University invites applications for the following four positions at the Assistant through Professor level:

**Plant Systematist:** We seek an individual who is applying molecular phylogenetic tools to general questions on the evolutionary history of plants. The department is especially interested in individuals who are taking an integrative approach, with expertise in development, morphology, or other areas of plant biology. Interest in overseeing the curation of our herbarium is also desirable.

**Experimental Geneticist:** We seek an individual working with established non-mammalian genetic systems or with emerging or novel systems. The ideal candidate would combine genetic, molecular and genomic approaches to understanding key concepts of cell and/or organismal biology

**Microbial Physiologist/Ecologist:** We seek an individual using genomic and/or proteomic approaches to study the physiology and ecology of Archaea or Bacteria. The Department has specific interests in microbes and viruses from extreme environments.

**Plant Cell Physiologist:** We seek an individual with expertise that would span the fields of organismal and cellular physiology. We are particularly interested in candidates who are studying plant physiology in an environmental or evolutionary context.

Minimum qualification is a Ph.D. in the biological sciences, with priority given to candidates with postdoctoral experience and who have demonstrated success in developing a research program through publications and external funding. We encourage applications from individuals whose interests complement existing departmental strengths (see the departmental web site: ([www.bio.pdx.edu/](http://www.bio.pdx.edu/))). The successful candidate will be expected to develop an externally funded research program, be effective in teaching at the undergraduate level, and participate in the training of graduate students in our masters and Ph.D. programs. These are tenure-track, 9-month appointments to begin in the fall of 2005. Review of applications will begin 1 October, 2004, and will continue until the positions are filled. A curriculum vitae, statement of current and future research, and three letters of reference should be sent to: Chair, (Appropriate) Search Committee, Department of Biology, P.O. Box 751, Portland State University, Portland, Oregon 97207. Portland State University is an Affirmative Action, Equal Opportunity institution and, in keeping with the President's diversity initiative, welcomes applications from diverse candidates and candidates who support diversity.

– Mitchell B. Cruzan, Associate Professor Department of Biology P.O. Box 751 Portland State University Portland, OR 97207

<http://web.pdx.edu/~cruzan/>

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### SUNYStonyBrook ResTech

Research Technician, Stony Brook University

A full-time research technician is available in the Department of Ecology and Evolution at Stony Brook University. The technician will assist in generating DNA sequence data for projects related to the phylogeny and evolution of salamanders and frogs. The duration of the position is one year.

Duties will consist of running basic molecular lab procedures (e.g., DNA extraction, PCR amplification, and DNA purification), limited data analysis (e.g., editing DNA sequences), and ordering supplies.

Minimum requirement is a completed undergraduate degree, preferably in biology, biochemistry, or microbiology. Desirable qualifications include: experience with relevant molecular lab techniques, good organizational skills, and an ability to work well with others. The ap-

plicant should also be able to work independently and maintain good records of work completed.

Expected starting date will be in October 2004.

Interested persons should contact John J. Wiens ([wiensj@life.bio.sunysb.edu](mailto:wiensj@life.bio.sunysb.edu)) with a resume.

John J. Wiens Department of Ecology and Evolution State University of New York at Stony Brook Stony Brook, NY 11794-5245 E-mail: [wiensj@life.bio.sunysb.edu](mailto:wiensj@life.bio.sunysb.edu) Phone: 631-632-1101 FAX: 631-632-7626 Web: <http://life.bio.sunysb.edu/~ee/wienslab/homepage.html>

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### SanFranciscoStateU ResAssist

Research assistant position, San Francisco State University, Romberg Tiburon Center

An additional position is available at the Romberg Tiburon Center for Environmental Studies (<http://rtc.sfsu.edu/>) and the Biology Department at San Francisco State University (<http://www.sfsu.edu/~biology/>). Two EPA and Sea Grant-funded 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 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 work experience, as well as good organizational and communication skills. Experience with microsatellite fragment sizing and other more advanced genetic techniques (either laboratory or computer) is additionally desirable, though not essential.

Candidates should contact Sarah Cohen, preferably by email ([sarahcoh@sfsu.edu](mailto:sarahcoh@sfsu.edu)) and include a cover letter and CV.

To officially apply, please send a CV with your social security number and job posting number 7946.49. to the following address:



San Francisco State University, Human Resources, 1600 Holloway Ave., ADM 252, San Francisco, California 94132. (No email, no faxes). AA/EOE/ADA – Sarah Cohen Assistant Professor Romberg Tiburon Center for Environmental Studies and the Biology Department San Francisco State University 3152 Paradise Drive Tiburon, CA 94920

sarahcoh@sfsu.edu <http://rtc.sfsu.edu/> <http://online.sfsu.edu/~sarahcoh/>

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## SouthwesternU EvolBiol

### JOB OPENINGS: BIOLOGY

#### Lillian Nelson Pratt Endowed Chair

The Department of Biology at Southwestern University invites applications from broadly trained Evolutionary Biologists for the Lillian Nelson Pratt Endowed Chair in Biology. Preference will be given to applicants with expertise in developmental and/or molecular approaches. Appointment will be at a rank commensurate with the experience of the individual filling the position, to begin August 2005. A PhD in a relevant discipline, a strong commitment to undergraduate teaching, and a record of distinction in both teaching and research are required.

Teaching responsibilities will include upper-level Evolutionary Biology for majors, participation in the Introductory Biology sequence, and possible additional courses as required by Departmental needs. The successful candidate may elect to participate in Southwestern's interdisciplinary Environmental Studies Program. The successful candidate will be expected to maintain a research program that actively involves undergraduates.

Interested persons should send a letter of interest, curriculum vitae, statements of teaching and research philosophies, graduate and undergraduate transcripts (unofficial), and three current letters of recommendation to:

Kendra Clovis, Faculty Secretary Biology Search  
Southwestern University P.O. Box 770 Georgetown,  
TX, 78627-0770

Applications received by October 22, 2004 will receive full consideration. Southwestern University is an Equal Opportunity Employer. EOE/M/F For more information, contact the Biology Department Chair, Dr. Re-

becca Sheller, shellerr@southwestern.edu.

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## SyracuseU EvolBiocomplexity

ECOLOGIST. – The Department of Biology at Syracuse University invites applications for a tenure-track position (Assistant to Full Professor) to be filled by August 2005. The successful candidate will have, or will develop, a strong, extramurally funded and highly innovative research program in ecology to join an emerging interdisciplinary research group in biocomplexity. The successful candidate will be one who uses terrestrial or aquatic systems to investigate questions related to plant ecophysiology, plant ecology, microbial ecology, trophic interactions, or ecosystem dynamics. Successful applicants will complement current research strengths within the department and university related to functioning of complex biological systems in different environments. The Department and the University place a high priority on effective teaching. Successful candidates will be expected to teach at undergraduate and graduate levels.

Successful candidates will join a highly productive faculty with strong links to other programs at Syracuse University, including engineering, environmental policy, biochemistry and earth sciences. The Department is in the midst of an exciting growth period, having hired seven new faculty in the past four years. We anticipate hiring six-ten more new faculty over the next five years. Specific information about individual Biology faculty research programs may be found on our website:

<http://biology.syr.edu/facultyresearch/-facultyresearch.html>

The Syracuse biocomplexity group also has close intellectual ties to more than 60 other faculty at several other universities including the nearby State University of New York Environmental Science and Forestry school (SUNY-ESF) and Cornell University. Collaborations among the faculty in this group would allow successful applicants to explore several new interdisciplinary funding initiatives at NSF, including NSF's Biocomplexity Initiative, Emerging Frontiers, and Biology & Mathematics programs.

Applicants should forward a curriculum vitae, a description of past research accomplishments, a clearly focused description of his/her proposed future research goals and a statement of teaching interests. We also request that applicants have at least three letters of reference sent. Please include the name, address, phone

number and e-mail address of each of your references. We invite applicants to submit materials electronically as a single PDF file to: [biosearch@cas.syr.edu](mailto:biosearch@cas.syr.edu). The position will be open until filled, but to be assured your application receives full consideration, we urge that you arrange to have all necessary materials to us by October 15, 2004.

Applications and reference letters should be addressed to:

Larry Wolf, Chair, Biocomplexity Faculty Search Department of Biology 130 College Place Syracuse University Syracuse, NY 13244

Syracuse University is an affirmative action/equal opportunity employer with a strong commitment to equality of opportunity and a diverse workforce.

REPORTS: Reports to Executive Director and oversees several program staff managers.

QUALIFICATIONS: Medical degree or doctorate in clinical microbiology, epidemiology, pharmacology, medicine and/or related discipline, preferably with a specialty in infectious diseases; supervisory experience; strong track record in peer reviewed publication; and high rate of successful grant development. Modeling and risk analysis experience and infectious disease experience a plus.

Application: Please forward resume/CV to Human Resources, APUA, 75 Kneeland Street, Boston, MA 02111. Email: [apua@tufts.edu](mailto:apua@tufts.edu). See [www.apua.org](http://www.apua.org) for more information.

Kelly Chang <[kelly.chang@tufts.edu](mailto:kelly.chang@tufts.edu)>

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## TuftsMedSchool EvolAntibiotics

POSITION DESCRIPTION: Senior Research Director  
The Alliance for the Prudent Use of Antibiotics (APUA) is a global organization dedicated to improving antimicrobial use through research and education. Founded in 1981 and located on the Tufts Medical School Campus in Boston, APUA conducts its public health programs in coordination with affiliated chapters in over 50 countries and the leading national and international public health organizations.

RESPONSIBILITIES: Takes primary lead on organization's research activities. Serves as principal investigator on NIH projects and manager of international scientific consortia and staff engaged in applied research and grant writing concerning infectious diseases.

DUTIES: 1. Advises the Board and Executive Director on scientific/clinical objectives in strategic planning 2. Involves APUA's scientific advisory board in the design of the projects 3. Analyses data on incidence and prevalence of infectious diseases 4. Interprets laboratory data 5. Develops statistical methodologies for analyzing data 6. Takes the lead in large scientific meetings 7. Prepares and presents reports and articles for peer review 8. Prepares and oversees grant proposals 9. Represents organization at various national and international meetings 10. Develops global and organizational partnerships to meet organizational goals 11. Tracks research opportunities at the federal and international levels 12. Interfaces with grantee agency

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## TuftsU MolEvolInfDisease

Research Assistant Position announcement: TuftsU\_MolEvolInfDisease A position is available to work on the molecular evolution of agents of infectious disease and their hosts in the laboratory of Stephen Rich at Tufts University School of Veterinary Medicine. The research assistant is needed to work as part of a research team, doing PCR, automated sequencing, SNP assays, data analysis and other duties. The primary project at the moment is to elucidate the population structure of *Plasmodium falciparum* in malaria endemic regions in the world's tropics.

QUALIFICATIONS: The successful applicant will have strong skills and documented experience in molecular biology (for example, DNA extraction, PCR, cloning, DNA sequencing, SNP assays, etc) and the computer analysis of biological data. The applicant will also be highly organized, have an attention to detail, and be able to work as an independent part of a team. Background and interest in evolutionary theory and/or infectious diseases is also highly favorable.

The incumbent would join a unique research group within the Division of Infectious Diseases at the TUSVM. The campus is located in a rural setting approximately 30 miles west of Boston and 6 miles east of Worcester, Mass..

The start date is flexible, but preferably by 15 October 2004.

To apply, please send a CV, a short statement of re-

search interests and experience, and contact information for three references to:

Stephen M. Rich Associate Professor Division of Infectious Diseases Tufts University School of Veterinary Medicine North Grafton, MA 01536 Phone: 508-887-4749 E-mail (preferred means of communication): stephen.rich@tufts.edu

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## UBielefeld MathGenetics

Postdoc position in Mathematical genetics University of Bielefeld

A position of 'Wissenschaftlicher Mitarbeiter' (maybe best described as a mixture of postdoc and lecturer) is available at the University of Bielefeld, in the biomathematics group recently established within the Technical Faculty. We seek an individual who is interested in theoretical/mathematical aspects of genetics, preferably population genetics. No specific project is predefined – it will be tailored according to the individual's personal interest, ideas and scientific background.

The applicant could either be

- a mathematician with genuine interest in genetics (for example, genetic stochastic processes)
- a biologist with a strong theoretical interest and solid mathematical background.

Apart from research, the individual is obliged to teach (4 hours per week during term).

A PhD is required; some knowledge of German is desirable. The position is for two years with possible extension, starting in March 2004. Salary will be according to BAT IIa, which is about 40.000 - 50.000 Euro per year before tax (depending on age, marital status etc).

Informal inquiries and applications should be sent to the address below before Oct. 20, 2004. Applications via email are welcome.

Bielefeld University offers an excellent research environment, its particular strength being due to close interaction between biomathematics, mathematics, bioinformatics, and biology (all in one huge building!).

Bielefeld University is an equal opportunity employer. Women and members of minority groups including disabled persons are strongly encouraged to apply.

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Prof. Ellen Baake, Technische Fakultät, Universität Bielefeld, Postfach 100131, 33501 Bielefeld, Germany phone (+49) 521 106 4896 email: ebaake@techfak.uni-bielefeld.de URL: <http://www.TechFak.Uni-Bielefeld.DE/ags/bm/>

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## UCDavis TheoPopGenet

Theoretical Population Genetics, 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, ASSOCIATE or FULL PROFESSOR level. Candidates must have a Ph.D. (or equivalent) in the biological sciences or related fields. Candidates should have a strong record of research in theoretical population genetics, focusing on questions of interest to molecular population geneticists and molecular evolutionists. The successful candidate will be expected to teach an undergraduate course in introductory biology or evolution and to participate in the Core Course required of all first-year graduate students in the Population Biology Graduate Group. Applicants should send the following items (as pdfs) to the Chair of the Theoretical Population Genetics Search Committee at bashaneyfelt@ucdavis.edu: curriculum vitae, description of current and projected research, summary of teaching interests and experience, and up to five publications. Applicants should also arrange to have three letters of recommendation sent by e-mail to bashaneyfelt@ucdavis.edu. Closing Date: Open until filled, but all application materials, including letters of recommendation, must be received by November 1, 2004 to assure full consideration. – David Begun Section of Evolution and Ecology and Center for Population Biology University of California Davis, CA 95616 ph 530-754-6362 FAX 530-752-1449 FAX 530-752-1449

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## UCaliforniaSanDiego EvoEcol

Senior Ecologist The University of California, San Diego Section of Ecology, Behavior & Evolution Division of Biological Sciences <http://biology.ucsd.edu/>

The EBE Section invites applications for a senior position in ecology with the rank of Professor or advanced Associate Professor. All qualified applicants are encouraged to apply, including minorities and women.

The area of scholarship is open. We seek candidates who will complement our existing strengths in evolutionary and conservation biology, and who will foster research involving organismic ecology in natural populations or communities. Applicants should have outstanding records of research achievement, and strong, extramurally supported research programs. The appointee is expected to participate fully in departmental affairs and teaching.

Applications will be reviewed upon receipt beginning November 1 and accepted until the position is filled. Mail hard copies of curriculum vitae, publication list, synopsis of professional goals, research and teaching interests, and three letters of reference (mailed directly from referees) to: EBE Search Committee, Biology-0116-I, UCSD, 9500 Gilman Drive, La Jolla, CA 92093-0116.

UCSD is an Equal Opportunity-Affirmative Action Employer with a strong institutional commitment to the achievement of diversity among its faculty and staff.

dwoodruf@ucsd.edu dwoodruf@ucsd.edu

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### UCentralFlorida PopGenetics

Population Geneticist: The Department of Biology at the University of Central Florida invites applicants for a tenure-track Assistant Professor-level position in the area of population genetics. Candidates should have a strong focus on laboratory or field-based organismal research, and use cutting-edge molecular and computational tools. The successful candidate will be expected to establish and maintain an extramurally funded research program in evolutionary biology that complements an active and expanding faculty. The new faculty member will have the opportunity to participate in Ph.D. programs in Conservation Biology and Biomolecular Sciences, and contribute to undergraduate education in Biology. Startup funds and teaching load are competitive. Candidates must have a Ph.D. and appropriate post-doctoral training. Please submit a CV, brief statements of research plans and teaching philosophy, and arrange for three letters of recommendation to be sent directly to: Dr. C. L. Parkinson, Chair, Population Geneticist Search Committee, Department

of Biology, University of Central Florida, 4000 Central Florida Blvd., Orlando, FL 32816-2368. Review of applications will begin November 15, 2004 with an anticipated start date of August 2005. The University of Central Florida maintains a strong research emphasis and is one of the largest universities in the USA (2nd largest in Florida). Please see <http://biology.ucf.edu/~clp/fps.html> for more details. The University of Central Florida is an Affirmative Action/Equal Opportunity Employer. As a member of the Florida State University System, all application materials and selection procedures are available for public review.

Christopher L. Parkinson, Ph.D. Dept. of Biology University of Central Florida 4000 Central Florida Blvd. Orlando, FL 32816-2368 office: 407-823-4847 fax: 407-823-5769 <http://biology.ucf.edu/~clp/> E-mail [cparkins@pegasus.cc.ucf.edu](mailto:cparkins@pegasus.cc.ucf.edu)

Chris Parkinson <[cparkins@pegasus.cc.ucf.edu](mailto:cparkins@pegasus.cc.ucf.edu)>

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### UColorado EvolBiology

#### ECOLOGY AND EVOLUTIONARY BIOLOGY

The Department of Ecology and Evolutionary Biology at the University of Colorado seeks to fill two positions at the Assistant Professor level as the first of six anticipated new hires over the next three years. These are 1) an Ecologist and 2) an Evolutionary Biologist working in any area of the disciplines. The individuals will be expected to pursue active research programs and to teach in their area of expertise. Applicants should submit a current curriculum vitae, statements of research and teaching interests, and the names and addresses of four references to: Ecology Search Committee or Evolutionary Biology Search Committee, 334 UCB, University of Colorado, Boulder CO 80309. Review of applications will begin on November 1, 2004. The University of Colorado at Boulder is committed to diversity and equality in education and employment.

Andrew Martin Dept of Ecology and Evolutionary Biology [am@colorado.edu](mailto:am@colorado.edu)

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### UHawaiiHilo ResTech

Bulletin Board Posting: 8/31/04

RCUH Website: 8/31/04

PCSU RESEARCH PROJECT TECHNICIAN - ID# 24450. Pacific Cooperative Studies Unit (PCSU), Biocomplexity of Introduced Diseases in Hawaii, and University of Hawaii at Hilo. Regular, Full-Time, RCUH Non-Civil Service position, located in Hawaii Volcanoes National Park on the island of Hawaii and University of Hawaii at Hilo. Continuation of employment is dependent upon program/operational needs, satisfactory work performance, and availability of funds. Minimum Monthly Salary: Commensurate with qualifications. Duties: Assists the Co-Principal Investigators with molecular genetic studies of native, indigenous, and invasive species in Hawaii and the Pacific, including parasites and pathogens, and the application of molecular methods to disease diagnostics. Duties include, but are not limited to: application of basic laboratory skills, assist in ordering, purchasing and inventory of supplies, maintaining and replenishing chemical solutions for routine use, DNA extraction and qualification, genetic analyses using Polymerase Chain Reaction (PCR), gel electrophoresis, computer-based data analyses, summarizing laboratory data for reports. Minimum Qualifications: Bachelor's Degree from an accredited four (4) year college or university in Biology, Zoology, Wildlife Science, or other Biological discipline. Six to twelve (6-12) months of research experience using molecular genetics techniques including but not limited to extraction and quantification of DNA, and PCR set up and troubleshooting in a laboratory setting. Basic knowledge in the principles of molecular genetics, including but not limited to, a working knowledge of computer programs used for DNA sequence analysis. Able to organize and complete multiple laboratory procedures on a daily basis. Able to safely handle chemicals and work with high attention to detail for completion and verification of laboratory procedures. Willingness to assist in routine laboratory functions, including ordering and inventory of supplies, and maintenance of laboratory equipment. Able to complete genetic analyses using PCR. Ability to maintain and update databases for records and data storage. Able to successfully perform multi-task duties as described. Desirable Qualifications: One to three (1-3) years of research experience (paid or volunteer) involving the application of molecular methods to biologically related issues, including experience with real-time PCR, micro/spotted array methodology or familiarity with use of robotics workstation. Inquiries: Dr. Susan Jarvi, 974-7358 (Hilo). Application Requirements: The preferred method of applying for this job is through our on-line application process. Please go to

[www.rcuh.com](http://www.rcuh.com), click on "Employment" and navigate to "Job Announcements/Apply for a Job." However, if you do not have access to the Internet, you may apply by submitting resume; cover letter including ID#, referral source, narrative of your qualifications for position and salary history; names, phone numbers and addresses of three supervisory references and copy of degree(s)/transcripts/certificate(s) to confirm your credentials by fax (808) 956-5022 or mail to Director of Human Resources, Research Corporation of the University of Hawaii, 2530 Dole Street, Sakamaki Hall D-100, Honolulu, HI 96822 before the closing date. Closing Date: September 15, 2004. EEO/AA Employer.

Sue Jarvi Biology University of Hawaii 200 West Kawili Street Hilo, HI 96720 808 974-7358 FAX 808 974-7693 jarvi@hawaii.edu

Sue Jarvi <jarvi@hawaii.edu>

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## UHouston EvoIBiol

### FACULTY POSITIONS IN EVOLUTIONARY BIOLOGY

The Department of Biology and Biochemistry at the University of Houston invites applications for two tenure-track Assistant, Associate or Full Professor position in Evolutionary Biology to complement existing strengths within the Division of Ecology and Evolution. Candidates are welcomed from all areas of evolutionary biology, including those using theoretical, molecular, ecological, or experimental approaches. The position requires an earned doctorate and postdoctoral experience. The successful candidate is expected to maintain a nationally competitive externally funded research program and participate in graduate and undergraduate teaching. The Department has spacious laboratories and offers competitive startup packages. Please submit curriculum vitae, list of publications, statement of research interests, and arrange for three letters of recommendation to be sent directly to: Dr. Dan Graur, Chair, Evolutionary Biology Search Committee, Department of Biology and Biochemistry, University of Houston, Houston, TX 77204-5513 (E-mail: [dgraur@uh.edu](mailto:dgraur@uh.edu)). All materials must be received by October 1, 2004.

UH is an Equal Opportunity/Affirmative Action Employer. Minorities, women, veterans and persons with disabilities are encouraged to apply.

– Dan Graur, Ph.D. John and Rebecca Moores Professor Department of Biology & Biochemistry University of Houston Houston, TX 77204 USA

email: dgraur@uh.edu Tel: 713-743-7236 Fax: 713-743-2636 Homepage: nsm.uh.edu/~dgraur

Dan Graur <dgraur@uh.edu>

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## UIowa EvolEcol

Evolutionary Ecology and Evolutionary Theory

The Department of Biological Sciences and the Roy J. Carver Center for Comparative Genomics at The University of Iowa

Applications are invited for two tenure track positions; one at the Associate Professor level, and the second position at the Assistant Professor level. Successful candidates are expected to have an internationally visible research program that strives to understand the molecular basis of significant questions in evolutionary biology using either empirical or theoretical approaches. In the area of Evolutionary Ecology, we are particularly interested in individuals whose research focuses on understanding the genetic basis of environmentally relevant phenotypic variation. In the area of Evolutionary Theory, we are interested in individuals developing novel approaches to the analysis of evolutionary processes, ranging from population genetics to phylogenetics and especially at their interface. The Department is committed to expanding its internationally recognized program in evolution and comparative genomics. More about the department and the Center for Comparative Genomics may be found at <<http://www.biology.uiowa.edu/ccg>>. Candidates should have post-doctoral experience and a recognized record of accomplishment as reflected in publications in leading journals. Successful candidates will be expected to establish and maintain an extramurally-funded research program. Recently renovated space and competitive start-up packages will be made available. Applicants should send a curriculum vitae, statement of research objectives, selected reprints, a description of teaching interests, and the names of three references to: Evolutionary Search Committee, c/o Becky Birch, Department of Biological Sciences, 143 Biology Building, The University of Iowa, Iowa City, Iowa 52242-1324. Review of applications will begin October 1, 2004. The University of Iowa is an affirmative action/equal opportunity employer. Women and minorities are especially encour-

aged to apply.

John M. Logsdon, Jr. Assistant Professor 319 335 1082 office University of Iowa 319 335 1083 lab Department of Biological Sciences 319 335 1069 FAX Carver Center for Comparative Genomics 319 335 1050 dept. 310 Biology Building Iowa City, IA 52242-1324

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

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## UKansas TheoEcol

THEORETICAL ECOLOGIST

The Department of Ecology & Evolutionary Biology at the University of Kansas invites applications for a tenure-track position as an Assistant Professor of theoretical ecology beginning 18 August 2005. Required qualifications: research program in theoretical ecology, with a demonstrated capability of developing mathematical models; Ph.D. (by date of appointment) required; commitment to excellence in research, service, and undergraduate/graduate education; ability to teach courses in theoretical ecology and principles of ecology, statistics, or general biology, as well as seminars in areas of expertise; commitment to seeking extramural funding for research. Preferred qualifications: demonstrated ability to secure extramural funding; teaching experience; post-doctoral experience; commitment to collaborative, interdisciplinary research and teaching. To apply, send curriculum vitae (with e-mail address), reprints, statement of current and future research plans, statement of teaching philosophy and interests, and have at least three letters of recommendation sent to: Dorothy Johanning, University of Kansas, Department of Ecology and Evolutionary Biology, 1200 Sunnyside Avenue, Rm 2041, Lawrence, KS 66045-7534. Review of applications will begin 29 October 2004, and will continue until the position is filled. For more information visit <http://www.ku.edu/~eeb/>. This position is contingent on final budgetary approval. EO/AA Employer

Dorothy Johanning [jdorothy@ku.edu](mailto:jdorothy@ku.edu)

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## ULausanne Bioinformatics

The Faculty of Biology and Medicine of the University of Lausanne invites applications for the position of

Assistant Professor (tenure track) Or Associate Professor (tenured) in bioinformatics

As part of the vigorous development of the life sciences and in parallel with the creation of the Center for Integrative Genomics at the University of Lausanne, we offer a full-time position in bioinformatics starting in Autumn 2005. Candidates should have demonstrated their potential to develop an innovative research program in bioinformatics with a strong interest in biological or medical applications. Specific research areas include genomics, molecular sequence analysis, molecular evolution, protein structure, gene expression, network analysis, computational proteomics, computational genetics, or structural and functional genomics and data visualization. The successful candidate is expected to conduct an independent research program funded by external resources, to establish strong collaborations within the Faculty, and to become affiliated to the Swiss Institute of Bioinformatics. He/she will be responsible of coordinating the teaching of bioinformatics to biology and medical students at the under- and post-graduate levels. Teaching in French is required, but a period of adjustment can be granted. Specifications are listed at: <[http://www.unil.ch/fbm/-page2295\\_fr.html](http://www.unil.ch/fbm/-page2295_fr.html)>[www.unil.ch/fbm/page2295\\_fr.html](http://www.unil.ch/fbm/page2295_fr.html). For further information, please contact Prof. J. Dubochet (jacques.dubochet@lau.unil.ch). Applications including a full CV, a list of publications with a copy of the 5 most relevant ones, a brief statement of the research program and teaching experiences, and at least three names of reference, should be addressed before November 15th 2004, to Prof. P. Mangin, Dean of the Faculty of Biology and Medicine, Bugnon 21, CH-1005 Lausanne. Applications from female candidates are strongly encouraged.

Prof. Jerome GOUDET Dep. Ecology & Evolution, Biol. Building Uni. Lausanne, CH-1015 Lausanne Switzerland NEW <http://www.unil.ch/dee> <http://www.unil.ch/popgen> Tel: +41 21 692 42 42 Fax: +41 21 692 42 65 Secr: +41 21 692 42 60 NEW [jerome.goudet@unil.ch](mailto:jerome.goudet@unil.ch)

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## UMO-Columbia FieldAssist

Hello,

I need a field assistant to help me conduct research in Southern Brazil. I would like to find someone who could be there the whole time I am there (mid October to early February), but time frames are flexible. I would be most appreciative of help in October and November. I would like to find someone in or from Brazil, but it may not be necessary (as long as your passport is valid and immunizations are current). Expenses would be covered (travel, room and board), but I cannot cover a stipend on top of the expenses. This would be a great experience. The work focuses on measuring and manipulating nectar traits.

Please contact me ASAP if you are interested.

Thank you,

Rainee Kaczorowski University of MO-Columbia  
rlk0f5@mizzou.edu

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## UOttawa Systematics Genomics

University of Ottawa FACULTY OF SCIENCE, DEPARTMENT OF BIOLOGY

Assistant Professors - Regular Faculty JOB FUNCTIONS The Department seeks to build on our interdisciplinary strength in environmental genomics and expand into the area of prediction of ecosystem responses to stress using genomic, proteomic and ecoinformatic data. We seek candidates in areas complementary to this theme. These include (but are not limited to) cell biology and microscopy, ecotoxicology, animal physiology, bioinformatics, genetics, molecular biology, plant biology, microbiology, and mathematical biology.

Assistant Professor JOB FUNCTIONS This position will be shared between the University and the Canadian Museum of Nature. This position should focus on systematics of lower plants using molecular techniques. Responsibilities will include research, teaching, public outreach and curatorial work.

Nominee - NSERC University Faculty Award JOB

FUNCTIONS We are seeking a candidate to be sponsored for an NSERC University Faculty Award, a program intended to increase representation of women and Aboriginal peoples in faculty positions. For details, see: [http://www.nserc.gc.ca/professors\\_e.asp?nav=profnav&lbi=c7](http://www.nserc.gc.ca/professors_e.asp?nav=profnav&lbi=c7)

Nominee - Tier II Canada Research Chair JOB FUNCTIONS The department has recently received major funding from the Canada Foundation for Innovation to establish a Centre for Advanced Research in Environmental Genomics. We have excellent laboratory facilities for cDNA microarray analysis and bioinformatics, as well as facilities for many types of environmental analyses. The Research Chair will be encouraged to participate in the activities of the Centre. For more information, please visit [www.chairs.gc.ca](http://www.chairs.gc.ca) Nominee - NSERC Industrial Research Chair JOB FUNCTIONS The successful candidate will be expected to establish collaborative research with industrial partners and to arrange for matching industrial funds. For more information, please visit the NSERC website at [www.nserc.gc.ca/professors\\_e.asp?nav=profnav&lbi=c1](http://www.nserc.gc.ca/professors_e.asp?nav=profnav&lbi=c1)

SELECTION CRITERIA FOR ALL POSITIONS Appointments will normally be at the Assistant Professor level, but applications from candidates at higher ranks may be considered. Successful candidates will participate in undergraduate and graduate teaching in programs in Biology, Biopharmaceutical Sciences and/or Environmental Sciences. Candidates must have a PhD and a strong, independent research program. As the University is a bilingual institution, candidates for regular faculty positions will be expected to teach in both French and English. Successful candidates for the chairs and awards will have reduced teaching and administrative responsibilities during the tenure of their awards. For these positions, bilingualism is an asset.

Applicants should send a description of their teaching interests and their proposed research program, as well as a curriculum vitae, and the names of four referees before October 1, 2004, to: Search Committee, Department of Biology, University of Ottawa, Box 450, Station A, Ottawa, Ontario K1N 6N5 Canada. Fax: (613) 562-5486. According to government policy, all qualified candidates are invited to apply. However, preference will be given to Canadian citizens and permanent residents. The University of Ottawa is an equal opportunity employer. We strongly encourage applications from women, Aboriginal peoples, persons with disabilities and members of visible minorities.

Located in the heart of Canada's capital, offering a broad range of outstanding research and teaching programs to 30,000 students in both of our country's offi-

cial languages, thriving on its growing diversity and its national outlook, the University of Ottawa is Canada's university.

- Dr. Guy Drouin Département de biologie Université d'Ottawa 150, rue Louis Pasteur C.P. 450 Succursale A Ottawa, Ontario Canada K1N 6N5

tel: (613) 562-5800 ext. 6052 FAX: (613) 562-5486 E-Mail: [gdrouin@science.uottawa.ca](mailto:gdrouin@science.uottawa.ca)

Web: <http://www.bio.uottawa.ca/scripts/mbr-f.php?id=8> (en français) <http://www.bio.uottawa.ca/scripts/mbr-e.php?id=8> (in english)

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## UPierreMarieCurie EvolParasitology

Professorship in Evolutionary Ecology of host-parasite interactions

A full professorship in evolutionary parasitology is available at the Department of Evolutionary Parasitology at the University of Pierre et Marie Curie in Paris.

We have a special interest in scientists conducting field experiments on host-parasite coevolution or parasite evolution. However, research achievement is more important than the specific research area.

Teaching responsibilities will vary from introductory courses for 1st year students to specialized courses in our graduate program in biodiversity and ecology. Introductory courses must be taught in French.

The starting date is September 2005.

As French regulations require that professors first qualify with the National Council of Universities, the application is set up in two stages: - Qualification: application from 10 September 2004 to 19 October 2004 (see [http://www.education.gouv.fr/personnel/enseignant\\_superieur/enseignant\\_chercheur/antares.htm](http://www.education.gouv.fr/personnel/enseignant_superieur/enseignant_chercheur/antares.htm) section 'Qualification') - Final procedure: application to the University in early 2005

For more information, contact Jacob Koella ([jkoella@snv.jussieu.fr](mailto:jkoella@snv.jussieu.fr)) and see the department's web page (<http://parasito-evolutive.snv.jussieu.fr/>)

Jacob Koella Laboratoire de Parasitologie Evolutive Université P. & M. Curie 7 quai St. Bernard, CC237 75252 Paris Cedex 5 France



Tel 0033 1 44273809 Fax 0033 1 44273516 <http://parasito-evolutive.snv.jussieu.fr/>

24-25, Haus 26, D-14476 Potsdam, Germany, Email: [tiedeman@rz.uni-potsdam.de](mailto:tiedeman@rz.uni-potsdam.de)

Ralph Tiedemann <[tiedeman@rz.uni-potsdam.de](mailto:tiedeman@rz.uni-potsdam.de)>

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## UPotsdam EvolBiol

Research Scientist position (BAT-IIa-O) in Evolutionary Biology for 3 years (prolongation possible), University of Potsdam

At the Institute of Biochemistry and Biology, University of Potsdam, Unit of Evolutionary Biology/Systematic Zoology, we look for a qualified Research Scientist to be appointed for 3 years (prolongation possible), starting as soon as possible (1st of February 2005 at the latest).

The successful applicant is expected to perform independent research compatible with the scope of the Unit of Evolutionary Biology/Systematic Zoology. He/she will be involved in undergraduate and graduate teaching. For undergraduates, the applicant has to give courses in animal species determination as well as zoological field courses. He/she should work on an actual topic of evolutionary biology and hold a profound zoological knowledge.

Applicants must hold a university degree (Diploma or Master of Science) and a PhD of a relevant topic. They should appreciate interdisciplinary research and cooperation within the Unit of Evolutionary Biology/Systematic Zoology as well as with international cooperation partners. Familiarity is desired with techniques of at least one of the following fields: molecular genetics, expression analysis, immunology, cytogenetics/karyology, as well as their application in evolutionary research.

The University of Potsdam is an equal opportunity employer. If equally qualified, disabled applicants will be preferably considered. The University of Potsdam aims at increasing the number of female researchers and encourages qualified females to apply.

Appointment is pending on financial approval.

Please send your application with details of your research concept, external funding (if any), statement on possible cooperation within the Unit of Evolutionary Biology/Systematic Zoology, and a list of your teaching experience before 21st of September 2004 to: Prof. Dr. Ralph Tiedemann, University of Potsdam, Institute of Biochemistry and Biology, Evolutionary Biology/Systematic Zoology, Karl-Liebknecht-Str.

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## URochester EvolBiology

FACULTY POSITIONS Assistant/Associate/Full Professors of Biology

The Department of Biology at the University of Rochester is continuing its major hiring initiative, with faculty positions in Developmental, Cell, Molecular, and Evolutionary Biology. We anticipate making at least five new tenure-track appointments over the next several years. We are interested in individuals who would value being in a Department that includes scientists studying both molecular mechanisms and evolution. Special consideration will be given to candidates who bridge the traditional disciplines of developmental, cell, molecular, and evolutionary biology. We will consider outstanding candidates in all areas of biology, and positions are available at all levels. Send curriculum vitae, a statement of research interests, and the names of three references to: Faculty Search Committee, Department of Biology, University of Rochester, Rochester, NY 14627-0211. Review of applications will continue until positions are filled. The University of Rochester is an Equal Opportunity Employer.

H. Allen Orr Department of Biology University of Rochester Rochester, NY 14627

phone: 585-275-3838 fax: 585-275-2070 <http://128.151.242.156/~orrlab/ORRHOME-2002.HTML>

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## UStThomas BehavioralBiol

The Department of Biology at the University of St. Thomas invites applications for a tenure-track position at the assistant professor level for a behavioral biologist, to start September 2005. Individuals whose research integrates the study of molecular/physiological mechanisms with ecological/evolutionary approaches are particularly encouraged to apply. Teaching opportunities exist in behavior, conservation biology, and advanced

courses in behavioral ecology, evolution, or related areas of expertise. Some contribution to teaching majors introductory courses is also expected. The successful candidate is expected to develop a vigorous, fundable research program involving undergraduates. Faculty research is supported by ongoing course-release time and start-up funds to establish a research laboratory. Ph.D. is required, and post-doctoral experience is preferred.

The University of St. Thomas seeks to develop morally responsible individuals who combine career competency with cultural awareness and intellectual curiosity. A Catholic and urban university, St. Thomas continues to develop outstanding regionally and nationally recognized academic programs and support services as it strengthens its ties to the local community, particularly the vibrant and ethnically diverse cities of Minneapolis and St. Paul. The Biology Department is housed in the 200,000 sq. ft. Frey Science and Engineering Center, which opened in 1997 and is equipped with state of the art instructional and research facilities. Biology website: [www.stthomas.edu/biol/](http://www.stthomas.edu/biol/) Send a cover letter (refer to position #200073), curriculum vitae, statement of teaching philosophy and research experience and goals, and three letters of recommendation electronically to: [www.hr.stthomas.edu](http://www.hr.stthomas.edu), or mail to: UST, Mail #AQU217, 2115 Summit Ave., St. Paul, MN, 55105. For full consideration, application materials should be received by November 1, 2004.

The University of St. Thomas is an Affirmative Action/Equal Opportunity Employer.

Simon K. Emms, Chair, Department of Biology, OWS 390, University of St. Thomas, 2115 Summit Avenue, St. Paul, MN 55105

skemms@stthomas.edu 651 962-5228

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## UTennessee LandscapeEcolEvol

### TWO POSITIONS AT TENNESSEE: LANDSCAPE ECOLOGY, EVOLUTION

The Department of Ecology and Evolutionary Biology at UT seeks applicants for two positions at the assistant/associate professor level to start August 1, 2005.

Landscape Ecologist: Field or laboratory experience is required. We encourage applicants who wish to develop a research program based in part on regional ecosystems. Teaching will include an upper division landscape ecology course, a graduate course in the appli-

cant's specialty, and eventual participation in a lower division ecology course. Committee chair: Dr. Dan Simberloff.

Evolutionary Biologist: We seek applicants who integrate theoretical and empirical approaches to study evolutionary processes in natural populations. Research areas might include gene flow, speciation, co-evolution, or phylogeography. Teaching will include an upper division population genetics course, a graduate course in the applicant's specialty, and eventual participation in a lower division genetics course. Committee chair: Dr. Gary McCracken.

For more information visit [eeb.bio.utk.edu](http://eeb.bio.utk.edu). Candidates should apply to the appropriate committee chair at the Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996. Applicants should send a CV, statements of research and teaching goals, and arrange for three reference letters to be submitted. Applications will be reviewed beginning Oct. 25, 2004. The University of Tennessee is an Equal Employment Opportunity/Affirmative Action/Title VI/TitleIX/Section 504/Americans with Disabilities Act/Age Discrimination in Employment Act institution in the provision of its Education and Employment programs and services.

Randall Small Dept. of Botany, 437 Hesler Biology The University of Tennessee Knoxville TN 37996 USA

phone: 865-974-6207 fax: 865-974-2258 e-mail: [rs-small@utk.edu](mailto:rs-small@utk.edu) <http://web.utk.edu/~rsmall> Randy Small <[rsmall@utk.edu](mailto:rsmall@utk.edu)>

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## UTexasArlington EvolBiol

The Department of Biology at the University of Texas at Arlington seeks four geneticists/genomicists to contribute to an active research group in these areas. We are very interested in candidates whose research is at the interface of genetics or genomics, and evolution or ecology. Salaries and start-ups will be highly competitive. Candidates at all ranks are encouraged to apply.

The Department offers both Master's and Ph.D. degrees, and the majority of our graduate students (about 70 in total) conduct research in evolution and ecology. The Department is very research-oriented, is well equipped for molecular work with an ongoing, major expansion in this area, has an extensive, newly constructed animal care facility, and offers ample labo-

ratory space. UTA is the second-largest and fastest-growing component of the University of Texas system, with approximately 25,000 students, about 1,600 of whom are undergraduate Biology majors.

Arlington is a medium-sized city of about 300,000, located midway between Dallas and Fort Worth. It has a wide diversity of neighborhoods and housing styles, and the cost of living is very low relative to the vast majority of comparable metropolitan areas in North America. Arlington lies at the center of the Dallas/Fort Worth metroplex, about a 20 minute drive from DFW International Airport, 20 minutes from downtown Fort Worth, and 30 minutes from downtown Dallas. Arlington, Dallas, and Fort Worth each have very distinct characters; all are vibrant cities that offer extensive cultural and recreational opportunities.

The following ad for these positions currently is online in Science.

#### FOUR POSITIONS IN GENETICS, GENOMICS, MOLECULAR BIOLOGY

The University of Texas at Arlington

The Department of Biology at The University of Texas at Arlington invites applications for four tenure-track positions at the rank of Assistant Professor. Exceptional candidates at other ranks will be considered. We seek eukaryotic and prokaryotic genomicists to contribute to the department's focus in genetics and genomics. Additional hires will add to this core group or complement it. We are interested in individuals using prokaryotic or eukaryotic systems to address questions in population, evolutionary or ecological genetics/genomics; quantitative or developmental genetics; molecular evolution and related areas. Applicants must have a Ph.D. and a demonstrated record of research productivity commensurate with their experience. The successful candidates will be expected to establish vigorous, extramurally funded research programs and participate in both graduate and undergraduate education. The Department offers several degrees including a Ph.D. in quantitative biology. Located in the Dallas/Fort Worth metropolitan area, UTA is a fast-growing, comprehensive university that is the second largest in the University of Texas system. Hiring will be contingent on the completion of a satisfactory criminal background investigation for security-sensitive positions. Additional information is available at the website: <http://www.uta.edu/biology/>. Applicants should submit curriculum vitae; copies of up to five significant publications; statements of research and teaching interests and philosophy; and the names, e-mail addresses, and telephone numbers of four persons who can provide letters of reference. Review of completed applications

will begin October 15, 2004, and will continue until the positions are filled. Send applications to: Genetics Search Committee, Department of Biology, University of Texas at Arlington, Box 19498, 501 South Nedderman Drive, Arlington TX 76019-0498.

UTA is an Equal Opportunity/Affirmative Action Employer.

Paul T. Chippindale Associate Professor Department of Biology, University of Texas at Arlington Phone: (817) 272-2703/2521, Email: [paulc@uta.edu](mailto:paulc@uta.edu)

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### UTexasAustin LabTech

#### Job: FULL-TIME RESEARCH TECHNICIAN

A full-time research position is available at the University of Texas at Austin to work on a study of natural selection in three-spine sticklebacks. The position is full-time and is anticipated to start in early January 2005 and last for two and a half years. The technician will be responsible for data collection from preserved specimens, including morphological measurements, diet analysis, stable isotope ratio analysis, nucleic acid extraction, and genetic analysis, as well as being responsible for training undergraduate assistants. The research technician will also participate in one to two months of field research each year to collect specimens from natural populations on Vancouver Island, British Columbia. Applicant will therefore have to be able to spend between 1 and 2 months each year in moderately remote areas of Vancouver Island. A 1-page summary of the project goals can be found at <https://webspace.utexas.edu/dib73/Bolnicklab/summary.pdf>

Candidates having a B.S. or graduate degree are invited to apply. Training will be provided, so experience with the specific techniques to be used in this study are less important than responsibility, a high level of motivation, and attention to detail. A background in evolution and ecology is preferred, as is experience with field and/or laboratory research.

Yearly salary will depend on education and experience, starting between \$23,000 and \$25,000 per year plus benefits.

Interested applicants should send a brief letter outlining their background, research experience, and long-term goals; a CV; and names and addresses (including telephone number and email addresses) of three references to: Dr. Dan Bolnick Section of Evolution and Ecology

Storer Hall University of California at Davis Davis, CA 95616 USA (530) 752-6784 danbolnick@mail.utexas.edu

Informal inquiries are welcome and should be directed to Dan Bolnick.

Applications will be reviewed starting September 30. Applications will be considered until a suitable candidate is found. The University of Texas is an EOAA Institution committed to cultural diversity and compliance with the ADA.

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

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## UToronto EvolEcol

**FUNCTIONAL ECOLOGY** The Botany Department of the University of Toronto invites applications for a tenure-track position in Functional Plant Ecology at the Assistant Professor level, starting July 1, 2005. The successful candidate should have a Ph.D. and post-doctoral experience. We seek a scientist studying mechanisms of ecological function. Individuals from any area of ecology are welcome to apply. We particularly welcome applicants whose research integrates multiple levels of ecological enquiry, and who use novel techniques including molecular, biochemical, isotopic, physiological and/or comparative approaches. Teaching responsibilities will include participation in core undergraduate courses in ecology and environmental biology, and a course in the successful candidate's area of expertise. Applicants should arrange to have three letters of reference sent directly to the address below. In addition, the applicants should send their curriculum vitae, copies of significant publications, and statements of research and teaching interest to the Chair, Functional Ecology Search Committee, Department of Botany, University of Toronto, 25 Willcocks Street, Toronto, ON M5S 3B2 Canada before November 15th, 2004. Inquiries should be directed to Professor Spencer Barrett at barrett@botany.utoronto.ca

Spencer C.H. Barrett Professor, FRSC & FRS Canada Research Chair

Department of Botany, University of Toronto, 25 Willcocks Street, Toronto, Ontario, Canada M5S 3B2

Phone 416-978-4151/5603, FAX 416-978-5878 E-mail Barrett@botany.utoronto.ca [www.botany.utoronto.ca](http://www.botany.utoronto.ca)

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. The University of Toronto offers the opportunity to teach, conduct research and live in one of the

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## UToronto MicrobialInteractions

### MICROBIAL INTERACTIONS

#### DEPARTMENT OF BOTANY UNIVERSITY OF TORONTO

The Botany Department of the University of Toronto invites applications for a tenure-track position in Microbial Biology at the Assistant Professor level, starting July 1, 2005. The successful candidate should have a Ph.D. and preferably post-doctoral experience.

Candidates area of expertise should be in plant-microbe interactions, microbe-microbe interactions, or microbe-environmental interactions, with an emphasis on prokaryotes. Candidates addressing mechanistic or evolutionary questions using genomic approaches are particularly encouraged to apply.

Teaching responsibilities will include participation in core undergraduate courses in cellular or molecular biology, and a course in the successful candidates area of expertise.

Applicants should arrange to have three letters of reference sent directly to the address below. In addition, the applicants should send their curriculum vitae, copies of significant publications, and statements of research and teaching interest to the Chair, Microbial Interactions Search Committee, Department of Botany, University of Toronto, 25 Willcocks Street, Toronto, ON M5S3B2 Canada before October 15th, 2004. Inquiries should be directed to Prof. David Guttman at david.guttman@utoronto.ca.

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. The University of Toronto offers the opportunity to teach, conduct research and live in one of the most diverse cities in the world and is strongly committed to diversity within its community. The University especially welcomes applications from visible minority group members, women, Aboriginal persons, persons with disabilities, members of sexual minority groups,

and others who may contribute to the further diversification of ideas.

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## WesternKentuckyU 2 EvoNeuroscientist

Neuroscientist Assistant Professor

Western Kentucky University, Department of Biology, invites applications for a nine-month, tenure-track appointment in Neuroscience. Ph.D. required, post-doctoral experience preferred. Additional qualifications include ability to teach and mentor students (undergraduate and M.S.) with a high level of effectiveness, excellence in research, and commitment to pursuit of extramural funding. Partially supported by Kentucky's NIH-INBRE program <http://www.kbrin.louisville.edu/index.html>. Teaching responsibilities may include neurobiology, introductory biology, and advanced course in area of expertise. Submit CV, separate statements of teaching and research interest and three letters of recommendation to: Neuroscience Search Committee, Department of Biology, Western Kentucky University, Bowling Green, KY 42101-3576. Review of applications begins 25 October 2004 and will continue until the position is filled. Preferred start date, January 15, 2005. For more detailed information visit <http://bioweb.wku.edu>.

Biotechnology Center Coordinator

Western Kentucky University, Department of Biology also seeks experienced Laboratory Coordinator to operate the Biotechnology Center Core Facility. Candidate must have a M.S. degree or a B.S. degree with equivalent experience, and broad experience in molecular and cellular techniques. Must be: well organized, able to manage laboratory services and equipment effectively, able to direct student workers and student researchers in the safe application of biotechniques. Salary commensurate with experience. Permanent twelve-month full-time position. For more information on the position visit <http://biotech.wku.edu/>. Submit letter of application and a resume illustrating experience and skills along with three references to the Department of Human Resources, Wetherby Administration Building, Room 42, Western Kentucky University, 1 Big Red Way, Bowling Green, KY 42101-3576. Internet URL: <http://www.wku.edu/Dept/Support/HR/>. Applications are accepted until the position is filled.

All qualified individuals are encouraged to apply, includ-

cluding women, minorities, persons with disabilities and disabled veterans. Western Kentucky University is an Affirmative Action/Equal Opportunity Employer.

Dr. Jeffrey M. Marcus Assistant Professor Department of Biology 1 Big Red Way Western Kentucky University Bowling Green, KY 42101 -3576 (270) 745-2043 FAX (270) 745-6856

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## WesternKentuckyU ResAssist ButterflyGenet

Western Kentucky University is seeking applicants for a Research Assistant in the Biology Department. This is a full-time 5-year National Institutes of Health grant-supported position in a butterfly and fruit fly genetics laboratory. The technician will work with other members of the lab to understand the genetics, development, and evolution of butterfly color patterns. Specific responsibilities of the position will include supervising the daily activities of the laboratory, performing experimental protocols, insect care, assisting in the supervision and training of lab personnel, supply ordering and inventory, preparing stock solutions, data acquisition and analysis, and general laboratory upkeep. Occasional fieldwork and travel may be required. Additional information about the laboratory can be found at: <http://bioweb.wku.edu/faculty/-Marcus/default.html> and questions can be addressed to [jeffrey.marcus@wku.edu](mailto:jeffrey.marcus@wku.edu)

Qualifications: Bachelor's Degree in Biology or a related discipline. Applicants must have laboratory research experience. Experience desired in molecular biology techniques, *Drosophila* genetics, insect culture, or Lepidopteran field collection. Grant writing experience is desirable. Strong communications skills are a plus.

Interested candidates should submit a cover letter describing their qualifications and experience, resume, and three professional letters of reference to: Human Resources Department, Search Committee - Research Assistant (Genetics Laboratory), Western Kentucky University, Wetherby Administration Building, Room 42, 1 Big Red Way, Bowling Green, KY 42101-3576. Applicants may track the status of this position at: <http://www.wku.edu/Dept/Support/HR/>. Review of application materials will begin on October 5, 2004 and will continue until the position is filled.

All qualified individuals are encouraged to apply includ-

ing women, minorities, persons with disabilities and disabled veterans.

Western Kentucky University is an Affirmative Action/Equal Opportunity Employer.

Dr. Jeffrey M. Marcus Assistant Professor Department of Biology 1 Big Red Way Western Kentucky University Bowling Green, KY 42101 -3576 (270) 745-2043 FAX (270) 745-6856

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### WoodsHoleMA ResAssist BacterialMutualists

RESEARCH ASSISTANT POSITION, Molecular Evolution of Bacterial Endosymbionts, Woods Hole, MA.

A full-time Research Assistant (Technician) position is available in the lab of Jennifer Wernegreen at the Marine Biological Laboratory (MBL) in Woods Hole, Mass. Individual will contribute to projects using comparative, molecular approaches to study the evolution of bacterial mutualists associated with insects. Applicants should have strong interests in molecular evolution, genomics, symbiosis and/or microbiology, and a genuine drive to perform basic research. The Wernegreen lab is housed within the MBL's Josephine Bay Paul Center (<http://jbpc.mbl.edu/>), a collaborative research group focused on molecular evolution, comparative genomics, computational biology, and microbial diversity.

**Job Responsibilities:** Project duties will include high-throughput sequencing, extraction of nucleic acids from microbial cultures and insect samples, Polymerase Chain Reaction, cloning of PCR products, gel electrophoresis, and quantitative PCR. RA will also contribute to general lab organization and maintenance (e.g., making and autoclaving general solutions, ordering reagents, etc). Analytical duties include DNA sequence alignment, phylogenetic analysis, design of PCR and sequencing primers, and the use of molecular databases.

**Requirements:** This position requires an independent, organized, and motivated individual with demonstrated skills and experience in molecular techniques. Educational requirements include a B.A., B.S., or M.S. in molecular biology or a related field and prior experience in an active research lab. Familiarity with Mac OS, a working knowledge of UNIX/LINUX operating systems, experience in computer programming includ-

ing PERL, and knowledge of microbiology are pluses. Applicants must have excellent written, verbal and interpersonal skills, a superb work ethic, and exceptional organizational skills. Position level and salary will depend upon education and experience.

**To Apply:** The application consists of: (1) a letter describing your interests and prior research experience, detailing your specific experience with any of the job responsibilities listed above; (2) a curriculum vitae, (3) copies of your transcripts from undergraduate and, if applicable, graduate work; (4) a reference letter from an individual who acted as your supervisor in a previous research position/experience, and the contact information of two additional references. Send all materials to: Marine Biological Laboratory, ATTN: Human Resources reference code [RAI II GME], 7 MBL Street, Woods Hole, MA 02543; phone, 508/289-7422, email: [resume@mbl.edu](mailto:resume@mbl.edu). Please ask referees to send letters directly to the MBL and to note the position code RAI II GME.

**Deadline:** Screening of applications will begin October 18, 2004 and will continue until a suitable candidate is identified.

Questions about projects or the position should be directed to [jwernegreen@mbl.edu](mailto:jwernegreen@mbl.edu).

The MBL is an Equal Opportunity/Affirmative Action/Non-smoking workplace.

Jennifer Wernegreen <[jwernegreen@mbl.edu](mailto:jwernegreen@mbl.edu)>

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### YaleU EvolBiol

Yale University

Faculty Positions in Ecology and Evolutionary Biology

The Department of Ecology and Evolutionary Biology at Yale University invites applications for several faculty positions at either the senior or junior level. We have a special interest in the following fields:

(1) theory, both evolutionary and ecological, including computational approaches; (2) phylogenetic and other historical approaches to ecological questions; (3) comparative biology that involves intimate acquaintance with organisms and active use of the Peabody Museum collections; (4) interactions, including symbioses, mutualisms, and host-pathogen interactions.

A record of outstanding achievement and a promising research program are more important than the spe-

cific research area. Interested candidates should submit their CVs, three relevant reprints or manuscripts, a brief research and teaching statement, and the names and addresses of four potential evaluators by 30 September 2004. Send materials to:

Department of Ecology and Evolutionary Biology, Yale

University, P.O. Box 208106, New Haven, CT 06520-8106 USA attn: Francine Horowitz.

The Department is described at [www.eeb.yale.edu](http://www.eeb.yale.edu). Yale University is an equal opportunity/affirmative action employer. Men and women of diverse racial/ethnic backgrounds and cultures are encouraged to apply.

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### AFLP controls

Hi

I am currently working on AFLP's of butterflies, and have had a lot of problems with my negative controls. Blanks which have been through both the preselective and selective PCR steps often have a number of peaks, whereas controls that are only put through the selective PCR are normally clear. I have recently been told that this sometimes happens and not to run blanks through

both PCR stages. Can anybody verify this, and if so does anyone have an explanation for why this might occur? Alternatively, I would also like to hear from people who have clean controls!

I am dubious about eliminating negative controls from the whole process, and would have thought that if peaks occur in blanks than spurious bands will also be present in samples. I am interested in any comments or suggestions.

Thanks

KateE-mail: kate.holehouse@ioz.ac.uk

Thank you very much,

Andrey

Andrey Rzhetsky, Ph.D. Assistant Professor Department of Biomedical Informatics and Columbia Genome Center Columbia University 1150 St. Nicholas Ave., Russ Berrie Pavilion, Informatics, room 121H New York, NY 10032

Voice: (212) 851-5150 Fax: (212) 851-5149

<http://genome6.cu-genome.org/andrey> Andrey Rzhetsky <ar345@columbia.edu>

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## ALFPs

Dear EvolDir members,

We've recently started working with AFLPs in our lab and have been using universal fluorescent labeled primers (as per Schuelke 2000).

I was curious to know whether anyone else has been using this approach with AFLPs and whether their results have been consistent when a sample is run repeatedly.

Our problem appears mostly to be an issue of peak quality (samples are run on an ABI 3100 Avant sequencer) as opposed to differential fragment amplification. Any suggestions of how to assure uniform peak heights across runs and samples would be greatly appreciated.

Thanks, Steve srauth@lamar.colostate.edu -----  
Steven J. Rauth Ph.D. Candidate Dept. of Bioagricultural Sciences and Pest Management Plant Sciences Building Colorado State University Fort Collins, CO. 80523 lab: (970)491-5984 Email: srauth@lamar.colostate.edu

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## Allele distribution

Could you please provide me with a quick pointer to sources addressing the distribution shape of the number of (slightly) deleterious mutations per genome? That is, what is the probability to sample a (human or non-human) genome and discover exactly \*K\* deleterious polymorphisms?

---

## Bonferroni corrections

Dear all,

I need to perform the standard Bonferroni correction to my data following the same procedure that FSTAT v.2.9.3 does. They say they divide the nominal level (usually 5%) by the number of tests that are being carried out, but they don't explain how they estimate the number of tests. They give the following example: "In FSTAT, with 20 samples and 10 loci, 400 tests are carried out if the option 'testing, HW within sample and locus' is selected". I was hoping someone would help me to understand how this calculation is performed: is it the nr of samples times the number of loci times 2 alleles...? And if I perform a HW test only within samples, how should I perform the calculation in this situation? I would appreciate immensely if someone could give me a help with this.

Best regards,

Joana C. Silva lady\_bird@netcabo.pt

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## Branch Lengths

Dear All,

Does anyone know a program that gives pairwise branch lengths between taxa (NOT branch lengths from a taxon to a node)? We would need a program to be able to read a tree file rather than compute a tree.

Thanks in advance, Natalia Martinkova martinkova@brno.cas.cz



Natalia Martinkova Institute of Vertebrate Biology  
Academy of Science of the Czech Republic Stude-  
nec 122 675 02 Konesin Czech Republic mar-  
tinkova@brno.cas.cz

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## Capillary Sequencer

HI All,

We are in the market for a capillary sequencer for sequencing, microsatellite genotyping and AFLP. We have been considering the Megabase 500 and would like to hear any feedback about the system....We are also curious if the fragment analysis data can feed into the ABI genotyper software package.

If you have a capillary system other than ABI that you would recommend, then we would be interested in hearing about that.

Thanks,

Lisette – 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 <http://www.uidaho.edu/cfwr/fishwild/lwaits.htm>

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## Coefficient differentiation

I am looking to learn more about the coefficient of differentiation applied to cytochrome b gene sequences. are there any documented congruence between this parameter and determination of species boundaries as with the genetic distance (Bradley and Baker, 2001).

thanks for time

freddupuid

fred dupuis <freddupuid@yahoo.fr>

---

## Coefficient differentiation answers

Dear Evoldir readers,

As some people asked to read answers to my question on coefficient of differentiation applied to cyt.b gene sequences, here are answers. However, its not respond exactly to my query and other answers would be welcom. I thank all the people who took their time to reply (or will do).

Best wishes,

Fred

1- Tiawanna Taylor

Dear Fred

Re your evoldir message.

Sorry cannot advise although have read the Bradley Baker paper I would be very grateful to hear what people say if you don't put the answers on evoldir as it is of interest.

2- Carol Lee

I don't know if this answers your question, but check out these papers:

Lee, C. E., and B. W. Frost. 2002. Morphological Stasis in the Eurytemora affinis species complex (Copepoda: Temoridae). *Hydrobiologia* 480:111-128.

Lee, C. E. 2000. Global phylogeography of a cryptic copepod species complex and reproductive isolation between genetically proximate "populations". *Evolution* 54:2014-2027.

They compare genetic distance, morphological distance with patterns of reproductive isolation

best wishes,

3- Heidi Schwaninger :

Hi Fred

I don't have answers ... but I am interested in the responses you get To your query of coeff. of differentiation and species boundaries. A posted summary will be widely appreciated. Thanks already.

Heidi

fred dupuis <freddupuid@yahoo.fr>

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## CommercialMicros answers

A week ago I posted a request for a commercial lab that isolates microsatellites for population genetic stud-

ies. Here the list, ranked according to the number of positive e-mails:

Travis Glenn's group at the Savannah River Ecology Lab. They are bit cheaper and have different options depending on your available funds. <[http://www.uga.edu/srel/Msat\\_Devmt/Microsatellites-home.htm](http://www.uga.edu/srel/Msat_Devmt/Microsatellites-home.htm)>[http://www.uga.edu/srel/Msat\\_Devmt/Microsatellites-home.htm](http://www.uga.edu/srel/Msat_Devmt/Microsatellites-home.htm) Ecogenics: <<http://www.ecogenics.ch/>><http://www.ecogenics.ch/>. They provide certain guarantees of what you will get for the money (I think it's ten loci with at least four alleles each).

Gennifer, in Ferrara, Italy (gennifer@unife.it)

Wildlife Genetics International (<<http://www.wildlifegenetics.ca/>><http://www.wildlifegenetics.ca/>) they do really good work

Genetic Identification Services <<http://www.genetic-id-services.com/>>[www.genetic-id-services.com](http://www.genetic-id-services.com/) and they are great

At Sheffield: <<http://www.shef.ac.uk/misc/groups/molecol/smgf.html>><http://www.shef.ac.uk/misc/groups/molecol/smgf.html> contact Deborah Dawson

And a website that lists many more: <<http://www.uga.edu/srel/Microsat/Microsat-L.htm>><http://www.uga.edu/srel/Microsat/Microsat-L.htm> Thanks for your collaboration.

Francesco Nardi

----- FRANCESCO NARDI

Dep. Evolutionary Biology University of Siena

via Aldo Moro 2 53100 Siena Italy Ph: +39.0577.234420  
Fax: +39.0577.234476 nardifra@unisi.it -----

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## DNA quantitation

Dear All, I am looking for cheap (up to 4000Euro/5000\$), sensitive and easy to operate DNA quantitation tool. As I am working very often with samples containing small quantities of DNA thus I need it to be rather sensitive. I also wonder what method you use for quantitation of degraded DNA. Any suggestions are welcome. Maciek Konopinski

---

## DNA quantitation answers

Dear All, Three weeks ago I have posted a question about cheap DNA quantitation system suitable for samples with low concentrations of nucleic acids or strongly degraded DNA. Most of you advice Nanodrop-1000 as it needs only 2ul of DNA solution (<http://www.nanodrop.com/>). Another solution is fluorometer - more sensitive but as far as I know it is more expensive as it needs special reagents. Because neither spectrophotometers nor fluorometers does not distinguish between degraded and good DNA it is still necessary to check the DNA on gel. I wonder what's the use of buying ultrasensitive device... I was also advised to read: Hardie DC, Gregory TR, Hebert PDN. 2002. From pixels to picograms: A beginners' guide to genome quantification by Feulgen image analysis densitometry. J. Histochem. Cytochem. 50(6):735-749. Thank all of you for your suggestions. All the answers I received you will find below. Best regards Maciek

----- Eppendorf/Brinkmann makes a spec that is reasonably inexpensive (3-5\$K if I remember right) but it still requires 50ul of fluid in the cuvette, and the cuvettes are a dollar each(or more). You can dilute your sample of course, but it's not as accurate that way.

But I highly recommend the Nanodrop spec. It is about \$8000US (after you include taxes) but it takes only 1 ul of fluid, and requires no cuvettes. So over the long term, it's much more accurate, gives a full spectrum of wavelengths which will help you figure out how much and what kinds of contaminants you might have in there, and works out to be cheaper, I think. If you do a google search on "nanodrop 3.0" you should find the vendor.

----- You need a fluorometer (not a spectrophotometer). I use a smaller version (which I am not sure they still sell) of this one: <http://www.turnerdesigns.com/t2/instruments/td700.html> -----

My suggestion might be slightly out of your price range (~\$6000), however I can affirm it has been a phenomenol piece of equipment for our lab. It's the Nanodop ND-1000 spectrophotometer. This spec uses 1-2 ul of solution (which can be retrieved without contamination after a reading has been taken) and provides a spectrogram from 200-600nm in 15 seconds. Refer to the website for more details <http://www.nanodrop.com/> . I can also attest that the cus-

tomers service at Nanodrop has been superb. I always enjoy the opportunity to share my great experiences with this wonderful piece of equipment. I hope his helps. \_\_\_\_\_

In my work, I need very fast/efficient quantification of low (pre-PCR) concentrations of RNA and DNA. I recently discovered a product by a company called Nanodrop, then ND-1000 spectrophotometer. It is more expensive than the range you are asking for (\$7500 US) but it will save you money over time because it does not require cuvettes, which can break and are expensive to replace. The ND-1000 is supposed to be more precise and read to lower concentrations (down to 1 ng/ul) +/- 0.5 ng/ul I think. It only requires 1 or 2 microliters (ul) of sample, which are placed directly on an optical lens with a pipettor, and wiped off with a kemp wipe or other small tissue paper. This is faster, and uses little of your sample. I have not used it yet, but have heard great things, and am just ordering one now. \_\_\_\_\_

I haven't found a good way to do that... I struggled for months with a Fluorometer (Biorad?) and hated it. Though purported to be amazingly sensitive, I found that the readings were amazingly inconsistent. UV spec reading worked better, but not by much. My favorite way is simply to run it on an agarose gel with a size marker. If you use some of that fancy dye, green-something, I think you can visualize pretty small quantities, but I've never tried it. If you have a computer program hooked up to your camera, you can digitally compute the concentration of DNA. Let me know if you find out something else! \_\_\_\_\_

Our core lab recently got a nanodrop <http://www.nanodrop.com/> It is a spectrophotometer, but you only need to load 1ul of sample, and since it doesn't get diluted, it is much more sensitive than the typical spec, where you need to have a large volume of liquid to fill up a cuvette.

Folks in the lab seem to be pretty happy with it.

For degraded dna - i dont think the nanodrop will distinguish btw degraded dna and good dna. You probably need to run your sample on a gel to see how degraded it is. Then you can do eyeball quantification by comparing to a mass ladder. \_\_\_\_\_

We have found Pico Green to be state of the art (has high affinity for dsDNA and uses very little product). I do not know the exact amt for the fluorometer, but cost to maintain is relatively easy and it is much

— / —

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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## Drosophila Genome

Brian -

Could you please redistribute a recent posting to Flybase concerning genome assemblies for the new Drosophila genomes <<http://www.flybase.org/docs/news/Genomes.html>>. The posting links to a page containing preliminary whole genome shotgun assemblies for *D. ananassae*, *D. mojavensis*, *D. virilis* and other public resources not available elsewhere <<http://rana.lbl.gov/drosophila/multipleflies.html>> . Many thanks, Casey Bergman, Ph.D.

Department of Genetics University of Cambridge  
Downing St CB2 3EH Cambridge, UK

tel: +44 (0)1223 766336 fax: +44 (0)1223 333992

email: [cbergman@gen.cam.ac.uk](mailto:cbergman@gen.cam.ac.uk) <http://www.gen.cam.ac.uk/casey>

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## Effective pop size

Has any research been done correlating  $N_e$  (long-term evolutionary effective pop size) to typical pop sizes for a variety of organisms?

Lynch & Conery (The Origins of Genome Complexity, Science 302:1401-1402) seem to assume that large  $N_e$  correlates with a large actual pop size and I can imagine the two as completely uncoupled, since you could have selective sweeps of beneficial alleles in a very large population. The paper does briefly mention this fact, but then still goes on to correlate and make statements about the genome sizes of organisms (prokaryotes through multicellular eukaryotes) relating to the population size as affected by selection and drift.

Do Selection and drift act differentially on populations with different  $N_e$  or just different pop sizes? My understanding is selection & drift act differently on ACTUAL pop sizes, but correct me if I'm wrong. I could not quickly locate any reference that actually correlated  $N_e$  with pop size across a wide range of organisms. Let

me know if anyone has any references or insight into this.

Thanks! Wendee Holtcamp

Wendee Holtcamp ~ ~ ecowriter@ev1.net Freelance  
Writer & Photographer ~ ~ [www.greendzn.com](http://www.greendzn.com) Ph.D.  
Student, Rice University, Ecology & Evolutionary Bi-  
ology

Do not go where the path may lead. Go instead where  
there is no path and leave a trail. – Ralph Waldo Emer-  
son

### Effective pop size answers

Thanks to all who replied to my question about the  
relationship between  $N$  and  $N_e$ . Here is a summary  
of replies because several people were interested. Best,  
Wendee Holtcamp ————— As you'll recall  
from Jody Hey's talk, his chimpanzee's had a very large  
effective population size and they actually have a very  
low census size. This not uncommon in a conservation  
biology context where you have historically large popu-  
lations having recently gone through a bottleneck. I've  
just reviewed a paper on red pandas that had the same  
effect. I've attached a paper of mine that goes through  
some of the different estimators and what they are ac-  
tually estimating [Crandall, K.A., D. Posada, and D.  
Vasco. 1999. Effective population sizes: issuing mea-  
sures and missing concepts. *Animal Conservation*. 2:  
317-319). It turns out that there are even different ef-  
fective population sizes and that they can estimate very  
different things. Hope this helps.

Dr. Keith A. Crandall Brigham Young University ———  
—

One difficulty with  $N_e$  and  $N$  is that the former is mea-  
sured in a number of different ways. In my talk I was  
talking about a long term measure based on the rate  
of genetic drift over the depth of genealogies. You'll  
get something very different if you just go out and esti-  
mate the actual rate of drift from one generation to the  
next. We often end up talking about the effective size  
experienced by individual loci - loci with fast drift have  
small  $N_e$ , those with slow drift have high  $N_e$ . In this  
light, loci with HGT may have a much larger  $N_e$  than  
loci that do not. Again this is quite an abstraction and  
pretty far removed from an  $N$  based on census numbers.

Jody Hey, Rutgers University —————  
Dear Wendee,

One such analysis is summarized in Fig. 2.9 and accom-  
panying sections of the text (especially pp. 49-60) in  
my Phylogeography book (2000; Harvard Univ. Press).  
Perhaps you might find that of some help or interest.  
I'm sure the approach could be greatly extended.

John Avise University of Georgia ————— Take a  
look at

Gillespie JH (2001) Is the population size of a species  
relevant to its evolution? *Evolution Int J Org Evolution*  
55:2161-9

It is a brilliant paper and discusses the questions you  
seem to be interested in. Dmitri A. Petrov Stanford  
University —————

John Gillespie discusses some of these issues in his book,  
*The Causes of Molecular Evolution* (Oxford, 1991), pp.  
52-55, and gives some references to some older studies  
of the sort you mention. You might also have a look at:

Gillespie, JH. 2001. Is the population size of a species  
relevant to its evolution? *Evolution* 55(11): 2161-2169.

Cheers, Jay Taylor University of Edinburgh —————  
—

I do not think that I can answer your question. How-  
ever, in thinking the behavior of weakly selected mu-  
tations, the paper I attach here may be of some help.  
The effective population size is a difficult concept, but  
so often used because of the convenience.

[Ohta, T. 2002. Near neutrality in evolution of genes  
and gene regulation. *PNAS*. 99: 16134-16137]

Tomoko Ohta National Institute of Genetics, Japan —  
————— > —————

Hi Wendee,

I'm doing my dissertation on environmental influences  
on effective population size and haven't come across  
the kind of reference you are looking for [correlating  $N_e$   
with typical pop sizes for a variety of organisms] yet.

seems to me that I ran across a conservation paper that  
may have touched on this a bit, and I thought Russ  
Lande may have been involved in writing it but on a  
casual look I'm not finding it. I'll keep looking.

While large  $N_e$  needs to have a large  $N$  (census size), it  
is also possible to have large  $N$  with small  $N_e$ . While  
your observation of selective sweeps is correct, the type  
of selection going on would have to be hard selec-  
tion and reduce  $N$  substantially in order to affect  $N_e$ .  
And eventually in evolutionary time,  $N_e$  would increase  
again so your window of time for seeing a small  $N_e$  in  
a large population that had gone through a selective  
sweep would actually be pretty short, in evolutionary

terms.

Drift is more efficient and selection less so in populations that have small  $N_e$  to begin with. Selection is more efficient in populations with large  $N_e$ . It gets confusing in the evolutionary literature because they don't really make distinctions between  $N_e$  and  $N$  and mostly they're talking about  $N_e$ , I think.

I'm more of an ecologist and have only recently delved into the population genetic models we're talking about here, but if I can help you any further, please don't hesitate to contact me.

Erin Espeland UC Davis —————

Frankham, R. 1995. Effective population size/adult population size ratios in wildlife: a review. *Genetical Research* 66:95-107.

John Orrock National Center for Ecological Analysis and Synthesis —————

Wendee Holtcamp ~~~ ecowriter@ev1.net

— / —

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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## Fragment analysis techniques

Some time ago I posted a question about reducing costs of fragment analysis. I got many great responses and posted a summary on the directory. Many of you asked me about one idea which was to make your own size standard. I did not have further details at the time, but have just been made aware of details on the technique which has just been published online and will be in print soon:

Symonds and Lloyd (2004) A simple and inexpensive method for producing fluorescently labelled size standard. *Molecular Ecology Notes*

To find it do an author search on *Molecular Ecology Notes'* web site.

Hope this helps everyone!  
chaine@biology.ucsc.edu

Alexis

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## Fragment analysis techniques 2

For those interested in making your own size standard, see also:

DeWoody J.A., Schupp J., Kenefic L., Busch J., Murfitt L. & Keim P. (2004) A universal method for producing ROX-labeled size standards suitable for automated genotyping. *Biotechniques* 37, 348-352.

"DeWoody, James Andrew" <dewoody@purdue.edu>

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## GeneDiversity StdErrs answers

Dear members

I am grateful to all of you who took the time to reply to my question. Here are the answers that I received:

Hi,

If your sampling design is relevant, you may test a difference in  $H_s$  and  $H_o$  between groups of samples (i.e. groups of 'sub-populations') by permuting samples among groups; this procedure is implemented in FSTAT (Goudet 1995, 2001). This doesn't strictly answer your question, but I thought it may help. Could you please forward other answers ?

Regards,

Thomas Broquet.

Hello I have a C program computing gene diversity variance based on bootstraps on individuals and loci. If you are interested, I can send it to you and if necessary, I can add the calculation of observed heterozygosity. How many markers do you have? S. Mariette

Dear Paulo,

The variances or standard errors of heterozygosity or gene diversity can be computed by the program DISPAN or POPTREE, which can be downloaded from the section of Software or MEP of my website listed at the end of this message.

Masatoshi Nei

Hi,

I just want to let you know that now I have the executables of my bootstrapping program for both Mac and Window on the web at

<http://chkuo.name/software/GDB.html> Cheer,

Chih-Horng <chkuo@uga.edu> <http://chkuo.name/>-  
Department of Genetics The University of Georgia

Thanks

Paulo

Paulo Antonio Russo Almeida Departamento de Zootecnia Univ. Tras-os-Montes e Alto Douro Apartado 1013 5000-911 Vila Real PORTUGAL e-mail: prusso@utad.pt tel: +351-259350432 fax:+351-259350482

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## GenecleanKit

Dear Members,

I am interested in hearing comments about the use of SPIN Modules (filters) with the Geneclean II Kit from Bio101 Systems/Q-BIOgene. These columns are supposed to be used when purifying high molecular weight DNA (up to 300kb). We have only used the kit without the SPIN Modules, although this kit is supposedly only good for DNA up to 20 kb. Does anyone have experience with this kit and the SPIN Modules? Can you comment on the benefit of using the filters over just using the kit without these SPIN Modules for DNA over 20 kb?

I am grateful for any responses. Gabriela Ibarguchi

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Gabriela Ibarguchi

Department of Biology, Queen's University Kingston, Ontario, Canada, K7L 3N6

ibarguch@biology.queensu.ca or gibarguchi@biology.ca  
tel (613) 533-6000 ext. 75051 fax (613) 533-6617

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## Genetic relatedness

Dear colleagues,

We are using the software RELATEDNESS (Queller &

Goodnight, 1989) to calculate genetic relatedness between individuals of known pedigree, using microsatellite loci, for two species of endangered birds. The population sizes are small and genetic diversity is low: only a few loci (five and six, respectively) were polymorphic in each species. One species has only biallelic loci also.

Firstly, we would like to know how to evaluate the statistical power of the relatedness values that we generate, given that genetic diversity is so low. For example, in the species with only 5 biallelic loci, there are only 243 possible genotypes. This is likely to influence the validity of comparing 60 individuals all with each other (~1,800 comparisons), but how can the degree of this influence be evaluated?

Also, RELATEDNESS is generating values lower than -1 (as low as -8), and we are unsure how this is possible. Is this also a factor of low genetic diversity?

Furthermore, upon evaluating the overall pair-wise genetic relatedness of pairs with pedigree relatedness of 0.5 (parent-offspring, sib-sib) we found an average value of 0.3, with a very high variance (0.17). We are unsure how to interpret such a lower value than expected, when this is an inbred population and we may predict a result that is even higher than the "expected" value of 0.5.

We have tried using the same data in the program KINSHIP, and generated very similar values, although they are slightly lower (by around 0.02).

We would appreciate the advice of anyone who has performed a similar analysis.

Thank you,

Nicolas Margraf and Catherine Grueber

nicolas.margraf@stonebow.otago.ac.nz Department of Zoology, University of Otago, New Zealand.

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## GraduateStudents

Hi,

we are in the process of evaluating our strategies for recruiting new graduate students for our graduate programs (M.S. and PhD). I was wondering if anyone has developed any successful strategies that have increased number and also quality of applicants. Any information or suggestions are welcome.

If any students or recent graduates are reading this message I would like to know what attracted you to a spe-

cific graduate program.

Thanks!

Andrea

Dr. Andrea Schwarzbach Assistant Professor and Curator of the Herbarium Department of Biological Sciences Kent State University Kent, OH 44242

aschwarz <aschwarz@kent.edu>

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### Guitarfish samples

Greetings to all,

We are conducting a study on the phylogeny of guitarfishes (Rhinochordata) and we are in great need of tissue samples (fixed in non-denatured ethanol for DNA sequence analyses) from at least one individual of the species listed below .

Rhina ancylostoma Zanolobatus schoenleinii Rhynchobatus luebberti Zapterix brevirostris Rhynchobatus djiddensis Platyrrhina sinensis Platyrrhina limboonkengi Trygonorrhina melaleuca Rhynchobatus australiae

We hope that someone in the list may be able to give us a hand with this directly or at least refer us to someone who might, any help will be tremendously appreciated.

Apologies for cross-postings

Best regards and happy fishing

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Axayacatl Rocha-Olivares, Ph.D. CICESE Biological Oceanography Department P. O. Box 434844 San Diego, CA, 92143-4844

DOMESTIC: Apartado Postal 2732 Ensenada, Baja California, CP 22800 Mexico

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Office: +52(646)175-0500 (ext. 24240) Fax: +52(646)175-0545

Email: arocha@cicese.mx <http://dob.cicese.mx/pag/-arocho.htm> Axayacatl Rocha <arocha@cicese.mx>

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### Hybrid clonality

Dear all

I have been analysing a microsatellite data set on two species of tree and their hybrid. All three taxa show certain levels of apparent clonality i.e. several individuals with identical multilocus genotypes.

While I have used MLGsim to test if these MLGs are due to clonal spread or the product of sexual reproduction. Unfortunately, I don't think I can use this approach for the hybrid individuals.

Does anyone have any suggestions on how I can determine if identical MLGs in hybrids are due to clonal spread or possible multiple hybridization events.

Many thanks

Andy

PLEASE NOTE NEW PHONE NUMBER

Dr Andrew King School of Biosciences Cardiff University PO Box 915 Cardiff CF10 3TL

Tel: 029 2087 6806

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### Intelligent Design

HI, can you post this message. Thanks

I am teaching a graduate/advanced undergraduate course in Molecular Evolution. I have a student who is a believer in Intelligent Design (based on what he has read on web sites). I have not really kept up with exactly what the Intelligent Design people are up to and am wondering how the best way to deal with this student.

How have others dealt with this situation? Any suggestions for what I can read or suggested reading for my student?

Thanks Liz Waters – Elizabeth R. Waters, Ph.D. Assistant Professor Biology Department San Diego State University 5500 Campanile Dr. San Diego, CA 92182-4614 Phone: (619) 594-7036 ewaters@sciences.sdsu.edu FAX: (619) 594-5676

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### Intraspecies genealogies

dear evoldir members

some time ago I posted a mail to the list asking for any reference to a /method/software to infer/test correlation between intraespecies trees / genealogies.

I have already forwarded the answers to those of you who emailed me showing an interest in this question, but further emails asked me to post them in the list, so here they are. Hope they are useful.

all the best

santos

1.- One idea would be to correlate the distances but I guess that could fail to detect important differences.

2.- I can recommend Page 2003, Tangled trees. The University of Chicago Press. In particular, there is a chapter by Hulsenbeck, in which he describes a Bayesian approach. See also, TreeMap (by Page).

3.- You could use CAIC. It is either [www.caic.org.au](http://www.caic.org.au), or else [www.bio.ic.ac.uk/evolve/software/caic/](http://www.bio.ic.ac.uk/evolve/software/caic/) 4.- There are of course very different elements to 'correlations' of the types you talk about, notably the topologies of phylogenies as opposed to the depths. The works of Rod Page and Mike Charleston are worth a close look, and some other people have hands-on solutions around these issues. Here are some starting points:

Page RDM, and Charleston MA. 1998. Trees within trees: phylogeny and historical associations. Trends in Ecology & Evolution 13: 356-359. Schneider CJ, Smith TB, Larison B, and Moritz C. 1999. A test of alternative models of diversification in tropical rainforests: Ecological gradients vs. rainforest refugia. PNAS 96: 13869-13873. Sullivan J, Arellano E, and Rogers DS. 2000. Comparative phylogeography of mesoamerican highland rodents: Concerted versus independent response to past climatic fluctuations. American Naturalist 155: 755-768.

5.- I don't have an answer for your query as such but I know that there are many methods to compare different trees in the field of 'supertrees', i.e. the combining of many small trees into one large consensus tree containing all the taxa. It is hard to say without knowing exactly what you need to do but one of the methods used by the supertree people may be applicable in your case. There is a guy in Ireland (James McInerney) who works on supertrees and, if you like, I could forward on some details to him and see if he can suggest a solution.

6.- I don't know if I exactly understood your problem. However, there are quite some methods that compute distances between trees (i.e. something similar to correlation). My first try would be component from Rod Page which implements several

distance metrics and is available for windows: <http://taxonomy.zoology.gla.ac.uk/rod/cpw.html> and macintosh: <http://taxonomy.zoology.gla.ac.uk/rod/eplite/guide.html>. Also, there is the excellent website of Joe Felsenstein, which provides links to many programs related to phylogenies and tree comparison: <http://evolution.genetics.washington.edu/phylip/software.html#Consensus> 7.- Have you tried looking at something like Brooks parsimony? there's a chapter in the recent Joe Felsenstein book about testing for concordance between trees I think... You might want to take a look at that.

8.- I guess this can be broken down into two questions:

1. Do the trees for the genes have the same phylogeny, i.e. are they evolving together within lineages? 2. If they are evolving together, are there any site that show coevolution between the two?

I'm afraid my experience is largely with interspecies trees, where the answer to question 1 is a much clearer 'yes' because they are evolving along the same species lineages. With your intra-specific trees is there likely to be lots of recombination etc. between the two proteins, or are your different humans (/populations?) sufficiently separate that the two proteins should be evolving together? (I mean this in the sense that they are being inherited together rather than that they are directly influencing each other's evolution.) If they are, then I guess you could draw a tree from the concatenated sequences and then use a method such as the one below to scan for coevolving sites across the different sequences. I am not sure, however, whether there would be enough information within a species to perform these kinds of tests. You may be better off looking for coevolution using interspecific trees and then mapping those sites onto your intraspecific data to see if it still fits?

If it is question 1 that you are asking then I think there are maximum likelihood tree-drawing programs (possibly MrBayes) that can assign a posterior probability to an input tree given the data, which you may be able to use to see how much worse the receptor tree is if you make it look like the ligand tree, for example. Again, though, I think these will be designed

— / —

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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## Molecular Data Analysis

I would like to calculate automatically the number of different haplotypes detected in the set of lines I have examined. I would be grateful if you could let me know if there is a program that can count the number of different haplotypes.

Best regards

Livia

Livia Tommasini <liviati@botinst.unizh.ch>

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## Molecular Data Analysis answer

DAMBE (<http://aix1.uottawa.ca/~xxia/>) has a “feature” of scornfully telling you:

“Some sequences are identical. Identical sequences should be represented by just a single sequence and a single sequence name. Do you wish to keep only unique sequences in DAMBE’s buffer?”

If you hit “Yes”, ...

You could then count what you had left!

Jim Mallet

At 07:12 02/09/2004, you wrote:

>I would like to calculate automatically the number of different >haplotypes detected in the set of lines I have examined. >I would be grateful if you could let me know if there is a program that >can count the number of different haplotypes. >>Best regards >>Livia >>>Livia Tommasini <liviati@botinst.unizh.ch>

Jim Mallet <http://abacus.gene.ucl.ac.uk/jim/>

---

## Molecular Data Analysis answer2

>I would like to calculate automatically the number of different >haplotypes detected in the set of lines I have examined. I would be >grateful if you could let me

know if there is a program that can count >the number of different haplotypes. >>Best regards >Livia Tommasini <liviati@botinst.unizh.ch>

The TOPALi (pronounced Toe-Pal-Eye) program can input an alignment and select a unique subset by keeping one member of each group of identical sequences. However, even better, try this....

Use TOPALi to construct a phylogenetic tree: you can then ask TOPALi to shade clusters according to similarity, so TOPALi will do exactly what you want.

You can download TOPALi (GUI, runs on PCs, MAC X, Linux, etc) from:

<http://www.bioss.ac.uk/~iaimm/scri.html> Instructions for using TOPALi to shade clusters of identical sequences New Project Choose location for project file (which holds data and results) Load alignment

Analysis > Settings (choose F84+Gamma/Neighbor Joining) Analysis > Create phylogenetic tree (with or without bootstrapping - you choose)

Go to tree graphic window - choose second last icon (states “Group cluster” when mouse is over it) Click on “Group Clusters” icon Choose threshold limit for similarity (0.0 for identical sequences) TOPALi will now shade clusters (in different colours)

Best Wishes,

Frank Wright

TOPALi development team [topali@bioss.ac.uk](mailto:topali@bioss.ac.uk)

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## MolecularClock answers

Dear EvoDir members,

following my recent queries on molecular clock issues I received four answers and several people requested that I post the answers. I think some very interesting issues were raised and I would like to thank all the people who took their time to answer. With my best wishes, Lukas

1) Paul O. Lewis Doing two separate searches (one with clock constraints enforced and the other without constraints on branch lengths) would be the best approach if the likelihood ratio test did not require models to be nested. Using the same tree topology, the “clock” model is a constrained version of the “non-clock” model and the LR statistics will be approximately chi-squared. If the topology changes between clock and non-clock hypotheses, all bets are off with respect to the goodness of

the chi-squared approximation because the two models being compared are no longer nested. (Different tree topologies represent different non-nested models.)

If one is going to conduct a test then and look up the LR statistic in a chi-squared table to assess significance, you need to keep the topology the same. Usually the null hypothesis is the simpler one (i.e. more constrained) so it seems that the search should be done under the constrained (i.e. clock) model and then the constraints relaxed (but keeping the topology the same) to obtain the unconstrained likelihood for comparison. I would be interested to hear arguments from others, however, on a possible rationale for performing the topology search under the non-clock model.

2) Ziheng Yang In theory, you should use the correct tree (the tree that represents the biological relationships among the sequences) to calculate the lnL under the clock and non-clock models. If the correct tree is unknown, I suspect (a) is a better choice than (b) if you are going to use the chi square. You might use two or three trees to check that the test results are not sensitive to the tree topology assumed. If you use (b), you should not use the chi square since the two models are not nested. I am not sure about the r8s program, but the LRT can be done using a number of programs such as phylip, paup, and paml. You should watch out for the likelihood calculations under the clock as some programs might have problems.

If you have difficulty in deciding whether the clock should be rejected, there is probably no point in doing rate smoothing. You could just assume the clock for date estimation. Often the clock is so wrong that there is no need for a formal test. If the tree is really clock, a sensible method should be able to deal with it, so I can't see anything wrong in applying the algorithm on a clock-like tree. Also the rate smoothing algorithms require estimates of branch lengths without the clock, so the likelihood calculation under the clock should not be a limitation.

3) Kenneth Kozak With regards to question 2, the reason to use NPRS or PL is to obtain ultrametric branch lengths when the data reject a molecular clock. The methods for generating molecular clock trees you mentioned result in ultrametric trees. So, there is no need to transform the branch lengths using NPRS or PL because the branch lengths will already be proportional to time.

On another note, you can use Mr. Bayes to do and MCMC search under the restriction of a molecular clock. My experience with this approach is that it goes much faster than doing a ML search with a molecular clock enforced.

Mr. Bayes version 3.04 will do searches with a molecular clock enforced. One thing that might be worth exploring is doing an unconstrained search and then a search with the molecular clock enforced. If the data are consistent with a molecular clock, then the 95% posterior probability distributions for the likelihood scores of these two analyses should overlap.

4) Toby Johnson Your observation that (b) gives better likelihood scores than (a) is general, because (a) is a special case of (b). That is, the space you are maximising the likelihood over with option (a) is a sub-space of the space you are maximising over with option (b), and therefore option (b) is guaranteed to have greater or equal likelihood.

Option (b) seems to me the right approach to take. BUT If you use different topologies (option (b)) you cannot use a LRT. This test can only be used when you have a nested sub-model in continuous parameter space (because it relies on asymptotic normality of the ln-likelihood function). That is, the simpler model (clock) must be obtained from the more general model (no clock) by setting continuously varying parameters to predetermined values. Branch lengths are continuous, tree topologies are not.

Akaike's Information Criterion (AIC) or the Schwarz Criterion (BIC) can in principle be used to choose between non-nested models. You might also be able to estimate the Bayes Factor between the two models using a program like MrBayes.

My original questions:

— / —

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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## PAUP problems

I am having trouble using Paup4.0beta10 win in Windows XP Professional and was wondering if anyone had experienced similar problems. Whenever I try to use any of the commands begin data; begin character; begin distances or begin taxa; the program crashes. The program can still complete a parsimony or likelihood analyses with no apparent problems. I have tried using different file formats but this has made no difference. Any suggestions would be greatly appreciated.

Cheers

Claire McClusky PhD Student Deakin University Warrnambool, Australia [clairefi@deakin.edu.au](mailto:clairefi@deakin.edu.au)  
[clairefi@deakin.edu.au](mailto:clairefi@deakin.edu.au)

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## PCR evaporation

Dear All, My question maybe is trivial but I would like to know if you also encounter this problem and if there is any good solution (a perfect supplier?). Sometimes during long cycles one or more reactions evaporates - I have two MJResearch PTC-200 cyclers (block 96x0,2ml) and usually work with 10ul mixes. I have tried different suppliers (e.g. Merck, Biozym, Axygen, MJResearch) - some tubes/plates are completely useless and most that do not let the liquid evaporate are very hard to open - I am always afraid I will mix products while opening them. Using oil or wax would surely help but... come on, it is XXI century now! :) Is there a perfect sealing system? I also wish to know your opinions on different suppliers and their products - maybe someone already did a kind of rakning of plasticware? Best reagrads Maciek Konopinski

[konopinski@iop.krakow.pl](mailto:konopinski@iop.krakow.pl)

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## PCR evaporation answers

Dear All, Many thanks for the answers to one of the most trivial questions about PCR anyone could ever ask: How to keep the liquid inside the tube? I have noticed that during PCR, reaction mixtures evaporate from some tubes. I have asked you if there is some perfect solution for sealing tubes, or perfect plastic-ware.

The conclusions are:

1. Oil is valuable as always but troublesome too (don't annoy weapon inspectors :)
2. Silicon seals are almost perfect, however, I have serious doubts about using them when dealing with museum material - it is hard to be too careful. They are simply too expensive for single use and the only reusable thing I allow to contact with PCR tubes (already sealed!) is thermocycler.

3. Sealing tapes are good if applied properly. One can also tighten the seal with silicon mate between the tape and heating cover. During longer storage some leakage may take place.

4. Larger reaction volumes are good (25-50ul instead of 5-10ul) but when the number of reactions is large, it is also too expensive.

5. It seems that this problem is more likely to occur in MJResearch machines (which I love truly) than in Perkin-Elmer/ABi or Eppendroff.

Some of you have asked me to post the answers. There you are!

— Did you tried rubber seals for your plates or just the sticker ones?? rubber seals work fine in Applied biosystems machines and I heard that the same is valid for MJ PCRs

— Here, we use oil! Could you send us, after a while, a summmary of the answers?

— Our lab uses MJ thermocyclers too. I've tried a lot of combinations of plates and sealing films, and some work and some don't. One hint is to always lay a flat silicone mat (we use Axygen brand) on top of sealing film. It helps make a better seal than the metal of the heated bonnet.

— I have encountered this problem before and it is indeed frustrating. In general, I have liked the eppendorf single tubes, although it has been a while since I have run a reaction that goes more than 10 hrs or so.

— I would be very interested in hearing your responses for both of the questions you posted on EvoDir. Because we have pressure fit lids on our thermocyclers (we use MJ Research PTC-100 and Eppendorf thermocyclers), we currently use rubber mats (distributed by ISC BioExpress, cat #T-3161-1) to seal our 96-well plates for PCR (our plates are skirtless ones from Denville), and rarely have problems with evaporation. However, these mats do not work without pressure fit lids, and do not seal reactions well following PCR. After our PCRs are completed, we use sealing tape (also distributed by ISC BioExpress, cat #T-3021-7). We are not extremely pleased with the ability of the tape to seal the reactions for long periods of time post-PCR. As for tubes, we use flat-topped PCR tubes from Denville, and they have worked pretty well for us. If you are worried about opening tubes, you could try microcentrifuge tube openers (check any major supplier).

— I'm not familiar with the machine you are using. The first question is whether it has a hot top. If not, there is nothing you can do to prevent evaporation, and you're stuck with wax or oil, even in the XXI century

;-) If you already have a hot top, I'd suggest that you use a larger volume. Ten microL is darn little in a 0.2 ml tube (I'm guessing), go up to 50 microL of reaction and see whether this takes care of your troubles.

— We have two PCR machines, an Eppendorf Master Cycler (Gradient) and an Applied Biosystems PE 9700. We currently use strip tubes distributed by Sarsted (not sure if they also manufacture them or not) and are moving to Axygen plates. The strip tubes never evaporate unless they are not sealed tightly by the researcher. I had a few difficulties with the plates in the beginning but have now found that using the clear sealing film works perfectly (as long as the user seals the plates completely with the film). We use a small wallpaper roller to get a good seal.

Hope this helps, but if there is a wider scale, more standardized comparison available I'd like to know about it.

— evaporation sometimes occurs. But in general, it should not be a problem. I use cheap 96 well plates (fisher brand, cheapest) with a silicone plate sealer. Most plate sealers are junk and allow evaporation. But there is one style, made or at least distributed by a couple of vendors, that works. It has a button shaped semi-circular nub that projects into the well, and a small thin point on top that gets pushed down when you tighten the lid. The combination of pushing this sealer onto the plate adequately, and tightening the lid down sufficiently has resulted in almost no cases of evaporation for me. I've even done 5 ul reactions with no loss. Make sealer vendors send you samples until you find one that works. Test them with 5 ul of water in every well and run it all the way through your cycle.

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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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## Peer reviewed creationist

Dear all, With the unfortunate publication of a creationist article in a peer reviewed journal (see this weeks Sept. 9th Nature, page 114), I was wondering if there is anything we can or should do about it. It appears that the journal in question (The Proceedings of the Biological Society of Washington) has been hijacked by

a creationist editor who has now provided them with unfounded legitimacy by being able to cite a peer reviewed journal.

Some responses we might think about:

- 1) Get our libraries to cancel any orders for this journal.
- 2) Boycott peer reviewing and citation of any papers of the journal.
- 3) Put a list of the members of the The Biological Society of Washington on the Evolution Directory so that we can let them know that it is irresponsible for them to chose such an editor. This should be a warning to all of us who belong to various societies to pay attention and to take the responsibility of running journals very seriously.

I think that most would agree that this society and the journal has made all of lives more difficult with this slip up. Maybe doing nothing is better and simply dismissing it as a fluke would be the best strategy at this point. Some of the suggestions above might be too extreme and only heighten the impact in their favor, but I would at least hope that those of you in this society will reconsider your choice of editors, and that if you know someone in the society you will have a conversation with them about taking their professional responsibilities more seriously.

Best,

Joel Parker

Dr. Joel Parker Department of Ecology and Evolution University of Lausanne, BB CH-1015 LAUSANNE Switzerland Tel: (+41 21) 692 41 93 Fax: (+41 21) 692 41 65 E-mail: [Joel.Parker@ie-zea.unil.ch](mailto:Joel.Parker@ie-zea.unil.ch) Web site: <http://www.unil.ch/dee/page7722.html>

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## Peer reviewed creationist 2

Dear Joel,

I understand your concern about this, but I think the best thing to do would indeed be to ignore the incident. We all know peer review isn't perfect, and that science is – after all – a human activity. But we don't need to give more ammunition to creationists by mounting a boycott campaign.

On the other hand, of course, the journal in question has lost credibility (so does Cambridge Press, for analogous reasons, which is much more worrisome), so each

of us is perfectly entitled not to submit papers to them. Your warnings about taking choices of editors and publishers more seriously, of course, are also right on the mark.

Cheers, Massimo Pigliucci pigliucci@yahoo.com

— evodir@evol.biology.mcmaster.ca wrote:

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I think that most would agree that this society and the journal has made all of lives more difficult with this slip up. Maybe doing nothing is better and simply dismissing it as a fluke would be the best strategy at this point. Some of the suggestions above might be too extreme and only heighten the impact in their favor, but I would at least hope that those of you in this society will reconsider your choice of editors, and that if you know someone in the society you will have a conversation with them about taking their professional responsibilities more seriously.

Best,

Joel Parker

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### Peer reviewed creationist 3

Hi Joel (and others),

As an administrator of the internet site (<http://www.pandasthumb.org/>) that first broke the news of

this paper, I can tell you that we are working on it. The people who actively watch and fight against the anti-evolution movement have well addressed the “paper.” The issue now is countering and publicizing the spin that anti-evolutionists are doing. NCSE is working with the journal to get them to draft a more strongly worded denial of the paper. You can follow developments and debate about the paper at The Panda’s Thumb (<http://www.pandasthumb.org/>).

Addressing a couple points you mentioned:

The editor in question published Meyer’s paper as the last thing he did before he resigned. He is no longer in charge, and the journal is institution a more structured editorial policy. There is no evidence that the BSW knew that their former editor was a creationist. There is evidence that he intentionally hid this from them. They are in a tough position and simply not experienced enough to handle the anti-evolution political game. It is very clear from the vast scientific errors in the paper and from the fact that its topic was outside the scope of the journal that it did not receive critical peer review. It has also come to light that about 40% of the paper had been previously published by the author and colleagues.

I will also point out that there is another peer-reviewed paper by anti-evolutionists that we are working on addressing. The reference is “Behe MJ & Snoke DW (2004) Protein Science. Aug 31 [Epub ahead of print].” This one is not as egregious as the first, and is just an unremarkable, rather flawed, theory paper. We can see how it got published, since questionable papers do get published from time to time.

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Reed A. Cartwright Phone: (706) 542-1448 Doctoral Student Fax: (706) 542-3910 University of Georgia Department of Genetics <http://www.dererumnatura.us/> C232 Life Sciences Bldg <http://www.pandasthumb.org/> Athens, GA 30602-7223 <http://www.georgiascience.org/> Cuiusvis hominis est errare, nullius nisi insipientis in errore perservare. –Cicero

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### Peer reviewed creationist 4

[http://www.ncseweb.org/resources/news/2004/ZZ/608\\_bsw\\_repudiates\\_meyer\\_9.7.2004.asp](http://www.ncseweb.org/resources/news/2004/ZZ/608_bsw_repudiates_meyer_9.7.2004.asp) STATE-

MENT FROM THE COUNCIL OF THE BIOLOGICAL SOCIETY OF WASHINGTON

The paper by Stephen C. Meyer in the Proceedings ("The origin of biological information and the higher taxonomic categories," vol. 117, no. 2, pp. 213-239) represents a significant departure from the nearly purely taxonomic content for which this journal has been known throughout its 124-year history. It was published without the prior knowledge of the Council, which includes officers, elected councilors, and past presidents, or the associate editors. We have met and determined that all of us would have deemed this paper inappropriate for the pages of the Proceedings.

We endorse the spirit of a resolution on Intelligent Design set forth by the American Association for the Advancement of Science ([www.aaas.org/news/releases/2002/1106id2.shtml](http://www.aaas.org/news/releases/2002/1106id2.shtml)), and that topic will not be addressed in future issues of the Proceedings. We are reviewing editorial policies to ensure that the goals of the Society, as reflected in its journal, are clearly understood by all. Through a web presence ([www.biolSOCwash.org](http://www.biolSOCwash.org)) and contemplated improvements in the journal, the Society hopes not only to continue but to increase its service to the world community of taxonomic biologists.

The Council of the Biological Society of Washington 7 September 2004

[http://pharyngula.org/index/weblog/comments/-microdissecting\\_meyer/](http://pharyngula.org/index/weblog/comments/-microdissecting_meyer/) It's not as extensive as the Panda's Thumb review, but I like it just as much. <http://www.pandasthumb.org/pt-archives/000430.html> Tom Schneider's review: <http://www.lecb.ncifcrf.gov/~toms/paper/ev/#Meyer> is too criptic and centered on Tom Schneider's own work, in my opinion.

Brian Foley <btf@lanl.gov>

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**Peer reviewed creationist 5**

The Council of the BSW should consider recalling the ID paper. That aproach has been taken by other journals when irregularities have been detected.

Harold Kerster <kersterh@saclink.csus.edu>

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**Peer reviewed creationist 6**

Dear Colleagues, I am glade that the Proc. Biol. Sci. Wash. have explained how the publication of the paper by Meyer was mistake— which I take as equivalent to retracting the paper. However, I am worried about the strength of the reaction of part of the Scientific Community to the publication of the paper in question.

We have different options for dealing with Creationists: We can boycott them and prevent them from publishing, we can also ignore them, or we can open bridges of discussion with them and even give them space in our tribunes.

In my opinion, boycotting is the wrong thing to do; mainly because they will easily interpret it, and instrumentalize it as proof of their persecution— they will be the 'poor victims' of the 'evil Evolutionists'. I also think that the boycott of ideas is a dangerous and scary thing, and it does not agree with the open and critical mind of an Evolutionist.

Ignoring Creationist opinions does not resolve the problem neither. Ignored Creationists will use it as a proof of their strength and claim that Evolutionists are unable to 'face' them and answer their criticism.

However, I think that being more 'tolerant' with them will invalidate their excuses and instrumentalizations. It will also attract those of them who still can have a mind critical enough to admit that hiding is the only power of their supposed intelligent designer. We have also to recognize that, in addition to the criticism made by Evolutionists to contributions of their fellow Evolutionists, some of the criticism made by creationists have stimulated more work on Evolution, and contributed to improve the Theory, or at least speed-up its improvement.

Cheers,

Mohammed Bakkali

~~~~~ Institute of Genetics Queen's Medical Centre University of Nottingham Nottingham NG7 2UH England ~~~~~ Mobile: +44 (0) 7800 785 349 Fax: +44 (0) 1159 709 906 Web: <http://www.ugr.es/~mbakkali> Web: <http://www.ugr.es/~mbakkali>

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### Peer reviewed creationist 7

I recently received this from our good scientific buddies the Raelians, the same group that claims a close acquaintance with space aliens, and made a big splash with unsubstantiated claims of human cloning two years ago. They believe that life on earth was engineered by aliens.

On the one hand, I suspect this is a preview of what we will hear from many creationist groups.

On the other hand, the fact that the Raelians want to pile on should help illustrate the range of craziness that we deal with. This fact can be a very useful pro-science, anti-creationist tool, as pointed out by Massimo Pigliucci in his recent book Denying Evolution.

>Date: Tue, 14 Sep 2004 02:47:56 -0500 >To:  
>Subject: Press Release - Scientific creation recognized officially as a >scientific theory for the origin of life >From: "Raelian Movement" <usa@rael.org>  
> >SCIENTIFIC CREATION RECOGNIZED OFFICIALLY AS A SCIENTIFIC THEORY FOR THE >ORIGIN OF LIFE > >Press release, September 14, 2004 - The Raelian Theory about the creation >of all life on Earth by intelligent beings has long been dismissed as >unscientific despite the great number of scientists who have joined the >Raelian Movement after having carefully reviewed the other available theories. > >This "Raelian Theory" is also gaining more and more interest in the >scientific community as a similar theory is being developed called the >"Intelligent Design theory", which hypothesizes that no new living entity >can appear by chance. > >On August 4th, 2004 an article by Dr. Stephen C. Meyer, Director of >Discovery Institute's Center for Science & Culture appeared in a >peer-reviewed biology journal published by the National Museum of Natural >History at the Smithsonian Institution in Washington D.C., the Proceedings >of the Biological Society of Washington (volume 117, no. 2, pp. 213-239). >In this article, entitled "The Origin of Biological Information and the >Higher Taxonomic Categories", Dr. Meyer argues that no current theory of >evolution can account for the origin of the information necessary to build >novel animal forms. He proposes intelligent design as an alternative >explanation. > >This article represents a major breakthrough as being published in a peer >reviewed journal, it can be used

as a reference and free the numerous >scientists who were obligated to refer to evolution in explaining their >discoveries. > >Raelians are rejoicing over this event and will make sure that more >articles are published in that domain so that biologists can look at >living entities not as the result of random mutations but more as >sophisticated creations in which every detail has been thought of and has >a reason to exist. > >"Biology will go so fast once biologists stop being blinded by the >evolution theory and I am sure that in ten years from now scientists will >look back and wonder why they accepted evolution for so long" said Dr. >Boisselier, spokesperson of the Raelian Movement. > ><<http://www.rael.org/-www.rael.org> > > > > > >- > >To update your preferences visit ><<http://www.rael.org/-PHPList/contacts/?p=preferences&uid/-09e19eb21ab0b570a83b53efcf8e96>>this >link > >powered by <<http://www.phplist.com>>phplist v 2.9.1, © ><<http://tincan.co.uk/powered>>tincan ltd

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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### Peer reviewed creationist 8

Dear colleagues,

I agree with Mohammed Bakkali that censorship based on a disagreement about how we think the world works is unwise at best and unscientific at worst. Since the proponents of ID claim to be willing to play by the rules of scientific research, I would encourage them do so: show us good, solid science and we will be happy to listen. The issue then boils down to a very simple matter: the quality of the science.

It seems that the paper that started all this got published without peer review. In my opinion it shouldn't be retracted because it comes from an ID proponent, it should be sent out for review and judged on the basis of its scientific merit. If the science is bad, then it shouldn't be published.

Bad science should be kept out of journals, not matter who is responsible for it. We have all seen papers in top tier journals that have made us pull our hair, and no one has ever suggested to boycott the journal or to have the editors retract it. Making ID proponents stick

to the rules of the scientific process is all we really need. And if they ever manage to do it, so be it.

Cheers! isabel novella Medical College of Ohio

Isabel Novella <isabel@mco.edu>

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## Peer reviewed creationist 9

A number of years ago (5?) I attended an AAAS SWARM meeting in Flagstaff. I was surprised to see that individuals who still believe in the ether theory to explain physical experimental results that are better explained by Relativity were given presentation time. I believe the organizer who allowed this either may not have known (or appreciated) how discredited ether theories are, or has a belief in the free expression of ideas. I believe having given etherists a forum in such an important scientific organization as the AAAS was very inappropriate, but I never heard of any repercussions, perhaps because it is not such an emotionally charged, social, and political issue as creationism.

Stan stan\_gorodenski@asualumni.org

evolDir@evol.biology.mcmaster.ca wrote:

>[http://www.ncseweb.org/resources/news/2004/-ZZ/608.bsw\\_repudiates\\_meyer\\_9\\_7\\_2004.asp](http://www.ncseweb.org/resources/news/2004/-ZZ/608.bsw_repudiates_meyer_9_7_2004.asp) > >  
STATEMENT FROM THE COUNCIL OF THE BIOLOGICAL > SOCIETY OF WASHINGTON >  
> The paper by Stephen C. Meyer in the Proceedings ("The origin of >biological information and the higher taxonomic categories," vol. 117, no. >2, pp. 213-239) represents a significant departure from the nearly purely >taxonomic content for which this journal has been known throughout its >124-year history. It was published without the prior knowledge of the >Council, which includes officers, elected councilors, and past presidents, >or the associate editors. We have met and determined that all of us would >have deemed this paper inappropriate for the pages of the Proceedings. > > We endorse the spirit of a resolution on Intelligent Design set forth by >the American Association for the Advancement of Science >([www.aaas.org/news/releases/2002/1106id2.shtml](http://www.aaas.org/news/releases/2002/1106id2.shtml)), and that topic will not be >addressed in future issues of the Proceedings. We are reviewing editorial >policies to ensure that the goals of the Society, as reflected in its >journal, are clearly understood by all. Through a web presence >([www.biolsoewash.org](http://www.biolsoewash.org)) and contemplated improvements in the journal, the

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>[http://pharyngula.org/index/weblog/comments/-microdissecting\\_meyer/](http://pharyngula.org/index/weblog/comments/-microdissecting_meyer/) > >It's not as extensive as the Panda's Thumb review, but I like it >just as much. ><http://www.pandasthumb.org/pt-archives/-000430.html> > >Tom Schneider's review: ><http://www.lecb.ncifcrf.gov/~toms/paper/ev/#Meyer> >is too criptic and centered on Tom Schneider's own work, >in my opinion. > > > >Brian Foley <btf@lanl.gov>  
> > > >

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## Quotation

Hello

Does anybody know who coined the term "The ghost of competition past"? And can you give me a reference?

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

Phone: +41 1 635.47.55 Fax: +41 1 635.47.80 e-mail: wolfman@zoolmus.unizh.ch

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## Quotation answer

For those of you who want to know the answer about the original quote. most respondents agree that the original quote is

> Connell JH. 1980. Diversity and the coevolution of competitors, or the > ghost of competition past. Oikos 35:131-8. >

THANKS!

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

Phone: +41 1 635.47.55 Fax: +41 1 635.47.80 e-mail: wolfman@zoolmus.unizh.ch



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## Saturation test program

I am looking for a computer program that calculates and /or plots uncorrected pairwise distances using transitions and transversions versus corrected distances. The program must be able to handle large data sets (eg 100 000 comparisons) and various substitution models. I would be grateful if you could let me know if there is such a program.

Best regards, Maarit Jaarola

maarit.jaarola@cob.lu.se

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## Selection contents

The journal Selection has published papers of outstanding researchers mainly in population genetics, game theory, adaptive dynamics, and language evolution. Sadly, the journal did not enjoy good circulation and ceased after its third volume.

Yet many of these papers are much too valuable to slip into obscurity. I circulate the contents of the journal to let you find if you need some of them (in author email addresses, [\*] replaces the funny character to defend against spammers). Special issues on adaptive dynamics and on language evolution are in the second and third volumes, respectively. Free abstracts and pay pdfs are available on the publisher's website ([http://www.akkrt.hu/kerdesek/-reszletes\\_hjour.jsp?id6&language=en](http://www.akkrt.hu/kerdesek/-reszletes_hjour.jsp?id6&language=en)).

Eva Kisdi (eva.kisdi[\*]utu.fi)

SELECTION Volume 1 (2000)

John Maynard Smith Festschrift

Crow, J. F. <jfcrow[\*]facstaff.wisc.edu> An Insatiable Appetite for Ideas

Broom, M.; Cannings, M.; Vickers, G. T. <m.broom[\*]sussex.ac.uk> Evolution in Knockout Contests: The Variable Strategy Case

Cressman, R.; Tao, Y. <rcressma[\*]wlu.ca> The Discrete-time Two-species ESS Concept

Dor, D.; Jablonka, E. <daniel[\*]post.tau.ac.il> From

Cultural Selection to Genetic Selection: A Framework for the Evolution of Language

Shapira, H.; Eshel, I. <Illan[\*]math.tau.ac.il> On the Volunteer Dilemma I: Continuous-time Decision

Griesemer, J. <jrgriesemer[\*]ucdavis.edu> The Units of Evolutionary Transition

Hofbauer, J. <jh[\*]banach.mat.univie.ac.at> From Nash and Brown to Maynard Smith: Equilibria, Dynamics and ESS

Lenski, R..E.; Velicer, G. J. <lenski[\*]msu.edu> Games Microbes Play

Michod, R. E.; Roze, D. <michod[\*]u.arizona.edu> Some Aspects of Reproductive Mode and Origin of Multicellularity

Pen, I.; Weissing, F. J. <penir[\*]biol.rug.nl> Sexual Selection and the Sex Ratio: An ESS Analysis

Poore, A. G. B.; Fagerström, T. <Torbjorn.Fagerstrom[\*]adm.slu.se> Intraclonal Variation in Macroalgae: Causes and Evolutionary Consequences

Scheuring, I. <shieazsf[\*]ludens.elte.hu> Avoiding Catch-22 of Early Evolution by Stepwise Increase in Copying Fidelity

Svenstrup, M.; Christiansen, F. B. <freddy[\*]biology.au.dk> Biker's Dilemma: Cooperation between Foes

Taylor, P. D.; Irwin, A. J.; Day, T. <taylorp[\*]post.queensu.ca> Inclusive Fitness in Finite Deme-structured and Stepping-stone Populations

Ujhelyi, M. On the Evolution of the Capacity for Mirror-Self-Recognition

von Kiedrowski, G.; Szathmáry, E. <kiedro[\*]jernie.orch.ruhr.uni-bochum.de> Selection versus Coexistence of Parabolic Replicators Spreading on Surfaces

Waxman, D.; Peck, J. R. <D.Waxman[\*]sussex.ac.uk> The Outcome of Evolution when Mutations are Highly Pleiotropic

Lemire, M.; Lessard, S.; Tao, Yi <lessards[\*]dms.umontreal.ca> Evolutionary Stability in Two-sex Two-locus Models

Regular Papers

Wool, D.; Agami, T. <dwool[\*]post.tau.ac.il> Response to Selection and Genetic Regulation of Esterase Activity Variation in *Tribolium confusum*

Marks, R. W.; Ptak, S. E.

<susan[\*]charles.stanford.edu> The Maintenance of Single-locus Polymorphism. V. Sex-dependent Viabilities

Waxman, D. <D.Waxman[\*]sussex.ac.uk> Dynamics of a Multilocus Trait

Book Review Jablonka, E. <jablonka[\*]post.tau.ac.il> The Evolution of the Common Good

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Volume 2 (2001)

Adaptive Dynamics

Proulx, S. R.; Day, T. <proulx[\*]proulxresearch.org> What can Invasion Analyses Tell us about Evolution under Stochasticity in Finite Populations?

van Doorn, G. S.; Weissing, F. J. <doorngs[\*]biol.rug.nl> Ecological versus Sexual Selection Models of Sympatric Speciation: A Synthesis

Matessi, C.; Gimelfarb, A.; Gavrilets, S. <matessi[\*]igbe.pv.cnr.it> Long-term Buildup of Reproductive Isolation Promoted by Disruptive Selection: How Far Does it Go?

Leimar, O. <olof.leimar[\*]zoologi.su.se> Evolutionary Change and Darwinian Demons

Champagnat, N.; Ferrière, R.; Ben Arous, G. <champagn[\*]clipper.ens.fr> The Canonical Equation of Adaptive Dynamics: A Mathematical View

Vincent, T. L.; Brown, J. S. <vincent[\*]u.arizona.edu> Evolutionarily Stable Strategies in Multistage Biological Systems

Greenwood-Lee, J. M.; Taylor, P. D.; Haig, D. <taylorp[\*]post.queensu.ca> The Inclusive Fitness Dynamics of Genomic Imprinting

Maire, N.; Ackermann, M.; Doebeli, M. <doebeli[\*]zoology.ubc.ca> Evolutionary Branching and the Evolution of Anisogamy

de Jong, T. J.; Geritz, S. A. H. <deJong[\*]rulsfb.leidenuniv.nl> The Role of Geitonogamy in the Gradual Evolution towards Dioecy in Cosexual Plants

Meszéna, G.; Szathmáry, E. <geza.meszena[\*]elte.hu> Adaptive Dynamics of Parabolic Replicators

Kisdi, É.; Jacobs, F. J. A.; Geritz, S. A. H. <eva.kisdi[\*]utu.fi> Red Queen Evolution by Cycles of Evolutionary Branching and Extinction

Regular Papers

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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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## SnowVole samples

Dear Evoldir members,

we are currently looking for tissue samples of snow voles (including *Chinomys nivalis*, *C. gud* and *C. roberti*) from various geographical areas for a phylogenetic and phylogeographic analysis. Samples could be soft tissues (fur, muscles, liver, kidney...) but also hard tissues (teeth and bones) notably from owl pellets.

Thanks in advance,

Christelle Tougard. –

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<http://www.u-bourgogne.fr/BIOGEOSCIENCE/-TougardCVT.html>

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## Software SeqGen v1 3

I have just uploaded a new version of Seq-Gen to our web site:

<http://evolve.zoo.ox.ac.uk/software/seqgen/> Seq-Gen is a program that will simulate the evolution of nucleotide or amino acid sequences along a phylogeny, using common models of the substitution process. A range of models of molecular evolution are implemented including the general reversible model. State frequencies and other parameters of the model may be given and site-specific rate heterogeneity may also be incorporated in a number of ways. Any number of trees may be read in and the program will produce any number of data sets for each tree. Thus large sets of replicate simulations can be easily created. It has been designed to be a general purpose simulator that incorporates most of the commonly used (and computationally tractable)

models of DNA sequence evolution.

The new version allows the simulation of amino acid sequence (previously in our separate program, PSeq-Gen) but also includes some additional models of AA substitution.

Thanks, Andrew

–

Andrew Rambaut, EMAIL - andrew.rambaut@zoo.ox.ac.uk Zoology Department, WWW - <http://evolve.zoo.ox.ac.uk/> University of Oxford, TEL - +44 1865 271261 South Parks Road, Oxford, UK FAX - +44 1865 271249

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## Software Transformer-2

Dear colleagues,

We are announcing the release of TRANSFORMER-2, a computer program for the analysis of molecular population genetic data which is suitable for codominant (allozyme or microsatellite) data for at least 60 enzyme/primers with up to 10 loci (each containing a maximum of 10 alleles) per enzyme/primer in 66,000 diploid individuals.

Through saving a lot of research time while increasing accuracy, Transformer-2 permits the effective implementation of urgency in the growing number of practical applications of molecular population genetic information.

This program is the result of a collaborative effort between the Jardín Botánico Canario Viera y Clavijo and the Departamento de Ingeniería del Software of the Instituto Tecnológico de Canarias (ITC). It can be downloaded without charge at the web page of the Jardín Botánico Canario Viera y Clavijo

<http://www.jardincanario.org> (under the link Genética de la Conservación),

and may be distributed freely if and when (i) it does not undergo any modification, (ii) the manual and the two example files transf-draw.xls and transf-gntp.xls are attached without changes, and (iii) it is adequately cited in all papers and communications.

Caujape-Castells J, Baccarani-Rosas M (2004) Transformer-2: a program for the analysis of molecular population genetic data. Jardín Botánico Canario Viera y Clavijo and Instituto Tecnológico de Canarias,

Las Palmas de Gran Canaria, Spain.

### DESCRIPTION

At present, you can feed Transformer-2 with the drawings of the interpretations of your molecular patterns (a utility that will probably be most welcome by those using allozymes) or with a matrix of genotypes.

For those using the drawing utility, Transformer-2 offers a versatile and intuitive data entry interface that makes corrections and manipulations fairly easy to implement. The major advantage of drawing the interpretations is that, once you are done, quantitative data for any possible configuration of populations and loci will be a few seconds away. However, there are at least three additional reasons to use this tool of Transformer-2:

1. You can forget about genotyping individuals, as the program will do it for you from the drawing. Therefore, you are less prone to make the mistakes that are so frequent when you interpret by hand.
2. You may correct or modify your interpretations by moving, inserting or deleting any number of individuals, alleles, loci or spaces easily at any point of the interpretation process.
3. You will have a permanent visual record of the interpretations which is much easier to scan and check than a whole table of genotypes and which can be used nicely in presentations (see the attached file «transf-draw.xls»).

Either if you draw your interpretations or if you enter a Table of genotypes, Transformer-2 automatically generates the necessary files to run six genetic analysis programs of widespread use in population genetics (Biosys, GeneStat, Bottleneck, PopGene, GenePop and Ntsys), and calculates all the parameters related to the probabilities of allelic loss (sensu Bengtsson et al. 1995) FOR ANY GROUPINGS OF POPULATIONS YOU MAY BE INTERESTED IN. Thus, the program allows you to define population subsets, compare independent groups of populations, include the same population (s) in more than one group and make all possible data combinations you can think of just with a few easy mouse clicks.

Transformer-2 is already being improved to include a much wider range of possibilities and calculations. A new version that will accept RAPD and AFLP data is already in the pipeline, and we hope to have it ready before spring 2005. In a longer term, we plan to have a Transformer that performs most of the calculations involved in the analysis of molecular population genetic data while keeping the versatility of the present version.

Cheers,

Juli and Mario

Dr. Juli Caujape-Castells Laboratorio de Biodiversidad Molecular Jardín Botánico Canario "Viera y Clavijo" Ap. de Correos 14 de Tafira Alta 35017 Las Palmas de Gran Canaria Spain

email: [julicaujape@grancanaria.com](mailto:julicaujape@grancanaria.com) phone: ##34 928219421 ext. 4770 fax: ##34 219581

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### Video animal tracking

Hi there

I wish to quantify movement of beetles from digital video. They are black in colour and can be filmed individually against a pale background, and I want to know how far they move and at what speed over a given time period. Does anyone know of any freely available software to calculate this? It's a fairly simple problem: just find the x and y coordinates of a black spot once per frame, and output it to a text file along with a time stamp. There's obviously lots of commercial packages, but I don't really want to shell out the thousands necessary for an ethovision license. Any advice gratefully received.

Rob Knell

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### Windows PAUP

I am having trouble using Paup4.0beta10 win in Windows XP Professional and was wondering if anyone had experienced similar problems. Whenever I try to use any of the commands begin data; begin character; begin distances or begin taxa; the program crashes. The program can still complete a parsimony or likelihood analyses with no apparent problems. I have tried using different file formats but this has made no difference. Any suggestions would be greatly appreciated.

Cheers

Claire McClusky PhD Student Deakin University Warrnambool, Australia [clairefi@deakin.edu.au](mailto:clairefi@deakin.edu.au)

Claire McClusky <[clairefi@deakin.edu.au](mailto:clairefi@deakin.edu.au)>

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### WoodsHole VisitingScholars

As seen in the 10 September issue of Science:

Visiting Scholars in Global Infectious Diseases Marine Biological Laboratory, Woods Hole, MA

The Marine Biological Laboratory (MBL) announces the 2005 Visiting Scholars Program in Global Infectious Diseases. The goal of this program is to encourage the application of genomic and functional genomic approaches to the study of parasitic diseases. Applications are invited from graduate students, post-doctoral fellows and independent investigators to join year-round investigators in the Global Infectious Diseases Program to conduct studies on the basic biology of pathogens and complex host-pathogen interactions. Individuals working in developing countries are encouraged to apply. The visiting scholarships provide short-term support (typically 2-3 months) including research support, travel, housing and meals at the MBL. Applications should include a brief Curriculum Vitae, a two page description of the proposed research to be conducted and the names and contact information for three references.

Global Infectious Diseases Laboratories at the MBL: Stephen Hajduk -Molecular biology and biochemistry of parasites; Andrew McArthur -Global gene expression and computational biology in eukaryotic pathogens; David Patterson-Biodiversity informatics; Robert Sabatini-Epigenetic regulation of gene expression in kinetoplastids; Mitchell Sogin-Genomics and molecular evolution of parasites; Jennifer Wernegreen-Bacteria-insect symbiosis.

Please send applications to Dr. Stephen L. Hajduk c/o Trish Halpin, [thalpin@mbl.edu](mailto:thalpin@mbl.edu) Global Infectious Diseases Program Marine Biological Laboratory, 7 MBL Street Woods Hole, MA 02543

Applications reviewed beginning September 30, 2004.

See <http://jbpc.mbl.edu/> for more information about the GID research programs listed above and other labs in the MBL's Josephine Bay Paul Center for Comparative Molecular Biology and Evolution.

Jennifer Wernegreen <[jwernegreen@mbl.edu](mailto:jwernegreen@mbl.edu)>

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## PostDocs

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### CornellU CanineGenomics

Post-doctoral positions in canine genomics.

Two post-doctoral positions are available to study the genetic & biologic basis of abnormal cardiac innervation, ventricular arrhythmias and sudden cardiac death in German shepherd dogs. Study of these animals will provide important insights into inherited cardiac diseases in animals and humans. These studies are part of a collaborative effort between Drs. Sydney Moise and Teresa Gunn in the Departments of Clinical Sciences and Biomedical Sciences in the College of Veterinary Medicine at Cornell University (Ithaca, NY) and Dr. Karen Vikstrom in the Department of Pharmacology at SUNY-Upstate Medical University (Syracuse, NY).

Our German shepherd dogs have an inherited predisposition to abnormal cardiac innervation, ventricular arrhythmias and sudden cardiac death. Although the mode of inheritance has not been well defined, it is consistent with a major susceptibility locus that is influenced by modifier loci. The aim of our research is to

determine the genes involved and understand the biological pathway(s) that are disrupted to cause this disease. Two projects are available: 1) Screening German shepherd dogs from affected and unaffected dogs from our colony for genetic markers and performing linkage analysis to map modifier loci, followed by analysis of candidate genes. Funding is provided for 2 years with possibility of extension. 2) Microarray analysis of archived heart tissue from affected and unaffected German shepherd dogs using canine Affymetrix arrays, followed by validation and analysis of gene expression differences. Funding is provided for 18 months with possibility of extension. Some of the work will be performed at SUNY-Upstate.

Position requirements: Ph.D. or equivalent degree with a focus on genetics, molecular biology or related field of study. Candidates should submit a current CV, a statement of research experience, and the names of three individuals who could provide letters of reference to

Dr. Teresa Gunn Department of Biomedical Sciences  
T2006B VRT Cornell University Ithaca, NY 14853

email (preferred): [tmg25@cornell.edu](mailto:tmg25@cornell.edu) fax (607) 253-4212

Cornell University is an affirmative action, equal opportunity employer. Applications from women and minorities are encouraged.

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## CornellU HumanPopGenetics

Postdoctoral position in computational human population genetics at Cornell Carlos Bustamante, Rasmus Nielsen, Tara Matise and Andy Clark seek an energetic postdoctoral fellow to engage in NIH-funded research on the analysis of dense, genome-wide SNP genotype data such as that being produced by the HapMap project. We are pursuing a series of investigations that center around the following four aims: 1. SNPs used in these large projects have been ascertained in separate re-sequencing projects. We plan to investigate the consequences to a variety of inferences of failing to consider this ascertainment bias, and methods for correcting this bias. 2. Positive, purifying, and balancing selection, as well as demographic changes, all are expected to influence the site frequency spectrum, patterns of linkage disequilibrium, and other aspects of SNP variation. We will be developing methods to infer the impact of natural selection on genomic regions, testing their validity and robustness, and applying them to dense genotype data. 3. Population genetics theory shows that local rates of recombination are expected to have an impact on the efficacy of natural selection, which in turn influences linkage disequilibrium, frequency spectrum, and other population genetic attributes of SNPs. We are developing formal statistical approaches to parameter estimation and hypothesis testing, centering on the null hypothesis that variability among genomic regions in local population genetic attributes is explicable by the local recombination rate. This entails analysis of the data, both direct and indirect, supporting inferences about local recombination rate.

4. The dense LD map provided by HapMap enables us to simulate disease associations so as to quantify the power whole-genome LD association inference. These tests will help identify the attributes of local LD that best predict the power of association tests, and will serve as additional guidance to identify regions requiring more dense SNP coverage. Our research groups provide a lively and stimulating research environment. Facilities include a 50 dual-G5 processor cluster (run by our group), and access to the Cornell Theory Center Velocity Cluster. Please email your resume, statement of research interests and contact information for three

references to Andrew Clark (ac347@cornell.edu) and/or Carlos Bustamante (cdb28@cornell.edu). The position is available immediately, but we can be flexible.

ac347@cornell.edu

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## GeorgiaInstTech EvolBiol

A POSTDOCTORAL POSITION in evolutionary biology is available in the laboratory of Todd Strelman at the Georgia Institute of Technology. The candidate for this position will be expected to carry out independent research contributing to the major focus of the laboratory: the genetic basis of functional and phenotypic diversity in cichlid fishes from Lake Malawi, East Africa. In the past few years, the cichlid community has built an array of genomic resources (<http://hogs.unh.edu/-cichlid/>) to complement decades of natural history information. Using these tools in the context of wild cichlid populations, the Strelman lab aims to understand the evolutionary genesis of complex organismal designs. We study cichlids in the field, in the laboratory, and in the tropical aquarium facilities at the GIT. Research is presently focused on the evolution of jaws, teeth and color pattern because these traits have been important to cichlid diversification (for representative publications, see <http://www.biology.gatech.edu/professors/-strelman.htm>).

Candidates working in evolutionary ecology, biomechanics, quantitative genetics or evolutionary development, are especially encouraged to apply. The Georgia Institute of Technology offers exciting avenues for collaboration with biomedical engineers, biomechanicians, developmental biologists and systems ecologists.

The start date for this position is flexible, and funding is available for at least two years. The salary is competitive and commensurate with experience. Interested individuals should send a CV, a brief description of research and professional goals, and the names and addresses of 3 references to Todd Strelman, by e-mail (todd.strelman@biology.gatech.edu) or regular mail (School of Biology, 310 Ferst Drive, Georgia Institute of Technology, Atlanta, GA 30332-0230).

J.T. Strelman Assistant Professor School of Biology The Georgia Institute of Technology 310 Ferst Drive Atlanta, GA 30332-0230 404-385-4435 (office) 404-385-4436 (lab) 404-894-0519 (fax department) 404-897-3395 (fax home) E-mail: todd.strelman@biology.gatech.edu <http://www.biology.gatech.edu/professors/->

strelman.htm <http://www.biology.gatech.edu/professors/strelman.htm>

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## GoteborgsU AlgalPopGenetics

Position available at Göteborgs University 2004-09-01  
Department of Marine Ecology Tjärnö Marine Biological Laboratory

POST-DOCTORAL RESEARCHER in Population genetics/Molecular Ecology

A Post-doctoral researcher is required for a project on population genetics and molecular ecology in bladderwrack (*Fucus vesiculosus*, a marine macro algae) during the period October 2004 to August 2006, at the Department of Marine Ecology, Göteborg University.

The project is funded by grants to Kerstin Johannesson & Lena Kautsky

The position is available at Tjärnö Marine Biological Laboratory, a research station at Göteborg and Stockholm universities, on the west coast of Sweden.

The project will use microsatellites to evaluate population structure in the marine brown algae *Fucus vesiculosus* and particularly in populations of the Baltic. *Fucus vesiculosus* is a keystone species of shallow marine hard-bottom communities in the Baltic. Preliminary studies show a high degree of substructure as well as reproductive isolation between the normal and a dwarf morph confined to northern parts of the Baltic. Moreover, the dwarf morph reproduce asexually using proliferations growing from the stem. This is an hitherto unknown strategy and one aim of this project is to investigate this strategy in more detail to unravel how and where it has evolved and why. We will also assess the distribution and taxonomic status of the dwarf morph to clear out if it is endemic to the Baltic. Clonal reproduction is present also in the normal morph suggesting that this is a unique adaptation to extreme environmental conditions, such as low salinities.

The successful applicant should have a proficiency in microsatellite analyses and DNA sequencing methods. It is also essential that the applicant has a proper theoretical background in population genetics and is experienced with computer-based tools of analysis. Knowledge in screening of genomic (BAC) libraries, cloning and subcloning and making cDNA libraries is valuable for the proper development of this and related projects and will be judged as a merit.

For further information please contact Kerstin Johannesson (kejo@tmbl.gu.se). For a general information about the research station please consult [www.tmbl.gu.se](http://www.tmbl.gu.se) Application Applications, including CV, a choice of three-five relevant publications, the names, postal and e-mail addresses of two academic referees, should be sent to: Registrator, Göteborg University, Box 100, S-405 30 Göteborg, Sweden, stating reference number E36 3356/04, no later than 22 of September 2004.

Union representatives: SACO Jan Berggren, tel +46 31 773 1078, SEKO Lennart Olsson, tel +46 31 773 1173, OFR-S Eva Sjögren, tel +46 31 773 1169.

Dean of the faculty

Kerstin Johannesson <Kerstin.Johannesson@tmbl.gu.se>

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## JohnsHopkinsU MosquitoPopGenet

Applications are being accepted for a full-time, non-tenure track post-doctoral associate in the Department of Molecular Microbiology and Immunology, Bloomberg School of Public Health, Johns Hopkins University. Project entails the development, evaluation and analysis of genetic markers in the mosquito *Culex tarsalis*. These markers will be used to conduct population genetics and QTL analysis in this mosquito to investigate its role as a vector of West Nile Virus in North America. The position is available immediately. Funding is available for 3 years contingent on satisfactory performance. Salary will follow NIH guidelines. Benefits included. Applicants should have a Ph.D. in ecology, population biology, genetics or related field. Experience in entomology and vector insects is helpful but not required. Candidate must have experience in population genetics, QTL analysis and development/use of genetic markers such as microsatellites, RAPD's, ISSR's and AFLP's. The ideal candidate will have a competitive publication record, experience with modeling, epidemiology and general molecular laboratory techniques. The successful candidate will be given the opportunity for independent grant writing and attendance at national/international conferences. Applicants should send a detailed CV, statement of research goals, contact information (name, phone number and email address) for 4 professional references, and up to 4 re-prints to:

Jason L. Rasgon, Ph. D. Assistant Professor, The W. Harry Feinstone Department of Molecular Microbiology

and Immunology, Room E4626 Bloomberg School of Public Health, Johns Hopkins University 615 N. Wolfe Street E4626 (410) 502-2584 jrasgon@jhsph.edu <http://faculty.jhsph.edu/?F=Jason&L=Rasgon> Jason Rasgon <jrasgon@jhsph.edu>

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## MarieCurieRes SexEvol

Marie Curie Research training network (MRTN) SEXASEX - 4 postdoc positions available

Students and researchers interested in the paradox of sex in evolutionary biology are strongly encouraged to send an expression of interest to work in the European Union Marie Curie Research Training Network SEXASEX that is co-ordinated by Prof. Dr. Koen Martens, RBINSc, Brussels. Criteria of eligibility include: EU citizenship, less than 4 years of research experience for Young Researchers (YR), less than 10 years for Experienced Researchers (ER), and a willingness to work in a European country other than the country of origin. We seek candidates who are enthusiastic about evolutionary biology, travelling and living abroad, learning in a multidisciplinary research environment and working in teams. All appointments will be for 3 years, YR are offered PhD positions, ER post-doc positions. YR will be expected to obtain a PhD at the end of the project. The application of female candidates is especially encouraged; detailed information on child care facilities at the different institutions will be provided upon request. Aid can be sought if accompanying spouses also require employment abroad.

Project overview: Sex is the queen of evolutionary problems. It will be tackled by SEXASEX in a multidisciplinary approach, providing training and transfer of knowledge for a total of 360 person-months. 10 network researchers (6 young researchers (YR) and 4 experienced researchers (ER)) will receive training in 9 institutions across as many countries. A wide array of research tools will provide excellent training opportunities, for example through individual career development plans, individual tutoring and secondments, which will be supplemented by participation in courses and external workshops. Network-wide training will exploit the extensive experience of the partner institutions through five courses and summer schools for all network researchers. Complementary skills such as management and communication (verbal, written) will be developed, and gender awareness will be raised, in two network-wide meetings. The network's theoretical and empiri-

cal research will apply 13 major approaches, including novel genomic and karyological approaches, intraspecific phylogeography, ecology, behavioural studies, GIS analyses and theoretical modelling. With this multidisciplinary toolkit, SEXASEX will investigate why sex exists at all, given its evolutionary costs, using the model organism *Eucypris virens*, a non-marine ostracod species with both sexual and asexual reproduction. What determines its gender, what are the genomic consequences of long-term asexuality, what is the cohesiveness of a species with mixed reproduction, how do asexuals and sexuals compete and what is their historical zoogeography? The pluralistic approach of SEXASEX is unique and timely, using highly novel methodologies and dealing with cutting edge science based on European excellence and tradition.

If you are interested, please contact Dr Isa Schön, Royal Belgian Institute of Natural Sciences, Freshwater biology, Vautierstraat 29, B-1000 Brussels, Belgium

E-mail ([Isa.schoen@naturalsciences.be](mailto:Isa.schoen@naturalsciences.be)) or fax (0032 2 62 74 113).

Correspondence by email is preferred.

For PhD position 3 and Postdoc position 1, a full application is asked before the 20th of September 2004. For all other positions, expressions of interest are invited. Applications or expression of interest should include a letter, a CV and addresses of two potential referees. Please state clearly in the letter which position(s) interest you, and why. If there is more than one, rank them according to your preference.

The following 4 Postdoc positions will become available in the course of the network:

**POSTDOC POSITION 1: AGE ESTIMATION AND MUTATION ACCUMULATION IN ASEXUAL AND SEXUAL LINEAGES OF *E. VIRENS*** Starting date: 1st November 2004 Duration: 36 months (2x 18 months) Salary: country-specific plus tax-free mobility allowance Persons in charge: Prof. Dr Koen Martens, Dr Isa Schön, Belgium Prof. Dr Roger Butlin, UK

Locations: Brussels, Belgium & Sheffield, UK Places of work: Royal Belgian Institute of Natural Sciences, Freshwater Biology University of Sheffield, Department of Animal and Plant Sciences Methods to be applied: Development of microsatellite and sequence-based markers, application of these markers and assistance in the training and supervision of YR applying them, plus a central role in data analysis and publication of results. Candidate profile: PhD degree in evolutionary genetics/molecular ecology, or equivalent practical experience; strong track record in the areas of practical molecular biology, associated data analy-



sis and publication. Only persons without Belgian and British nationality are eligible.

POSTDOC POSITION 2: REPRODUCTIVE ECOLOGY OF ASEXUAL AND SEXUAL LINEAGES OF EUCYPRIS VIRENS. Starting date: 1st May 2005

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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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### MichiganStateU EvoAquaticPathogens

Post Doctoral Researcher - Ecological and Molecular Genetic Approaches to Epidemiological Studies of Aquatic Pathogens in Great Lakes Fishes

A 3-year post doctoral research position is available to study molecular genetic and ecological factors associated with the epidemiology of *Renibacterium salmoninarum* (RS) in salmonid fishes of the Great Lakes basin. Research will also include assessment of the importance of natural population structure, environmental and anthropogenic factors mediating disease prevalence, transmission, and persistence. Research will be conducted through the Departments of Fisheries and Wildlife and Department of Pathology and Diagnostic Investigation at Michigan State University (MSU), with an interdisciplinary team composed of Drs. Kim Scribner (Ecological Genetics), Mohamed Faisal (Pathology), Robert Templeman (Quantitative Genetics; Dept. Animal Sci.) and Ruth Phillips (Molecular and Evolutionary Genetics; Washington State University-Vancouver). Duties will include working with project co-PI's and supervising technical staff in each of several areas including: 1) quantitative genetic analyses of gene expression associated with RS infection in different life history stages of salmonid fishes, 2) investigation of relationships between genotype at candidate antigen-processing genes and disease phenotypes, 3) controlled experimental studies of the effect of genotype, environment and disease susceptibility. Population genetic, phylogeographic, and immuno-pathological data bases are available for numerous co-distributed species from across the Great Lakes to extend results from experimental analyses to natural populations. Requirements include a PhD

and molecular skills in either disease, epidemiology, molecular and population genetics, or allied disciplines. Background in the use of microarray technology and some quantitative skills in analysis and interpretation of expression data would be desirable. The position is available as early as mid-October. Send resume, letter of research interests and contact information for 3 references to either: Kim Scribner, PhD, Departments of Fisheries & Wildlife and Zoology, Michigan State University, 13 Natural Resources Building, East Lansing, MI 48824-1222, Tel: (517)-353-3288, e-mail: <<mailto:scribne3@msu.edu>>scribne3@msu.edu or Mohamed Faisal (DVM), Departments of Fisheries & Wildlife and Diagnostic Investigation, Michigan State University, Tel: (517)-432-8259, e-mail [faisal@cvm.msu.edu](mailto:faisal@cvm.msu.edu)

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### PortlandStateU BacterialPhylogenomics

Postdoctoral position available in bacterial taxonomy and phylogenomics. Research will focus on the taxonomy and of the Aquificales. The availability of 4 whole genome sequences, and multiple strains and clones of this group, provides an excellent model system for exploring microbial species concepts and biogeographical questions. Experience in anaerobic culture techniques, microarray analysis, and molecular phylogenetic analysis is desirable. Please send CV, brief statement of research interests and names of three references to Anna-Louise Reysenbach, Biology Department, P.O. Box 751, Portland State University, Portland, OR 97201; fax, (503)725-8570; [reysenbacha@pdx.edu](mailto:reysenbacha@pdx.edu). Webpage [www.alrlab.pdx.edu](http://www.alrlab.pdx.edu) Anna-Louise Reysenbach Phone: (503) 725 - 3864 Fax (503) 725 - 8570 Portland State University Department of Biology, SB2 Rm 246 1719 SW 10th Ave Portland, Oregon 97201

[www.alrlab.pdx.edu](http://www.alrlab.pdx.edu) Phd stipends at <http://-oregonstate.edu/dept/igert/index.html> <http://-www.asm.org/Meetings/index.asp?bid=19177>

Anna-Louise Reysenbach <[reysenbacha@pdx.edu](mailto:reysenbacha@pdx.edu)>

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## RichmondVA SNPs

Virginia Institute of Psychiatric and Behavior Genetics and Center for the Study of Biological Complexity, Virginia Commonwealth University

A postdoctoral position is available with flexible start date. Our research focuses on (1) data mining single nucleotide polymorphism (SNP) patterns in the mammalian genomes and (2) the bioinformatics for the projects in psychiatric genetics. We are currently investigating the neighboring nucleotide compositions of SNPs in the genomic categories and developing computational tools for the data analysis and management in the psychiatric genetics. The successful candidate may participate in one or both of the projects above and join the research program in the Center for the Study of Biological Complexity. The candidate will work in a dry lab environment. The university is located in Richmond, the state capitol of Virginia, within 90 minutes from the mountains, the beach, and Washington, D.C. More information can be found at the website <http://bioinfo.vipbg.vcu.edu/>.

Qualified candidate should be highly motivated in the research and have background in molecular biology and/or computational biology. Experience in one of the programming languages (C/C++, Perl, SQL, Java) is desirable, and experience in database management and/or Linux OS is a plus. Applicants should send a CV, brief statement of research interests, and reference to: Zhongming Zhao (zzhao@vcu.edu).

Contact for more information:

Zhongming Zhao

Assistant Professor Virginia Commonwealth University PO Box 980126 Richmond, VA. US  
 Phone: (804) 828-8129 Fax: (804) 828-1471  
 Email: <<mailto:zzhao@vcu.edu>> zzhao@vcu.edu  
 Web: <<http://bioinfo.vipbg.vcu.edu/>> <http://bioinfo.vipbg.vcu.edu/>

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## RockvilleMD Bioinformatics

Post-doctoral positions (2) for research at the interface

of Bioinformatics and Molecular Evolution

Two UMBI Research Associate (post-doc) positions in bioinformatics and molecular evolution are available at the Center for Advanced Research in Biotechnology (Rockville, Maryland)\*. We seek highly motivated individuals to continue an NIH-funded project developing a software system for phyloinformatic analysis, and applying this system to resolving questions regarding the origin and evolution of split genes (see Qiu, et al., Mol. Biol. and Evol. 21:1252).

Applicants must have a PhD in a relevant field, expertise in computer programming, and relevant research experience. We are particularly interested in applicants whose primary interest is in evolution, and who have expertise in either i) statistical inference using probabilistic models of character evolution, or ii) design and implementation of software systems such as databases, analysis pipelines, or code libraries. These are 1-year positions with the opportunity for renewal in subsequent years (dependent on availability of funds), and salaries of \$40-55 K per year, depending on experience.

To apply, send a cover letter, curriculum vitae, and contact information for three personal references to the address below. Review of applications will begin immediately and will continue until the positions are filled.

Dr. Arlin Stoltzfus (stoltzfu@umbi.umd.edu), <http://www.molevol.org/camel> Center for Advanced Research in Biotechnology 9600 Gudelsky Drive, Rockville, Md 20850 Tel: (301) 738-6208 Fax: (301) 738-6255

— \*The Center for Advanced Research in Biotechnology ([www.carb.nist.gov](http://www.carb.nist.gov)) is a joint research center of the National Institute of Standards and Technology (NIST) and the University of Maryland Biotechnology Institute (UMBI). Rockville is in the heart of Maryland's biotechnology corridor, about 15 miles from Washington, DC. Basic research at CARB is both theoretical and experimental, and focuses on macromolecular structure and function. CARB is an EEO/AA Employer. Women and minority candidates are especially encouraged to apply.

————— Arlin Stoltzfus (arlin.stoltzfus@nist.gov)  
 Research Biologist, NIST; Adj. Asst. Prof., UMBI  
 CARB, 9600 Gudelsky Drive, Rockville, Maryland  
 20850 tel 301 738 6208, fax 301 738 6255, web home  
[www.molevol.org/camel](http://www.molevol.org/camel)

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## TexasAnMU PopGenetics

Postdoctoral Research Associate \* Population Genetics/Molecular Ecology Department of Wildlife and Fisheries Sciences Texas A&M University College Station, Texas 77843-2258 Responsibilities: Position responsibilities involve development and assay of nuclear-encoded microsatellites and assay of mitochondrial DNA sequences for projects involving population genetics and molecular ecology of marine fishes. Primary responsibilities include data acquisition and analysis, and preparation of reports and publications. Qualifications: Dissertation or postdoctoral work in molecular population genetics and/or molecular ecology is required, as is experience with microsatellite and/or mtDNA data acquisition and analysis. Experience with major software programs (e.g., Arlequin, Genepop etc.) also is required. Salary: Salary will depend on experience. Benefits are included. Position is for 12-24 months. Closing date: Position will remain open until filled. Contact: Send curriculum vitae, description of research experience, and names, addresses, phone numbers, and e-mail of three references to: Dr. John R. Gold, Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, Texas 77843-2258. Electronic submissions are acceptable: goldfish@tamu.edu. International applicants will be considered if they hold the correct visa(s). Texas A&M University is an Equal Opportunity/Affirmative Action/Equal Access Employer.

John Gold <goldfish@tamu.edu>

as depending on the interests of the candidate. A strong bioinformatics and phyloinformatics background is required. Experience of automated DNA sequencing would be a bonus. The researcher will work in association with Trevor Hodkinson (Principal Investigator; [www.tcd.ie/Botany/Staff/THodkinson.html](http://www.tcd.ie/Botany/Staff/THodkinson.html)), Nicolas Salamin ([www3.tcd.ie/~salamin](http://www3.tcd.ie/~salamin)) and Vincent Savolainen (Royal Botanic Garden, Kew, England). They must also be able to work independently and would be expected to help support existing researchers on this project and contribute to the research group in general.

To apply or to obtain further information, please send a CV including research interests, a publication list and contact details of two referees and a letter of motivation to [salamin@tcd.ie](mailto:salamin@tcd.ie) (Phone 00 353 1 6083740) by October 15th 2004.

– Nicolas Salamin

Molecular Systematics Lab Department of Botany University of Dublin Trinity College Dublin 2 Ireland

tel: +353 1 608 3740 fax: +353 1 608 1147 email: [salamin@tcd.ie](mailto:salamin@tcd.ie) web: <http://dnabank.bot.tcd.ie/~salamin> <http://www3.tcd.ie/~salamin> <http://evolution.gs.washington.edu/salamin>

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## UAuckland 2 Bioinformatics

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### TrinityCollegeIreland PlantBioinformatics

Job vacancy - Postdoctoral researcher Plant bioinformatics and phyloinformatics

Department of Botany, Trinity College, University of Dublin, Ireland Salary c.32-35,000 Euro Starting date: January 2005. Finishing date: end January 2006 Closing date for application: 15th October 2004

A postdoctoral researcher is required to work full time for c.13 months on an Enterprise Ireland funded Basic Research Project entitled 'Large trees, supertrees, and the grass phylogeny: a high performance computing approach'. The work will be primarily computer based but could involve some DNA sequencing. We expect the postdoc to work on our grass dataset to examine taxonomic relationships of taxa, molecular evolution and positive selection on genes of interest. However, there is also scope to pursue other ar-

Dear colleagues

We are pleased to advertise the following two positions. Both close on 1 Oct 04. I would appreciate it if you could bring these positions to the attention of suitably qualified candidates. Thank you.

Allen Rodrigo Bioinformatics Institute University of Auckland

Position 1 – Vacancy Number A516-04 We are seeking a postdoctoral research fellow with experience in statistical learning methodology, pattern recognition and class prediction to join the SCOPE (Screening for Pregnancy Endpoints) team researching novel methods of predicting the major diseases of late pregnancy. This is a two year appointment in research fellow/lecturer grade, subject to experience.

Location: Auckland Term of Contract: 2 years Closing Date: 1 October 2004

Position Overview A postdoctoral research position for an experienced statistician/bioinformaticist to join the

SCOPE team is available in the Bioinformatics Institute, University of Auckland. The primary focus of the research is to identify novel biomarkers in the proteome of human sera to predict the three major complications of pregnancy, preeclampsia, fetal growth restriction or preterm birth. This project is part of an international SCOPE project to develop effective methods of predicting these conditions, and involves collaboration with universities in UK, Australia and USA, including the University of California, San Francisco. The research will utilise a unique pregnancy biobank established through the SCOPE screening study of 3000 pregnant women, conducted under the auspices of the Department of Obstetrics and Gynaecology, University of Auckland. Preferably the candidates should have experience in machine learning methods including neural networks and support vector machines, as well as proficiency with standard statistical techniques such as model selection and averaging, tree-based methods and boosting. Familiarity with Bayesian methods would also be an advantage.

Applicants should have good verbal and written communication skills. They should be able to work independently and operate effectively within the SCOPE research team.

Salary and level of appointment is commensurate with qualifications and experience.

For further information about this position please contact Associate Professor Robyn North Department of Obstetrics and Gynaecology School of Medicine and Health Sciences r.north@auckland.ac.nz

Professor Allen Rodrigo Director, Bioinformatics Institute University of Auckland a.rodrigo@auckland.ac.nz

Position 2 – Vacancy No A517-04 A vacancy exists for a two-year postdoctoral research fellow to work on computational and statistical methods for integrating population genetics with population dynamics models of whales (see Baker and Clapham, 2004, TREE 19:365-371). Location: Auckland Term of Contract: 2 years Closing Date: 1 October 2004

Position Overview A vacancy exists for a two-year postdoctoral research fellow to work on computational and statistical methods for integrating population genetics with population dynamics models of whales (see Baker and Clapham, 2004, TREE 19:365-371). Ideally, the candidate will have a PhD in Evolutionary Biology, Population Biology, Computational Statistics, Bioinformatics or a related discipline, with a significant computing and modelling component. The researcher will be familiar with Markov chain Monte Carlo methods for Bayesian inference, and an understanding of genealogy-

based population genetics. In addition, familiarity with modelling using differential equations will be an advantage. Knowledge of Java, C++, or C is essential.

Applicants should have good verbal and written communication skills and they should be able to work independently.

Salary and level of appointment is commensurate with qualifications and experience.

For further information about this position please contact Professor Allen Rodrigo Professor of Computational Biology and Bioinformatics Director of Bioinformatics Institute a.rodrigo@auckland.ac.nz

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## UBasel HostParasiteEvol

Universitat Basel, Switzerland Zoologisches Institut

2 Postdoc positions in host-parasite evolution

are available in the division of Evolutionary Biology, Institute of Zoology at Basel University. I am looking for 2 highly motivated post-docs with interest in the evolutionary biology of host-parasite interactions. These positions are funded to work on the evolutionary genetics and epidemiology of *Daphnia* and its microparasites (bacteria and microsporidians). A good background in evolutionary genetics, including knowledge of molecular methods is helpful. Statistical skills are helpful, previous experience with *Daphnia* is not essential. Excellent written, verbal, and interpersonal skills, a superb work ethic, and the ability to think creatively and critically are desired. Starting date is flexible, from January 2005 onwards. The positions are initially for 2 years but can be extended.

The post-docs will be part of Dieter Ebert's group working on the evolution of host-parasite interactions, focusing on the *Daphnia* system. The group is currently at Fribourg University but will move to Basel University in October 2004. Details about the groups activities can be found under: <http://www.unifr.ch/-biol/ecology/ebert/index.html> Please send application by E-mail to Dieter Ebert. Applications should include a CV, a list of publications and a short description of your research interests. Applications received before 22. October 2004 will be given full consideration.

Contact information: Prof. Dr. Dieter Ebert, Universität Basel, Zoologisches Institut, Biozentrum/Pharmazentrum, Klingelbergstrasse 50 4056

Basel, Switzerland, Email: dieter.ebert@unibas.ch  
Tel.(Sekretariat) +41-(0)61-267 16 26; Fax +41-(0)61-267 16 27

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Dieter Ebert [ Mailto:dieter.ebert@unifr.ch ]

until 30 Sept. 2004: Université de Fribourg, Département de Biologie, Ecologie et Evolution, Chemin du Musée 10 1700 Fribourg, Switzerland <http://www.unifr.ch/biol/ecology/index.html> Tel. +41-(0)26-300 88 69, Fax +41-(0)26-300 96 98

Mail address from 1. October: Universität Basel, Zoologisches Institut, Biozentrum/Pharmazentrum Klingelbergstrasse 50 4056 Basel, Switzerland Tel.(Sekretariat) +41-(0)61-267 16 26 Fax +41-(0)61-267 16 27

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## UCaliforniaRiverside EvoInteractions

Postdoc, Evolution of Tritrophic Interactions

A postgraduate research position is available for a highly motivated individual to join an NSF-funded research project to study the evolution of a tritrophic interaction. The primary objective is to test the working hypothesis that the indirect effects of the glandular trichomes of *Datura wrightii* on the natural enemies of *D. wrightii*'s herbivores oppose the direct effects of the trichomes on those herbivores. These indirect effects may constrain the increase in the frequency of plants with glandular trichomes in natural populations. Measurements of plant fitness in the field in the presence and absence of herbivores and/or natural enemies will be emphasized. The successful candidate will participate in planned field and laboratory experiments and also will have the opportunity to develop related projects. Applicants must have a PhD. degree before hiring, and research experience and knowledge in insect ecology and behavior, the design and analysis of field experiments, insect identification and a genuine interest in the evolution of tritrophic interactions. Excellent oral and verbal communication skills are also required.

Postdoctoral positions start at a salary of \$31,044 per year, plus benefits. The starting date is negotiable but will be no later than February 1, 2005. Screening of applications will begin November 1, 2004. The initial appointment will be for one year with reappointment for up to two additional years contingent upon satisfac-

tory performance. To apply, send a curriculum vitae, relevant reprints or manuscripts in press, a description of research interests within the *Datura* system, and the names and e-mail and postal addresses of three references to:

Dr. J. Daniel Hare Department of Entomology University of California Riverside, CA 92521

For more information, send an e-mail to [daniel.hare@ucr.edu](mailto:daniel.hare@ucr.edu). A list of previous publications on *D. wrightii* can be found at <http://faculty.ucr.edu/~harejd/>.

The University of California, Riverside is an Equal Opportunity, Affirmative Action Employer.

Dr. J. Daniel Hare Telephone: (951) 827-3858 Professor FAX: (951) 827-3086 Department of Entomology and e-mail: [daniel.hare@ucr.edu](mailto:daniel.hare@ucr.edu) Evolution and Ecology GRU University of California Riverside, California 92521 <http://www.entomology.ucr.edu/people/hare.html>

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## UConnecticut MolEvol

POSTDOCTORAL FELLOWSHIP IN MOLECULAR EVOLUTION AND EVOLUTIONARY GENOMICS, UNIVERSITY OF CONNECTICUT

A NASA-funded postdoctoral fellowship is available starting after January 2005 for a period of up to three years (initial appointment is for one year and renewed based on satisfactory performance) in the laboratory of J. Peter Gogarten, Department of Molecular and Cell Biology, University of Connecticut. This is a collaborative interdisciplinary project between Gogarten's lab and the lab of Lutz Hamel, Computer Science and Statistics Department, University of Rhode Island to improve and develop new tools for analyses of microbial genomes based on unsupervised machine learning techniques, and to work on deciphering the early evolution of life as provided in the molecular record.

The successful candidate should be a highly motivated individual with a Ph.D. in molecular evolution, computational biology, bioinformatics, or a related area, with programming experience, experience with phylogenetic analyses and at least working knowledge of the UNIX operating system and databases. Some background in mathematics and/or statistics is a plus.

Salary is \$35,000 plus benefits.

Send CV, key publications, a brief statement of research interests and career goals, and the names of at least two referees (or two letters of reference) to:

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

Phone: (860) 486-4061 Email: bioinf@carrot.mcb.uconn.edu  
 Web: <http://gogarten.uconn.edu> University of Connecticut is an equal opportunity employer. This position will remain opened until filled.

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J. Peter Gogarten Professor of Molecular and Cell Biology University of Connecticut Biology/Physics Building, Rooms 404/426/427 Unit 3125 91 North Eagleville Road Storrs CT 06269-3125 USA

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

### UEdinburgh Butterfly Speciation

A three year Leverhulme funded postdoc is available at the University of Edinburgh.

You will carry out a study of the role of niche divergence in the speciation of ithomiine butterflies. The project will involve collecting ecological information on microhabitat, flight height and larval host plants for two Ecuadorean communities of butterflies. A phylogenetic hypothesis will then be generated for the species using nuclear and mitochondrial molecular sequence data, and used to test for the correlated evolution of mimicry and habitat use, and for the role of these traits in causing speciation. You will have a PhD in a relevant field. Experience in comparative phylogenetic analysis, molecular systematics and ecological fieldwork would all be desirable, although it is not expected that candidates will have experience in all of these areas. The relative time spent on different aspects of the project will depend on the interests of the candidate.

This project is a collaboration with Keith Willmott at the University of Florida and Eldredge Bermingham at the Smithsonian Tropical Research Institute in Panama

For more information and to apply please follow this link: <https://www.jobs.ed.ac.uk/jobs/>

[index.cfm?action=jobdet&jobid=3002832](http://index.cfm?action=jobdet&jobid=3002832) And for more information about my research see <http://neruda.cap.ed.ac.uk/> And please email me directly if you have any questions or simply to express interest. [Chris.Jiggins@ed.ac.uk](mailto:Chris.Jiggins@ed.ac.uk)

Chris Jiggins Institute of Evolutionary Biology School of Biology University of Edinburgh Edinburgh EH9 3JT Scotland UK Tel: (+44)(0)131 650 8624 Fax: (+44)(0)131 650 6564 <http://neruda.cap.ed.ac.uk/> Chris Jiggins <[chris.jiggins@ed.ac.uk](mailto:chris.jiggins@ed.ac.uk)>

### UEdinburgh Parasitoid Evolution

A 35-month NERC-funded post-doc is available at the Institute of Evolutionary Biology of the University of Edinburgh (Salary scale: £19,640 - £29,128 pa)

The successful applicant will work on the population genetic structure of natural populations of parasitoid wasps. The project will focus on the chalcid communities associated with oak cynipid galls, and use microsatellites (1) to assess the extent to which parasitoid populations are structured by host gall traits, and (2) to infer the mechanisms by which parasitoids recruit to invading gallwasp hosts. The project will make use of existing samples, but there will also be opportunities for involvement in fieldwork. The project will be supported by a full time technician, and will use new lab and automated ABI genotyping facilities at IEB. Applicants must have a Ph.D. in a relevant field, with experience in the use of automated genotyping and in the analysis of population genetic datasets. The applicant will be expected to show project management skills, and interest in entomology is an advantage.

This project is in collaboration with Dr. Karsten Schönrogge at the the NERC Centre for Ecology and Hydrology, Winfrith, Dorset U.K.

Fixed term: up to 35 months Salary scale: £19,640 - £29,128 pa Please quote Ref: 3002833 Closing date: 12 October 2004

For more information and to apply please follow this link: <https://www.jobs.ed.ac.uk/jobs/-index.cfm?action=jobdet&jobid=3002833> And for more information about my research see <http://www.homepages.ed.ac.uk/amegilla/home>

All formal applications must be made via the Edinburgh jobs website above, but feel free to contact me directly for further details or if you have any questions.

Graham.stone@ed.ac.uk

Graham Stone Institute of Evolutionary Biology  
School of Biology University of Edinburgh Edinburgh  
EH9 3JT Scotland UK Tel: (+44)(0)131  
650 7194 Fax: (+44)(0)131 650 6564 [http://-](http://www.homepages.ed.ac.uk/amegilla/home)  
[www.homepages.ed.ac.uk/amegilla/home](http://www.homepages.ed.ac.uk/amegilla/home)

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## ULausanne EvoGenomics

Postdoctoral position: Evolutionary Genomics University of Lausanne, Switzerland

We are seeking a highly motivated postdoctoral researcher who is interested in evolutionary genomics to work on the analysis of genome sequence data of the arbuscular mycorrhizal fungus *Glomus intraradices*. The genome sequencing project on this fungus is currently underway at the Joint Genome Institute (for general project information see Martin F et al. 2004. *New Phytologist* 161: 330-335) and it will provide the first genome sequence of a putative ancient asexual organism and will also be the first genome of a eukaryotic symbiont to be sequenced. Because of this, and also because of the controversy about the origin and organization of genetic variation in these fungi, there are many potentially exciting avenues of evolutionary research using the genome sequence data. The successful candidate should be completely familiar with up-to-date computer based techniques for genome annotation, assembly and analysis. He/she should also be able to interact with the other group members who have lab-based projects on evolution and population biology of mycorrhizal fungi (see list of recent papers).

The successful candidate will be located in the Department of Ecology and Evolution at the University of Lausanne (Switzerland) and will be expected to collaborate with the groups of the other steering committee members situated in New Mexico State University, Michigan State University, Oak Ridge National Laboratory, University of Alabama, Cornell University, INRA Dijon (France), plus others. The Dept. of Ecology and Evolution in Lausanne is situated on the shores of Lake Geneva and provides a pleasant & exciting research environment comprising 17 different research groups. A genomics research centre has also been recently established at the same site.

The position is initially for a one and a half year period with the possibility of extension, depending on performance. Starting date is negotiable. Applicants

should contact Ian Sanders, Dept of Ecology and Evolution, University of Lausanne, Switzerland. Email: [ian.sanders@unil.ch](mailto:ian.sanders@unil.ch) Tel: +41 21 692 4261. More details can be found about our group at: <http://www.unil.ch/dee/page7238.html> Recent group publications:

Kuhn G, Hijri M, Sanders IR. (2001). Evidence for the evolution of multiple genomes in arbuscular mycorrhizal fungi. *Nature* 414: 745-748. Sanders IR. (2002). Ecology and evolution of multigenomic arbuscular mycorrhizal fungi. *American Naturalist* 160: S128-S141. Gandolfi A, Sanders IR, Rossi V, Menozzi P. (2003). Evidence of recombination in putative ancient asexuals. *Molecular Biology and Evolution* 20: 754-761. Corradi N, Kuhn G, Sanders IR. (2004). Monophyly of beta-tubulin and H<sup>+</sup>-ATPase gene variants in *Glomus intraradices*: consequences for molecular evolutionary studies of AM fungal genes. *Fungal Genetics and Biology* 41: 262-273. Hijri M, Sanders IR. (2004). The arbuscular mycorrhizal fungus *Glomus intraradices* is haploid and has a small genome size in the lower limit of eukaryotes. *Fungal Genetics and Biology* 41: 253-261. Koch AM, Kuhn G, Fontanillas P, Fumagalli L, Goudet I, Sanders IR. (2004). High genetic variability and low local diversity in a population of arbuscular mycorrhizal fungi. *PNAS* 101: 2369-2374. Corradi, N.; Hijri, M.; Fumagalli, L.; Sanders, I.R. (in press). Arbuscular mycorrhizal fungi (Glomeromycota) harbour ancient tubulin genes that resemble those of the chytrids (Chytridiomycota). *Fungal Genetics and Biology*.

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

Tel (direct): +41 (0)21 692 4261 Tel (secretary): +41 (0)21 692 4260 Fax: +41 (0)21 692 4265 [http://-](http://www.unil.ch/dee)  
[www.unil.ch/dee](http://www.unil.ch/dee) New email!: [ian.sanders@unil.ch](mailto:ian.sanders@unil.ch)

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## UMontpellier EvolutionaryEcol

Postdoctoral position available in theoretical community ecology:

A postdoctoral position is immediately available in theoretical ecology at the University of Montpellier, south of France, in collaboration with Michael Hochberg and Nicolas Mouquet. The objective is to study species interactions in a spatial context either in competitive metacommunities or in the context of food web theory.

The consequences of explicit migration/emigration processes on single species population dynamics can also be envisaged. Applicants must have demonstrated experience and publications in community ecology and modelling. This position will be funded by the European community for up to 14 months (salary based on experience). If interested, please send your CV, list of publications, and the names of at least two references to: Nicolas Mouquet ([mouquet@isem.univ-montp2.fr](mailto:mouquet@isem.univ-montp2.fr)).

Dr. Nicolas Mouquet

UMR 5554 - ISEM, Université Montpellier II Place Eugène Bataillon, CC 065 34095 Montpellier Cedex 5, France

Phone 33 4 67 14 93 57 Fax 33 4 67 14 36 37

Reprints at : <http://nicolasmouquet.free.fr/>

Nicolas Mouquet <[mouquet@isem.univ-montp2.fr](mailto:mouquet@isem.univ-montp2.fr)>

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### UNewHampshire MarineBiodiversity

Post-Doc Position Available Applications are invited for a postdoctoral position on an NSF-funded project documenting the biodiversity of marine flatworms. We are looking for an applicant with a strong academic record in invertebrate zoology, who is accustomed to working independently and in remote locations. Expertise in field collecting, taxonomy, morphological and histological techniques, and phylogenetic analyses is required. Knowledge of molecular techniques is helpful but not necessary. SCUBA certification is preferred. The project involves specimen collection, in situ photography, sample processing for histology and DNA sequencing, development of on-line databases and identification keys, and the description of new species.

Please, submit your CV, a statement of research interests, and the names, titles, and e-mail addresses of three people that can be contacted for letters of recommendation to:

Dr. Marian K. Litvaitis Department of Zoology Rudman Hall University of New Hampshire Durham, NH 03824, USA e-mail: [m.litvaitis@unh.edu](mailto:m.litvaitis@unh.edu)

Electronic applications are preferred.

Marian Litvaitis <[m.litvaitis@unh.edu](mailto:m.litvaitis@unh.edu)>

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### UParis MetabolicSystems

Post-doctoral position on genetics and evolution of metabolic systems

A postdoctoral position is immediately available in quantitative genetics/system biology in the group Fundamental Quantitative Genetics (INRA-University Paris XI-CNRS-INA PG) in Gif-sur-Yvette, France. The project is part of a research program on the genetic and evolution of metabolic systems. Metabolic fluxes are quantitative traits controlled by all enzyme parameters genetically variable. In particular, enzyme concentrations could play a key role in the variation and evolution of such systemic variables, which are related to fitness components and other complex traits. Relying on the background of the metabolic control theory, our laboratory has recently developed theoretical and experimental models of evolutionary optimization of fluxes. The post-doc project will deal with the effect of selection on the flux, using in vitro reconstruction of metabolic pathways and experimental evolution approach: - Enzyme concentrations may vary non-independently, due to competition and/or co-regulation. As theoretically shown, the co-regulations have an evolutionary cost, since they decrease the maximum possible flux in a context of limited resources. This prediction will be tested on glycolysis reconstituted in vitro, by varying enzyme concentrations according to various models of co-regulations. - In order to study the effects of selection on the enzyme concentrations and their correlations, yeast strains will be cultivated on various sources of carbon. The variation of concentrations of glycolytic enzymes will be followed over generations by quantitative proteomics, and the glycolytic flux and growth rate will be measured. Such information will shed light on the influence of regulatory processes in evolution. Applicants could have skills in any of several areas of evolutionary biology, biochemistry, system biology and/or genetics. This position will be funded by the French Institut National de la Recherche Agronomique for one or two years, and is opened to non-French citizens only. If interested, please send your CV, list of publications, and the names of at least two references to: [devienne@moulon.inra.fr](mailto:devienne@moulon.inra.fr) Pr. Dominique de Vienne, Université Paris-Sud, UMR de Génétique Végétale, INRA-UPS-CNRS-INA PG 91190 Gif-sur-Yvette, France <http://www.moulon.inra.fr> References



of the group related to the proposal Bost B., Dillmann C., de Vienne D. (1999). Fluxes and metabolic pools as model traits for quantitative genetics. I. The L-shaped distribution of gene effects. *Genetics* 153: 2001-2012. de Vienne D., Damerval C., Leonardi A., Bost B., Piégu B., Dillmann C., and Zivy M. (2000). Genetics of the maize proteome. In *Genomes* (J. P. Gustafson, Ed.), pp. 123-139, Kluwer Academic / Plenum, New York. de Vienne D., Bost B., Fievet J., Dillmann C. (2001) Optimisation of enzyme concentrations for unbranched reaction chains : the concept of combined response coefficient. *Acta Biotheoretica* 49: 341-350. Bost B., de Vienne D., Moreau L., Hospital F., Dillmann C. (2001). Genetic and non genetic bases for the L-shaped distribution of QTL effects. *Genetics* 157: 1773-1787. de Vienne D., Bost B., Fiévet J., Zivy M., Dillmann C. (2001). Genetic variability of proteome expression and metabolic control. *Plant Physiology and Biochemistry* 39: 271-283. Fiévet J, Dillmann C, Lagniel G, Davanture M, Negroni L, Labarre J, de Vienne D. 2004. Assessing factors for reliable quantitative proteomics based on two-dimensional electrophoresis. *Proteomics*, 4: 1939-1949. Lion S., Gabriel F., Dillmann C. Fiévet J., Bost B., de Vienne D. (2004). Taking into account correlations between enzymes concentrations: an extension to the metabolic control theory. *Eur. J. Biochem.* (accepted with revisions). Fiévet J, Dillmann C, Curien G, de Vienne D. Practical modelling of metabolic pathways for flux prediction and optimisation : lessons from an in vitro reconstruction of the upper part of glycolysis (submitted). Fiévet J. Dillmann C., Bost B, Sicard D., Curien G., de Vienne D. Test tube genetics supports a metabolic model for heterosis (submitted).

devienne@moulon.inra.fr

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## UPotsdam EvolBiol

PostDoc position in Evolutionary Biology for 12 months, University of Potsdam

In an EU financed project we look for a qualified PostDoc to be appointed for 12 month, starting as soon as possible (1st of January 2005 at the latest).

In this project, the successful applicant will have to perform molecular genetic research on population structure and immuno-competence of amphibians. Main objective is to provide qualified advice for management decisions.

Applicants must hold a university degree (Diploma or

Master of Science) and a PhD of a relevant topic. They should appreciate interdisciplinary research and cooperation with international project partners. Familiarity with modern molecular genetic techniques (PCR, cloning, marker development) is desired. Experience in research on MHC is beneficial.

The University of Potsdam is an equal opportunity employer. If equally qualified, disabled applicants will be preferably considered. The University of Potsdam aims at increasing the number of female researchers and encourages qualified females to apply.

Please send your application before 15th of September 2004 to: Prof. Dr. Ralph Tiedemann, University of Potsdam, Institute of Biochemistry and Biology, Evolutionary Biology/Systematic Zoology, Karl-Liebknecht-Str. 24-25, Haus 26, D-14476 Potsdam, Germany, Email: tiedeman@rz.uni-potsdam.de

Prof. Dr. Ralph Tiedemann Universitaet Potsdam Institut fuer Biochemie und Biologie Evolutionsbiologie/Spezielle Zoologie Karl-Liebknecht-Str. 24-25, Haus 26 D-14476 Potsdam Germany Tel: +49-331-977-5249, -5253 (Sekretariat) Fax: +49-331-977-5070 Email tiedeman@rz.uni-potsdam.de <http://www.bio.uni-potsdam.de/spezzoo/index.htm>

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## UReading StatPopGenetics

A postdoctoral position is available in statistical population genetics at the University of Reading, UK. The post is funded at GBP 26,327 (depending on experience), and is for a duration of 28 months. The objective is to develop methods for inferring selection from genome scans in structured populations, particularly with a view to testing models of speciation and adaptation in the face of gene flow.

Applicants should have experience in, or, at the very least, publications that demonstrate technical capacity to implement, computer-intensive statistical methods (e.g. MCMC, importance sampling, etc). Ideally, also, they should have a background in population genetics.

For further information please contact Mark Beaumont (m.a.beaumont@reading.ac.uk) Kevin Dawson (kevin.dawson@bbsrc.ac.uk)

– Mark A. Beaumont, School of Animal and Microbial Sciences, University of Reading, Whiteknights, P.O. Box 228, Reading RG6 6AJ, UK

Tel 0118 378 7707 Fax 0118 931 0180 Email:  
 m.a.beaumont@reading.ac.uk WWW: <http://www.rubic.rdg.ac.uk/~mab/>

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## USEnvProtAgency 2 EvolPopBiol

I would like to call your attention to two postdoctoral positions currently advertised at the US Environmental Protection Agency's Molecular Ecology Research Branch in Cincinnati, Ohio. Application details, salary, etc are available at <http://www.epa.gov/nerl/postdoc/postdoc.html> Only US citizens or permanent residents are eligible for these positions. You can contact me for more details about the research projects and research environment (bagley.mark@epa.gov). The timeframe for receipt of applications is short (September 24)!

Project EERD-2004-06, Spatially explicit models for assessment of population sustainability

Assessments of ecological condition must ultimately be linked to long-term population outcomes through development of predictive population models. This research will relate near-term ecological assessment data based on population genetic structure and community composition to estimates of long-term ecological sustainability under alternative environmental conditions. The researcher will evaluate EPA's existing genetic and ecological data to develop population models applicable to one or more of these research areas: fish/invertebrate community structure, invasive aquatic species, biotechnology risk assessment, landscape genetics.

Educational Requirements: Ph.D. in population biology, population genetics, quantitative ecology or other related scientific field. Specialized training and/or experience preferred: Mastery of theoretical population biology and mathematical modeling, as well as a high level of understanding of landscape ecology and population genetics.

Project: EERD-2004-05, Biotechnology Impact on Target and Non-target Insect Populations

The candidate will aid in the assessment of (1) the risk of resistance development in insect pests targeted by Bt-crops and (2) long-term risks of Bt-crops to non-target populations. The work will involve characterization of genetic patterns and responses to Bt-crops in laboratory and field populations western corn rootworm and several nontarget insect species. Estimates of

demographic and genetic parameters for these species will aid EPA in evaluating long-term ecological risks of genetically modified crops.

Educational Requirements: Ph.D. in population genetics or a related scientific discipline. Specialized training and/or experience preferred: Mastery of theoretical population biology and quantitative genetics, as well as familiarity with modern genomics and population genetics methods. A background in agricultural entomology is highly desirable.

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## USheffield EvolBehaviour

University of Sheffield

Post Doctoral Research Associate in Quantitative Behavioural Genetics and Speciation

Department of Animal and Plant Sciences

P.I.'s: Dr. Rhonda R Snook, University of Sheffield, and Prof. Allen Moore, University of Manchester

A postdoctoral position is available to join a NERC-funded project examining the consequences of mating system structure on genetic architecture and reproductive isolation in *Drosophila pseudoobscura*. We are currently involved in an experimental evolution study in which we have manipulated the mating system of this naturally promiscuous species, by enforcing monogamy and elevating promiscuity. These selection lines are being used to elucidate the adaptive significance of sperm heteromorphism (production of multiple sperm types within a male) and the nature of sexual conflict in this species.

We seek to complement these studies by quantifying how mating system evolution influences the genetic architecture of morphology and behavioural traits that are relevant to reproductive success. This component of the research will employ a quantitative genetics approach using a half-sib design to calculate additive genetic (co)variances within and between the sexes and to determine the relationship to mating system. We will also determine the role of sexual selection and sexual conflict in promoting reproductive isolation by examining pre- and post-copulatory success between and within the selection lines having different mating systems. The project will also take into account any effects of inbreeding by characterizing the effect of selection on genetic diversity using molecular markers.

The Evolution and Behaviour group at Sheffield has been at the forefront of several recent developments in evolutionary and behavioural ecology, including the integration of mechanistic and functional approaches. The postdoc would interact with this large group. Additional interaction would occur with the Integrative Animal Biology group at the University of Manchester, members of which are experts in quantitative genetics.

Candidate requirements:

The desired candidate will have a strong background in evolution, preferably quantitative behavioural genetics. Applicants with experience in one or more of the following will be preferred: microscopy, measurement and dissection techniques; the use of microsatellites. Experience in *Drosophila* culturing is helpful but not essential. The project is based in Sheffield and will require some weekend work.

The closing date for applications is September 8th, 2004. This full time post can be filled immediately although start date is negotiable and is for 1 year initially, renewable for up to a total of 3 years. The proposed salary range is £18,893 - £24,097, commensurate with experience.

For further details and application packs see the University of Sheffield jobs website (posted by August 16th):

<http://www.shef.ac.uk/jobs/> For informal inquiries and further details of the project, please contact either Rhonda Snook (44 114 222 0126; [r.snook@shef.ac.uk](mailto:r.snook@shef.ac.uk)) or Allen Moore (44 161 275 7221; [allen.j.moore@man.ac.uk](mailto:allen.j.moore@man.ac.uk)).

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## VirginiaTech MolSystematics

Postdoc

A postdoctoral position is available in the molecular systematics and evolution of angiosperms. The study is part of the Angiosperm Tree of Life consortium. The candidate should have a Ph.D. and experience in molecular systematics tools and phylogenetic data analysis. Duties include generating sequence information from genes from across angiosperms, data analysis, and interaction with other ATOL labs. The position is for one year with potential renewal to three years. Preferred starting date is January 15, 2005. Send letter of application, curriculum vita, and names and addresses of three references to Dr. Khidir W. Hilu, Department of Biology, Virginia Tech, Blacksburg, VA 24061. e-mail:

[hilukw@vt.edu](mailto:hilukw@vt.edu) Phone: 540-231-5407. Virginia Tech is An Equal Opportunity /Affirmative Action Institution.

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Sincerely yours,

Khidir Hilu Professor of Botany

Department of Biology Virginia Tech Blacksburg, Va 24061 USA Phone: 540-231-5407 Fax: 540-231-9307  
<http://www.biol.vt.edu/faculty/hilu/>

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## WoodHoleMA EndosymbiontEvol

POSTDOC POSITION, Genome Evolution in Bacterial Endosymbionts, Woods Hole.

We seek a highly motivated individual to join a research project on bacterial endosymbionts in Jennifer Wernegreen's lab at the Marine Biological Laboratory, Woods Hole, MA. This Postdoctoral Fellowship will integrate genomic, computational, and evolutionary biology to examine mechanisms and outcomes of bacterial-insect associations. Current research in the lab includes comparative genomics of free-living and endosymbiotic bacteria, analyses of evolutionary forces shaping bacterial sequence variation, and studies of mutualism-parasitism transitions. The Postdoctoral Scientist will contribute to one or more of these efforts.

The Wernegreen lab is part of the MBL's Josephine Bay Paul Center, a collaborative research group focused on comparative genomics, molecular evolution, and microbial diversity. The Bay Paul Center houses shared facilities for automated DNA sequencing, microarray analysis, and computational biology, including three Beowulf clusters running LINUX. See <http://jbpc.mbl.edu/> for more information about the Wernegreen lab and the Bay Paul Center. Visit <http://www.mbl.edu> for general information about the MBL and Woods Hole area.

Requirements: This position requires an independent and highly motivated individual with demonstrated expertise in statistical and computational analyses of DNA sequences and full genomes. The successful applicant will have strong programming skills (e.g. PERL) and a working knowledge of UNIX/LINUX operating systems and genome databases. Educational requirements include a Ph.D. in biology, genetics, bioinformatics, computer science or a related field. Applicants should also have experience with phylogenetic methods, evolution and population genetics, comparative genomics, and a knowledge of bacterial physiology and

evolution. Experience in entomology and molecular biology, including gene expression analyses and high-throughput molecular techniques, are pluses. General requirements include excellent written, verbal, and interpersonal skills, a superb work ethic, and the ability to think creatively and critically.

To Apply: The application consists of a letter describing your professional interests and skills, CV, relevant reprints, and the contact information of three references. Send all materials to: Marine Biological Laboratory, ATTN: Human Resources reference code [PDS

LSME], 7 MBL Street, Woods Hole, MA 02543; phone, 508/289-7422, email: resume@mbl.edu. For more information about research projects and responsibilities of this position, please contact jwernegreen@mbl.edu.

Screening of applications will begin October 18, 2004 and will continue until a suitable candidate is identified.

The MBL is an Equal Opportunity/Affirmative Action/Non-smoking workplace.

Jennifer Wernegreen <jwernegreen@mbl.edu>

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## WorkshopsCourses

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### Berlin GeneAnnotation Dec13-14

Workshop on Gene Annotation Analysis and Alternative Splicing December 13th - 14th, 2004 Harnack-Haus, Ihnestr a 16-20, 14195 Berlin.

Detailed information can be found at <http://www.medizin.fu-berlin.de/molbiochem/bioinf/-Konferenz.04/Start.html> Contact: Dorothea Bauer (BCB / Charite, Campus Benjamin Franklin) Institut fuer Molekularbiologie und Bioinformatik Arnimallee 22, D-14195 Berlin phone: +49/30/8445-1510 , fax: -1504 email: dorothea.bauer@charite.de

twiehe@uni-koeln.de

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### Curacao CoralReefs Spring

Hello All:

We have two openings left in a new course we will be teaching the Spring of 2005. It is a 6 credit semester-long, graduate course where 10 weeks will be spent at CARMABI Marine Laboratory on Curacao (Netherlands Antilles) learning to do field research. This graduate course is open to seniors with adequate background coursework (see list of pre-requisites). It will consist of 5 modules taught by different faculty, and a 3-week period at the end for students to focus on their individual research projects. Undergraduates can concurrently enroll in BIO 480 Field Biology for an additional 6 credits to be fully enrolled (12 credits). Diving certification is required. The full information about the course, the syllabus, the cost structure, as well as the applications forms can be found on my web page [see address in my signature]. Partial scholarships, and special out-of-state tuition rates are available to qualified applicants. The deadline has been extended to August 30th (on web page states Aug 15th). Interested students should contact me immediately.

Thank you for your help in directing this information to students that might be interested in this new offering.

We are especially interested in attracting minorities and students from the Caribbean.

Alina Szmant

Dr. Alina M. Szmant Coral Reef Research Group UNCW-Center for Marine Science Presently in Field: 371 Bahia Dr, Key Largo FL 33037 Tel & Fax: (305)453-4792 Cell: (910)200-3913 email: szmanta@uncw.edu Web Page: <http://people.uncw.edu/szmanta>

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## EMBO Phylogenetic Analysis Nov1-7

Hi folks,

EMBO are funding the registration fee, accommodation and food for a small number of students that wish to attend the EMBO World programme course on the theory and practice of Phylogenetic Analysis and its application in a high throughput framework.

Before applying, please take a look at the website for the course:

<http://bioinf.may.ie/EMBO/> EMBO might also fund the travel costs, but this will be a separate application to EMBO. The closing date for applicants is October 1st. We are especially trying to encourage the participation of students from South and Central America.

The course contents include:

Lectures = 17.5 hours = 33% Practical work = 25 hours = 47% Demonstrations = 3 hours = 5.5% Student presentations = 2 hours = 3.5% Seminars = 6 hours = 11% Total = 53.5 hours

Monday 1st November 0900-1000 Introduction Prof T. Martin Embley. 1000-1030 Coffee and discussion 1030-1200 Multiple sequence alignment Dr. James McInerney 1200-1300 Student introduction and poster presentation (I). 1300-1400 Lunch 1400-1800 Practical Alignment and high throughput alignment methods. 1800-1900 Seminar Dr. Mark Wilkinson. 2000 Dinner.

Tuesday 2nd November 0900-1000 Distance Matrix Methods Prof T. Martin Embley 1000-1030 Coffee and discussion 1030-1200 Maximum Parsimony Dr. Mark Wilkinson. 1200-1300 Student Introduction and poster presentation (II). 1400-1800 Demonstration PAUP software. 1500-1800 Practical Phylogenetic Analysis Using PAUP 1800-1900 Seminar Dr. Robert Hirt. 2000 Dinner

Wednesday 3rd November 0900-1000 Maximum Likelihood Dr. Peter Foster. 1000-1030 Coffee and discussion. 1030-1300 Bayesian Inference Dr. Peter Foster. 1300-1400 Lunch 1400-1800 Practical (Likelihood and Bayesian Inference). 1800-1900 Seminar Dr James McInerney 2000 Dinner.

Thursday 4th November 0900-1000 Protein Phylogenies Dr. Robert Hirt. 1000-1030 Coffee and Discussion 1030-1300 Protein Phylogenetics Dr. Robert Hirt. 1300-1400 Lunch 1400-1700 Practical Protein Phylogenetics. 1700-1800 Demonstration Phylogenetic Analysis: beginning to end. 1800-1900 Seminar Dr. Gilson Manfrio. 2000 Dinner.

Friday 5th November 0900-1000 Robustness of data and Hypotheses Dr. Mark Wilkinson. 1000-1030 Coffee and Discussion. 1030-1300 Phylogenetic Supertrees and total evidence Dr. Mark Wilkinson and Dr. James McInerney. 1300-1400 Lunch 1400-1800 Practical Phylogenetic Supertrees 1800-1900 Seminar Prof T. Martin Embley. 2000 Dinner.

Saturday 6th November 0900-1000 High throughput Phylogenomics (i) Dr. James McInerney 1000-1030 Coffee and Discussion 1030-1300 High throughput Phylogenomics (ii) Dr. James McInerney 1300-1400 Lunch 1400-1500 Demonstration Phylogenomic pipeline development. 1500-1800 Practical Phylogenomics. 1800-1900 Seminar Dr. Peter Foster. 2000 Course Dinner

Sunday 7th November 0900-1000 Round table discussion (I). 1000-1030 Coffee and discussion. 1030-1300 Round table discussion (II). 1300-1400 Lunch. 1400-1800 Practical - Student data analysis and clarification of practical points All lecturers. 1800 Course ends.

– Dr. James O. McInerney, Bioinformatics Laboratory, Department of Biology, National University of Ireland, Maynooth, Co. Kildare, Ireland. P: +353 1 708 3860 F: +353 1 708 3845 E: james.o.mcinerney@may.ie – Take a look at our website — <http://bioinf.may.ie/> –

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## UAzores MarineMolMarkers Sep1-6

IMAR Institute of Marine Research (DOP-University of the Azores) is organising the following workshop: “use of molecular markers for the study of marine biodiversity” from 1-6 September 2004 and it will be held in Horta (Azores).

This workshop is FREE OF CHARGE for students but please, sort out your flight and accommodation. For fur-

ther informations and applications, please contact Sergio Stefanni at [sstefanni@notes.horta.uac.pt](mailto:ssstefanni@notes.horta.uac.pt)

This workshop aims to lead PhD students and young scientists through traditional and more up-to-date methodology of analysing molecular data for the study of marine biodiversity. This subject has become an important issue in the scientific community and the use of molecular tools is of invaluable help. Therefore, with this workshop, we gather together several world-leading experts of marine molecular ecology to give a unique opportunity to students to analyse their own datasets. Seminars followed by tutorials should make the students familiar with the use of designed software's, and the variety of subjects presented by the invited speakers will cover a large spectrum of organisms inhabiting or associated to the sea. Applicants are strongly advised to bring their own datasets as they will analyse them during the workshop. The selection of the candidates is done to equally fill each of the fields of expertise: marine invertebrates (sea urchins, deep sea and hydrothermal vents), fish, sea turtles, marine mammals and seabirds.

The structure of the workshop is as follows: Introduction to mathematical models and building trees/networks techniques applied on molecular data (sequences and microsatellites) Practical exercises on specially prepared datasets for the students. Daily seminars with practicals on the different group of marine or sea associated organisms. Small groups of students, divided according to type of molecular markers used in their projects, with the aim of analysing their own datasets under the supervision of the related field experts. Presentation of students' work based on elaboration of their own datasets is expected to conclude the workshop.

Workshop schedule: Sept 1 9:15-9:30 opening session and welcome (R.S. Santos, Director of Dept. of Oceanography and Fisheries, University of the Azores) 9:30-12:00 lectures (Giorgio Bernardi & Giacomo Bernardi): - The neo-selectionist theory of evolution: An ultra-Darwinian view - Evolution of coral reef fish *Thalassoma* spp. (Labridae). Molecular phylogeny and biogeography 14:30-17:30 lecture and tutorial (Giacomo Bernardi): - Structural approaches to sequence evolution: Molecules, networks, populations Sept 2 9:00-12:00 lectures (T. Patarnello & H.A. Lessios): - Messinian crisis: macro and micro-evolutionary processes that affected Mediterranean marine fauna - The use of mitochondrial DNA to detect global-scale barriers to Gene Flow of Shallow Water sea urchins 14:30-17:00 lectures (A.R. Hoelzel + S. Querouil): - Molecular ecology of marine mammals - Social organization and population genetics of bottlenose dolphins and sperm whales around the Azores Sept 3 9:00-12:00 lec-

tures (S.A. Karl & D.R. Dixon): - Complex population structure in sea turtles - Molecular characterisation of pelagic larvae & molecular biology of hydrothermal vent organisms 14:30-17:00 Tutorials on students' data sets and students' questions Sept 4 10:00-12:00 lectures (R. Bettencourt & S. Stefanni): - Genes that fight infection: what Bivalves say about innate immunity - Phylogeography of two blennies, *Lipophrys pholis* and *Coryphoblennius galerita* and the prospects of two new endemisms for the Azores 14:30-17:00 Tutorials on students data sets and students questions Sept 5 Excursion Sept 6 9:00-12:00 lectures (T.M. Burg & J. Bried): - Review of Seabird Genetics - Combining genetic and demographic data to determine genetic variability and population structure in the wandering albatross (*Diomedea exulans*) 14:30-17:00 presentations by students and closing session

List of invited speakers: Giacomo Bernardi Associate professor of Molecular Ecology and Evolutionary Biology at the University of California, Santa Cruz. Giorgio Bernardi President of Stazione Zoologica Anton Dohrn, Naples, Italy T. Patarnello Professor of Zoology, Department of Biology, University of Padova, Italy. H.A. Lessios Staff Scientist, Smithsonian Tropical Research Institute, Box 2072, Balboa, Panama, R.A. Hoelzel Reader in Molecular Ecology, Dept of Biological Sciences, University of Durham, UK. S.A. Karl Associate professor Molecular Ecology, Evolution and Conservation Biology at the University of South Florida. D.R. Dixon Group leader of the molecular genetics group, George Deacon Division for Ocean Processes, Southampton Oceanography Centre, University of Southampton, United Kingdom. T.M. Burg Post-doctoral researcher, Dept. of Biology, Queen's University, Kingston, Canada.

List of local speakers: S. Stefanni

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## UGroningen SympatricSpeciation

### ANNOUNCEMENT

One-day symposium on Sympatric Speciation Friday October 15, University of Groningen, Academy build-

ing, room A901, Broerstraat 9, Groningen, The Netherlands

The research group Theoretical Biology at the University of Groningen organizes a one-day symposium on Sympatric Speciation on the occasion of the PhD thesis defence by Sander van Doorn. Attendance of the symposium is free but, due to the limited capacity of the conference room, \*\*\*advance registration is compulsory\*\*\*. For more information and registration (before October 12), you can contact Han Verkiel (h.verkiel@biol.rug.nl).

#### PROGRAM

09:00-09:30 Coffee & Tea

09:30-10:15 Sergey Gavrilets (Univ. of Tennessee, USA) - Sympatric speciation and costs of being choosy

10:15-11:00 Ulf Dieckmann (IIASA, Austria) - Linking pattern and process in modern speciation theory

11:00-11:15 Coffee & Tea

11:15-12:00 Sander van Doorn (Univ. of Groningen) - Sexual selection and sympatric speciation

12:00-12:45 Lunch

13:15-14:15 PhD thesis defence

14:15-15:30 Reception

15:30-16:15 Trevor Price (Univ. of Chicago, USA) - Phenotypic plasticity, genetic assimilation, and speciation

16:15-17:00 Olof Leimar (Stockholm Univ.) - A new perspective on the theory of adaptive polymorphism

17:00-17:45 Hans Metz (Univ. of Leiden) - Thoughts on the geometry of macro-evolution

The symposium is financially supported by the Dutch Society for Theoretical Biology (NVTB) and the Centre

for Ecological and Evolutionary Studies (CEES).

F.J.Weissing@biol.rug.nl

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## ULisbon Phylogeography Oct22-23

#### Workshop:

The Workshop “THE QUATERNARY LEGACY - Phylogeography and climatic changes in Southern Europe” will be held in Lisbon, in the Faculty of Science of the University of Lisbon ([www.cba.fc.ul.pt/](http://www.cba.fc.ul.pt/)) in the 22nd and 23rd of October 2004. The official language of the Workshop is English.

The main theme concerns the role of the Southern European Peninsulas in maintaining the genetic variability by functioning as ice age faunal refugia, and the consequent phylogeographic patterns that were generated during the Quaternary climatic oscillations.

By organizing this meeting we are aiming to create a discussion forum to solve impasses resulting from different points of view and as well to favour the development of joint research programmes and collaborations. The Scientific Programme includes talks by invited speakers and poster presentations. Posters will be displayed for two days during the meeting. Information about the workshop: <http://www.cba.fc.ul.pt/-workshop/index.html> Local Organizing Committee

Centre for Environmental Biology & Department of Animal Biology Faculty of Science, University of Lisbon Campo Grande, 1749-016 Lisboa, Portugal

anaritagrosso@netcabo.pt

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## Instructions

Instructions: To be added to the EvoDir mailing list please send an email message to [Golding@McMaster.CA](mailto:Golding@McMaster.CA). At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). In addition, if it originates from ‘blackballed’ addresses it will be sent to me at [Golding@McMaster.CA](mailto:Golding@McMaster.CA). These messages will only

be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

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

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains 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.