
E v o l D i r

June 1, 2006

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

Forward

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

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

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



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BanarasHinduU Evol Oct14-16

To: US Citizen members of Evoldir

A proposal is being prepared to support travel to the following symposium, which is by invitation only. The prospective funding agency has indicated that it would be eager to support the travel of young investigators (graduate students, postdoctoral fellows, and assistant professors), particularly women and under-represented minorities. US citizenship or resident alien status required. It is expected that those funded would participate in the meeting but would not speak. If the proposal is funded, funding would be announced on 20 Sept, so participants would need to be able to abide by this schedule.

If you are interested, please reply with: 1. Name 2. US citizen or resident alien? 3. Status (grad student, post-doc, junior faculty)? 4. Female? 5. Underrepresented minority? 6. A few sentences on your research interests and how you might contribute to the symposium

International Symposium on Environmental Factors, Cellular Stress and Evolution at Banaras Hindu University, Varanasi, India (October 14-16, 2006) Stress, in one form or the other, affects every biological system. The proteome induced by cellular stresses has been studied intensively during the past 3-4 decades.

These studies have provided deep insights not only into some of the basic cellular processes like protein folding, gene regulation, cellular homeostasis etc but have also stimulated biotechnological and clinical applications. At a more basic biology level, it is clear that environmental stress factors have been key players in shaping organic evolution. However, this aspect has received relatively less attention than molecular biology of the stress responses. There is a strong need for understanding the roles of stress proteins and stress responses from an integrative biological perspective. One of the ways to achieve this is to provide a common platform for interactions between those studying stress responses and stress proteins in relation to evolutionary biology, ecology, molecular biology or biotechnology points of view. Keeping this objective in mind, a 2 day international symposium on "Environmental Factors, Cellular Stress and Evolution" is planned at the Banaras Hindu University, Varanasi, India on 14th and 15th October 2006 in conjunction with a meeting of the Officers of the IUBS on 12th and 13th October 2006 at the same place. In this part of the world, the environmental conditions are very diverse, and so is the biological diversity. These factors provide very good models for studying interactions between stress responses/proteins and evolutionary forces. However, it is also true that due to financial constraints, the scientific community in this region is generally unable to interact with leading scientists in the field and, therefore, not often able to work at the forefront of field. A major objective behind organizing the above meeting in India is, therefore, to

have leading experts present extensive reviews in their own areas of research to a large audience comprising young faculty members and researchers/graduate and under-graduate students from different parts of India and neighboring countries. This meeting will have only invited lectures of about 40-45 min each. The speakers have been asked not to concentrate only on their research but to review their chosen topic and to discuss future directions keeping the philosophy of Integrative Biology in mind. About 40 young faculty and researchers will be invited from India and neighbouring countries as participants. Undergraduate and graduate students and faculty members from different departments of the Banaras Hindu University will also attend the lectures.

Dr. Martin E. Feder E-Mail: m-feder@uchicago.edu

Professor Department of Organismal Biology & Anatomy The University of Chicago 1027 East 57th Street Chicago, IL 60637 USA E-Mail: m-feder@uchicago.edu Telephone: 773 702-8096 Fax: 773 702-0037 http://pondside.uchicago.edu/~feder/Martin_Feder.html m-feder@uchicago.edu

BiRC Bioinformatics Jun15-18

Dear

This Summer BiRC hosts 2 big events:

15 - 18 June Bioinformatics 2006 Conference. Deadline for registration is 31 May

Updated programme and further info at

<http://www.birc.au.dk/bioinformatics2006/> 24-28 July Scandinavian Institute in Statistical Genetics. The early registration and payment deadline is Friday, 16 June

For further info

<http://www.biostat.washington.edu/sisg06/-index.php?menu=main&location=europe> christiandurr@gmail.com

Firenze Italy Sibe-Iseb Sept4-7

Dear Friends and Colleagues,

It gives us great pleasure to announce the 2nd Congress of Italian Evolutionary Biologists (1st Congress of the Italian Society for Evolutionary Biology), which will be held in Firenze, Italy, at the beginning of September (4-7), 2006.

The scientific program will include oral and poster presentations and four keynote lectures by Laurent Keller, William Martin, Remy Petit and Svante Paabo. Social events will enable free interaction among all participants.

The deadline for early registration and abstract submission is May, 31.

Prizes for the best communication, poster, and scientific publication will be available for young scientists. A limited amount of financial support will be also available for young scientists with the highest travel expenses.

Detailed instructions (in English) on the conferences are available at the URL <http://www.unifi.it/sibe2006>

The website of the Italian Society for Evolutionary Biology (only in Italian) is <http://www.sibe-iseb.it> David Caramelli, Renato Fani (Meeting Organizers)

Giorgio Bertorelle President of SIBE

David Caramelli University of Florence Department of Animal Biology and Genetics Laboratory of Anthropology via del Proconsolo 12, 50122 Florence Italy Tel +390552743021 Fax +390552743038 www.unifi.it/antropologia david.caramelli@unifi.it

Halifax SMBE June24-28 2007

SMBE ANNUAL MEETING–June 24-28, 2007

You are invited to attend the 2007 Annual Meeting of the Society for Molecular Biology and Evolution (SMBE), to be held at Dalhousie University in Halifax, Nova Scotia, Canada, June 24-28. The meeting will be held in conjunction with the Evolutionary Bi-

ology Program of the Canadian Institute for Advanced Research.

Meeting Organizers:

John Archibald, Ford Doolittle & Wanda Danilchuk
Department of Biochemistry and Molecular Biology,
Dalhousie University

Information about speakers, registration, travel, accommodation, etc. will be available shortly at the SMBE website:

<http://www.smbc.org/> — John M. Archibald, Ph.D.
Genome Atlantic and CIAR Evolutionary Biology Program
Department of Biochemistry and Molecular Biology
Dalhousie University Sir Charles Tupper Medical
Building 5850 College Street, Halifax, Nova Scotia B3H
1X5, Canada

jmarchib@dal.ca Phone: (902) 494-2536 Fax:
(902) 494-1355 Archibald Lab Webpage: <<http://myweb.dal.ca/jmarchib/>> —

John Archibald <jmarchib@dal.ca>

KansasCity EcoGenomics Nov3-5

Plan now to attend the 4th Annual “Genes in Ecology, Ecology in Genes” Symposium on November 3, 4 & 5, 2006, in Kansas City. The Symposium will begin on Friday at 6:00 p.m. and conclude on Sunday at noon. Information will be posted on our website, <<http://www.k-state.edu/ecogen>> [www.K-State.edu/ecogen](http://www.k-state.edu/ecogen), as details are finalized.

Ecological Genomics is a field at the interface of ecology, evolution and genomics that seeks to place the functional significance of genes and genomics into an ecological and evolutionary context. The following is a partial list of Symposium speakers. Each is doing research at the forefront of Ecological and Evolutionary Functional Genomics.

Featured Speakers: Ian T. Baldwin, Max-Planck Institute for Chemical Ecology, “Using transformed plants to study ecological interactions” May R. Berenbaum, University of Illinois at Urbana-Champaign, “Cytochrome P450 genes and genomics in insect-plant interactions: Necessity or nimety?” Justin Fay, Washington University, “Evolution of gene expression” Maria J. Harrison, Cornell University, “Towards an understanding of the arbuscular mycorrhizal symbiosis: Functional genomics approaches” Michael W. Nach-

man, University of Arizona, “The genetic basis of reproductive isolation in mice” Katie Peichel, Fred Hutchinson Cancer Research Center, “Genetics of reproductive isolation in sticklebacks” Loren Rieseberg, Indiana University, “Genomics of invasive sunflowers” John H. Willis, Duke University, “Genetic analysis of adaptation and reproductive isolation in *Mimulus*” Patricia Wittkopp, University of Michigan, “Genetic basis of regulatory variation” The list of speakers continues to expand. Please refer to our website for announcements of additional speakers.

Participants are invited to share their own research with the group through a poster session on Friday night and Saturday. Poster topics should be related to the field of Ecological Genomics. A limited number of submitted poster abstracts will be selected for oral presentations. Please check our <<http://www.k-state.edu/ecogen/PosterAbstractGuidelines2006.htm>> website for abstract submission guidelines. Participants will also learn about the Ecological Genomics Institute at Kansas State University and the research being conducted by its members.

Please share this announcement with colleagues and students who are interested in learning more about the field of Ecological Genomics. If you have questions, please contact us at (785) 532-3482 or ecogen@ksu.edu. Additional information about this interdisciplinary research initiative is available at <<http://www.k-state.edu/ecogen>> [www.K-State.edu/ecogen](http://www.k-state.edu/ecogen).

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

Ecological Genomics Institute Directors: Dr. Loretta Johnson Dr. Michael Herman Kansas State University, Division of Biology 231 Ackert Hall, Manhattan, KS 66506-4901 (785) 532-3482, <<http://www.ksu.edu/ecogen>> www.ksu.edu/ecogen

dmerrill@ksu.edu

LundU EvolvertebrateAnimals June01-03

Final announcement- INTERNATIONAL SYMPOSIUM ON THE EVOLUTION OF VERTEBRATE ANIMALS

We are happy to announce the second international symposium on the evolution of vertebrate animals held at Lund University, Sweden.

The symposium will take place on 1-2 June 2006, with an excursion in Southern Sweden on the 3rd of June.

Distinguished speakers on human evolution, mammalian phylogeny, vertebrate relationships and genome analysis have been invited to give talks. These include:

Michael Benton, University of Bristol, UK Emmanuel Douzery, Université Montpellier 2, France Gaston Gonnet, Institute for Computational Sciences, Switzerland Arndt von Haeseler, Center for Integrative Bioinformatics, Austria Wilfried de Jong, Univ. of Nijmegen, The Netherlands Herve Philippe, Université de Montréal, Canada Martin Pickford, Museum National d'Histoire Naturelle, France Brigitte Senut, Museum National d'Histoire Naturelle, France Cecilia Saccone, CNR - Istituto di Tecnologia Biomedica, Italy Yoshinori Kumazawa - Nagoya University, Japan Jan Klein - Pennsylvania State University, USA Hans Zischler - University of Mainz, Germany

In conjunction with the symposium there will also be a poster session. The registration deadline was 30 April 2006, but it is still possible to attend. The symposium carries only a small registration fee of 20 euros.

Please consult the webpage, <http://www.biol.lu.se/-isev2006> for information about registration, accommodation and travel.

Axel Janke & Ulfur Arnason

isev.2006@cob.lu.se. Evolutionary Molecular Systematics, Lund university, Sölvegatan 29, S-223 62 Lund Sweden. Tel: +46 46 222 7862, Fax: +46 46 147 874

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<http://phylo.gen.lu.se/> Email: axel.janke@cob.lu.se Tel.: +46/46/222 7849 FAX: +46/46/147874

axel.janke@cob.lu.se

Marseilles 10EvolBiol Sep20-22 Registration

10th Evolutionary Biology Meeting at Marseilles-France-20/22 September, 2006

Deadlines registrations: 30th June, 2006! This is in one

month!!

News about Social events, Awards as well as Updated Abstracts are available on: <http://www.evolutionary-biology.org> We remember you that registrations and abstract submissions for the 10th Evolutionary Biology Meeting at Marseilles are on line and until June 30th, 2006.

The general scheme of the conference will be similar to the one proposed the former years. The following topics will be discussed: Systematic, Biodiversity, Comparative genomic and post-genomic (at all taxonomic levels), Functional phylogeny, Environment and evolution. This year, we would also like to touch on: - Evolutionary biology concepts for biological annotation. - Probabilistic models and statistic tools for concepts in evolution.

For more information, please see the web site <http://www.evolutionary-biology.org> Or, contact us at egee@up.univ-mrs.fr

egee@up.univ-mrs.fr

Montreal ComparativeGenomics Sept24-26

SECOMD CALL FOR PAPERS, Fourth Annual RECOMB Satellite Meeting on Comparative Genomics

SUBMISSION DEADLINE: June 5, 2006

September 24-26, 2006, Montreal, Canada

MEETING WEBSITE: <http://www.crm.umontreal.ca/Genomics06/> NEW: Expanded versions of conference papers will be invited for submission to a special issue of the Journal of Computational Biology.

ORGANIZERS: Guillaume Bourque, Genome Institute of Singapore, Singapore Nadia El-Mabrouk, University of Montreal, Montreal, Canada Jens Lagergren (Stockholm Bioinformatics Centre & KTH) Aoife McLysaght (Trinity College Dublin) David Sankoff (University of Ottawa)

KEY DATES: June 5, 2006 Paper submission deadline June 21, 2006 Notification of paper acceptance July 5, 2006 Final manuscript due August 21th, 2006 Poster submission deadline September 24-26, 2006 Workshop

THEME AND SCOPE: Large-scale genome sequencing projects are generating vast amounts of data for a

multitude of organisms including mammals and other vertebrates, invertebrates, fungi, plants, bacteria, and viruses. As the data increase so do the opportunities and the challenges for scientists to interpret them. By endeavouring to make sense of the process and pattern of genome evolution, comparative genomics lies at the forefront of this challenge. The core of comparative genome analysis is the establishment of the correspondence between genes (orthology analysis) or other genomic features in different organisms. It is these intergenomic maps that make it possible to trace the evolutionary processes responsible for the divergence of two genomes. A multitude of evolutionary events acting at various organizational levels shape genome evolution. At the lowest level, point mutations affect individual nucleotides. At a higher level, large chromosomal segments undergo duplication, lateral transfer, inversion, transposition, deletion and insertion. Ultimately, whole genomes are involved in processes of hybridization, polyploidization and endosymbiosis, often leading to rapid speciation. The complexity of genome evolution poses many exciting challenges to developers of mathematical models and algorithms, who have recourse to a spectrum of algorithmic, statistical and mathematical techniques, ranging from exact, heuristic, fixed parameter and approximation algorithms for problems based on parsimony models to Monte Carlo Markov Chain algorithms for Bayesian analysis of problems based on probabilistic models. The RECOMB Satellite Workshop on Comparative Genomics is a forum on all aspects and components of this field, ranging from new quantitative discoveries about genome structure and process to theorems on the complexity of computational problems inspired by genome comparison.

SUBMISSIONS: Papers should not exceed 10 pages (all inclusive) and must be submitted via the conference website <http://www.crm.umontreal.ca/Genomics06/>. Submissions must be received in electronic form by 11:59pm (Montreal local time) of June 5th, 2006.

Papers submitted for review should represent original, previously unpublished work. At the time the paper is submitted to the conference, and for the entire review period, the paper should not be under review by any other conference or scientific journal. Note that accepted papers will be considered as preliminary work, and may be submitted to a journal publication after notification of acceptance.

Successful submissions will be invited for a 25-minute presentation, and the paper will be printed in the conference proceedings, which will be published by Springer in the "Lecture Notes in Bioinformatics" series.

Expanded versions of conference papers will be invited for submission to a special issue of the Journal of Computational Biology.

Address any questions to the program committee chairs, Guillaume Bourque (bourque@gis.a-star.edu.sg) or Nadia El-Mabrouk (mabrouk@iro.umontreal.ca).

REGISTRATION: Registration is available at the conference website <http://www.crm.umontreal.ca/Genomics06/>
PROGRAM COMMITTEE CO-CHAIRS: Guillaume Bourque, Genome Institute of Singapore, Singapore Nadia El-Mabrouk, University of Montreal, Montreal, Canada

PROGRAM COMMITTEE: Lars Arvestad, Robert Beiko, Anne Bergeron, Michael Brudno, Cedric Chauve, Avril Coghlan, Miklós Csürös, Dannie Durand, Niklas Eriksen, Rose Hoberman, Tao Jiang, Aoife McLysaght, Bernard Moret, Laxmi Parida Yves van der Peer, Ben Raphael, Cathal Seoighe, Eric Tannier, Glenn Tesler, Stacia Wyman.

David Sankoff <sankoff@uottawa.ca>

Montreal RECOMB ComparativeGenomics Sep24-26

CALL FOR PAPERS

Fourth Annual RECOMB Satellite Meeting on Comparative Genomics September 24-26, 2006, Montreal, Canada

Submission Deadline: June 5, 2006

TWO WEEKS LEFT

MEETING WEBSITE: <http://www.crm.umontreal.ca/Genomics06/>
KEY DATES: June 5, 2006 Paper submission deadline June 21, 2006 Notification of paper acceptance July 5, 2006 Final manuscript due August 21th, 2006 Poster submission deadline September 24-26, 2006 Workshop

ORGANIZERS: Guillaume Bourque, Genome Institute of Singapore, Singapore Nadia El-Mabrouk, University of Montreal, Montreal, Canada Jens Lagergren (Stockholm Bioinformatics Centre & KTH) Aoife McLysaght (Trinity College Dublin) David Sankoff (University of Ottawa)

SUBMISSIONS:

Papers should be submitted via the EasyChair system. Submissions must be received in electronic form

by 11:59pm (Montreal local time) of June 5th, 2006.

Submissions should be no more than 12 single-spaced A3 or A4 pages with 1.25-inch margins all around, everything included (title, authors, addresses, abstract, references, figures, tables), in at least a 10-point font. An optional short appendix may contain details or additional data to be consulted at the discretion of the program committee. Note that authors of accepted papers will have to reformat them for the proceedings using the Springer LNCS style, which has even wider margins. It may save the authors' some work if this format is used from the outset. The submission must include the corresponding author's email address.

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Successful submissions will be invited for a 25-minute presentation, and the paper will be printed in the conference proceedings, which will be published by Springer in the "Lecture Notes in Bioinformatics" series.

Expanded versions of conference papers will be invited for submission to a special issue of the Journal of Computational Biology.

Address any questions to the program committee chairs, Guillaume Bourque (bourque@gis.a-star.edu.sg) or Nadia El-Mabrouk (mabrouk@iro.umontreal.ca).

PROGRAM COMMITTEE CO-CHAIRS:

Guillaume Bourque, Genome Institute of Singapore, Singapore
Nadia El-Mabrouk, University of Montreal, Montreal, Canada

PROGRAM COMMITTEE:

Lars Arvestad, Robert Beiko, Anne Bergeron, Michael

Brudno, Cedric Chauve, Avril Coghlan, Miklós Csűrös, Dannie Durand, Niklas Eriksen, Rose Hoberman, Tao Jiang, Aoife McLysaght, Bernard Moret, Laxmi Parida, Yves van der Peer, Ben Raphael, Cathal Seoighe, Eric Tannier, Glenn Tesler, Stacia Wyman.

David Sankoff <sankoff@uottawa.ca>

OeirasPortugal Coalescent Jun21-24

Dear All,

Please note the workshop announced below, taking place here in Portugal in a month from now. The deadline for applications is 31 May.

Thank you very much, Constantin Fesl

Workshop on Coalescent Theory and its perspectives in human genetics and complex trait mapping

Time: June 21-24, 2006 Place: Instituto Gulbenkian de Ciência (IGC), Oeiras, Portugal

Coalescent theory, an approach to reconstruct genealogical relationships of a population sample with given information on extant gene diversity, was originally developed in the context of evolutionary genetics, where patterns of past demography, selection and genetic drift have been inferred. Recently, it is becoming a possible tool in human genetics, comprising the estimation of distributions of recombination rates and particularly population-based mapping of genotypes underlying complex traits.

The workshop is addressed to all researchers, postdocs and students working on or interested in the subject, and particularly to human geneticists. Two days of lectures and discussion will be followed by practical exercises with diverse available software for coalescent modeling.

Particular subjects: Demographic history and selection in coalescent models - Bayesian inference and MCMC algorithms - Perspectives for human gene mapping.

Confirmed speakers: Richard Hudson, University of Chicago (USA) Sebastian Zöllner, University of Michigan (USA) Graham Coop, University of Chicago (USA) Lounès Chikhi, Université Paul Sabatier, Toulouse (France)

----- Program:

Wed June 21, morning: R. Hudson (Introduction)

Wed June 21, afternoon: L. Chikhi (Inferring demographic history from genetic data) G. Coop (Selection) Discussion

Thu June 22, morning: S. Zoellner (Bayesian inference and MCMC algorithms) L. Chikhi (Bayesian inference for demographic history)

Thu June 22, afternoon: S. Zoellner (Human gene mapping) R. Hudson (Fine-scale mapping) Discussion on perspectives

Friday 23 and Saturday 24 June: Practical software exercises -----

Number of participants: 40

Participation is free of charge. For further information, please consult: www.igc.gulbenkian.pt [Events/Other Events]

Please send your applications, including a CV and a short letter of motivation, until May 31st, 2006 to:

Constantin Fesel (IGC), Email: cfe-sel@igc.gulbenkian.pt

cfe-sel@igc.gulbenkian.pt

Prague EvoDevo Aug16-19 Deadline

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Reminder: deadline for registration and abstract submission is 1 May 2006!

*

<http://natur.cuni.cz/evodevo/> *_**

Euro-Evo-Devo

*Prague**, 16-19 August 2006*

You are invited to participate in, and contribute to, the First and Founding Meeting of the *European Society for Evolutionary Developmental Biology (EED)* in Prague, August 16-19, 2006.

Call to participate You are invited to participate in, and contribute to, the First and Founding Meeting of the European Society for Evolutionary Developmental Biology in Prague, August 16-19, 2006. The scientific program will consist of plenary sessions, symposia, contributed talks and a poster session, see our website: *_<http://natur.cuni.cz/evodevo/>_* *Call for abstracts* You are invited to submit an abstract <<http://www.conference.cz/evodevo/>> for a contributed talk

or poster. Online submission will be possible March 6, 2006. Please submit your abstract before *May 1, 2006*

Registration The early registration fee for students is 120,-, for non-students 200,- and for partners 25,-. Registration <<http://www.conference.cz/evodevo/>> can start 1 March 2006 and the deadline for early registration is 1 May 2006.

The organizing committee looks forward to seeing you in Prague!

Keynote speakers:

- Philippe Janvier /(Paris, France)/

- Pat Simpson /(Cambridge, U.K.)/

- Günter Theissen /(Jena, Germany)/

- Hervé Philippe /(Montreal, Canada)/

- Jukka Jernvall /(Helsinki, Finland)/

- Barbara Gravendeel /(Leiden, the Netherlands)/

//

Symposia:

-/"Evo-Devo History"/ (organizer: Scott Gilbert)

-/"Homeobox genes in evolution and development"/ (organizers: Dave Ferrier, Jordi Garcia Fernandez)

-/"Modularity"/ (organizer: Chris Klingenberg)

-/"Stem groups and the integral role of paleontology in evolutionary developmental biology"/ (organizers: Graham Budd, Phil Donoghue)

-/"Head Evo-Devo"/ (organizers: Lennart Olsson, Michael Depew)

-/"Insect Evo-Devo"/ (organizer: Urs Schmidt-Ott)

-/"Plant Evo-Devo"/ (organizer: Günter Theissen)

-/"Evolutionary Novelties"/ (organizers: Gerhard Schlosser, Shigeru Kuratani)

-/"Lamprey, shark, and vertebrate Evo-Devo"/ (organizers: Didier Casane, Sylvie Mazan)

-/"Theoretical approaches to pattern formation, variation and innovation"/ (organizers: Isaac Salazar-Ciudad, Tom van Dooren)

-/"Evo-Devo of late development"/ (organizers: Eckhard Witten, Ann Huysseune)

-/"Limb Evo-Devo"/ (organizer: Michael Richardson)

*Information: *

<http://natur.cuni.cz/evodevo/>

friet-

son.galis@gmail.com*_**

Frietsen Galis PhD Institute of Biology Leiden University PO Box 9516, 2300RA Leiden The Netherlands tel.: -31.(0)71.5274911 fax: -31.(071).5274900 email: Galis@rulsfb.leidenuniv.nl <mailto:Galis@rulsfb.leidenuniv.nl> website: <http://biology.leidenuniv.nl/~galis/> <<http://biology.leidenuniv.nl/%7Egalis/>> website Euro-Evo-Devo society: <http://natur.cuni.cz/evodevo/vdooren@rulsfb.leidenuniv.nl>

RutgersU Phylogenetics June21-22

DIMACS WORKSHOP ON PHYLOGENETIC TREES AND RAPIDLY EVOLVING PATHOGENS June 21 - 22, 2006, DIMACS Center, CoRE Building, Rutgers University

Organizers: Allen Rodrigo, University of Auckland, a.rodrigo@auckland.ac.nz

Mike Steel, University of Canterbury,

M.Steel@math.canterbury.ac.nz Presented under the auspices of the Special Focus on Computational and Mathematical Epidemiology. We have an excellent line up of speakers, and we invite you to attend the workshop. If you wish to present a poster, please contact Allen Rodrigo or Mike Steel by email before 1 June 06. Please consult

<http://dimacs.rutgers.edu/Workshops/PhylogeneticTrees/> for registration, accommodation, and other information. We look forward to seeing you there. Allen Rodrigo Mike Steel

a.rodrigo@auckland.ac.nz

SanJuanIsland MarineGenomics Sept9-12

We are organizing a "Genomics and the Life Aquatic" symposium at the beautiful Friday Harbor Labs on San Juan Island from September 9-12, 2006. We anticipate a small but interactive meeting that will bring together scientists who are really doing "functional genomics" in aquatic systems to address a diversity of questions, from the origins of multicellularity to the evolution of

new species. We have invited a number of great speakers! For more information, please check the website:

<http://depts.washington.edu/fhl/centsymp/2006genomics.html> We are currently soliciting applications from graduate students and postdocs to give them a chance to present their work as an oral presentation and to interact with leaders in the field. Please pass this information along to any grad students or postdocs you know who might be interested. If you would like to apply, please use the website and click on the application form for grad students and postdocs. You will need to submit a 250 word abstract, as well as a 250 word description of your research interests and why they are relevant to the symposium. Applications are due by July 15 and we will notify people by the end of July.

We plan to cover lodging and food while at the conference for all attendees. We are still working on soliciting more support for the meeting, but will try to cover at least some amount of travel expenses for all attendees.

If you would like any more information, please send either myself (cpeichel@fhcrc.org) or Chris Amemiya (camemiya@benaroyaresearch.org) an email.

We look forward to seeing you at Friday Harbor in September.

Katie Peichel and Chris Amemiya -- Katie Peichel, PhD Assistant Member, Division of Human Biology Fred Hutchinson Cancer Research Center 1100 Fairview Ave North Mailstop D4-100, PO Box 19024 Seattle, WA 98109-1024 (206) 667-1628 (206) 667-2917 (fax) <http://www.fhrc.org/science/labs/peichel/wjs18@u.washington.edu>

StAndrews PhDEvolBiol Sept5-8 2

Dear PhD Students in Evolutionary Biology,

This is a reminder that registration for EMPSEB XII opens at 12 noon (BST) May 1st, and will close May 10th.

You will be required to submit an abstract of your work (200 words or fewer) when you register and to state whether you will be presenting a talk or a poster. Please note that preference will be given to delegates offering talks over those offering posters.

Please be sure to register as soon as possible as places are limited.

For more details please visit the meeting website: <http://www.biology.ed.ac.uk/public/conferences/-evolbiol2006/> Hope to see you in St Andrews! – Pedro Vale EMPSEB XII committee

Pedro Vale <pedro.vale@ed.ac.uk>

StonyBrookU SSESSBASN2006 Jun23-27 mentors

DIVERSITY AT SSE/SSB 2006:

Call to graduate students, postdocs and faculty for volunteer mentors.

The Undergraduate Mentoring in Environmental Biology (UMEB) program will take place again at the 2006 meeting this June in Stony Brook, New York. Fifteen individuals have generously volunteered to serve as mentors, but the program will work best if we can get this number up to thirty four. Duties will include meeting with a pair of undergraduates in the program, attending and demystifying a half-day of talks with them, joining them for a meal, introducing them to colleagues and in general befriending them in ways that make evolutionary biology seem like a welcoming discipline. No costs for travel, housing or registration are covered. Please spread the word about this very rewarding activity.

Please send an email to Rich Kliman (rmkliman@cedarcrest.edu) if you would you like to be a mentor.

Rmkliman@cedarcrest.edu Rmkliman@cedarcrest.edu

Sydney SocConservBiol July10-13

Mark your calendars: the Australasian section of the Society for Conservation Biology invites you to its inaugural regional meeting of conservation scientists

When: July 10-13, 2007

Where: University of New South Wales, Sydney, Australia

Topic: The Biodiversity Extinction Crisis, a Pacific and Australasian response

The world faces its sixth great extinction event, driven mainly by humans. Our region faces special challenges including: island ecology, rising sea levels, changing rainfall, and land and water degradation. These issues are overlaid by the general problems of habitat loss and fragmentation, invasive species, pollution and overharvesting.

This conference identifies the major problems for biodiversity conservation in our region, existing and potential solutions and links to the global biodiversity initiatives. Real opportunities can be found in the nexus between conservation science and policy-makers, managers and the community. There will be five major themes: (1) Regional challenges (particular issues for our part of the world); (2) Managing threatening process of universal importance; (3) Case studies of conservation in action, including biodiversity monitoring and assessment; (4) Conservation science and policy and; (5) Conservation science and the community (non-government organisations, indigenous people).

Information on the meeting, as well as registration and abstract submission will be forthcoming.

We look forward to seeing you in Sydney in 2007

Richard.kingsford@unsw.edu.au

On behalf of the SCB-Australasia 2007 Conference Organizing Committee

Dr Karen Firestone Conservation Biologist Adjunct Lecturer Australasian Conservation Genetics Centre Rm 565 School of BEES Zoological Parks Board of NSW University of NSW PO Box 20 Sydney, NSW 2052 Australia Mosman, NSW 2088 Australia P: +61 (02) 9385 3446 (office) P: +61 (02) 9978 4608 P: +61 (02) 9385 8236 (lab) F: +61 (02) 9978 4613 F: +61 (02) 9385 1558

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Tuebingen HermaphroditeEvol Aug4-6

Final announcement

H E R M A P H R O D I T E M E E T I N G T U E

B I N G E N HerMeeT

We are organising an informal meeting on the evolutionary ecology of hermaphrodites in Tuebingen (Germany) from Fri 4 until Sun 6 August 2006.

(<http://www.evolution.uni-tuebingen.de/herma-meeting/>)

This is the third meeting of its kind. It is meant as a forum for all levels of Ph.D. students, post-docs or seniors to exchange ideas and to discuss recent findings. The scope can range from genes to behaviour, and includes theory, plants or animals (with some bias towards the latter).

Preliminary programme Thu evening/Fri morning: Arrival Fri afternoon: Start of presentations at 3pm Fri evening: social evening in the historic city centre Sat: Presentations and extended discussions Sat evening: social evening in the historic city centre Sun: Departure day, with option for further discussions, lab visits, etc. We offer a lot of time for informal interaction (long breaks). Talks will be max 20 min + 10 min discussion (or shorter). Posters possible.

All attendants cover their own costs. Cheap student accommodation is available and we can help you with bookings (if you register in time).

For registration and further information send an Email to nils.anthes@uni-tuebingen.de <<mailto:nils.anthes@uni-tuebingen.de>> before 16 June 2006, including: - Name and contact details - Preference for oral or poster contribution - Title of contribution - Number of nights in Tuebingen - Preferred accommodation (hotel, guesthouse, youth hostel, floor space, not required) - Vegetarian or other special requirements

Looking forward to seeing you in Tuebingen.

Nils Anthes & Nico Michiels

Nils Anthes <Nils.Anthes@uni-tuebingen.de>

**UAlaskaAnchorage Sticklebacks
Jul30-Aug4 AbstractCall**

Greetings -

This is the final call to submit abstracts for the Fifth International Conference on Stickleback Behavior and Evolution, to be held in Anchorage, Alaska July 30-August 4, 2006. In addition to invited talks, we have

received over sixty abstracts from researchers working in dozens of institutions in twelve countries from Japan to Finland and points in between. As of today, 73 people have registered to attend. We have just a few more spots available for presentations, and therefore we have decided to extend the abstract deadline to May 7th to provide the opportunity to present to anyone who may have missed the May 1st deadline. The registration will stay open until the start of the meeting (but costs do rise incrementally), so even if you don't submit an abstract you can still take part in an exciting meeting.

Best Regards, Bill

William A. Cresko Assistant Professor of Biology Center for Ecology and Evolutionary Biology University of Oregon, Eugene, Oregon wresko@uoregon.edu

WashingtonDC Retrovirus Oct8-11

This meeting will include sessions on viral emergence, evolution and genomics.

Dear Colleague,

On behalf of the organizing committee for the 8th International Feline Retrovirus Research Symposium to be held in Washington DC October 8-11, 2006, I am pleased to invite you to and members of your group to submit abstracts of your latest work. The conference promises to be an innovative and exciting blend of cat genomics, retroviral research and advances in the cat as a model of infectious disease.

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

This is an exciting time for feline infectious disease research and also feline genomics. The 2006 completion of the complete cat genome sequence holds great promise for expanding the role of the cat as a model of infectious disease. We anticipate a unique blend of talks at the conference and your participation would be a wonderful contribution.

Please visit the conference website at <http://ifrrs8.ncifcrf.gov> for additional information, submission of abstracts, and registration. Please note the deadline

for abstracts is July 15, 2006 and an early registration discount deadline is June 1, 2006. Please feel free to contact Dr Jill Pecon-Slattey or Dr. Naoya Yuhki of the local organizing committee with any questions.

Best wishes

Stephen J. O'Brien, Chief Laboratory of Genomic Diversity, National Cancer Institute-Frederick, Frederick MD USA on behalf of the International Organizing

Committee (see <http://ifrrs8.ncifcrf.gov> for complete list)

Local Organizing Committee: Jill Pecon-Slattey, Ph.D slattey@ncifcrf.gov 301-846-5882 Fax: 301-846-6327 Naoya Yuhki Ph.D. yuhki@ncifcrf.gov Alfred Roca, Ph.D. roca@ncifcrf.gov Meredith Brown, DVM brownmer@ncifcrf.gov

roca@ncifcrf.gov roca@ncifcrf.gov

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DalhousieU PatagonianFish

PhD position in Comparative Phylogeography/Conservation Genetics of Patagonian fish

Support for a PhD position is expected to become available at Dalhousie University (Halifax, Nova Scotia, Canada) for research in comparative phylogeography and conservation genetics of fish in Patagonia. The student will develop a research project that uses molecular genetic and phenotypic approaches to the examine issues in phylogeography, adaptive radiation and/or conservation genetics. The successful candidate should have experience with molecular techniques and should have a strong interest in population genetics and statistics. Fieldwork in Patagonia will take place in collaboration with scientists from Argentina and Chile. The

position is expected to start in the 2006/2007 academic year, pending funding approval and is contingent upon acceptance to the Department of Biology graduate program.

For more information please contact: Daniel E Ruzzante, Associate Professor and Canada Research Chair in Marine Conservation Genetics, Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4J1.(email: daniel.ruzzante@dal.ca, <http://myweb.dal.ca/~ruzzante>)

Daniel Ruzzante, Associate Professor Canada Research Chair in Marine Conservation Genetics Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4J1 phone: (902) 494-1688 fax: (902) 494-3736 e-mail: daniel.ruzzante@dal.ca

<http://myweb.dal.ca/ruzzante> Canada Research Chairs <http://www.chairs.gc.ca>
Daniel.Ruzzante@Dal.Ca

ETHZurich
ExperimentalEvolRecombination

EXPERIMENTAL EVOLUTION OF RECOMBINATION

The new Institute of Integrative Biology (IBZ) at ETH Zurich (group of Paul Schmid-Hempel) is looking to fill a

PhD position

on the topic of

³Host-parasite co-evolution vs. meiotic recombination²

In most organisms, offspring are produced sexually involving meiotic recombination. Recombination generates genetic diversity in populations, but because the parent's successful genetic make-ups are thus destroyed, the process is difficult to understand in evolutionary terms. Theoretical models suggest that recombination should be selected against under a very wide range of conditions, yet empirical evidence is scarce. This project therefore addresses the problem by experimentally testing the consequences of host-parasite co-evolution using populations of the Red Flour Beetle (*Tribolium castaneum*), in the presence of co-evolving parasites and other relevant selection regimes. The experimental populations will be screened by molecular methods to identify genotypes of individuals etc., and so to test some main hypotheses.

Please send application (CV, names and addresses of referees) to Prof. Paul Schmid-Hempel, ETH Zurich, Institute of Integrative Biology (IBZ), ETH-Zentrum / Universitätsstrasse 16, CH-8092 Zurich Switzerland; or by email (psh@env.ethz.ch). Applications are being reviewed starting 23 June 2006, or until post is filled. Employment according to standard regulations of ETH. Start of project: autumn 2006 or by mutual agreement. More information on our web page (www.eco.ethz.ch).

Prof. Paul Schmid-Hempel ETH Zurich Institute for Integrative Biology (IBZ) ETH-Zentrum CHN CH-8092 Zurich ph: +41 44 633 6048 / 6033 fax:+41 44 632 1271 psh@env.ethz.ch www.eco.ethz.ch Paul Schmid-Hempel <Paul.Schmid-Hempel@env.ethz.ch>

ETH Zurich EvoImmuneDefence

PhD position: Evolutionary Ecology of Immune Defence

Institute of Integrative Biology (IBZ) at ETH Zurich, Switzerland

Joachim Kurtz and Paul Schmid-Hempel seek a graduate student interested in doing a PhD on the topic of the evolutionary ecology of immune defence. The project will focus on the evolution of phenotypic plasticity in immunity. The major goals are (1) to investigate the extent of phenotypic plasticity in the immune response of an invertebrate (the flour beetle *Tribolium castaneum*), (2) to experimentally test its benefits, costs and health impacts with regard to pathogenic and nutritional environmental conditions, (3) to use an experimental evolution approach for studying the evolutionary significance of phenotypic plasticity. Since the project will include the study of long-term phenotypic adaptation, which might be transferred between generations, it will touch the recently highly debated field of epigenetic change.

For more information please contact: Joachim Kurtz (joachim.kurtz@env.ethz.ch) ETH Zurich, Institute of Integrative Biology (IBZ), ETH-Zentrum, Universitätsstrasse 16, CH-8092 Zurich, Switzerland. Phone: + 41 44 63 36 032

For application please send your CV and addresses of 2-3 potential referees until 18 June 2006. Employment will be according to standard regulations of the ETH. Start of project: August 2006 or by mutual agreement. More information on our research can be found at [http:// www.eco.ethz.ch](http://www.eco.ethz.ch) . ***

Dr. Joachim Kurtz

ETH Zurich Experimental Ecology Universitätsstr. 16
ETH-Zentrum, CHN J12.1 CH-8092 Zurich Switzerland

Phone: + 41 44 63 36 032 Fax: + 41 44 63 21 271

E-mail: joachim.kurtz@env.ethz.ch

WWW: <http://www.eco.ethz.ch> <http://www.mpil-ploen.mpg.de/english/evoleco/staff/kurtz.htm>

joachim.kurtz@env.ethz.ch joachim.kurtz@env.ethz.ch

ErasmusU HumanPopGenetics

PH.D. STUDENT POSITION IN HUMAN POPULATION GENETICS (4 YEARS) AVAILABLE

Department: Forensic Molecular Biology, Erasmus MC - Medical Faculty of the Erasmus University Rotterdam, The Netherlands

Period: 4 years

Salary: gross 1.702 Euro in the first year up to ? 2.283 in the fourth year via University employment

Project: Investigating human genetic diversity for identification of geographic ancestry and externally visible characteristics.

Prerequisites: M.Sc. or equivalent degree, solid background knowledge in theoretical population and evolutionary genetics as well as biostatistics, practical benchwork experience in molecular genetic techniques incl. genotyping. Skills in computer programming are highly welcome.

Additional: The Department of Forensic Molecular Biology performs fundamental research in human genetics / human biology with potential future applications to forensics (<http://www.erasmusmc.nl/fmb/>) and has strong collaborations with other biomedical departments of Erasmus MC such as genetics, cell biology, epidemiology, bioinformatics, clinical genetics (<http://www.erasmusmc.nl/medical.genetics/>), the Netherlands Forensic Institute (<http://www.forensischinstituut.nl/NFI/nl>) and many international partners in human and forensic genetics. The successful applicant will be integrated into the postgraduate research school Medical Genetic Center Southwest Netherlands - MGC (<http://www.medgencentre.nl/>). Rotterdam (<http://www.medgencentre.nl/>) is a modern and highly international city at the North Sea and is situated in close connection to the most attractive cities of Western Europe (Amsterdam, Paris, Brussels, Antwerp, London, Cologne, etc.).

Application: CV, publication list, research interest and motivation, e-mail addresses and phone number of three references should be submitted to Prof. Manfred Kayser, Department of Forensic Molecular Biology, Erasmus University Medical Centre, Medical-Genetic Cluster, PO Box 1738, NL-3000 DR Rot-

terdam, The Netherlands, preferentially via e-mail: m.kayser@erasmusmc.nl

Application dead-line: June 15, 2006

Manfred Kayser, Ph.D. Professor of Forensic Molecular Biology Head, Department of Forensic Molecular Biology Erasmus University Medical Centre Rotterdam PO Box 1738, 3000 DR Rotterdam, Netherlands tel. ++31-10-4638073, fax. ++31-10-4089300 <http://www.erasmusmc.nl/fmb/> "M.H. Kayser" <m.kayser@erasmusmc.nl>

FrankfurtU EvolMulluscs

PhD position at Frankfurt University in Evolutionary Ecology of molluscs

available, starting as soon as possible. The position (salary BAT IIa/ 2) is in the group of Professor Dr. Bruno Streit (Institute of Ecology, Evolution and Diversity) and will be given for 3 years. Prerequisites: Diploma or master thesis in the field of ecology, limnology or mollusc biology. Knowledge in molecular genetic techniques are required. The successful candidate should be willing to cooperate in current projects, but may also present his/her own PhD project. Further duties include teaching and administration; therefore an adequate knowledge of German is required.

Further information on our research and on cooperating groups may be found on www.bio.uni-frankfurt.de/ee. Send CV and referee names (closing date May 26, 2006) to: Prof. Dr. Bruno Streit, Frankfurt University, Biologie-Campus, Building A, Siesmayerstrasse, D-60054 Frankfurt am Main, Germany.

streit@zoology.uni-frankfurt.de

LeibnizInst FishPopDynamics

Job Opening Modelling the Population Dynamics of Human-Exploited Fish Populations

The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB) of the Forschungsverbund Berlin e.V., Department Biology and Ecology of Fishes, in cooperation with the International Institute for Applied Sys-

tems Analyses (IIASA) in Laxenburg (Austria) (PD. Dr. Ulf Dieckmann) invites applications for the following position within the framework project "Adaptive Dynamics and Management of coupled social-ecological recreational fisheries (ADAPTFISH)" granted by the Pact for Research and Innovation of the Leibniz-Society (WGL).

PhD student

Topic: This project aims at modelling and analysing the population dynamics of angler-exploited freshwater fish stocks. The impacts of selective recreational fishing mortality on yield, stock structure and salient life-history traits shall be modelled depending on fisheries intensity, varying regulations (e.g. size limits) and considering different population parameters (e.g. growth rate). Moreover, eco-genetic models to analyse the potential of recreational fishing to induce evolutionary changes are expected to be constructed and analysed. The projects ultimately aims at deriving recommendations for fisheries management and conservation.

Qualifications: M.Sc. degree in Natural Sciences such as Theoretical Biology, Applied Mathematics, Fisheries Biology, Computer Sciences or comparable degree with a focus on quantitative approaches to understand the population dynamics of exploited animals; experiences with programming (e.g., C++) and mathematical software (e.g., Matlab) are explicitly requested; experiences with quantitative population models or fish stock assessment; good working knowledge of English; above average communication skills and team spirit; ability to work independently; high motivation; familiarity with recreational angling would be a benefit.

The position is open until filled. It is limited to three years and will be paid according to TVÖD (service class wage agreement, depending on age and marital status roughly 25.000 Euro per year gross income, health insurance covered, the wage is equivalent to 0.5 the wage of a full time scientist). It is anticipated that the successful candidate will split attendance between residence at IGB and IIASA. Applications by females are particularly encouraged. Disabled persons with identical qualifications will be favoured.

Please send your application, preferably by email, with the usual material (expression of interest, CV, copies of certificates, if available representative reprints of published work) including a short statement of personal research aims and interests and a summary of the M.Sc. thesis ideally not later than May 30, 2006 to:

Leibniz-Institute of Freshwater Ecology and Inland Fisheries Dr Christian Wolter Müggelseedamm 310 12587 Berlin, Germany, wolter@igb-berlin.de

– Echte DSL-Flatrate dauerhaft für 0,- Euro*! "Feel free" mit GMX DSL! <http://www.gmx.net/de/go/dsl>
Robert Arlinghaus <rarlinghaus@gmx.de>

McMasterU ToxicologyFatheadMinnows

Graduate Student Opportunity - Genotoxicology of Fathead Minnows exposed to contaminated sediments in situ.

We seek a M.Sc. student for a collaborative study of fathead minnows that we will cage in situ near a historical coal tar spill (Randle Reef) and at reference sites near by in Hamilton Harbour, Lake Ontario, and then return to the laboratory for follow-up evaluation. The longer-term goal is to assess the genetic damage, long-term developmental effects, and reproductive effects in fish caused by exposure to Randle Reef water and sediment before, during, and after the Randle Reef clean-up operation. The student will gain experience exposing fathead minnows to sediments, and rearing fish offspring to assess heritable mutations. As well, we will examine germ-line mutations in tandem repeat DNA, vitellogenin levels, developmental deformities, and survival of the exposed adults' fry. Transfer to a Ph.D. program may be possible depending upon the timing of the spill clean-up. The student will be based in the Biology Department at McMaster University and will work part of the time with collaborators Drs. Jim Sherry and Joanne Parrott, Environment Canada Scientists, at Canada Centre for Inland Waters. Please send a statement of interest, CV, Transcripts, and list of references to the following address.

Dr. James S. Quinn, Biology Department, McMaster University, 1280 Main Street West Hamilton, ON, L8S 4K1, e-mail (quinn@mcmaster.ca)

James S. Quinn, PhD Biology Department McMaster University Hamilton, ON L8S 4K1 (905) 525-9140 ext 23194 quinn@mcmaster.ca <http://www.science.mcmaster.ca/biology/faculty/quinn/-quinn.htm> jim quinn <quinn@mcmaster.ca>

CONCERNS: 3-Years PhD position available at the Roscoff Marine Station, Team: Plankton Evolution and Paleoceans.

The group Plancton Oceanique at the SBR in Brittany, France, is a one of the world leader in the fields of molecular ecology, evolution, and physiology of marine unicellular plankton (<http://www.sb-roscoff.fr/Phyto/>). The new team Plankton Evolution and Paleoceans (PI: Colomaban de Vargas; Research Engineer: Ian Probert; PhD students: Miguel Frada and Hui Liu) explores key aspects of the biological, functional, and ecological diversities within the two main groups of pelagic micro-calcifiers: the coccolithophores and foraminifers. Having build kilometer-thick, exceptionally well preserved carbonate deposits at the ocean floor, these protists have played a fundamental role in the ecology and geology of Earth System for the last ~200 My. The biological (genomics, physiology, ecology, biogeography), chemical (isotopics, trace elements within the micro-skeletons), and morphological (optic and electron microscopy) information we extract from living species are used to assess their mode and rate of evolution, and re-interpret their fossil record and impact on biogeochemical cycles.

PhD project: Role of Red-Queen selection, life cycle, and sex in the evolution of marine pelagic viruses and their hosts (coccolithophores).

This project will be co-supervised by Colomaban de Vargas (SBR) and Willie Wilson (Plymouth Marine Laboratory, <http://www.pml.ac.uk/pml/>). It is part of ESTeam, a new European PhD program of excellence in marine genomics and molecular ecology, hold at the SBR (<http://www.sbroscoff.fr/ESTeam/>).

Project Abstract: Modern optical and genomic techniques have revealed extremely abundant and diverse marine planktonic viruses. Although the influence of viruses on marine geochemical cycles (via the regulation of host populations), and prokaryote evolution (via lateral gene transfer), is well recognized, the processes creating and maintaining such huge oceanic viral diversity, including its rate of evolution, are largely unknown. Mechanisms of co-evolution between hosts and their viruses, where both are fighting to respectively decrease and increase virulence, are certainly playing critical roles. We propose to test two main hypotheses, using the coccolithophore *Emiliana huxleyi* as model: (A) virulence in pelagic host-virus interactions is highly specific, constrained by the boundaries between species, sub-species, or strains; (B) virulence is not species specific, but life-stages specific, and thus constrained by the sexual alternation between haploid and diploid populations. Experiments will test if Red-

Queen processes are driving ecological/evolutionary diversification in coccolithoviruses and their hosts, and will address whether host evolution is driven by rapid genomic mutations, or rather by genomic restructuring through haploidization and/or genetic recombination associated with sex. Results will enhance our understanding of the nature and tempo of evolution of planktonic host-virus interactions.

The complete project can be downloaded @: http://www.sb-roscoff.fr/ESTeam//Theses/ESTeam_DeVargas.pdf Application deadline: May 26th 2006; Interviews: June 15-16th 2006; Starting date: Fall 2006. Salary: 1532,94 Euros net/month; in addition: travel allowance, 750 /year; mobility: 523,50 /month; career exploration: 2000 /fellow. Further detail about the ESTeam program can be found @ <http://www.sb-roscoff.fr/ESTeam/>. Application form can be found @ <http://www.sb-roscoff.fr/ESTeam/> and will be sent, together with a CV, a letter of motivation, and 2 recommendation letters, to houbin@sb-roscoff.fr, i.e. Mrs Celine Houbin, ESTeam operational manager, SBR/CNRS-UPMC, BP74, F-29682 cedex, FRANCE. A copy of the documents should be emailed to the Dr. Colomaban de Vargas, vargas@sb-roscoff.fr; Any questions? Do not hesitate to call: 00 33 2 98 29 25 28. vargas@marine.rutgers.edu

StationBiologiquedeRoscoff Evol

9 PhD fellowships on marine sciences (from oceanography to genetics) are available at Station Biologique de Roscoff, France funded by the European Commission under FP6-Marie Curie Actions/EST. Deadline: May 26, 2006.

The SBR is leader of the network of excellence Marine Genomics Europe and is a european leading training centre in marine molecular biology. The salaries are attractives, the application are open to european and non european fellows and Women are highly encouraged to apply

registration at: <http://www.sb-roscoff.fr/ESTeam/>
Deadline: 26 May 2006 Interview: 15-16 June 2006
Start : September - November 2006

information at: houbin@sb-roscoff.fr

Michèle Barbier, PhD European Project Manager NoE Marine Genomics Europe CNRS SDV/INSU - FR 2424 Station Biologique, BP 74 F- 29682 Roscoff cedex,

France

E-mail: barbier@sb-roscoff.fr Tel: + 33 (0) 2.98.29.23.45 Fax: + 33 (0) 2.98.29.23.80

Here are the PhD fellowships involved in Evolution. Out of 14 proposals, 5 are dealing with macro- and micro-evolutive processes. These proposals are:

Genetic and genomic analyses of sporophyte/gametophyte alternation during the life cycle of the brown alga *Ectocarpus siliculosus* the PhD thesis will be performed in the "Algal Genetics" laboratory directed by J. M. Cock

Genomic, transcriptomic and genetic studies of photoacclimation and light stress response in *Synechococcus* spp. the PhD thesis will be performed in the "Oceanic Plankton" laboratory directed by D. Vault

Role of red-queen selection, life cycle and sex in the evolution of marine pelagic viruses and their hosts the PhD thesis will be performed in the "Evolution of plankton & PaleoOceans" laboratory directed by C. de Vargas

Thermal and oxydative stresses in the hydrothermal vent polychaete *Alvinella pompejana*: a study of adaptive polymorphisms using candidate genes and micro-arrays the PhD thesis will be performed in the "Evolution & Genetics of Marine Populations" laboratory directed by M. Valero

Evolution of respiratory adaptations in deep-sea hydrothermal vent scaleworms the PhD thesis will be performed in the "Ecophysiology: Adaptation & Molecular Evolution" laboratory directed by F. Zal

People can get all information on proposals including a one page abstract of each proposal at the address <http://www.sb-roscoff.fr/ESTeam/> Thank you for adverting these european Marie-Curie Fellowships

Best regards

Didier Jollivet

Didier JOLLIVET, CNRS CR1 Station Biologique de Roscoff, Evolution & Génétique des Populations Marines Place Georges Teissier, BP74, 29682, Roscoff cedex tel. 33 2 98 29 23 67 fax. 33 2 98 29 23 24

[didier.jollivet <jollivet@sb-roscoff.fr>](mailto:didier.jollivet@sb-roscoff.fr)

CONCERNS: 3-Years PhD position available at the Roscoff Marine Station, Team: "Evolution & Génétique des Populations Marines".

The group "EGPM" (resp. M. Valero) at the SBR in Brittany, France, is actually well-recognized in the fields of molecular ecology, evolution, population genetics. The group is sub-divided into 4 main research topics: Life cycles, reproductive strategies and population structure (C. Destombe), Selection & adaptations (D. Jollivet), Dispersal & phylogeography (M. Valero) and Genetics and microevolution of invasive species (F. Viard). The group is investigating macro- and micro-evolutionary processes that shape populations over various spatial scales in algae and marine invertebrates. Among these four main topics, "Selection & adaptations (PI: D. Jollivet) explores key aspects of the thermal and chemical adaptation of the deep-sea hydrothermal vent fauna using both transcriptomic (micro-arrays) and candidate gene (allele coalescence) approaches. The ultimate goal is to found specific adaptive eukaryot molecular signatures associated with "high" temperatures and anoxia and to understand how adaptive polymorphisms could be maintained in such a heterogeneous and instable environment.

PhD project: Study of thermal and oxidative stress in the hydrothermal vent polychaete *Alvinella pompejana*

This project will be co-supervised by Didier Jollivet (SBR), Arnaud Tanguy (SBR) and Franck Zal (SBR). It is part of ESTeam, a new European PhD program of excellence in marine genomics and molecular ecology, hold at the SBR (<http://www.sbroscoff.fr/ESTeam/>).

Project Abstract: Eurythermal eukaryotes associated with deep-sea hydrothermal vents are one of the most exposed organisms to highly fluctuant thermal regimes over small spatial scales. Using both transcriptomic and proteomic approaches, the aim of our project is 1) to identify enzyme systems involved in the response of *Alvinella pompejana*, the "Pompeii worm", to thermal and oxidative stresses, 2) to compare patterns of gene expression between colonists ("hot" conditions) and reproducers ("cool" conditions) in order to identify a set of stress-regulated genes that could provide useful candidate genes for the detection of adaptive polymorphisms and 3) to identify over a large set of genes, different-thermally adapted alleles in colonists (first young individuals that settle on new 'hot' chimneys) as opposed to reproducers (well-established individuals in aged populations from which thermal conditions are much more cooler).

The complete project can be downloaded @:<http://www.sb-roscoff.fr/ESTeam//Theses/>-

**StationBiologique de Roscoff MGE
Announcement 2**

ESTeam_tanguy_zal.pdf Application deadline: May 26th 2006; Interviews: June 15-16th 2006; Starting date: Fall 2006. Salary: 1532,94 Euros net/month; in addition: travel allowance, 750 €/year; mobility: 523,50 €/month; career exploration: 2000 €/fellow. Further detail about the ESTeam program can be found @ <http://www.sb-roscoff.fr/ESTeam/>. Application form can be found @ <http://www.sb-roscoff.fr/ESTeam/> and will be sent, together with a CV, a letter of motivation, and 2 recommendation letters, to houbin@sb-roscoff.fr, i.e. Mrs Celine Houbin, ESTeam operational manager, SBR/CNRS-UPMC, BP74, F-29682 cedex, FRANCE. A copy of the documents should be emailed to Dr. Didier Jollivet & Dr. Arnaud Tanguy jollivet@sb-roscoff.fr; Any questions? Do not hesitate to call: 00 33 2 98 29 23 67.

Didier JOLLIVET, CNRS CR1 Station Biologique de Roscoff, Evolution & Génétique des Populations Marines Place Georges Teissier, BP74, 29682, Roscoff cedex tel. 33 2 98 29 23 67 fax. 33 2 98 29 23 24

[didier.jollivet <jollivet@sb-roscoff.fr>](mailto:didier.jollivet@sb-roscoff.fr)

UCD Dublin MarinePopGenet

PhD position - UCD Dublin, Ireland

EU-nationals are invited to apply for a 3-year PhD scholarship in the MarBEE group at the UCD School of Biological & Environmental Science in Dublin, working with Dr Stefano Mariani in a newly-established group focusing on the evolutionary ecology and fisheries genetics of marine animals. The research is funded by Science Foundation Ireland, under the Research Frontiers Programme, and is aimed at understanding the population genetic consequences of sex change in marine fish, using molecular genetics, meta-analysis and computer modelling. The project will entail extensive molecular biology laboratory activity, fieldwork periods in the Mediterranean and South Africa, as well as intense computer-based work. Candidates should ideally already possess a Master-level degree in empirical population genetics or evolutionary biology, though we welcome applicants from other disciplines such as marine biology, zoology, ecology, as well as candidates with backgrounds in bioinformatics and applied mathematics, with a strong interest in biological systems. Proficiency in molecular laboratory techniques would be very advantageous, as would some experience of computer modelling. Strong enthusiasm for fieldwork in

marine coastal habitats and commitment to interdisciplinary research are critical.

The appointee will join the Marine Biodiversity, Ecology & Evolution Group and the Molecular Genetics Lab, which together comprise 12 PhD students, 2 Post-doctoral fellows and three academic staff, working on a broad range of topics from comparative genomics, molecular phylogenetics and population genetics, to fisheries science, community ecology and ecosystem management. For more details visit: <http://www.ucd.ie/zoology/marbee/> Application procedure: Please send a 1-page covering letter and a CV no longer than 2 pages, plus names and emails of three people who can be contacted for references, to: stefano.mariani@ucd.ie Closing date for applications: 30th June 2006 (interviews between July and August). Project start date: strictly 1st September 2006. Scholarship includes payment of university fees plus a monthly stipend of 1,300 EUR.

Committed to Equal Opportunities.

Feel free to contact me for any further information about the project and related issues.

Best,

Stefano Mariani

Dr Stefano Mariani MARine Biodiversity, Ecology & Evolution UCD School of Biological & Environmental Science and Education Research Centre (West) University College Dublin Belfield Dublin 4 Republic of Ireland tel. +353.1.716.2347 fax. +353.1.716.1152 <http://www.ucd.ie/zoology/marbee/> stefano.mariani@ucd.ie

UCD Dublin MarinePopGenet 2

PhD opportunity in marine population genetics at UCD, Dublin

With regard to the announcement posted yesterday, we would like to specify that non-EU applicants can still apply, but they have to be aware that - due to the higher cost of university fees for non-EU students - their salary would be thinned down to around 960 EUR per month.

thanks

Dr Stefano Mariani MARine Biodiversity, Ecology & Evolution UCD School of Biological & Environmental Science and Education Research Centre (West) University College Dublin Belfield Dublin

4 Republic of Ireland tel. +353.1.716.2347 fax. +353.1.716.1152 <http://www.ucd.ie/zoology/marbee/stefano.mariani@ucd.ie>

Andrew J. Leigh Brown Professor of Evolutionary Genetics University of Edinburgh Institute of Evolutionary Biology School of Biological Sciences Edinburgh EH9 3JT Scotland Tel: +44-131-650-5523 Web: <http://homepages.ed.ac.uk/eang09/LeighBrownGroup.html> A.Leigh-Brown@ed.ac.uk

U**Edinburgh** QuantGenet

MSc in QUANTITATIVE GENETICS AND GENOME ANALYSIS <http://www.qgen.co.uk>

NERC STUDENTSHIPS AVAILABLE FOR UK & EU APPLICANTS Full awards to UK residents with fees-only studentships for EU residents Details on eligibility and Masters funding at <http://www.nerc.ac.uk>

This world-renowned degree programme (12 months M.Sc./ 9 months Diploma) provides a unmatched foundation in population and quantitative genetics together with experience in relevant statistical methodologies. It includes options in evolutionary genetics , human genetics and animal breeding. There is a rapidly expanding demand for individuals with these combined strengths to apply quantitative genetics theory to practical problems in both biological sciences (eg conservation genetics), biomedical science (human gene mapping) and agricultural industries; and to undertake research on current problems in population genetics, genome analysis, and analysis of complex traits. This course provides an excellent platform for doctoral studies. Course details at <http://www.qgen.co.uk>

The course is based at the Institute of Evolutionary Biology at Edinburgh University <http://www.biology.ed.ac.uk/research/institutes/evolution/> with substantial input of teaching and research facilities provided by the Roslin Institute, Scottish Agricultural College, the Medical Genetics Section of the Department of Medical Sciences, and the MRC Human Genetics Unit. These are all internationally recognised centres for research in quantitative genomics and research training is an integral part of the course.

Applications invited from graduates in

1. Biosciences, Genetics, Agricultural Sciences, Medicine or Veterinary Medicine who have an interest in, and aptitude for quantitative biology, or
2. Mathematics, Statistics or Physical Sciences who wish to apply theory to genetic problems.

The application form can be downloaded from the Postgraduate Office web pages at <http://www.postgrad.ed.ac.uk> Informal enquiries and requests for further information to qgen@ed.ac.uk

U**Iceland** ExptPopGenet

U of Iceland Ph.D stipend in molecular population genetics and evolutionary biology

A three-year Ph.D stipend granted by the University Fund of The Iceland Steamship Company

Genes with small fitness effects: estimating effects of codon bias in sexually reproducing experimental populations of the yeast *Saccharomyces cerevisiae*.

The laboratory of Professor Einar Arnason, Institute of Biology, University of Iceland, is offering a three-year Ph.D. stipend.

The project, a combination of molecular biology and population/evolutionary genetics, is an experimental perturbation/reperturbation study of fitness effects of genes having small effects on Darwinian fitness. Codon usage and codon bias are excellent systems for experiments of this kind. Experiments will be conducted to estimate directly fitness effects of alternative silent-site mutations in codons of highly codon-biased genes. Theory and comparative molecular evolution studies predict small selection coefficients for such variation. The yeast *Saccharomyces cerevisiae*, a model organism par excellence, is the experimental organism of choice. The possibility of direct gene replacements, tagging of genes and very high meiotic recombination rate are among the important features making yeast the most suitable organism for studies on genes with small effects on fitness.

The population genetics/evolutionary biology laboratory is located in Askja, the new Natural Sciences Building at the University of Iceland. The laboratory shares facilities with molecular biology/genetics and cell biology/virology with state of the art equipment for molecular and cell biology. It also has high power computer facilities running various software for data analysis and simulation under Linux, Mac OS X, or Windows. The student will be part of a research team numbering between 20 and 30 students, post-docs and senior researchers.

We are searching for a highly motivated and quali-

fied student in a relevant field preferably with laboratory/research experience. We are looking for a student with a background in molecular biology and keen interest in population genetics/evolutionary biology, or, a student with a background in population/evolutionary biology and a keen interest in molecular biology. Studies will start in August 1, 2006 (or as agreed upon). The studies will be completed with a thesis defense at the end of the period.

For acceptance into the PhD program in the Faculty of Science at the University of Iceland the applicant must hold an MSc degree (3 year PhD program) or a BSc degree (4 year PhD program including courses) in a relevant field with a grade-point average of 7 out of 10 or equivalent. Relevant fields include population genetics, evolutionary biology, genetics, biochemistry, molecular biology. Available courses are few but small and high-level and with top-notch teachers. Graduate level courses in other Nordic or European countries and North America are also accepted. It may be possible that the student does 20% teaching and supervision of undergraduates which may extend the studies to approximately four or five years (for M.Sc. and B.Sc. students respectively). The stipend amounts to 2.5 million Icelandic kronur per annum for three years (approximately US\$ 33,000 at current exchange rates) before taxes and insurance.

Deadline for application is June 30, 2006. Applications should include copies of undergraduate and graduate transcripts, Curriculum Vitae, a short description of research interest and research experience, copies of published articles and thesis if any, and the names and addresses of two to three references who know the applicant's academic record and character. The applicant should arrange to have references send their evaluations of the applicant directly to Einar Arnason (who gives further information if requested: einararn@hi.is).

Applications shall be sent via mail or email by June 30 to:

Professor Einar Arnason einararn@hi.is Institute of Biology University of Iceland Sturlugata 7 101 Reykjavík Iceland

einararn@hi.is

UOxford AdaptiveEvol RNAviruses

Note: Funding is only available to applicants from the

UK and Europe only.

New deadline: 22 June 2006.

Department of Zoology University of Oxford Tinbergen Building, South Parks Road, Oxford Telephone: 01865 271234 Fax: 01865 310447

Application Enquiries to: Graduate Administrator but preferably to individual supervisors

Project Supervisor(s): Dr O Pybus Application Deadline: 22 June 2006 Funding is available to students from EUROPE (INCLUDING UK) ONLY

Investigating the Geographic Structure and Adaptive Evolution of RNA Viruses

Gene and genome sequences contain new and unique information about biological processes. The rapid and increasing accumulation of such data, together with recent advances in affordable computer power, means that more evolutionary hypotheses can be tested by computational analysis of biological sequences. Such analyses can help us to understand the behaviour of important human viral pathogens, including HIV, influenza, Hepatitis C virus, and Dengue virus.

This project aims to develop new methods and computer programs to infer the spatial location and geographic movement of viruses from gene sequence data. The theoretical foundation for this project is already fairly well-developed; given a set of virus gene sequences with known sampling dates and sampling locations, the models are used to calculate the probability of observing such data under a specified model of migration. From this can be obtained the best-fitting model of migration, in addition to estimates of migration rates among locations. A key technical challenge will be to develop and implement more realistic models of genetic geographic structure. Further epidemiological hypotheses can be tested by using the methods to track the movement of viral strains among different risk groups (instead of different locations). Lastly, the methods developed could be extended and used to investigate the dynamics of adaptive evolution in viral pathogens.

To apply please complete the University application form (available from: www.admin.ox.ac.uk/gsp/) and include two references from academic referees (follow procedure in Booklet A). Please submit two copies of the application form and all supporting material to the Graduate Administrator, Department of Zoology, University of Oxford, South Parks Road, Oxford OX1 3PS (and NOT the address detailed on the application form). Closing date: 22 June 2006

oliver.pybus@zoo.ox.ac.uk Department of Zoology South Parks Road Oxford, OX1 3PS, UK

Oliver Pybus <oliver.pybus@zoology.oxford.ac.uk>

UStAndrews EvolCompNeurosci

Dear EvolDir Members,

Please share the below graduate position advertisement with any interested parties.

Thank you, Anne Smith

A PhD student position is available in the laboratory of V Anne Smith at the University of St Andrews in Scotland, in computational neuroscience. My laboratory encompasses several computational biology approaches, from an evolutionary perspective. Please visit <http://biology.st-andrews.ac.uk/vannesmithlab/> for more information on the lab, and feel free to contact me at anne.smith@st-andrews.ac.uk with questions.

A pdf of the below PhD advertisement is downloadable from: <http://biology.st-andrews.ac.uk/vannesmithlab/CompNeuroPhD.pdf> PhD studentship in Neuroinformatics and Computational Neuroscience

How does the brain work?

The electrical activity of the billions of neurons in the brain accounts for our perceptions, thoughts, feelings and behaviours. Yet it is still unknown exactly what the link is between activity in these networks of neurons, and the cognitive or behavioural functions they serve. In this studentship, you will explore the possibilities of a new computational technique, Dynamic Bayesian Network (DBN) Inference Algorithms, to infer network connectivity and function in networks of neurons recorded from real brains. You will develop new algorithms and apply them to the analysis of multiple-single-unit recordings from the rat hippocampus, among others. You will also compare the abilities of the DBN to other, published information extracting algorithms. Your work will help us understand how information flows in the brain, and potentially lead to greater understanding of how this information flow relates to brain function.

This research is part of a larger consortium in Neuroinformatics (CARMEN: Code Analysis, Repository and Modelling for e-Neuroscience), which puts it at the cutting edge of Integrative Neuroscience. You will be connected in and interacting with a network of some of the UK's leading researchers in neuroinformatics and computational neuroscience.

The studentship will be based at the School of Biology at the University of St Andrews, and will be jointly supervised by Dr. V. Anne Smith (St Andrews) and Dr. Tom V. Smulders (Newcastle University). Applicants should have a background in Statistics, Mathematics or Computer Science; or in Biology/Neurobiology with strong computational interests. For more details, please contact anne.smith@st-andrews.ac.uk and/or visit: <http://biology.st-andrews.ac.uk/vannesmithlab/> EP-SRC funded: home/EU fees plus stipend

– Dr V Anne Smith School of Biology Sir Harold Mitchell Building University of St Andrews St Andrews, Fife KY16 9TS United Kingdom +44 (0)1334-463368 anne.smith@st-andrews.ac.uk biology.st-andrews.ac.uk/vannesmithlab/ biology.st-andrews.ac.uk/vannesmithlab/

USussex AdaptiveEvol

A 4-year PhD studentship is available to study adaptive evolution and the rates and fitness effects of new mutations in the lab of Adam Eyre-Walker at the University of Sussex in Brighton, UK. Unfortunately this studentship is only available to UK citizens or UK residents. Further information about the lab can be found at <http://www.lifesci.sussex.ac.uk/CSE/-members/aeirewalker/aeirewalker.htm>. Applications (CV + names and email addresses of 3 referees) or enquiries should be addressed to Adam Eyre-Walker at a.c.eyre-walker@sussex.ac.uk. Applications will be considered as they are received.

a.c.eyre-walker@sussex.ac.uk

UtahStateU Biodiversity

PhD Graduate Research Assistantship in Freshwater Biodiversity Assessment, Utah State University

Summary: A graduate research assistantship is available to support Doctoral Degree research in the area of conservation and bioassessment of freshwater ecosystems using molecular genetic techniques. This position is funded for four years and is associated with a collaborative project between the USU Department of

Biology, the Western Center for Monitoring and Assessment of Freshwater Ecosystems (USU Department of Aquatic, Watershed, and Earth Resources), and the US EPA Western Ecology Division in Corvallis, Oregon. The successful candidate will work jointly in the labs of Michael Pfrender (Department of Biology) and Chuck Hawkins (Aquatic, Watershed, and Earth Resources) and in collaboration with EPA scientists. The student may enroll in either the Department of Biology (PhD in either Biology or Ecology) or the Department of Aquatic, Watershed, and Earth Resources (PhD in either Ecology or Watershed Sciences).

Description: The central goal of this project is to improve biodiversity assessment in freshwater ecosystems through the development of molecular genetic assays. The student will be responsible for developing genetic assays of target invertebrate taxa, applying these assays in natural ecosystems, and integrating genetic marker information into a database.

Qualifications: A strong interest in conservation and the use of molecular genetic approaches to applied issues is required. Prior experience with basic molecular techniques including PCR, DNA sequencing, and gene expression analysis is desirable. This position will require well developed analytical and computational skills. A Master's degree is preferred but we will consider a highly motivated and qualified student with a Bachelor's Degree.

Department: Department of Biology (College of Science) / Department of Aquatic, Watershed, and Earth Resources (College of Natural Resources)

Stipend: \$20,000/yr

Closing Date: Review of applications will begin immediately and the position will remain open until July 31, 2006

Starting Date: No later than start of Fall term 2006.

We prefer a candidate that could start as early as June 15 - July 1.

Please send a cover letter including research interests (indicate Biodiversity Graduate Research Fellowship on cover letter), resume or curriculum vitae, and contact information for three references to:

Dr. Michael E. Pfrender Dr. Chuck Hawkins

Assistant Professor of Biology Director of the WC-MAFE

Department of Biology Aquatic, Watershed, and Earth Resources

5303 Old Main Hill Road 5210 Old Main Hill

Logan, UT 84322-5305 Logan, UT 84322-5210

e-mail: pfrender@biology.usu.edu e-mail: chuck.hawkins@usu.edu

Informative Websites:

Western Center for Monitoring and Assessment of Freshwater Ecosystems (<http://www.cnr.usu.edu/wmc>)

USU Department of Biology (<http://www.biology.usu.edu> <<http://www.biology.usu.edu/>>)

BLM/USU/ National Aquatic Monitoring Center (www.usu.edu/buglab)

USU College of Natural Resources (<http://www.cnr.usu.edu> <<http://www.cnr.usu.edu/>>)

USU Ecology Center (<http://www.usu.edu/ecology>)

Michael E. Pfrender Ph.D. Assistant Professor Department of Biology Utah State University 5305 Old Main Hill Road Logan, UT 84322-5303

Ph# 435-797-7623 Fax# 435-797-1575

pfrender@biology.usu.edu

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GeorgetownU SeqFacilityManager

Laboratory Technician Position, Shared DNA Sequence Facility Manager

A part or full-time research associate position is available in the Biology Department at Georgetown University, Washington, DC in the laboratory of Dr. Matthew B. Hamilton (bioserver.georgetown.edu/faculty/hamilton).

The position involves operation of an ABI 3100 sequencer for researchers in the Dept. of Biology as well as assisting in population and conservation genetics research. Duties include oversight of lab and instrument operations, collecting microsatellite and DNA sequence data, placing orders for supplies, and assisting with undergraduate and graduate laboratory training. The ability to trouble-shoot instrument problems, effectively schedule instrument time, help instrument users and work with independence is essential. Strong organizational and computer skills are required. There is the possibility to engage in research and co-author publications for highly motivated individuals.

This position is available July 1, 2006 for one year with continuation contingent on performance and availability of funds. Minimum requirements are a Bachelor's degree and experience in molecular biology, evolution, genetics or a related field. Previous laboratory experience with molecular biology and/or DNA sequencing is preferred. Individuals who have recently completed a degree in biology and are seeking further exposure to scientific research before graduate study are especially encouraged to apply. Salary will be commensurate with experience and includes benefits.

Please send a resume or CV and cover letter summarizing research interests and experience as well as three references with full contact information. Applications will be accepted until the position is filled. Georgetown University is an equal opportunity/affirmative action educator and employer.

Matthew B. Hamilton, Ph. D. (202) 687-5924 office Associate Professor (202) 687-5662 FAX Georgetown University hamiltm1@georgetown.edu Department of Biology Reiss Sciences Bldg. 406 3700 O Street NW Washington, DC 20057-1229 USA

“Matthew B. Hamilton”
<hamiltm1@georgetown.edu>

HarvardU CollectionsManager

Museum of Comparative Zoology Harvard University Collections Manager, Genetic Resources

Duties and responsibilities.-Reports to the MCZ's Manager, Collections Operations. Organize and curate new and existing frozen tissues collections and consolidate them into a centralized MCZ frozen tissue collection; develop protocols and procedures for multi-disciplinary collection and its use and preservation; incorporate and maintain tissue data into MCZ-wide collection database; prepare and monitor annual collection budget; implement standard record keeping and other administrative functions required for collecting, accessioning, and loan activities to comply with relevant laws and regulations; ensure compliance with all environmental, health and safety requirements, including training and documentation of facilities; and, in consul-

tation with the Manager, Collections Operations, and the museum's director, determine short- and long-term priorities for the MCZ's frozen tissue collection. The CMGR will be expected to participate in museum-wide and department-specific initiatives, and may assist in preparation of grant proposals for collection or facilities improvement.

Required education, experience and skills.-Advanced degree in biological sciences with emphasis in evolutionary genetics or genomics, or equivalent experience; practical skills in molecular biology; experience in laboratory/facility management, including supervising staff; experience in relevant occupational health and safety issues; demonstrated writing and organizational skills; excellent computer skills, including database management. Excellent interpersonal and communication skills required, as well as the ability to work both independently and in a busy team environment, and to coordinate tasks with multiple constituencies.

Background.-Harvard's Museum of Comparative Zoology contains the world's largest university-based zoological collections. These currently number around 21,000,000 specimens, including many thousands of primary type specimens. The collections are cosmopolitan in geographic scope, taxonomically comprehensive, and scientifically important; they document continuous research and teaching activity in comparative zoology for the last 150 years. The centralized frozen tissue collection will serve all ten of MCZ's departments, each with a faculty curator and full-time collections staff, and will be an active participant in ongoing research activities by faculty, postdocs, students, and visiting scientists.

For further information and to apply online.- Interested candidates may submit resume and cover letter by accessing the Harvard University Employment Website : <<http://employment.harvard.edu/>><http://employment.harvard.edu/> and entering Requisition # 26220

Harvard University is an Affirmative Action/Equal Opportunity Employer

- Linda S. Ford, Ph.D. Manager, Collections Operations Museum of Comparative Zoology Harvard University 26 Oxford Street Cambridge, MA 02138 USA

Tel: 617.495.3748 Fax: 617.495.5667

Chris Conroy <ondatra@berkeley.edu>

IndianaU EvolGenomics

EVOLUTIONARY COMPUTATIONAL GENOMICS
/ BIOINFORMATICS

ASSOCIATE/FULL PROFESSOR

INDIANA UNIVERSITY, BLOOMINGTON

The Department of Biology and the School of Informatics jointly seek an established scholar with a dynamic and innovative research program in the area of bioinformatics and/or computational biology. Successful candidates will be expected to contribute to and complement existing research and teaching strengths in comparative genomics, molecular evolution, and/or population genetics, although other areas of research expertise are not precluded. Indiana University is in a period of significant expansion in the life sciences, and candidates must have a demonstrated ability to promote an environment of collaborative scholarship and a vision for the development of future research and training activities. Candidates with a laboratory component to their research are encouraged to apply.

A complete curriculum vitae, a statement of current and future research interests, and contact information for at least three letters of reference should be forwarded to: Jeremy Bennett, Department of Biology, Indiana University, Bloomington, IN 47405 (hard mail) or jebennet@indiana.edu (pdf files). Direct inquiries about the position should be made to: Michael Lynch, milynch@indiana.edu. Review of applications will begin on May 1, 2006, and will continue until the position is filled.

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

Matthew Hahn Assistant Professor Department of Biology & School of Informatics 1001 E. 3rd St. Indiana University Bloomington, IN 47405 Phone: (812)856-7001 <http://www.bio.indiana.edu/facultyresearch/faculty/Hahn.html> <http://www.bio.indiana.edu/~hahnlab> Matthew Hahn <mwh@indiana.edu>

KewGardens Phyloinformatician

Phyloinformatician - European Distributed Institute of Taxonomy (EDIT)

DEPARTMENT: Jodrell Laboratory, Royal Botanic Gardens, Kew, London, UK

REF: PHY

HOURS OF WORK: Full time - 41 hours per week gross

JOB STATUS: 12 month Fixed Term Appointment

SALARY: from 26,225 British Pounds

JOB DETAILS: Within a European Network of Excellence entitled "the European Distributed Institute of Taxonomy (EDIT)", the jobholder will help design a user-friendly bioinformatics 'toolbox' for interpolating and processing phylogenetic trees, matrices, DNA barcodes and other relevant biodiversity data, to facilitate taxonomic research and conservation outcomes.

ESSENTIALS: The postholder will have a PhD (biology or computing) and have specialist training in computing, phylogenetics, GIS and statistics. Excellent oral and written communication skills essential in order to write high-profile scientific papers and give oral presentations at EDIT workshops. Proven, excellent team working skills.

CLOSING DATE: Monday 22 May 2006

More details and application pack, see:

<http://www.kew.org/aboutus/jobs/ref.phy.htm> Dr Vincent Savolainen Jodrell Laboratory Royal Botanic Gardens, Kew Richmond TW9 3DS, London UK Tel +44-(0)20-8332-5366 Fax +44-(0)20-8332-5310 v.savolainen@kew.org

v.savolainen@kew.org

KewGardens ResAssist Barcoding

Graduate or postgraduate research assistant to analyse plant DNA barcoding data.

Closing date: 14th April

We are seeking a data analyst for an international collaborative project devising new markers for plant DNA barcodes. You would compile sequence data generated by the project, implement phylogenetic and statistical analyses to judge the accuracy with which species can be identified, and prepare results for publication. The post would be ideal for a graduate interested in gaining research experience, someone with good bioinformatics skills or a postgraduate interested in strengthening their computing skills. You will have an undergraduate degree in biology, computing or related area and be familiar with phylogenetics, bioinformatics, or programming. You will also have excellent communication skills, problem solving ability, and team working experience.

The post will be based at the Royal Botanic Gardens, Kew or at the Silwood Park Campus of Imperial College London, with some flexibility on main location. It will last for 9 months from June 2006.

Application details are on <http://www.rbgkew.org.uk/aboutus/jobs/ref1255.htm> For more information on the project, see <http://www.rbgkew.org.uk/barcoding/index.html> or contact Tim Barraclough at t.barraclough@imperial.ac.uk.

Timothy Barraclough <t.barraclough@imperial.ac.uk>

KewGardensUK Cytogeneticist

Dear Colleagues,

We are currently advertising for a cytogeneticist to join the team at Kew, and we would be grateful if you could draw this to the attention of anyone that you think might be interested.

The details can be found below or at:

http://www.kew.org/aboutus/jobs/ref_293.htm or:

<http://www.newscientistjobs.com/viewjob.action?job.id=NS20062549033&index1> With best wishes and thanks,

Mike

You will be responsible for developing an independent high-impact research programme in cytogenetics as part of the Comparative Plant Biology programme. Using the tools of modern cytogenetics, you will investigate questions relating to plant genome evolution in

the broadest sense, building on the existing skills in the Cytogenetics Group. Through successful applications for funding, you will expand the range of opportunities for both national and international scientific collaboration.

With a PhD in a relevant subject and a strong research publication record, you will have experience in plant cytogenetics (including in situ hybridisation) and an understanding of the application of genetic data to population genetics and phylogenetics. Experience of teaching/ training students and research visitors and a track record in successful grant applications are desirable.

Salary is from £26,225 per annum depending on qualifications and experience and benefits include a choice of final salary or stakeholder pension, generous annual leave and a stunning work environment.

Application packs are available from our website www.kew.org (click on the link at the bottom of the homepage). Alternatively, please contact the HR Department, RBG Kew, on 020 8332 5184/5150 (24 hour answerphone). Please quote Ref 293.

Closing date: 19 May 2006.

Committed to equality through diversity.

Selection is on merit alone.

Dr Michael F. Fay Head of Genetics Jodrell Laboratory Royal Botanic Gardens Kew, Richmond Surrey, TW9 3DS UK Tel. (office) (+44) (0)20 8332 5315 Fax (+44) (0)20 8332 5310 email m.fay@kew.org

r.cowan@rbgkew.org.uk

LeidenU ScienceManager

Job opening

We are seeking to hire a science manager for a European Network of Excellence at the interface between biology and medicine. The Network centres on the relationship between development and ageing, and integrates experimental work on model organisms with key observations in human populations.

The successful candidate must have a solid training in biology and/or medicine, and must have an interest in the topics that are central to the Network. Importantly, the successful candidate should also have an interest in science management, and experience in management is at a premium, but is not required per se.

The science manager is expected to run the Network on a day to day basis, dealing with aspects ranging from finances to planning workshops and meetings for both content and practicalities.

We offer a varied position in a dynamic working environment that incorporates both biologists as well as medical scientists. We offer a one year contract, that, given satisfactory progress and working relations, can be extended to 5 years (the duration of the initial EC funding) and potentially beyond. We aim to fill the position the first of September 2006 at the latest.

Interested? Please contact Dr. Bas Zwaan at b.j.zwaan@biology.leidenuniv.nl (telephone +31 71 527 4877), or Prof. Dr. Rudi Westendorp at R.G.J.Westendorp@lumc.nl (telephone +31 71 526 6640) for more information and/or applications. Applications should include a letter explaining your interest for the position and full Curriculum Vitae. Applications should be sent by e-mail with "NoE science manager" in the subject field.

zwaan@rulsfb.leidenuniv.nl

MaxPlanckInst GroupLeaders

Group Leaders, Max Planck Institute for Chemical Ecology

The Department of Entomology in the Max Planck Institute for Chemical Ecology under the direction of Prof. David Heckel is seeking two Group Leaders, one in Insect Ecology and the other in Insect Population Genetics.

The Insect Ecology Group examines the traits involved in successful exploitation of host plants as food resources, focusing mainly on species- and hostrace-complexes in heliothine moths and other Lepidoptera.

The Insect Population Genetics Group applies QTL analysis, genetic mapping of selected genes or map-based cloning to identify genes involved in insect adaptation to host plants, and to subsequently track their changes over time at the population level.

More information on these research areas may be found under the Department of Entomology at the Institute's web page: www.ice.mpg.de. The Department invites applications from independent and highly motivated individuals, who should have 3 - 5 years of postdoctoral research experience in either of the two areas and will

likely be appointed for a period of 4 - 5 years.

The working language in the Institute is English, and the positions are open to all nationalities. The Max Planck Institute for Chemical Ecology is an Equal Opportunity Employer.

Applications and three reference letters should be submitted by June 20, 2006 to the attention of:

Ms. Ramona Taubert Max Planck Institute for Chemical Ecology Department of Entomology Hans-Knoell-Str. 8 07745 Jena Germany

Email: rtaubert@ice.mpg.de <http://www.ice.mpg.de>

Munich GraduateProgramCoordinator

The department of Biology, LMU Munich looks for a coordinator for a new graduate program (Master and PhD) in Evolution, Ecology, and Systematics. The ideal candidate should have a degree (preferably PhD) in Biology or a related field. S/he should be highly motivated have good communication skills. Proficiency in English and German is required. Any experience with administration or curriculum coordination is an advantage.

The coordinator will organize summer schools and workshops, contribute to the development of the curricula and function as an interface between university administration, teachers, and students.

The position is available at 50% (BAT IIa/2 according to German salary scale) from October 1st 2006 for initially three years. Informal inquiries and applications including letter of motivation, CV, and two references should be sent until end of May preferably by email to

Dr. Joachim Hermisson Department Biology II, LMU Munich Bio-Center, Grosshadener Str. 2 82152 Planegg-Martinsried

joachim.hermisson@lmu.de

NESCent Durham Bioinformatics

TWO INFORMATICS POSITIONS AT THE NATIONAL EVOLUTIONARY SYNTHESIS CENTER

Two informatics positions are available at the National Evolutionary Synthesis Center in Durham, North Carolina. These are non-academic positions, but they offer an excellent opportunity for programmers who wish to make a real contribution to evolutionary biology and bioinformatics and who thrive in an academic environment. Both positions offer generous compensation packages to highly qualified applicants.

Position 1: Database Programmer Job Description: A database programmer responsible for design, implementation and maintenance of databases used by both NESCent administration and evolutionary biology researchers and educators. The incumbent will collaborate with the Assistant Director of Informatics, as well as domain scientist and developers, to gather user requirements and translate those requirements into database tools. Education/Training: Degree in biology, computer science or related field. Proven ability to design and implement database technology. Proficient in the use of major open source relational database management systems (e.g., PostgreSQL). Proven team orientation. Outstanding interpersonal and communication skills. Required qualifications: - Thorough knowledge of relational data modeling, ERDs, and normalizing schemas, proven experience with translating domain models into relational schemas. - Thorough command of SQL, including DDL, and understanding of advanced elements of SQL (e.g., sub-queries, views, integrity enforcement) - Experience with a major open-source RDBMS (preferably PostgreSQL) or one or more of Oracle, Sybase, SQLServer, DB2 - Knowledge of and experience with object-relational mapping technologies (e.g., Class::DBI, CMP, JDO, Hibernate) - Proven ability to design and implement object models and middleware on top of databases in the Perl or Java programming language (preferably both), knowledge of design patterns and other best practices. - Experience with data warehousing principles (OLAP, Data Marts), SQL server-side programming (e.g., database triggers, PL/SQL, PL/pgSQL), and with modern middleware technologies (e.g., J2EE/EJB) is highly desirable. - Experience with designing and implementing web-based and stand-alone graphical user interfaces is a plus, as is experience with Web Services (e.g., SOAP, REST, RMI, CORBA), and Semantic Web technology. - Demonstrated ability to contribute to scholarly publications desired.

Position 2: Web/GUI Programmer Job description: A Web/GUI Applications Programmer responsible for development of graphical user interfaces (GUIs) to scientific software applications and databases developed

at NESCent. The incumbent will also have responsibility for website design and serve as the NESCent webmaster. Education/Training: Degree in biology, computer science or related field. Proven ability to design and implement sophisticated graphical user interface applications and web pages. Team orientation with outstanding interpersonal and communication skills. Required qualifications: - Thorough command of HTML/XHTML and CSS - Advanced knowledge of dynamic web-page technologies (DHTML, JavaScript, CGI), and experience in interfacing Unix command-line tools to the web using CGI scripting or web-services - Experience with (preferably) the web-server related part of the J2EE technology stack (JSP, JSTL, Servlet API), or the Template Toolkit in Perl - Experience with programming applets and stand-alone GUI applications in Java - Knowledge of and experience programming against authentication protocols (e.g., HTTP form, LDAP, Kerberos, JAAS) - Experience with dynamic content-management systems (e.g., Wiki, Plone) is desirable. - Experience with high-level dynamic web-content programming technologies (e.g., AJAX, Macromedia Flash), XML (XML-DOM), and with graphical design applications (e.g., Adobe Photoshop) is desirable. - Experience with Web Services (e.g., SOAP, REST, RMI, CORBA), and Semantic Web technology is a plus. as is experience with database design and implementation. - Demonstrated ability to contribute to scholarly publications desired

To apply to either position, please provide a cover letter, resume, and contact information for three references to Karen Henry (khenry@duke.edu). Questions concerning the positions should be addressed to Hilmar Lapp, Assistant Director for Informatics, at hlapp@duke.edu. Additional information on these positions is available on our website (www.nescent.org).

Todd Vision Associate Director of Informatics The National Center for Evolutionary Synthesis

tjv@bio.unc.edu tjv@bio.unc.edu

NHM London ResLeader

THE NATURAL HISTORY MUSEUM
RESEARCH LEADERS

Salary £26,652 - £55,000 per annum (or more for exceptional candidates)

The Natural History Museum (NHM) wishes to ap-

point a number of Research Leaders to grasp a unique opportunity to make a significant contribution to the future scientific research effort of this world-class institution. The NHM explores the diversity of the natural world and the processes that generate that diversity. Systematics and other collections-based investigations are at the heart of our research. We seek research leaders who can contribute to advances in our core science areas, collections development and pursuit of emerging areas, particularly our priority Research Foci (<http://www.nhm.ac.uk/research-curation/-science-directorate/science-policies-strategy/assets/-researchframework.pdf>) which stress interdisciplinary research. We are particularly interested in receiving applications from researchers in the following areas:

* Systematic Biology * Biodiversity, including * Response to Global Environmental Change * Population Genetics * Eukaryotic Microbial Biodiversity * Molecular Phylogeny, Co-phylogeny and Co-evolution * Evolution and Development

Appointments will be made to any of the four Life Sciences departments (Botany, Entomology, Palaeontology, Zoology) as appropriate. We are willing to appoint at any band on our research scale, subject to negotiation and forward planning of research income. We are happy to consider appointing a team of scientists working on a common theme. You will need to demonstrate a record of scientific publications in international journals, achievement in gaining external research funding, and scientific leadership.

Further details are available on request (fca@nhm.ac.uk). You are strongly recommended to make informal contact before application to one of the following Heads of Department:

Botany: Dr Johannes Vogel. Tel. +44 (0)20 7942 5282, Email j.vogel@nhm.ac.uk Entomology: Dr Martin Hall. Tel. +44 (0)20 7942 5715, Email mhall@nhm.ac.uk Palaeontology: Prof. Norman MacLeod, Tel. +44 (0)20 7942 5204, Email n.macleod@nhm.ac.uk Zoology: Prof. Phil Rainbow. Tel. +44 (0)20 7942 5275, Email p.rainbow@nhm.ac.uk

To apply, please send your CV, together with a covering letter, and the names and addresses of three referees to Frances Allen, Science Directorate, The Natural History Museum, Cromwell Road, London SW7 5BD; Email fca@nhm.ac.uk. Please indicate if you would prefer any of your referees not to be contacted prior to interview.

Closing date: 20th June 2006.

Please quote reference: NHM/RL/FA

Tony Maggio <t.maggio@nhm.ac.uk>

PacificGroveCA 2 techs

Research technician, part-time (75% FTE), benefits eligible position, at Stanford University's Hopkins Marine Station, in Pacific Grove, CA. Under the direction of the Principal Investigator the technician will assist with research related to genetic characterization of populations of marine vertebrates and invertebrates in the context of ongoing research into marine conservation and management. The primary responsibilities of the technician will include collecting larvae and adult specimens, extracting DNA and documenting genetic variation. This will require the use (or development) of many research skills using a variety of molecular genetic tools. In addition, the technician will participate in a variety of research activities including: field monitoring of multiple sites in central California, animal care, and laboratory maintenance. There is potential for extension of the technician position to other research projects as well as the possibility of co-authorship of at least one resulting publication.

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

If you are interested, contact Tim Knight at trknight@stanford.edu.

trknight@stanford.edu

Sweden MarineEvol

The Swedish Board of Fisheries is the central governmental institution responsible for fishery management in Sweden. The main goals are to promote sustainable use of fish resources; maintain biodiversity; promote

competitive fish enterprises; secure availability of high quality fish products and to increase public fishing opportunities.

Vacant position at the Institute of Coastal Research, Öregrund, as

PhD/Marine ecologist

focusing on environmental effects on coastal fish

Assignment: Your main task is to perform research on environmental effects on the fish fauna in coastal as well as offshore habitats. You will also be responsible for the Institute's commission regarding the evaluation of effects of establishment of marine windmill parks. Within the Environmental Analyses Group, you will participate in the development of models linking environmental variation to fish recruitment. In addition, you will contribute with expert knowledge in statistics and analyses of coastal fish resources in the common work at the Institute.

Qualifications: You have a PhD in marine ecology. Research experience in fish ecology and good knowledge of the Baltic Sea ecosystem is preferable. You should have good knowledge of statistics and be experienced in working with GIS. You are an energetic person who works independently, with good communication skills (in English), orally as well as in writing. Collaborative ability and personal suitability will be of significant importance for successful appointment.

More information can be obtained from the head of the Research and Development Department Ingemar Berglund, phone: +46-31-743 03 00, the head of the Institute of Coastal Research Magnus Appelberg or assistant head of the Institute Peter Karås, phone: +46-173-464 60.

Union representatives can be reached at: Stig Thörnqvist, ph. +46-31-743 04 08, ST-Fiske, or Karin Frohnlund, tel. +46-523-18714, SACO.

Our aim is an equal gender representation and high ethnical and cultural diversity.

Please send your application and CV to jobb@fiskeriverket.se or Fiskeriverket, Box 423, SE-401 26 GÖTEBORG, Sweden, on June 8th 2006 at the latest.

anssi.laurila@ebc.uu.se anssi.laurila@ebc.uu.se

TraceGenetics LabManager

Trace Genetics: Scientist/Lab Manager Trace Genetics is an identity genomics company that provides gene genealogical services and ancient/degraded DNA analysis. We are located in Richmond, CA and are seeking an enthusiastic and motivated individual to join our team as a lab manager/scientist. We value high customer satisfaction and strive to create an intellectually stimulating and enjoyable work environment for our employees. Our company, (www.tracegenetics.com <<http://www.tracegenetics.com/>>), is owned by DNAPrint Genomics, Inc. For information on our parent company, please see www.dnprint.com <<http://www.dnprint.com/>> . Our lab performs DNA analysis for DNAPrint related to ancestry (consumer), forensics and pharmacogenomics. Duties will include managing a DNA-based genotyping and sequencing laboratory with a staff of three scientists. We are looking for someone who has extensive experience in DNA extractions, CE sequencing, PCR, cloning, RLFP, electrophoresis, and SNP genotyping. The candidate should feel comfortable modifying and creating new protocols, designing experiments, analyzing and interpreting the results of an experiment. The position also requires communicating and coordinating with other labs, updating a growing sample database and maintaining the laboratory. Individuals who accept this position must be comfortable working in a high quality production environment and meeting promised deadlines. We are looking for smart, hardworking and interesting people to join our team. The position is full-time and includes health coverage and vacation/sick leave benefits. Requirements: - Ph.D. or equivalent in Molecular Biology, Cell Biology, Genetics, Anthropology, Evolution & Ecology, or a related field - Be detail oriented, organized, and proactive with responsibilities. - Be a quick learner and be interested in continually upgrading your skills. - Be able to multi-task. - Be able to work in a flexible team¹ and entrepreneurial environment. - Be able to manage staff scientists in an effective manner. - Have excellent writing skills and communication skills. - Have a solid knowledgebase in the lab about the biochemistry behind DNA genotyping and sequencing protocols. - Have experience using Microsoft Word, Excel, Access and Adobe Acrobat, Gene Mapper, and other genetic analysis software. To apply please email your resume and cover letter clarifying why you are interested in and qualified for this job to Ripan Malhi at ripan@tracegenetics.com by June 5th, 2006.

Ripan S. Malhi, Ph.D. Research Director Trace Genetics, Inc. 4655 Meade St., Suite 300 Richmond, CA 94804 www.tracegenetics.com

rmalhi@tracegenetics.com rmalhi@tracegenetics.com

UAlgarve BoneEvolution

Commencing date: As soon as possible, after the closing date
Place of work: Centre of Marine Sciences, University of Algarve, Campus de Gambelas, 8005-139 Faro, Portugal

Job description: To investigate the mechanisms of tissue mineralization in vertebrates through the identification of specific molecular determinants and studies on bone comparative biology and evolution, including the effect of protein mutagenesis. The successful candidate will be expected to integrate a group with strong experience on bone biology focused on the molecular determinants of tissue mineralization which includes 5 researchers, 5 PhD students, one technician and various undergraduate / masters students. Supervision of undergraduate/ graduate students and project writing in collaboration with members of the group will be expected. Candidate will have the opportunity to progressively develop his/her own line of work although maintaining some degree of internal collaboration.

Qualifications and experience: Candidates must hold a PhD in biochemistry or related areas, have a minimum of 3 years of postdoctoral experience and a strong motivation for group collaborative work. Qualifications must include experience in molecular and cellular biology and proven expertise in protein biochemistry including protein expression, purification, and mutagenesis. Knowledge of public biological databases and experience of *in silico* analysis of sequences and data mining will be a plus.

Further information can be obtained from Prof. Leonor Cancela: lcancela@ualg.pt

Contractual conditions: Initial 3-year contract, in accordance with current legislation (article 14a, Dec. Lei 125/99, 20 April) and for the implementation of the project.

Opening: 11th April 2006

Closing date: 23rd May 2006

To apply for this position, candidates should submit a detailed CV, with concise description of research experience and the names and addresses of at least two referees quoting ref. CIMAR/08/2006 to: efonso@ciimar.up.pt Centro Interdisciplinar de Investigação Marinha e Ambiental, Rua dos Bragas, n 289,

4050 ? 123 Porto, Portugal Fax: +351 223 390 608
 E-mail: eafonso@ciimar.up.pt
 smira@ualg.pt

UArizona ResTech HumanPopGenomics

Research Technician or Research Specialist Arizona Research Laboratories – Division of Biotechnology University of Arizona, Tucson, USA Full Time, Benefits Eligible

The Arizona Research Laboratories division of Biotechnology invites applications for a Research Technician/Specialist to work on NSF funded projects in the field of human population genomics: bridging evolutionary history, natural selection, and genetic disease. The selected candidate will take a lead role in the research group of Dr. Michael Hammer, performing a number of laboratory and computer tasks (e.g. preparation of DNA dilutions, evaluation of DNA sequence variation, etc.) and managing aspects of the daily running of the research group (e.g. student supervision, budgetary matters, product ordering). Applicants should be well-rounded individuals with a genetics background and strong management skills. The position will provide a rewarding career with unique opportunities to the right person.

Duties and Responsibilities:

*Molecular biology: Preparation of DNA dilutions, uni- and multiplex PCR, DNA sequencing, and DNA sequence analysis. Occasional use of robotics may be required, but training can be provided. *Computer work: Data analysis using a variety of software packages. Utilize molecular biology software (e.g. primer design, sequence alignment, database searches, etc.), and analysis of data using in-house software. Basic familiarity with the UNIX operating system is highly desired. *Laboratory management: Order supplies and reagents needed for experiments and data entry of requisitions. Keep track of bookkeeping and laboratory finances. Supervise and train undergraduate students in DNA sequence analysis and basic laboratory techniques. Attend and contribute to weekly research meetings. *Other: Collaborate with other members of the data analysis team both on-site and with collaborating research groups.

Minimum Qualifications:

Research Technician. Bachelor's degree in a field ap-

propriate to the area of assignment; OR, Four years research experience appropriate to the area of assignment; OR, Any equivalent combination of experience, training and/or education.

Research Specialist. Bachelor's degree in a field appropriate to the area of assignment AND two years related research experience; OR, six years research experience appropriate to the area of assignment; OR, any equivalent combination of experience, training, and/or education.

Preferred Qualifications Bachelor's degree in the area of biological sciences (molecular biology, evolution and ecology, genetics, etc.) AND two years of related research experience; OR, six years of appropriate research experience. * Strong leadership and organizational skills. * Demonstrated knowledge of modern research methods in molecular biology. * Excellent communication and reporting skills. * Experience working well in diverse groups. * A genuine interest in the subject matter is highly recommended, although specialty in this field is not required. Related interests may include: bioinformatics, biostatistics, computational biology, population genetics and/or evolutionary biology.

Outstanding UA benefits include health, dental, and life insurance; paid vacation, sick leave, and holidays; tuition reduction for the employee and qualified family members; access to UA recreation and cultural activities; state retirement; and more.

Job Number 35010 Quick Link
www.uacareertrack.com/applicants/-Central?quickFind=183202

-Murray

*** Dr. Murray Cox Arizona Research Laboratories - Biotechnology 1041 East Lowell Street, University of Arizona Bioscience West, Room 246B Tucson, AZ 85721, USA Tel: (520) 621-9791 URL: www.u.arizona.edu/~mpcox/ ***

mpcox@email.arizona.edu mpcox@email.arizona.edu

UGlasgow Biostatistics

UNIVERSITY of GLASGOW

FACULTY OF INFORMATION AND MATHEMATICAL SCIENCES

ROBERTSON CENTRE FOR BIostatISTICS

Senior Research Fellow/Reader 12226/DPF/A3
£33,646 - £43,850 per annum

Research Fellow 12225/DPF/A3 £20,044 - £30,002 per
annum

Biostatistician 12051/DPF/A3 £20,044 - £30,002 per
annum

Applicants for these posts in Biostatistics may have interests in any area of Biostatistics, including Statistical Genetics, Clinical Trials and Statistical Epidemiology. The successful candidates will be expected to have excellent records of academic achievement and a commitment to enhancing the strong research profile of the Centre. Applicants for the post of Senior Research Fellow/Reader will be expected to attract and secure research funding and build a research group in their area of expertise.

Informal enquiries may be directed to Professor Ian Ford (tel 0141-330-4744; email ian@stats.gla.ac.uk). Information on the Centre and the linked Department of Statistics is available on the Web at www.rcb.gla.ac.uk and www.rcb.gla.ac.uk. For an application pack please see our website at www.gla.ac.uk. Applications should be submitted to Ms Liz Anderson, Assistant Director, Robertson Centre for Biostatistics, Boyd Orr building, University of Glasgow, Glasgow G12 8QQ quoting the appropriate reference number. Applications should be received by 16 June 2006.

Catherine Young <c.young@admin.gla.ac.uk>

ULiverpool 2 EcolEvol

Two chairs available at University of Liverpool, UK

Behavioural Ecology/Evolutionary Biology Aquatic Biology

Application procedure: http://www.liv.ac.uk/working/job_vacancies/ School of Biological Sciences: <http://www.liv.ac.uk/biolsci/> Informal enquiries to Head of School of Biological Sciences, Prof. Steve Edwards (biolhos@liv.ac.uk) Closing date 23rd June

Chair in Behavioural Ecology/Evolutionary Biology - B/756

Department: School of Biological Sciences

Job Description: The University is keen to further develop its considerable strengths in aquatic biosciences and behavioural ecology within the School of Biological

Sciences. The School of Biological Sciences (rated 5 in RAE 2001) is the largest department in the University, with 71 academic staff covering the full range of biological sub-disciplines within a single research and teaching organisation (<http://www.liv.ac.uk/biosciences>). The School has recently moved into a new £23M Biosciences Research Building, which provides state-of-the-art laboratories, including a range of core facilities for live cell imaging, proteomics, genomics, cell culture and marine and freshwater aquaria/culture facilities. We are seeking to appoint an exceptional candidate who will help shape the future development of research and teaching of Behavioural Ecology and Evolutionary Biology in Liverpool, fully utilizing the superb research environment that is available. The successful candidate will have an outstanding research and publication record in behavioural ecology and/or evolutionary biology, and research specialisms that complement those of existing staff in the School are likely to be particularly welcome.

Salary: Negotiable

Further details; <http://uniwww.connect.org.uk/jobs/jb311481.html> Chair in Aquatic Biology - B/755

Department: School of Biological Sciences

Job Description: The University is keen to further develop its considerable strengths in aquatic biosciences and behavioural ecology within the School of Biological Sciences. The School of Biological Sciences (rated 5 in RAE 2001) is the largest department in the University, with 71 academic staff covering the full range of biological sub-disciplines within a single research and teaching organisation (<http://www.liv.ac.uk/biosciences>). The School has recently moved into a new £23M Biosciences Research Building, which provides state-of-the-art laboratories, including a range of core facilities for live cell imaging, proteomics, genomics, cell culture and marine and freshwater aquaria/culture facilities. We are seeking to appoint an exceptional candidate who will help shape the future development of research and teaching of Aquatic Biology in Liverpool, fully utilizing the superb research environment that is available. The successful candidate will have an outstanding research and publication record in aquatic biology, and research specialisms that complement those of existing staff in the School are likely to be particularly welcome.

Salary: Negotiable

Further details; <http://uniwww.connect.org.uk/jobs/jb311480.html> Steve Paterson
<S.Paterson@liverpool.ac.uk>

UMuenster EvolBiol

Junior professorship (W1) in Molecular or Experimental Evolution

The Faculty of Biology, University of Muenster, seeks an Evolutionary Biologist working on Molecular and/or Experimental Evolution at the Junior Professor (W1)-level, equivalent to a non-tenure track assistant professorship. The position, allocated at the Institute of Evolution and Biodiversity (IEB, www.uni-muenster.de/-evolution), is funded by the Volkswagen-Foundation initiative "Strengthening Evolutionary Biology in Germany" and starts on October 1st, 2006. Continuation after the initial three years is possible for another three years and depends on external review. Candidates are expected to lead an independent junior group with a strong research program.

Particularly welcome are applicants working on one or more of the following subjects:

- experimental evolution in short generation organisms (e.g., phages, bacteria, protists, unicellular algae, meiofaunal groups)

- molecular evolution of key genes

- population and comparative genomics using experimental and/or computational approaches

The successful candidate must have a PhD or doctorate in a biological discipline. Postdoctoral experience and a strong publication record are expected. The position includes teaching at the undergraduate (Bachelor) and graduate (Master) level in the field of evolutionary biology. To promote exchange of students, all teaching at the graduate level will be in English.

The IEB is equipped with a central molecular genetic laboratory, greenhouses, climate chambers and computational facilities. There will be some base funding, nevertheless the candidate is expected to participate in ongoing collaborative funding efforts of the Faculty of Biology and encouraged to acquire additional extramural funding.

Applications of women are particularly welcome. In the case of similar qualification, competence and specific achievements, women will be considered on preferential terms within the framework of the legal possibilities.

Handicapped candidates with equivalent qualifications will be given preference.

To apply for this position, please send a Curriculum Vitae in English, including a publication list, a summary of scientific achievements, teaching experience, acquired funding and a description of research plans until 10 June 2006 to: Dekan des Fachbereichs Biologie, Westfaelische Wilhelms-Universitaet, Hindenburgplatz 55, D-48143 Muenster, Germany.

Thorsten Reusch <treusch@uni-muenster.de>

UNCChapelHill Tech EvolGenetics

Evolutionary Genetics in the lab of Chris Willett at UNC-Chapel Hill

I am hiring a RESEARCH TECHNICIAN for my lab in the Department of Biology. Position is available this summer (July start preferred); initial appointment for one year (and likely can be extended to two years) with pay determined by experience level.

RESEARCH SUMMARY: My lab is currently focused on studies of speciation and adaptation using the intertidal copepod *Tigriopus californicus*. Experiments concentrate on genetic systems involved in reproductive isolation and their physiological consequences. Lab web page (<http://www.bio.unc.edu/-faculty/willett/>) has more information on research.

REQUIRED EXPERIENCE: A Bachelor's degree in biology or a closely related field and some experience in basic laboratory techniques are required. Additional qualifications desired: experience with molecular biology protocols, experience with handling of organisms, and experience supervising others.

RESPONSIBILITIES: 30% Isolation and molecular analysis of DNA using PCR and other techniques; 20% Physiological assays of enzyme performance in hybrid copepods; 20% Culture maintenance and crossing of copepods; 10% Supervision of undergraduates; 10% Data analysis of results from molecular sequencing; 10% Ordering and laboratory maintenance.

APPLICATION: Please submit a CV or resume, contact information for two references, and a cover letter summarizing your qualifications and interest in the position via email to Chris Willett at: willett4@email.unc.edu. Applications will be evaluated as they arrive.

–Apple-Mail-1-719054126 Content-Transfer-Encoding: 7bit Content-Type: text/enriched; charset=US-ASCII

Evolutionary Genetics in the lab of Chris Willett at UNC-Chapel Hill

I am hiring a RESEARCH TECHNICIAN for my lab in the Department of

Biology. Position is available this summer (July start preferred); initial

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RESPONSIBILITIES: 30% Isolation and molecular analysis of DNA using

PCR and other techniques; 20% Physiological assays of enzyme

performance in hybrid copepods; 20% Culture maintenance and crossing

of copepods; 10% Supervision of undergraduates; 10% Data analysis of

results from molecular sequencing; 10% Ordering and laboratory

maintenance.

APPLICATION: Please submit a CV or resume, contact information for

two references, and a cover letter summarizing your qualifications

and interest in the position via email to Chris Willett

at:

willett4@email.unc.edu. Applications will be evaluated as they

arrive.

UOttawa EvolBiol

Two teaching positions (5-year lectureships with the possibility of becoming permanent) are available in the Department of Biology at the University of Ottawa in Ottawa, Canada. Please Note: contact information for application materials is given below (do NOT send them to me). Individuals who can teach in French are especially encouraged to apply.

Sincerely, Howard Rundle

University of Ottawa / Université d'Ottawa Faculty of Science / Faculté des sciences

Lecturers in the Faculty of Science

With its strategic location at the heart of Canada's capital, its broad variety of teaching and research initiatives offered in the two official languages, the cosmopolitan environment, and its national perspective, the University of Ottawa is truly Canada's University.

The Faculty of Science at the University of Ottawa invites applications to fill eight limited-term lecturers positions starting August 1, 2006 in the areas listed below. The initial appointment is for a period of 3 years, renewable once for 2 years. In the fall of 2010, the University and the Association of the Professors of the University of Ottawa are to conduct a review to determine if these positions are to become permanent. If it is agreed, the individuals initially hired will be able to apply with their prior experience being recognized.

The workload of these Lecturer positions will normally involve teaching, academic service activities, and the expectation of continuing development as an educational professional through scholarly activities. They may have independent responsibilities for designing and teaching courses and laboratories or significant components of courses and laboratories. The salary scale is the same as the salary scale of Assistant Professors. Applicants should hold a doctorate in an appropriate field. Evidence of teaching excellence is required.

Specific details for each position are given below:

Biology (2 positions): The candidate will join a vibrant Department (<http://www.bio.uottawa.ca/eng/welcome.php>) with teaching and research strengths in bioinformatics, cellular/molecular biology, physiology, ecology, and evolution. The Department is also home to interdisciplinary initiatives provided through the laboratory facilities of the Center for Advanced Research in Environmental Genomics (<http://www.careg.uottawa.ca/>). The preferred candidates will have expertise in at least one of the core disciplines within the department (physiology and biochemistry, cell and molecular biology, and ecology and evolution). One of the two available positions must be filled by an individual who can teach in French. Bilingualism is an important asset for the other position. Chair: Dr. Steve Perry (sfperry@science.uottawa.ca)

Information about the Faculty of Science and the Departments can be found at <http://www.science.uottawa.ca/> Applicants should send a curriculum vitae, a statement on teaching excellence, and arrange for three confidential letters of recommendation to be sent to the Chair of the relevant Department (see above). The closing date for receipt of applications is July 15, 2006 or until the position is filled.

Chargés de cours; Faculté des sciences

Son emplacement stratégique au coeur de la capitale du pays, la grande variété de ses programmes d'enseignement et de recherche, offerts dans les deux langues officielles du Canada, sa diversité croissante ainsi que sa perspective nationale font de l'Université d'Ottawa " l'Université canadienne " par excellence.

La Faculté des sciences de l'Université d'Ottawa met au concours huit postes de chargés de cours à durée limitée, débutant le 1er août 2006, dans les domaines indiqués ci-dessous. Le contrat initial est de trois ans, renouvelable pour deux ans. A l'automne 2010, l'Université et l'Association des Professeurs de l'Université d'Ottawa détermineront si ces postes peuvent devenir permanents. Dans l'affirmative, les personnes embauchées initialement pourront poser leur candidature avec leur expérience sur ce poste reconnue.

La charge de travail des chargés de cours impliquera normalement de l'enseignement, des activités de service liées à l'enseignement, et une attente de formation continue en tant que professionnel de l'éducation, par des activités savantes. Ils pourront avoir des responsabilités en toute indépendance, pour enseigner et concevoir des cours et des laboratoires, en tout ou en partie. L'échelle salariale est celle de professeur adjoint. Les candidats ou candidates doivent avoir obtenu un Ph.D. dans la

discipline appropriée, et des évidences d'excellence en enseignement sont demandées.

Des détails spécifiques à chacun de ces postes sont fournis ci-dessous:

— / —

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>

UOxford Volunteer Badger ResAssist

Applications are invited for two 3-month volunteer positions to investigate cooperative breeding and mate choice in the European badger *Meles meles*. Research is office based, commences immediately, and involves behavioural analysis of CCTV footage of two social groups of badgers from Wytham Woods, Oxford. The dedicated volunteers will be trained to score behaviours according to an ethogram and enter data into an MS Access database. The volunteers will work with a team of behavioural researchers and will be based at the Wildlife Conservation Research Unit, University of Oxford. Our offices are in Tubney and transport from/to Oxford city centre can be provided, leaving at 9.15am and returning at 6.30pm.

The successful candidates must be available for at least 3 months (May - Aug 2006), willing to work 10am - 6pm, 5 days a week and have a strong academic interest in behavioural ecology. The volunteers must also be enthusiastic, self-motivated, committed, and based near Oxford, as accommodation unfortunately cannot be provided. However, £1,000 towards costs incurred during the 3 month post will be made.

To apply please email hannah.dugdale@zoo.ox.ac.uk to request a volunteer questionnaire form. Please complete this form and return it ASAP to hannah.dugdale@zoo.ox.ac.uk, along with your CV and a covering letter containing details of 3 academic or professional referees.

Hannah Dugdale Wildlife Conservation Research Unit
Dept of Zoology, Uni of Oxford Tubney House, Abingdon Rd Tubney, Abingdon OX13 5QL

Tel: 01865 393127 Fax: 01865 393101

hannah.dugdale@zoo.ox.ac.uk

han-

nah.dugdale@zoo.ox.ac.uk

USC ResTech ConservationGenet

Laboratory Research Technician, Req #20288 Marine Population and Conservation Genetics University of Southern California, Los Angeles

A full-time research technician position is available in the laboratory of Suzanne Edmands (<http://www.usc.edu/schools/college/faculty/-faculty1003223.html>) beginning as early as June 15. The technician will assist with projects involving the genetics of inbreeding and outbreeding depression using a marine copepod as a model. Specific duties will include maintenance of copepod cultures, morphometric assays, various molecular assays and routine lab management. The ideal candidate would have a bachelor's or possibly master's degree in biology, a strong interest in population genetics/evolution and research experience including molecular techniques such as PCR, DNA sequencing, microsatellites and AFLPs. Specific training will of course be provided. The position is initially for one year but may be extended. Starting salary is \$28-32K.

Please apply via the USC employment website under requisition # 20288: <http://www.usc.edu/bus-affairs/-ers/search.html> Applications should include a cover letter and resume/CV including contact information for three references. For specific questions please contact Suzanne Edmands at sedmands@usc.edu.

Review of applications will begin May 15 and continue until the position is filled.

Suzanne Edmands Associate Professor, Department of Biological Sciences 3616 Trousdale Parkway, AHF 314 University of Southern California Los Angeles, CA 90089-0371 Office: 213-740-5548 Lab: 213-740-9698 FAX: 213-740-8123

sedmands@usc.edu sedmands@usc.edu

USFWS Geneticist

The following position has been announced through USAJOBS: <http://www.usajobs.opm.gov/> Working for

the U.S. Fish and Wildlife Service is more than a career. It is also a commitment—one shared by more than 7,500 men and women representing a diverse range of professions, backgrounds, and specialties who are dedicated to conserving, protecting, and enhancing fish and wildlife and plants and their habitats for the continuing benefits of the American people.

The position is located at the Warm Springs Regional Fishery Center (WSRFC), Warm Springs Fish Technology Center in Warm Springs, Georgia. Incumbent serves as the Southeast Region's aquatic resource geneticist, performing genetic analysis and providing genetics expertise and recommendations to the Director of WSRFC and the Regional Directorate on international, national, and regional issues and policies concerning fish and aquatic organisms. Also serves as the primary liaison to the Fish and Wildlife Service, other Federal and State agencies, Tribal on the application of genetics to propagation, restoration, and conservation of aquatic organisms.

OPEN PERIOD: Wednesday, May 24, 2006 to Wednesday, June 21, 2006

SALARY RANGE: 63,719.00 - 98,500.00 USD per year

DUTY LOCATIONS: 01 vacancies - Warm Springs, GA

PROMOTION POTENTIAL: 13

Connie_KeelerFoster@fws.gov

UWisconsinEauClaire Genetics

Department of Biology

POSITION: Lecturer, Senior Lecturer or Visiting Assistant Professor to teach GENETICS We have an opening for a one-year Lecturer, Senior Lecturer or Visiting Assistant Professor position to teach Genetics in the Department of Biology beginning August 21, 2006.

QUALIFICATIONS: MS or PhD in Biology Preference given to individuals with experience teaching courses in genetics

RESPONSIBILITIES: Applicants will be expected to teach an upper level Genetics course, lecture and lab. The position is a one-year full-time position with 12 contact hours per week. Salary will be commensurate with teaching experience.

DEPARTMENT: The Department of Biology currently has 25 faculty and academic staff and approximately

500 undergraduate majors. The faculty are collegial, dedicated to teaching and are actively involved in research with students. Departmental facilities include a variety of teaching and research laboratories with standard molecular equipment, digital gel imaging systems and a Beckman Coulter CEQ 8000 capillary electrophoresis system. The department also has three greenhouses, an animal care facility, the James Newman Clark Bird Museum and shared access to transmission and scanning electron microscopes.

UNIVERSITY & EAU CLAIRE COMMUNITY: The University of Wisconsin-Eau Claire campus community consists of 10,500 students and 700 faculty and administrative/professional staff. Often described as Wisconsin's most beautiful campus, UW-Eau Claire's campus spans the banks of the Chippewa River in the heart of Eau Claire, western Wisconsin's largest city.

Eau Claire and the surrounding countryside have many scenic rivers, lakes, parks, bike trails and wooded areas where students and community members enjoy seasonal sports and a variety of outdoor recreational activities. It is a community of 60,000 people in a rural landscape, considered safe and affordable with outstanding schools for children and employment opportunities for family members. The Chippewa Valley offers a variety of community and cultural events, has major medical facilities and is within easy driving distance of major medical research centers. We are just 90 miles from Minneapolis-St. Paul, a vibrant cosmopolitan center.

APPLICATION PROCEDURE: Please send a letter of application describing teaching experience, specifically addressing the ability to teach genetics, a curriculum vitae and contact information for at least two references to:

Geneticist Search Department of Biology University of Wisconsin Eau Claire, Wisconsin 54702-4004

Contact Dr. Julie Anderson at anderju@uwec.edu with questions about the position or application process. The university reserves the right to contact additional references and applicant names are subject to public release unless confidentiality has been requested in writing. Names of all finalists must be released. We are an AA/EEO employer and encourage a diverse applicant pool to apply.

Chris H. Floyd, Ph.D. Assistant Professor Department of Biology Phillips Hall 354 University of Wisconsin-Eau Claire Eau Claire, WI 54701 Phone: 715-836-4163 Fax: 715-836-5089 floydch@uwec.edu

floydch@uwec.edu

WashingtonStateU LabManager

POSITION DESCRIPTION

Title: Laboratory Manager/ Technician

Location: School of Biological Sciences, Washington State University

Full-time, Grant funded, 1 year, renewable up to 3 years; Start Date: July or August, 2006

Salary commensurate with experience, including a full benefits package

DUTIES AND RESPONSIBILITIES: Laboratory manager in an evolutionary population genetics laboratory. The employee will work on a state-funded project to understand the effects of different timber harvest practices on amphibian population genetic variation and population structure.

Perform DNA extraction, quantification, PCR, real-time PCR, and microsatellite analysis. Perform population genetic analyses of data and maintain database. Prepare and/or review complex written progress reports concerning studies including assembly, organization, and interpretation of data and presentation of data to the lab group and/or the State of Washington. Responsible for laboratory maintenance and organization. Responsible for ordering and stocking supplies and maintaining order files for population genetics laboratory. Perform basic bookkeeping duties through use of spreadsheets to track laboratory expenditures and budget balances. Direct the work of undergraduate research associates.

Minimum Qualifications: Bachelor's Degree in an appropriate field of technology or science such as Biological Sciences, Molecular Biology or Genetics, PLUS one year of research experience OR one year of full-time post-baccalaureate college in an appropriate field of science or technology. MS Degree preferred. Experience with microsatellites is required. Professional level experience may be substituted, year-for-year, for the formal academic degree.

To Apply: Please send a letter of application outlining appropriate research experience, curriculum vitae, and the names and contact information for at least 3 references by June 13, 2006 to (email is preferred):

Andrew Storfer School of Biological Sciences Washington State University Pullman, WA 99164-4236

Email: astorfer@wsu.edu Phone: (509) 335-7922

WSU employs only U.S. citizens and lawfully authorized non-U.S. citizens. All new employees must show employment eligibility verification as required by the U.S. Citizenship and Immigration Services.

WASHINGTON STATE UNIVERSITY IS AN EQUAL OPPORTUNITY/AFFIRMATIVE ACTION EDUCATOR AND EMPLOYER. Members of ethnic minorities, women, special disabled veterans, veterans of the Vietnam era, recently separated veterans, and other protected veterans, persons of disability, and/or persons age 40 and over are encouraged to apply.

astorfer@mail.wsu.edu

WashingtonStateU PopGenet LabTech

POSITION DESCRIPTION

Title: Laboratory Manager/ Technician

Location: School of Biological Sciences, Washington State University

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Minimum Qualifications: Bachelor's Degree in an appropriate field of technology or science such as Biological Sciences, Molecular Biology or Genetics, PLUS one year of research experience OR one year of full-time post-baccalaureate college in an appropriate field of science or technology. MS Degree preferred. Experience with microsatellites is required. Professional level experience may be substituted, year-for-year, for the formal academic degree.

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astorfer@mail.wsu.edu

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ABI3130 costs

Our department has recently purchased an ABI 3130xl for DNA sequencing and fragment analysis. We expect that our usage of the instrument will vary, and there may be some weeks where it is only needed for a few runs. Given that, we would like to minimize our costs for consumable reagents, particularly polymer. ABI suggests changing any polymer bottle that has been on the instrument more than a week. Has anyone tried running the instrument with older polymer? If so, how old? Any adverse effects on the data or the instrument? Also, any other tips for saving on reagents during periods of inconsistent use would be greatly appreciated.

Thank you,

Dan Sloan Graduate Student Biology Department University of Virginia

dbs4a@virginia.edu

ARGOS costs

Dear all, can anyone give me a cost estimate of running an ARGOS transmitter on an animal? This is, the pure satellite-related costs, not the transmitter? Thanks, Stefan.

* Stefan Klose School of Integrative Biology University of Queensland, Goddard 317 Brisbane QLD 4072, Australia Fon: +61 7 3365 7591, Fax: Ext. 1655 Mobile: +61 406 334693 stefan.klose@uni-ulm.de www.evophys.com Skype: sklose1

Home affiliation: Department of Experimental Ecology (Bio III) University of Ulm Albert Einstein Allee 11 D-89069 Ulm, Germany Fon +49 731 50 22661 Fax +49 731 50 22683

* Peace Nobel Lecture 2005 - Mohamed ElBaradei: <http://nobelprize.org/peace/laureates/2005/-elbaradei-lecture.html> 'Imagine that such a world is within our grasp.'s.klose@gmx.de

s.klose@gmx.de

Arlequin question

Subject: Arlequin.question

Hi all

Have a question about the Arlequin program. Can you use allele frequencies only (or fq values converted to numbers); without genotype or haplotype data to estimate Fst's? In the manual it looks if you can do that but when I try to the program gives me an error.

I pasted my input file below. You will see I converted my fq to numbers and standard data, because in the fq format it gives the same error. (I use the newest version of Arl) . So, when I do a run with this input file; the settings under Pop comparisons are Copute Slakins Fst and I tried the "use conventional Fsts" (which the manual specifies that I must use in my case) and the other two options but all gives the following error:

```
#[ERROR # 1] : unable to read genotype frequency
#[ERROR # 2] : unable to read sample data
```

So to me it looks like Arlequin cannot compute Fst's from fq data only, the program looks for the extra file in which your haplotype/genotype data is usually stored if you're working with raw data. Am I correct or is there a way to estimate Fst's from fq data only?

Thank you

Carina

cshlebu@yahoo.com

#Arlequin input file

[Profile]

NbSamples=8

DataType=STANDARD

GenotypicData=1

GameticPhase=0

LocusSeparator=WHITESPACE

RecessiveData=0

MissingData='??'

[Data]

[[Samples]]

SampleName="Population SA White"

SampleSizeb7

SampleData= {

n00 123

n01 135

n02 86

n03 150

n04 133

{

SampleName="Population SA Bantu-speakers"

SampleSizea4

SampleData= {

n00 134

n01 122

n02 105

n03 150

n04 103

}

SampleName="Population SA Coloured"

SampleSize'2

SampleData= {

n00 134

n01 136

n02 93

n03 150

n04 89

}

SampleName="Population SA Indian"

SampleSizef6

SampleData= {

n00 134

n01 140

n02 101

n03 150

n04 141

}

SampleName="Population Beninese"

SampleSizeb8

SampleData= {

```

n00 138
n01 109
n02 105
n03 150
n04 126
}
SampleName="Population Cameroonian"
SampleSizeG5
SampleData= {
n00 107
n01 90
n02 72
n03 118
n04 88
}
SampleName="Population Congolese"
SampleSizeP1
SampleData= {
n00 113
n01 97
n02 74
n03 125
n04 92
}
SampleName="Population Pygmy"
SampleSizeA0
SampleData= {
n00 111
n01 67
n02 55
n03 111
n04 66
}
Carina.Schlebusch@nhls.ac.za

```

Asian Nicrophorus samples

Dear EvolDir members,

I am a Phd. student studying the biogeography of a group of Nicrophorus (Coleoptera: Silphidae) from the Asia/Australasia region. I am desperately trying to obtain specimens from Sumatra, Indonesia and Guadalcanal, Solomon Islands for DNA work. I am also interested in specimens from Taiwan, Vietnam, Laos, and the Philippines. If anyone is collecting in these regions, or knows of contacts, I would be extremely grateful for your collaboration.

Please reply to tmousseau@ucalgary.ca

Thanks for your help,

Tonya Mousseau

Tonya Mousseau Division of Zoology Department of Biological Sciences University of Calgary Calgary, AB T2N 1N4

Phone: (403) 220-8436 Email: tmousseau@ucalgary.ca
Email: tmousseau@ucalgary.ca

BeeDNA from Honey

Has anybody ever (successfully) tried to isolate the DNA of the bee from honey samples? If so, I would be very grateful to learn about your experiences. (I am a trained botanist and happend to work in a bee project.)
Nikolaus Hoffmann

[nikolaus.hoffmann <nikolaus.hoffmann@gmx.at>](mailto:nikolaus.hoffmann@gmx.at)

Biodiversity texts

Hi,

In a moment of insanity, I volunteered to develop and teach a new course for first year students (primarily aimed at non-majors) on the Evolution and Diversity of Life on Earth. The primary impetus is a growing realization that the current generation of students are growing up in an increasingly urban environment and have little or no appreciation for the vast diversity of living organisms that we are rapidly driving to extinction. My original plan was based loosely on Margulis et al., "The Illustrated Five Kingdoms", which is, well,

a coloring book. That in itself is not a problem with me, but it is organized ecologically, and my preference is a phylogenetic approach. I now need to decide on a textbook, and other resources to offer the course for the first time next fall. Has anyone out there developed such a course? Do you have any suggestions for useful texts and other resources? Any suggestions for how to approach such a course would be very much appreciated.

Sincerely, Andy Beckenbach Simon Fraser University
beckenba@sfu.ca

“Andy T. Beckenbach” <abeck@menten.mbb.sfu.ca>

Chicken data

Hi all,

We are a team that wants to develop a statistical procedure based on Bayesian Segregation and Linkage analysis to determine Major Genes affecting chicken production traits. This procedure has so many benefits that there is not any space to explain all of them. We are seeking some information for our project. We are requested all of the scientists and commercial chicken production companies to give necessary information. We will promise to share all of our findings and include their names in all of our publications.

Data specifications:

- 1- Phenotypic records for pedigreed populations for many (at least 10) generations.
- 2- Preferably, data would be related to commercial pure lines.
- 3- Molecular data (based on microsatellites, many and full coverage of the genome) for last two (GP and P) generations along with same phenotypic data.

If any further information are needed, please contact us.

With best regards,

S. Alijani & N. Pirany

– Nasrollah Pirany Assistant Professor University of Tabriz Faculty of Agriculture Dept. of Animal Science 29th Bahman Bolvard, East Azarbaiejan, Tabriz, Iran. Phone (Office):+98-411-3392060- Mobile:+98-9144177930

npirany@gmail.com

DNA extraction

Dear evoldir members,

I am looking for a DNA extraction protocol, either a kit or method, to extract from pine wood. I try to use the Quiagen DNeasy 96 tissue kit normally used for DNA extraction from tissues. But this was not be efficient .

Does anyone have some experience with this type of problem? Any other suggestions of good extraction protocols or DNA separation methods would also be appreciated.

Thank you all,

Pascal ASPE

Pascal.Aspe@orleans.inra.fr

DNA extraction in Solen

Dear evoldir members,

I have problems with DNA extraction too. Im working on the razor clam Solen marginatus. I have tried several methods and from different fresh tissues but the DNA is always degraded (I only got smear at the bottom of each lane). I have some experience working on the DNA of bivalves but I have never found something like this, it seems that there is something that degrades the DNA of this species. Does anyone know what could it be?

Thank you,

Miguel Angel Varela Muiño

mvarela@udc.es

DNAsampling HumanPopGenet

BEGINNING OF MESSAGE

RE: DNA SAMPLING STRATEGIES IN HUMAN

POPULATION GENETICS

Dear all,

We are thinking to organize a special session focussing on DNA SAMPLING STRATEGIES in human population genetics studies, being the session within a population genetics conference (3rd DNA POLYMORPHISMS IN HUMAN POPULATIONS likely to be held in Paris at the end of the year).

Possible issues can be: How many samples? Different strategies with different markers (mtDNA, Y-chromosome, autosomal markers)? What geographic resolution? What is the ideal case? What kind of sampling design should be absolutely avoided? Sampling and time-depth of markers: a same sampling with fast-mutating markers and with slow-mutating markers? Linguistic classifications? Ethnological classification? Ethical concerns How to mention the sampling in publications (longitude-latitude, linguistic classification, ethologic classification, etc)?

We are thinking to such a session because the literature on the subject is limited and we feel that there is a lack of investigation on this methodological issue that, to tell the truth, is the base of our articles.

We welcome any member of Evoldir able to contribute REFERENCES, suggest experts or provide suggestions concerning the points stated above. If you are the author of an important article focusing on DNA sampling strategies we may invite you in Paris for the conference. We stress that such call just concerns the SAMPLING since a further, more general, call for abstracts will follow later.

Best regards to all,

Please reply to:

Franz Manni Musée de l'Homme Paris manni@mnhn.fr

END OF MESSAGE

Dr. Franz Manni Maître de conférences / Lecturer
UMR 5145 - Eco-Anthropology Group National Museum of Natural History MNHN - Musée de l'Homme
17, Place du Trocadéro 75016 Paris - France Tel. 0033 1 44 05 72 84 Fax. 0033 1 44 05 72 41 Telex Musethno

Franz Manni <manni@mnhn.fr>

would appreciate it. I am looking for good data on 1. The distribution of allelic effects of new mutations in a known gene (presumably measured as mean effects, but I'd be interested in any other good measures that have been used) on some measured phenotype. I'd be interested in references to data sources, especially from naturally occurring organisms. I'm aware of many human disease gene data bases, which are useful except that they usually only include patients, and hence not all the naturally occurring mutations, and they only include those instances of a mutation that came to clinical attention.

2. Direct data on the empirical distribution of fitness effects of new mutations, studied in relation to a specific phenotype. I am aware of the extensive literature on indirect measures like Ka/Ks ratios and other indicators derived from genomic scans. I have John Endler's 1986 book on selection in the wild, but am in search of systematic studies that may have been done that have assessed fitness in relation to known mutations, and especially where multiple individual mutations are known for the same gene or trait. Data on any eukaryote species, including domestic or laboratory species would be of interest.

I know there is a large scattered literature on individual examples, but am trying to learn of systematic data that may exist.

Any comments or assistance would be appreciated. If I'm just highly ignorant of a large systematic literature, I'd be delighted to have my ignorance pointed out.....if you can do it politely!

Thanks for anyone who can help.

Ken

Kenneth M Weiss, PhD Evan Pugh Professor of Anthropology and Genetics Professor of Biology Department of Anthropology Penn State University 409 Carpenter Bldg University Park, PA 16802-3404

Phone: 814.865.0989 (office) 814.237.9405 (home)
Fax: 814.863.1474 Email: kenweiss@psu.edu
(old ID kmw4@psu.edu, still works) Web page:
<http://www.anthro.psu.edu/weiss.lab/index.html>
kmw4@psu.edu

Data on new mutations

Dianthus specimens

This may be a tall order, but if any readers can help I Dianthus samples

Dear EvolDir readers,

As part of my PhD project I am investigating the evolutionary radiation and diversification of the genus *Dianthus* (Caryophyllaceae). I will attempt to address diversification at the morphological and molecular level. At the morphological level I will be looking at nectar tube lengths and various pollination strategies. At the molecular level I will be constructing evolutionary trees from DNA markers. This will contribute to information present on this taxonomically difficult genus.

As *Dianthus* species occur in many countries it is not possible for me to visit every one to collect. I was wondering if anyone has any *Dianthus* specimens or know of recent herbarium specimens that may be available for my project.

Any help is greatly appreciated.

Best wishes, Samantha Wilkinson

Real Jardin Botanico de Madrid (CSIC) Plaza de Murillo 2 28014 Madrid España

wilkinson@ma-rjb.csic.es

Drosophila distribution maps

Hello all,

Does anyone know of species distribution maps for *D. pseudoobscura*, *D. persimilis*, *D. miranda*, and *D. athabasca*? Thus far, I have only found an older map in a book by Dobzhansky and Epling entitled "Contributions to the genetics, taxonomy, and ecology of *Drosophila pseudoobscura* and its relatives".

Thanks! Sam Yeaman

yeaman@zoology.ubc.ca yeaman@zoology.ubc.ca

European meadow grasshoppers

European meadow grasshoppers wanted. As I am writing a masters thesis about the meadow grasshoppers of Europe (Orthoptera: Acrididae) I will appreciate any voucher material collected in eastern or western Europe. Specimens should preferably be killed and preserved in 96% ethanol (or 70% if 96% is not available).

I am especially interested in specimens from the genus *Chorthippus*, *Omocestus*, *Sphingonotus* and *Oedipoda*, but other genera are also welcome. Please contact me for more information. I will really appreciate any submissions.

Sincerely, Carsten Kirkeby, University of Copenhagen, Denmark.

Carsten Kirkeby <ckirkeby@gmail.com>

Evol psychology

Dear colleagues,

I'm writing a chapter on how evolutionary psychology is conducted and perceived, and I've only gathered data on perceptions of the field via informal conversations. Thus, I'm very curious to learn what members of evoldir think of evolutionary psychology.

I would really appreciate it if you would send me an email indicating whether evolutionary psychology has proven to be helpful to your understanding of human behavior, and why or why not. I'd love to hear your thoughts on either side of this issue, even if it's just a two-word response.

Assuming sufficient interest, I'll create a table that summarizes the type and frequency of responses to this question, and post it to the list.

Best regards,

Bill

Bill von Hippel <w.vonhippel@unsw.edu.au>

EvolMeeting Registration

Could you please post this on evoldir, if you feel it is relevant?

Dear Evoldir members,

I am not able to attend the upcoming Evolution meetings in Stony Brook, NY. I am unable to get reimbursed by the meeting, but AM able to transfer my registration to another attendee. If you (or anyone you know) has not yet registered for "Evolution" but plans on at-

tending... please contact me for a registration slot, pay me for registration, and save yourself a late fee of 50 additional dollars.

Thank you! N.Martin nhmartin@uga.edu

Evolution schmevolution

All,

I'm looking for tapes, dvds or transcripts of the Jon Stewart/Comedy Central series on "evolution, schmevolution," which aired last year during the Dover, PA trial on Intelligent Design.

Believe it or not, this is for a book chapter on science, philosophy and pop culture. Any pointers would be appreciated, and of course I would pay for copying and shipping of the material.

Thanks much, Massimo Pigliucci

Dept. of Ecology & Evolution SUNY-Stony Brook, NY
massimo.pigliucci@stonybrook.edu

F Jacob quotation

I have been trying with limited success to locate the precise wording of, and citation for, a quotation attributed to Francois Jacob that I have always liked. The paraphrased version of the quote I heard was:

There are really only three questions in biology: how does it work? how does it develop? how does it evolve?

The closest version I have unearthed mentions only two questions:

"How does it work?, Where does it come from?" (p. 31, Jacob, F. 1982. *The Possible and the Actual*. The Jesse and John Danz Lectures. Parthenon, New York)

I would be grateful for any leads to the three-question version, or, alternatively, any assurances that I am on a wild (Canadian) goose chase and should remain content with the two-question version.

Regards, Rich Palmer –

A. Richard Palmer Systematics and Evolution Group
Department of Biological Sciences University of Alberta

Edmonton, Alberta T6G 2E9 CANADA phone: (780) 492-3633 message: (780) 492-3308 FAX: (780) 492-9234

<http://www2.biology.ualberta.ca/palmer/palmer.html>
(biological asymmetries, software, course notes)
Chair, Comparative Morphology & Development section,
Canadian Society of Zoologists. For info.
see: <http://www.biology.ualberta.ca/CMD/home.htm>
rich.palmer@ualberta.ca

FIS calculations

At the request of many Evoldir members, I will summarize the responses to my original inquiry, which was:

>Does anyone know of a program that will give confidence intervals >from bootstrapping over loci for F-IS, separately for every >population? > >I would like to compare F-IS values among populations for >microsatellite data. Most programs calculate only one overall F-IS >value for the entire set of populations. > >It would be tedious to create a set of single population input >files, and then analyze them separately. Although I have not >explored it thoroughly, I know that even this option will not work >in some cases. (Some programs will not calculate any F statistics >at all for an input file that has only one population.)

I would add two additional notes: First, in case the original posting was not clear, the specific goal is to have confidence intervals for F-IS for each individual population. Without these, one cannot say with any statistical certainty whether one population has more or less inbreeding than another population.

Second, most software programs test the null hypothesis of no population structure by permuting individuals, genotypes or gene copies over populations. (Or some similar "exact test".) But 1) this method does not provide confidence intervals, and 2) strictly speaking, I believe that permutation approaches do not test the same hypothesis as bootstrapping or jackknifing over loci (when multiple loci are available). I will leave a discussion of that distinction for someone to pick up in another thread...

Please email the group if there are any major corrections to the summary below.

Programs that will calculate population-specific CIs for F-IS: - - - - -
- GDA (<http://hydrodictyon.eeb.uconn.edu/people/plewis/software.php>) Will bootstrap over loci to gen-

erate confidence intervals. To get population-specific F-IS values in each population, exclude all but one population in the Misc menu. Very intuitive interface and menu system.

GENETIX <http://www.genetix.univ-montp2.fr/-genetix/genetix.htm> Will both bootstrap over loci and perform permutation analyses for F-IS values in each population. The software is in French, so get out your dictionary if necessary. In the FSTATS menu, TEST SUR FIS and choose the bootstrap or permutation option. You can choose all populations as well as all loci separately.

SPAGeDi <http://www.ulb.ac.be/sciences/ecoevol/-spagedi.html> I am told that this program will perform the desired analyses, but I have not verified this. The manual mentions one-delete jackknife procedures for estimating confidence intervals, but does not mention bootstrapping,

Programs that will not calculate population-specific CIs for F-IS: - - - - - FSTAT <http://www2.unil.ch/popgen/software/fstat.htm> TFPGA <http://www.marksgeneticssoftware.net/tfpga.htm> These two programs will calculate significance for overall F-statistics by bootstrapping over loci. However, they will not calculate locus-specific F-IS confidence intervals. They will not perform these calculations on a file with only one population.

GENEPOP ON THE WEB <http://wbiomed.curtin.edu.au/genepop/> Calculates overall and locus-specific F-IS values, but does not specifically test the significance of F-IS, or provide confidence intervals. (Options 1, 5, 6) Significance is assessed with permutation tests.

ARLEQUIN 3 <http://cmpg.unibe.ch/software/-arlequin3/> Runs permutation tests for an overall F-IS. Does not calculate locus-specific F-IS values. Does not bootstrap over loci. Laurent Excoffier has told me that the next version (late June) will compute FIS for each population, and test it by permutation, but no bootstrap CI will be provided.

Andy Bohonak -

Andrew J. Bohonak Associate Professor

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

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

bohonak@sciences.sdsu.edu

bo-

honak@sciences.sdsu.edu

Fluorescent mini probes

Hi, can anyone recommend a kit for fluorescently tagging minisatellite probes for routine size screening (i.e. not mapping studies)? I would rather avoid having to use radioactivity. I will of course post a compilation of replies. Thanks in advance, Bill

Dr Bill Hutchinson Genome Analysis Suite Manager Molecular Ecology & Fisheries Genetics, Biological Sciences, Hull University, HULL HU6 7RX United Kingdom

Tel:- 01482 465804 office 01482 465536 lab Fax:- 01482 465458 <http://www.hull.ac.uk/biosci/-staff/hutchinson.html> <http://www.hull.ac.uk/-GAS/> <http://www.microchecker.hull.ac.uk/> w.f.hutchinson@hull.ac.uk

Forensic medicine software

HI everyone, I was wondering if anyone could suggest any freely available software for studies of forensic medicine (to estimate population allele freqs, HWE, LD, paternity tests etc.) like DNATYPE which I haven't been able to get hold of. cheers Andrea

PER FAVORE RISPONDETE A QUESTO EMAIL verardino@gmail.com PLEASE REPLY TO THIS EMAIL verardino@gmail.com POR FAVOR CONTESTAR A ESTE EMAIL verardino@gmail.com

Dr Andrea Verardi Dipartimento di Genetica e Biologia Molecolare Università La Sapienza Roma mobile (+39) 340 97 17 555 email verardino@yahoo.com

andrea verardi <verardino@yahoo.com>

Gene deletion question

Dear All, This question was posed to me, and I have

no answer. I am hoping somebody out there may have an explanation.

There is a gene present in amphioxus, mouse, dog and humans. However, this gene is not present in zebra fish and chicken.

Any possible explanation for this phenomenon ?

Thanks

Sammy Aggrey, PhD Associate Professor Quantitative & Molecular Genetics/ Bioinformatics

Department of Poultry Science & Institute of Bioinformatics The University of Georgia Athens, GA 30602-2772

voice: 706-542-1354 Fax: 706-542-1827 Lab: 706-542-0295

“If we knew what we were doing, it wouldn’t be called research, would it ?” Albert Einstein:1879-1955

saggrey@uga.edu

GeneClean alternatives

Dear all,

Does anyone recommend a kit (with spin columns) to purify genomic DNA that ISN'T a Qbiogene GeneClean product, but contains glassmilk?

We have been using the Qbiogene (now MPBiomedicals) GeneClean Turbo kits to purify extracted genomic DNA following a phenol/chloroform procedure on fungal/oomycete-infected plant material. The kits provide glass milk-containing spin columns and two binding salt formulations - one for DNA fragments <3kb (ie. pcr products) and another for genomic DNA. I assume the difference in formulations is necessary. However, while they provide enough salt solution for PCR/fragments for the entire kit, they only provide 1/4 of the necessary 'GNomic' solution.

Qbiogene used to provide upon request extra bottles of the gnomic salt solution, to make full use of the kit, but now MPBiomedicals is refusing to do the same, won't sell them separately, and seems confused by our needs. I'm desperate to find an alternative kit that won't slow our extractions throughput (home-made glass milk might be too cumbersome) or compromise our DNA quality.

I'm extremely grateful for any comments or recommen-

dations. If i receive such I would be happy to repost them to the list.

cheers, ~a

– Amy Smith masmith@nature.berkeley.edu Environmental Science, Policy and Management 137 Mulford Hall - #3114 UC Berkeley Berkeley, CA 94720-3114 510-643-4282 (tel) 510-643-5436 (fax) <http://nature.berkeley.edu/garbelotto/english/index.php>

GeneDropping in GD

Dear EvolDir Members,

I am a PhD student at the University of Otago in New Zealand. I am investigating inbreeding and the losses of genetic diversity (GD) using molecular and pedigree methods. I am particular interested in whether species which have historically gone through severe bottlenecks and already have low GD, have a slower rate of further loss of GD (due to inbreeding or further bottlenecks) relative to species that have only experienced recent bottlenecks.

I have applied the pedigree method of gene-dropping (using PM2000) to investigate the relative losses of GD due to pedigree structure (in a genetically depauperate endangered bird, the takahe). As you may know, gene-dropping involves assigning two unique alleles to each founder, and performs simulations to estimate the relative loss of overall GD in the descendent popn. based on a given pedigree. I am interested in knowing whether it would be worthwhile to estimate the absolute losses using real microsatellite gene frequencies from the founder population and the descendants, after 7 regenerations of moderate inbreeding.

It is unclear whether we would expect any substantial differences between the relative losses (as measured by gene-drop) and absolute losses of GD. Is anyone aware of any studies that have investigated this question using genedropping?

Does anyone know of any software that will allow me to manually set the initial starting allele frequencies or genotypes for a genedrop analysis?

Thank you,

Catherine Grueber gruca565@student.otago.ac.nz

– Catherine Grueber, PhD candidate Email: gruca565@student.otago.ac.nz

Department of Zoology University of Otago PO Box 56
Dunedin New Zealand

Insect Sperm Sterilization

Dear All,

I am trying to find a method to sterilize honey bee sperm without affecting their mobility before artificial insemination. I am grateful for any kind of advice that you can give me, but particularly practical solutions from people in the Southeastern USA (North Carolina, anyone?) would be greatly appreciated.

Thank you,

Dr. Olav Rueppell Assistant Professor Department
of Biology, University of North Carolina, Greensboro
olav_rueppell@uncg.edu

Olav Rueppell O_RUPPEL <olav_rueppell@uncg.edu>

InsectDNA preservation answers

A few weeks back I asked about the use of propylene glycol (nontoxic, not flammable) to preserve insect tissues for DNA work. Thanks to all those who replied. Below I include a summary of the replies (after the original post) including a summary of my own results using my own focal group - silphid beetles.

The short answer is that there were few replies but most were positive about the value of PG.

ORIGINAL POST:

This paper recent paper on the use of 100% propylene glycol for preservation of spiders for later DNA extraction is exciting because propylene glycol is non-toxic (it's a food additive) and thus can be safely mailed and carried on planes etc. It effectively dehydrates the tissues.

The effects of preservatives and temperatures on arachnid DNA Author(s): Vink CJ, Thomas SM, Paquin P, Hayashi CY, Hedin M Source: INVERTEBRATE SYSTEMATICS 19 (2): 99-104 2005

I'd like to know if anyone has additional experience with this method of preservation. The authors used spiders

so one might assume the method would work for all arthropods - has anyone used it with insects?

I wonder specifically if larger bodied insects might not preserve as well in PG as in ethanol if the ethanol penetrates the tissues to dehydrate them faster than PG.

I'd also like to know if propylene glycol is a viable long-term alternative to high-grade ethanol for specimens stored at -80C.

Finally, I'm curious if there are any issues with DNA extraction - does the PG need to be thoroughly removed from the specimen for successful extraction? and if so, how is this done?

I'll collect replies off-list and summarize them for a later posting.

Thanks!

-Derek Sikes

REPLY 1:

Hey Derek

If you take a closer look at the paper, you will see that not only spiders were used, but also scorpions. And these were quite large scorpions. That may partly answer you questions. Just keep in mind that these results were for a month only of preservation. The longer term paper is coming along!

Cheers

Pierre

REPLY 2 (in part)

I was just going to follow what they did in the paper, that is to transfer the specimens back to ethanol, keep overnight in a refridgerator and then proceed with the extraction the next day as usual. I would normally transfer leg from ethanol to deionized water, let sit for about 20 minutes then dry out on kimwipe and proceed to extraction.

REPLY 3

Hi Derek,

Just to update you - I received my spiders in propylene glycol, transferred whole specimens to ethanol overnight at 4 degrees (in fridge). The next day I used 2 legs from each specimen, dried the legs on kimwipes before adding to lysis buffer (Qiagen-DNeasy kit) and extracted DNA as usual.

The results from my PCR using both mitochondrial COI primers and those for a single-copy nuclear locus were excellent for all specimens. Thus, it seems at least for spiders, the propylene glycol is not a problem if you transfer to ethanol for 24 hrs and dry out prior to ex-

tracting. Of course my specimens were only collected days earlier so it was very good starting material.

Anyway, hope this is helpful.

Take care,

Jessica Garb

Jessica E. Garb Post-doctoral Researcher Biology Department 900 University Avenue University of California Riverside, CA 92521 USA Ph: 909-787-7323 Fax: 909-787-4286

REPLY 4

Hello Derek Unfortunately we didn't include the specimens preserved in propylene glycol for our long term (1 year) storage experiment - we didn't expect propylene glycol to work so well. However, I see no reason why propylene glycol wouldn't be fine for long term storage provided they are kept at -20 or -80, which improves long term storage significantly. Propylene glycol does, however, shrivel soft tissue (eg genitalia).

The large scorpions we used were quite water-tight but there seemed to be no problem in the propylene glycol penetrating their tissues. We euthanized them by freezing to ensure they they didn't close their oral, anal and respiratory openings. Whenever I preserve any large or water-tight arthropods (eg weevils) I tend to pull off a leg or two and/or dissect/cut it to make sure the preservative reaches all the tissues.

Before DNA extraction of propylene glycol preserved specimens we transferred them to 95% EtOH for one day at 4 C (see Methods, Specimen preservation, 5) - this allowed the specimens to be dried prior to extraction.

Hope this of use.

cheers Cor

Cor Vink Scientist Biocontrol & Biosecurity AgResearch PO Box 60 Lincoln 8152 New Zealand

REPLY 5

Dear Derek

I did some assays with PG as a fixative several months ago. I used ascidian tissue and three fixation procedures: ethanol, ethanol plus change to PG after 3 days, and PG directly.

I extracted and sequenced the samples after ca 4 weeks, and sequenced a fragment of COI. In short, the best results were with the samples fixed in ethanol, the ones fixed in ethanol and afterwards

— / —

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>

Journal publishing

I'm forwarding this message that might be of your interest:

Carl Bergstrom (UW) has done a study of the cost effectiveness of journals; something to keep in mind when choosing a journal along with circulation and citation frequencies, etc. Go to his website and follow the links.

<http://octavia.zoology.washington.edu/publishing/>

Then consider punishing the costly journals by denying them your publications.

—

Daniel.Montesinos@uv.es www.danielmontesinos.es

Centro de Investigaciones sobre Desertificación-CIDE (CSIC-UV-GV) Camí de la Marjal, s/n <> 46470 - Albal <> València (Spain) Tel:(+34) 96 122 05 40 Fax:(+34) 96 127 09 67

Daniel Montesinos <Daniel.Montesinos@uv.es>

Live tortoise beetles

Hello-

I write to ask if anyone on the list is maintaining colonies of tortoise beetles, or knows of reliable suppliers that are maintaining tortoise beetle colonies (as unlikely as that possibility may be).

I'm looking for either the mottled tortoise beetle, *Deloyala guttata*, or the golden tortoise beetle, *Charidotella* (aka *Metriorhina*) *bicolor*.

Please respond to me directly; if there is sufficient interest, I'll post a summary of the responses I get.

—

John Stinchcombe Department of Botany University of Toronto, 25 Willcocks St. Toronto, ON Canada M5S 3B2

416-946-5986

<http://www.botany.utoronto.ca/ResearchLabs/-StinchcombeLab/> stinchcombe@botany.utoronto.ca

Long PCR protocol

Dear EvolDir Members,

Does anyone recommend a reliable protocol to set up long PCR on plant genomic DNA?

Thanks in advance,

andrea

Dr Andrea Carboni

ISCI - CRA Institute for Research on Industrial Crops Plant Breeding and Biotechnology Section via di Corticella, 133 - 40128 Bologna, ITALY E-mail: a.carboni@isci.it

a.carboni@isci.it a.carboni@isci.it

Microscope cameras

Hi all,

I am looking for advice about digital cameras for use with microscopes (with a C-mount for the lens). I am planning to use it to measure length traits on fruit flies and I don't know what sort of resolution will be sufficient and what sort of price to expect.

I have a quote from "Imaging Source" for a 1/3" CCD camera with 1024 x 768 pixels for USD \$695...is this sufficient/overkill for my needs? We already have a mount for the microscope and just need the camera.

Many thanks,

Sam Yeaman

yeaman@zoology.ubc.ca

ModelTest problems

I ran model test and the results for my rate matrix are

a bit troubling. my C-G rate was 0.0000 and Paup will not let me execute my data matrix because of this. Has anyone ever run into this before?

These are nematode ND4 and CO1 genes My other rates were as follows: A-C= 0.7366 A-G .6074 A-T= 1.7570 C-T= 9.4698 G-T= 1.0000

Thanks

Anson Koehler Department of Biology University of New Mexico Albuquerque, NM 87131

anson76@gmail.com

MultAlin Vs Sequencher Alignment

Dear EvolDir Members,

I have run into a snag while designing some primers. In comparing the alignments given by the Sequencher (software) and by MultAlin (online), I always receive different alignments for the same sequences. I was wondering if anyone knew how these two programs put gaps into their sequences? Which alignment is most correct? Which gaps do I believe? Perhaps there is a way to check against the protein sequence? however I am looking outside the coding region, so this may not be that helpful.

Any ideas would be much appreciated, or if anyone knows a definitive answer as to which program gives the most consistent, accurate multiple-species sequence alignment, that would be most helpful!

Thanks in advance for your time and help.

Shauna Kanel skanel@ucsd.edu

University of California, San Diego Department of Biology Center for Conservation and Research for Endangered Species Molecular Genetics

Shauna Kanel <skanel@ucsd.edu>

Mutation frequencies program

Dear All, Is anyone aware of a program that will compute the relative frequencies of specific mutations (ie GC->AT) for aligned DNA sequences (with or without a treefile)? Thanks, Miriam Barlow

mbarlow@ucmerced.edu

Miriam Barlow <mbarlow@ucmerced.edu>

Neotropical Raptors

Hi Everybody,

I am a Msc. student at a south-american University, studying phylogeny and population genetics of some groups of Accipitridae in the Neotropics. This study use a microsatellite (heterologous) markers designed for Imperial Eagle. I am currently in search of studies made with microsatellites in any other accipitridae. Apart from Begoña Martinez-Cruz, is there anybody currently developing accipitridae microsats and who is willing to collaborate in this study? I am also looking to check other Falconiforme microsats. The only information I need is the sizes of the alleles of the different markers. Is anybody aware of the existence of these or other unpublished falconiformes microsats? Could you please send replies directly to me at mafegomez@yahoo.com.

Thanks for your help,

María Gómez Asistente de Investigación Universidad de Los Andes Bogotá-Colombia fern-go2@uniandes.edu.co
mafegomez@yahoo.com

Nucleotide frequency software

Does anyone know of a method or a program to calculate the nucleotide frequencies at equilibrium from a nucleotide substitution matrix?

Thank you

Eran

eran elhaik <eranelhaik@gmail.com>

PAUP timing

Dear evoldir members-

Are there any current methods for estimating a ballpark amount of time it may take to perform a maximum likelihood procedure using Paup, given a specific set of conditions such as processor speed, number of taxa, length of sequence and number of variable sites? For instance, I want to estimate approximately (within a few days) how long it will take my computer to complete an analysis of a dataset that includes 113 individuals, 360 bases and an enormous level of sequence divergence.

Joel Anderson Natural Resource Specialist Perry R. Bass Marine Fisheries Research Station Coastal Fisheries Division, Texas Parks and Wildlife ph: (361) 972-5483 fax: (361) 972-6352 Joel.Anderson@tpwd.state.tx.us

Joel.Anderson@tpwd.state.tx.us

PeerReview Bias

I am a member of a working group sponsored by the National Center for Ecological Analysis and Synthesis (NCEAS) exploring issues associated with publication bias in ecology and evolution. We are conducting an on-line survey on the publication and review process. Please visit our web site to participate in the 4 minute survey <http://www.ecobias.org> Many thanks!

Yours

Tom Tregenza

- Dr T. Tregenza Royal Society Research Fellow Centre for Ecology & Conservation School of Biosciences University of Exeter Cornwall Campus Penryn TR10 9EZ

T.Tregenza@Exeter.ac.uk Tel: (+44) 1326 371862 Fax: (+44) 1326 253638

Reprints of publications can be downloaded from my website: <http://www.selfishgene.org/Tom/>

Phylogenetics book

Published Spring 2006

Awise, J.C. 2006. Evolutionary Pathways in Nature: A Phylogenetic Approach. Cambridge University Press,

New York (286 pp.)

Reconstructing phylogenetic trees from DNA sequences has become a popular exercise in many branches of biology, and here an award-winning geneticist explains why. Molecular phylogenies provide a genealogical backdrop for interpreting the evolutionary histories of many other types of biological traits (anatomical, behavioral, ecological, physiological, biochemical, and even geographical). Guiding readers on a natural history tour along dozens of evolutionary pathways, the author describes how creatures ranging from microbes to elephants came to possess their current phenotypes. If you want to know how the toucan got its bill and the kangaroo its hop, this is the book for you. This book also provides a definitive answer to the proverbial question: "which came first, the chicken or the egg?" This scientifically educational yet entertaining treatment of ecology, genetics, and evolution is intended for college students, professional biologists, and anyone interested in natural history and biodiversity.

javise@uci.edu javise@uci.edu

Publishing evolution

Dear Evolutionary Biologists

The Society for the Study of Evolution is reviewing the mode of publication of its highly-regarded international evolutionary biology journal *EVOLUTION*.

The Society has a commitment to intellectual and human diversity - one reflection of this is its office of non-North American Vice President. In that role, I would like to ask for your opinions on some issues regarding publication of evolutionary biology.

Please take a minute to answer the following questions. Please answer irrespective of your opinion - a random sample of opinions would be the best. Answers will be kept confidential, unless you specify otherwise.

Q1. If you have to pay page charges to publish in a good journal (typically in the order of USD60 per page), how much of a disincentive relative to other factors is this to submit to that journal?

Q2. Have you ever decided to not submit to a particular journal on the basis that you would incur page charges, and if so, how often (eg rarely, usually etc)?

Q3. Have you ever requested a waiver of page charges from any journal? Was it granted?

Q4. Are you aware that the Society for the Study of Evolution has low-cost membership fees, and that one of the benefits of membership is an allowance of 12 fee-free pages per year if your work is published in *EVOLUTION*?

Q5. Are you a member of the Society for the Study of Evolution, and if not, why not?

Q6. Have you published in *EVOLUTION*? How often?

Q7. What is the country/region from which your research funding comes?

Q8. Do your national funding bodies mostly allow application for publication charges?

Q9. Do you have any other comments on the subject of publication of evolutionary biology?

thank you for your time.

Paul Sunnucks

- Dr Paul Sunnucks Senior Lecturer in Zoology School of Biological Sciences Monash University, Melbourne Clayton Campus 3800 Victoria Australia ph + 61 3 9905 9593 fax + 61 3 9905 5613

email paul.sunnucks@sci.monash.edu.au

webpage: <http://www.biolsci.monash.edu.au/~staff/sunnucks.html> Paul Sunnucks
<Paul.Sunnucks@sci.monash.edu.au>

ReedWarblers SoundRecordings

Dear EvolDir members,

This summer I'm planning to do fieldwork on reed warblers and honeyeaters of Micronesia. In order to take blood samples, I will need to capture birds, and for this purpose I'd like to be able to lure them to my nets using play-back of vocalizations. I am looking for sound recordings of the Caroline reed warbler *Acrocephalus syrinx*, nightingale reed warbler *A. luscinius*, and the cardinal or Micronesian honeyeater *Myzomela (cardinalis) rubrata*. If you have recordings of one of these species and would be willing to share these, please contact me. Your help is much appreciated!

Many thanks,

Henri

Dr. Henri A. Thomassen
Hthomassen(at)rulsfb.leidenuniv.nl

Smithsonian fieldwork fellowships

Fellowships for Caribbean fieldwork at the Smithsonian The Smithsonian Tropical Research Institute is offering Graduate Student Fellowships in support of fieldwork to be conducted at STRI's Bocas Research Station (see www.stri.org/Bocas for information) on the Caribbean coast of Panama. Five \$2,000 fellowships will be awarded to applicants who plan to spend at least 2 months in residence at the Bocas Research Station between June 2006 and April 2007.

Priority will be given to first-time visitors to the Bocas del Toro Research Station. Research on any aspect of marine or terrestrial biology, geology or anthropology will be considered. Applicants are strongly encouraged to consult with STRI research scientists in the relevant field before submitting a formal application. Bios of the staff can be found at <<http://www.stri.org/english/-scientific-staff/index.php>>. Please inquire with a relevant STRI scientist for advice on the scientific merit of the proposed research, methodology and logistics.

Applicants should send (1) a CV, (2) a description of the research to be conducted in Panama and how the investigation connects to the applicants dissertation research, 5-page maximum, and (3) two letters of recommendation by e-mail to the Bocas Research Station's Director, Dr. Rachel Collin (collinr@si.edu). Evaluation of proposals will begin June 15th and will continue until all of the funds have been awarded.

–

Dra. Rachel Collin Director, Bocas Research Station Smithsonian Tropical Research Institute Apartado Postal 0843-03092 Balboa, Ancon, Republic of Panama collinr@si.edu <http://striweb.si.edu/collinlab/> Phone: +507-212-8766

Bocas del Toro Research Station <http://www.stri.org/-bocas> Rachel Collin <collinr@si.edu>

Software Geneious 3

SOFTWARE: Geneious 1.0 for organizing and ana-

lyzing sequences, alignments, phylogenetics trees and pubmed abstracts. Geneious 1.0 is free to academics and the full version has numerous improvements over the beta (0.9e) that were requested by the community, as well as many bug fixes. Among improvements is a faster database and direct access to NCBI BLAST searches. The sequence, annotation and alignment viewer have been improved and now include basic manipulation such as reverse complement and translation. We have also added access to the NCBI structure database as well as providing 3D interactive protein structure visualization via the open-source package Jmol. One of the main features of Geneious we received some good feedback on in the last release was its ability to continually update your local database once you set up a query.

Version 1.0 can now be downloaded from www.geneious.com. Geneious.version_1.0 runs on Mac OS X, Windows and Linux, and allows evolutionary biologists to access data more effectively, while integrating several tasks that are core to evolutionary biologists, including:

- * phylogenetic reconstruction (NJ with bootstrapping) & tree viewing
- * multiple & pairwise sequence alignment
- * sequence alignment
- * faster dot plots
- * sequence viewing, including sequence annotations from NCBI database
- * translating from DNA to amino acids and reverse complements
- * export to Endnote, Nexus, Newick, Fasta
- * import trees, sequences alignments and bibliographies in a variety of formats
- * adding user information and notes to sequences, alignments and trees
- * NCBI Blast
- * 3D protein structure viewing
- * Fast local database searching
- * PDF full text searching of publications

The process of downloading, sorting and analysing sequences has been simplified, so that you can spend more time on genuine research. By creating a searchable, continuously updating local database of sequences, you can perform more complicated searches and view data in more detail than NCBI and EBI readily allow.

To encourage community development, we will soon be publishing a public API for our product on our website. This means that bioinformatics developers can write plugins to Geneious. Any developers wanting to know more about this should contact us (contact@biomatters.com) for details.

Daniel Batten <daniel@biomatters.com> Daniel Batten <daniel@biomatters.com>

Software GlobalTreefinder

A new unpaid TREEFINDER version is online at:

www.treefinder.de TREEFINDER is a software to compute phylogenetic trees from molecular sequences.

New features include:

- global search from multiple start trees - user-definable start trees - start tree generator - export of tip distances - more tolerant data import - more compatible PostScript code - bootstrap analysis under topological constraints - confidence limits for all numerical results, including - confidence limits for divergence times - simplified tree calibration - minor bug fixes

Gangolf Jobb gangolf@treefinder.de

Gangolf Jobb <gangolf.jobb@treefinder.de>

the analysis of PTI, PSI and PSS pair type estimators for any number of traits (only limited by RAM memory). - It gives the significance of the above coefficients by bootstrapping and resampling methods using laboratory and natural data sets models.

The software and instructions are available from

<http://webs.uvigo.es/c03/webc03/XENETICA/XB2/-JMsoft.htm> Further details and references related to this software and these topics can be found in the related paper "Antonio Carvajal-Rodríguez and Emilio Rolán-Alvarez 2006. JMATING: a software for detailed analysis of sexual selection and sexual isolation effects from mating frequency data. BMC Evolutionary Biology 6: 40" available in the former web page

Antonio Carvajal-Rodríguez (acraaj@uvigo.es) and Emilio Rolán-Alvarez Departamento de Bioquímica, Genética e Inmunología Universidade de Vigo Spain acraaj@uvigo.es

Software MOL COANC

Software JMating

Dear evoldir members:

We wish to announce the new software JMATING (ver 1.0.7; May 2006) able to do a battery of analyses to study sexual isolation and sexual selection effects from mating frequency data. The program has a friendly user windows interface and it is implemented in Java.

The lists of the main features provided are: - It calculates the less biased sexual isolation coefficients available. In one of the former statistics gives a unique sexual isolation estimation for the whole table when more than two traits are studied. In addition, it also calculates the classical two trait indexes for all combinations of the traits being studied. The number of traits being used is only limited by the memory of the computer. - It allows to obtain the cross product fitness estimator (W; the maximum likelihood of a qualitative trait fitness) for sexual selection in male and females separately. - It gives the significance of all the above indexes by bootstrapping, using laboratory and natural data sets models. - It also gives the significance of the above effects (sexual selection and sexual isolation by maximum likelihood methods, as a G test partition for sexual selection and isolation components. - It allows

Dear all,

A very early version of the programme MOL_COANC is now available. This software implements the method developed by Fernandez and Toro (Molecular Ecology 15:1657-1667, 2006) to estimate coancestry from molecular information. A compiled version for Windows, as well as a brief manual and some example files, can be downloaded from my personal web page (see the bottom of the message). Any comments on the performance or utility on your own data will be very welcome. Suggestions, bugs found, etc please send them to me.

Regards

***** Jesús Fernández Martín Departamento de Mejora Genética Animal 34-91 3471487 Instituto Nacional de Investigación y 34-91 3572293 (FAX) Tecnología Agraria y Alimentaria (INIA) jmj@inia.es Crta. A Coruña Km. 7,5 28040 Madrid (SPAIN) <http://www.uvigo.es/webs/c03/webc03/XENETICA/XB2/-Jesus/Fernandez.htm> *****

jmj@inia.es

Software Mesquite1 1

Mesquite 1.1: a modular system for evolutionary analysis has been released at <http://mesquiteproject.org>. This software provides diverse analyses for phylogenetic and population biology.

There are more than 500 modules in the standard installation, so we can't hope to summarize all features here. Here are some of the basic analyses (* = new to 1.1):

Ancestral state reconstruction: Categorical data parsimony likelihood *stochastic character mapping Molecular data parsimony Continuous data parsimony/likelihood landmarks (geometric morphometrics) Processes of character evolution: Rates: Categorical data, 1 & 2 parameter models Correlation: Felsenstein's contrasts (via PDAP) Pairwise comparison *Pagel's 1994 method Molecular analysis *Alignment *manual alignment tools *ClustalW integration Simulations of sequence evolution (GTR, HKY85, etc.) *Charts of sequence distances (Jukes Cantor, F81, F84, K2P) Visualizations of sequence properties Gene tree/species tree Coalescence simulations Measures of fit deep coalescences *duplications/extinctions Geography phylogeographic visualizations (via Cartographer) tests of population structure Simulations and randomizations Trees Pure birth process (Yule) Coalescence Reshuffling terminals Random rearrangements Noise to branch lengths Characters Simulations of evolution DNA models (HKY85, GTR, etc.) Categorical (1 & 2 parameter) Continuous (Brownian) Reshuffling character states Parametric bootstrapping Integration with PAUP, MrBayes, etc. via Batch Architect Multivariate analysis Principle Components Analysis Evolutionary PCA Canonical Variates Analysis Tree comparison Robinson-Foulds metric (via TSV) Strict consensus (via TSV) Visualizations of tree space (via TSV) Instability of terminal taxa Tree reconstruction Tree Search to optimize: deep coalescences *duplications/extinctions other criteria Cluster analysis UPGMA, Single linkage *Jukes Cantor, F81, F84, K2P

The above list presents features in a simple paradigmatic way; many other novel analyses can be performed by combining modules together.

In addition there are many visualizations (tree windows, charts) and utilities for editing and manipulating data. Some other notable features new to this version

are:

- fusing matrices: you can now merge matrices (e.g., three different genes) even if each uses different taxon names, into a single matrix
- integration with MrBayes, including export of MrBayes style files (composite matrices) and live-updated reading of MrBayes tree files as they are being produced.
- installation for Windows considerably simplified
- distribution of source code via Subversion repository

Mesquite runs on Windows, Mac OS X, Mac OS 9, and Linux/Unix.

Wayne Maddison David R. Maddison Departments of Zoology and Botany Department of Entomology University of British Columbia University of Arizona Vancouver, BC V6T 1Z4 Tucson, AZ 85721 email: wmadisn@interchange.ubc.ca email: beetle@ag.arizona.edu

Mesquite: <http://mesquiteproject.org> MacClade: <http://macclade.org> Tree of Life: <http://tolweb.org>

Software Mosy

Dear EvolDir members,

I am pleased to announce a software that detects recent selective sweep and estimates its parameters in population with varying size.

A long-standing interest in evolutionary biology is to estimate the rate of adaptive substitution. Footprints of recent adaptation can be detected by identifying selective sweeps in the genome (in particular, valleys of reduced polymorphism). The purpose of the software is to detect these adaptive events in the genome when the population size is not constant. The basic idea is to set the neutral demographic scenario as the null hypothesis in the likelihood ratio test, and the hitchhiking model under the same scenario as the alternative hypothesis.

The software is available at <http://www.zi.biologie.uni-muenchen.de/~li/mosy/> Sincerely,

Haipeng Li

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muenchen.de

li@zi.biologie.uni-

tant Museum of Comparative Zoology Harvard University 26 Oxford St Cambridge, MA 02138 617-495-8971
wfarnum@oeb.harvard.edu

Software SGRunner 2 0 1

SG Runner 2.0.1: A Graphical User Interface for Seq-Gen

SG Runner is a simple Mac OS X application that provides a graphical user interface for Seq-Gen, the sequence simulation program from Rambaut and Grassly (2001). SG Runner does not incorporate any code from Seq-Gen, but instead acts as an intermediary, controlling Seq-Gen through a standard graphical interface. So, instead of typing:

```
/usr/bin/Seq-Gen -mHKY t2.7 -l1000 -n100 -a.43 -g4  
-f.23 .21 .29 . 27 <~/Documents/Simproj/tree.phy  
>~/Documents/Simproj/simout.txt
```

you fill in the model parameters in a graphical form. This approach provides three potential benefits: 1) fewer mistakes since the layout for model specification is very similar to PAUP and SG Runner checks that parameters entered are of the correct type, 2) easier management of multiple simulations through the built-in simulation management tools, and 3) broader use of Seq-Gen by people that may be frustrated by the command line interface.

SG Runner 2.0.1 is a bug fix release. Users are encouraged to download the new release.

SG Runner requires Mac OS X 10.2 or above.

SG Runner is available at:

<http://homepage.mac.com/tpwilcox/>
wilcox@mac.com

tp-

Takara Ex Taq

I am trying to optimize my primer concentration for use with Takara Ex Taq in order to amplify large pieces (2000-4000bp) of DNA. Does any one have any experience with this product that would be helpful.

Thank you for your help, Whit Farnum Curatorial Assis-

VideoSoftware for LeicaCamera

We need software to record fig wasp behaviour using a binocular microscope but have been unable to find a suitable package for the hardware we have available. If anyone has any suggestions they will be gratefully received.

The microscope we have access to is a Leica MZ6 with a Leica DFC 280 camera. The camera is connected to a Mac mini with a Mac OSX 10.4.6 operating system. We have tried the demo of Leica's Openlab software, but it doesn't work with the DFC280 camera. We get great real time images on the screen using Leica's Firecam software, but this does not enable us to capture a video of what the animals are up to.

Kind regards

Derek.

Derek Dunn Division of Biology Imperial College London Silwood Park Campus Ascot SL5 7PY, UK
d.dunn@imperial.ac.uk

Tel. 02075942249 Fax 02075942339

"Dunn, Derek W" <d.dunn@imperial.ac.uk>

VideoSoftware for LeicaCamera answers

Many thanks to all who replied to my original posting about capturing real-time moving images on a computer screen. I have included the original posting and the replies. The solution to the problem was the software SnapZpro, available from Ambrosia softwares website.

<http://www.ambrosiasw.com/utilities/snapzprox/>

This software enables a Mac user to easily record any activity on their screen as a movie file. The part of the screen to be recorded can be easily altered. The price of the software, \$69 US, compares quite favourably

with Leica's own product, \$1000 U.S., which doesn't work with the Leica camera we have available anyway. Unfortunately, it looks like SnapZpro is a Mac only product and doesn't work with PCs.

Derek Dunn.

Original posting: We need software to record fig wasp behaviour using a binocular microscope but have been unable to find a suitable package for the hardware we have available. If anyone has any suggestions they will be gratefully received.

The microscope we have access to is a Leica MZ6 with a Leica DFC 280 camera. The camera is connected to a Mac mini with a Mac OSX 10.4.6 operating system. We have tried the demo of Leica's Openlab software, but it doesn't work with the DFC280 camera. We get great real time images on the screen using Leica's Firecam software, but this does not enable us to capture a video of what the animals are up to.

Kind regards

Derek

Derek, Funny you posted on that. I just tested two camera's, one from Leica and the one at this webpage. And, I ended up buying the Unibrain.

<http://www.1394store.com/eshop/-product.asp?dept%5Fid=59&pf%5Fid=4417>

Haven't used it yet except as demo, but it takes stills and videos and has great resolution and its own software. The Leica software couldn't get us both capabilities although it has a pretty spiffy interface.

On closer reading, I see you don't want a camera, just software. I don't know if Unibrain would sell it separately and whether it would work on your camera....probably not.. Leica does sell separate video software for about \$1k. But, I think the sampling rate was low if I remember correctly.

I would be interested to know what you come up with.

Sarah Cohen

Hi,

I know a linux package made rather for video surveillance, but capable of interacting with many different cameras and hardware. Maybe its worth to try it - anyway, I do not know on which port your camera connects to the computer.

It available on <http://www.zoneminder.com> Good luck, Wolfgang Arthofer

Hello Derek, I have successfully used iMovie to capture live video feeds (in my case from a digital video camera. Have you tried this yet? The fact that you can see it on screen makes me think you can capture it. You can then export Quicktime movies at lower frame rates, import them into ImageJ and take various measurements. I have attached the instructions I use for my undergrads.

-Patrick Lorch

Derek, If you can get video on screen, you could use Ambrosia Software's SnapZ Pro to capture the video. <http://www.ambrosiasw.com/utilities/-snapzprox/> Hope this helps, Joshua Der

Dear Derek,

I have a similar setup (but with a DFC 320 and a PC) in my lab. However, I do have a Powerbook which I occasionally like to plug in. The setup suggested to me was to use the standard firecam streaming and then capture it with one of the following programs (listed in order of preference): Snapz Pro BTV Pro Media Capture

I haven't done this in a few months but, for a time, I had it working quite well. In any case, I'd be very interested to hear which solution you finally decide on.

Nathan Pike

"Dunn, Derek W" <d.dunn@imperial.ac.uk>

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BielefeldU EvolOfLearning

“Postdoc”

BehavioralBiologist.BielefeldUniversity.Germany

Behavioral biologist - Evolution of learning, memory, cognition in rodents

Post-doctoral / assistant professor position. Searching for a behavioural biologist from biology or experimental psychology to develop collaborative and independent research on questions relating to learning, memory or cognition in rodents in the newly set up cognitive neuroscience lab at Bielefeld University. The university position (BAT IIa/Ib) is at a non-tenured assistant professor level involving moderate teaching. It is available from September 2006 for initially three years. The candidate’s CV must reflect the ability to successfully secure outside funding. The candidate should have a research approach with a focus on experimental animal behaviour analysis within the wider field of the evolution of cognition. Available is a newly developed virtual-reality setup permitting free movement orientation of rodents in VR space and, in addition, state-of-the-art automated behaviour testing systems for rodents. Developing new, high-throughput technology for rodent behavioural phenotyping is another focus of the lab. Candidates should be open to cooperate with invasive neurobiology within the lab. Applicants should send an e-mail outlining research interest and motivations, including C.V., two suggested referees and contact details to: york.winter@uni-bielefeld.de. Further information can be obtained from www.uni-bielefeld.de/biologie/cog

Contact:

Prof. Dr. York Winter Chair of Cognitive Neuroscience School of Biological Sciences - Bielefeld University 33501 Bielefeld Germany

york.winter@uni-bielefeld.de

Canadian PlantBarcoding

Post-Doctoral Fellowships in Plant Barcoding

We seek qualified individuals with a Ph.D. and expertise in molecular techniques and a strong background in plant evolution or systematics for three post-doctoral fellowships to work with the Canadian Barcode of Life Network (CBOLN) to develop, evaluate and apply DNA barcoding to the vascular and non-vascular plants of Canada. The fellowships are for two years (salary \$Can-45K per year) and are funded by a grant from Genome Canada to the Canadian Barcode of Life Network (CBOLN). Post-docs will collaborate with members of the Canadian Plant Barcoding Working Group composed of Spencer Barrett (Botany, University of Toronto), Sean Graham (UBC Botanical Garden, Univ. of British Columbia), Brian Husband and Steve Newmaster (Integrative Biology, University of Guelph). We would like to fill the positions this summer preferably by June. The three hires will be located in the laboratories of Barrett, Graham and Husband, respectively, but we anticipate considerable cross-fertilization among lab groups.

Post-docs will work on two main objectives: 1) the analysis of a local flora; 2) clade-based testing of barcoding and the analysis of intra-specific variation in taxonomically problematic groups. Opportunities for addi-

tional projects related to barcoding and plant evolution are also available. Qualified applicants are encouraged to visit the websites of Barrett, Graham and Husband where further details of the research focus of each investigator can be found. Applicants should contact individual investigators by e-mail if they are interested in applying for these positions and send a CV and arrange to have three letters of recommendation submitted.

Spencer Barrett (barrett@botany.utoronto.ca <mailto:barrett@botany.utoronto.ca>)

<http://www.botany.utoronto.ca/ResearchLabs/-BarrettLab/index.html>

Sean Graham (swgraham@interchange.ubc.ca <mailto:swgraham@interchange.ubc.ca>)

www.ubcbotanicalgarden.org/research/grahamlab.php
<<http://www.ubcbotanicalgarden.org/research/-grahamlab.php>>

Brian Husband (bhusband@uoguelph.ca <mailto:bhusband@uoguelph.ca>)

www.uoguelph.ca/ib/faculty/faculty_husband.shtml

For further information on barcoding and CBOLN visit www.bolnet.ca <<http://www.bolnet.ca>> and the Barcode of Life site at www.barcodinglife.org <<http://www.barcodinglife.org>>

Spencer C.H. Barrett

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
barrett@botany.utoronto.ca

CornellU ComputationalPopGenet

Postdoctoral position in statistical/computational human population genetics at Cornell

Carlos Bustamante, Rasmus Nielsen, Simon Tavaré, Manolis Dermitzakis and Andy Clark seek a creative and energetic postdoctoral fellow to engage in NIH-funded research on the analysis of genome-wide SNP genotype data for purposes of identifying associations with measured phenotypes. We are pursuing a series of investigations that center around the following four aims:

1. Our first goal is to develop Bayesian classification models to identify genomic regions most likely to harbor

variation associated with phenotypic differences. We have full genome expression microarray data for the 270 human HapMap samples to serve as a terrific test bed for these models.

2. The second goal is to quantify the effects of ascertainment bias and departures from neutrality of the marker variation on association testing. SNPs used in genome-wide platforms went through an ascertainment process that gives them a skewed frequency spectrum and local population biases, and we need to understand when and how this makes a difference in association testing.

3. The third goal is to explore application of data reduction methods to both the SNP and the phenotype data. High dimensional regression methods have been developed over the past 20 years with the goal of identifying subsets of independent variables that can be dropped from the model prior to model selection procedures. The correlation structure of SNPs and the low portion of variance typically explained by each SNP necessitates tuning these methods to the problem of genome-wide association testing.

4. The final goal is to assess the power of the association tests under a wide variety of violations of model assumptions.

Our research groups make a lively and stimulating research environment. Facilities include a 101 dual-G5 processor cluster (run by the Cornell group), and access to the Cornell Theory Center Velocity Cluster. Please email your resume, statement of research interests and contact information for three references as an attachment to Andrew Clark (ac347@cornell.edu) and/or Carlos Bustamante (cdb28@cornell.edu). The position is available immediately.

ac347@cornell.edu ac347@cornell.edu

CornellU DrosophilaInnateImmunity

Postdoctoral position - Evolutionary Genomics of Innate Immunity at Cornell

Brian Lazzaro and Andy Clark seek an energetic postdoctoral fellow with experience in *Drosophila* to engage in NIH-funded research on the analysis of the evolution and regulation of the innate immune response. We are pursuing a series of investigations that center around the following four aims:

1. Analysis of innate immunity as a gene regulatory network The level of detailed knowledge of the genes involved in innate immunity is now sufficient to begin to investigate evolutionary constraints on this gene regulatory network. We have accumulated extensive data quantifying variation in immune-related transcript abundance over time following challenge with several pathogen elicitors. We will fit dynamical models of the immune system as a gene regulatory network, test the resilience and robustness of the system, and identify weak points that may be exploited by pathogens.

2. Functional variation and population structure in immunity genes Pathogen attack can present a particularly strong, population-specific form of natural selection. The degree and pattern of population structuring in innate immunity genes relative to non-immunity genes will be determined from a global survey of SNP genotypes. We will fit population genetic models to assess whether observed population subdivision in innate immunity genes is attributable to heterogeneity in selective pressures across populations, and test for differences in resistance to a series of pathogens to determine whether pathogen diversity may be responsible for maintenance of host polymorphism.

3. Physiological and fitness trade-offs to launching an immune response The fact that organisms do not simply maintain a constant state of active defense, but instead induce specific responses only after septic infection, suggests that there are physiological or fitness costs to maintaining a constitutive state of immune activation. We are starting a series of experiments to quantify these costs and their variation among *Drosophila* lines.

4. Comparative genomic analysis of multiple *Drosophila* species Detailed comparative analysis of the innate immune pathway across the 13 *Drosophila* species for which there is genome-wide data is revealing which genes face the strongest evolutionary pressures. These genes are also particularly amenable to analysis of evolutionary divergence in regulation, and alignments of 5' regulatory regions will be identifying genes with unusual rates and patterns of inferred regulatory divergence.

Our research groups enjoy a lively and stimulating research environment. Facilities include an outstanding DNA Core facility for sequencing and genotyping, a 101 dual-G5 Xserve computer cluster (run by our groups), and. Please email your resume, statement of research interests and contact information for three references as an attachment to Andrew Clark (ac347@cornell.edu) and/or Brian Lazzaro (bl89@cornell.edu). The position is available immediately.

ac347@cornell.edu ac347@cornell.edu

EBI Hinxton ComparativeGenomics

Two jobs in Nick Goldman's group at the EMBL-European Bioinformatics Institute (EBI), Hinxton, Cambridge, UK, will be advertised in Nature this week, and are already advertised online.

One position is described as "Research Associate in Molecular Evolution", and full details can be seen at <http://www-db.embl.de/jss/servlet/-de.embl.bk.emblGroups.JobsPage/0669.html> The second position is described as "Senior Research Associate in Comparative Genomics", and full details can be seen at <http://www-db.embl.de/jss/servlet/-de.embl.bk.emblGroups.JobsPage/0670.html> Please bring these positions to the attention of any talented researchers you think may be interested.

Nick Goldman

Nick Goldman tel: +44-(0)1223-492530 EMBL - European Bioinformatics Institute fax: +44-(0)1223-494468 Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK

goldman@ebi.ac.uk goldman@ebi.ac.uk

France TreePopulationDynamicsModeling

We have a post-doc position available immediately, or as soon as possible, to a non French citizen, both granted by INRA (National Institute of Agronomic Research, Research department "Forest, Grassland and Aquatic Ecology") for 6 months and by CIRAD (Centre for International Cooperation in Agronomic Research for Development, forestry department), for 6 months or more.

To study the effect of management on tree populations, we have developed demo-genetics models for several species, in temperate as well as tropical forests. Currently, the most achieved model is available for a tropical species - highly harvested in French Guyana - the angelique (*Dicorynia guianensis*). This work was possible thanks to many data available on the life cycle of the species (from seed production to tree mortality) and

on gene flow (with the genotyping of reproducing and young trees in a 40 ha stand). The model was implemented on the platform CAPSIS (Croissance d'Arbres en Peuplement avec Simulation d'Itinéraires Sylvicoles / Computer-Aided Projection of Strategies In Silviculture, see <http://coligny.free.fr/>) developed by INRA. The first simulations indicate that repeated harvesting on a 40 years cycle reduce regularly the number of trees but the genetic diversity remains constant.

During this post doc project, we would like: 1) to evaluate the validity of our first conclusions: (i) by using a sensitivity analysis of the model (ii) by studying how the hypotheses are going on with the model. 2) to compare the results obtained for angelique with oak (and *Quercus petraea*, sessile oak, in particular).

The post-doc candidate will first be working on the CAPSIS module for angelique to complete the study and to get familiar with the tool. She/he will improve some parts of the model, in particular seed and pollen flow dispersal description. An experimental plan for simulations will be set up, to measure the sensitivity of the model to the different entry parameters. The *Quercus* module will then be improved. Some simulations will be performed to study the impact of various forest management scenarios on the demo-genetic behaviour of oaks. Results will be compared to those obtained in angelique, to stress out differences, and to explain them. The goal would be to build a sensitivity analysis on species characteristics, by exploring how modifications of these characteristics will affect simulations.

The candidate should have qualification in computer programming, forestry, modeling. The work will be first located in Montpellier, a stay in Bordeaux is also possible. The monthly salary is around 2000 euros.

Please rapidly send applications, including CV, publication list, and major publications (if available also addresses of referees and statement of research interests) by email to addresses given below.

For more information please contact:

Sophie Gerber UMR1202 BioGEco - Biodiversity, genes and communities INRA-Université Bordeaux I 69 route d'Arcachon 33612 Cestas cedex - FRANCE tel (33) (0)5 57 12 28 30 fax (33) (0)5 57 12 28 81 gerber@pierroton.inra.fr

Sylvie GOURLET-FLEURY Département Forêts du CIRAD TA 10 / D Campus International de Baillarguet 34398 Montpellier Cedex 5 - FRANCE Téléphone : 04 67 59 38 83 Fax : 04 67 59 37 33 sylvie.gourlet-fleury@cirad.fr

Sophie Gerber <gerber@pierroton.inra.fr>

Gif sur Yvette Sex Chromosome Drive

A one-year Post-doctoral position in Genetics, sponsored by the Centre National de la Recherche Scientifique, is available at the Laboratoire Evolution, Génomes et Spéciation, at Gif sur Yvette (near Paris), France. The successful applicant will join the group of Catherine Montchamp-Moreau, working on the molecular basis and the evolutionary history of sex chromosome drive. The project aims at identifying the genes or genetic elements responsible for “/sex-ratio/” drive, a type of segregation distortion occurring in males of *Drosophila*. <>/Sex-ratio/ segregation distorters are linked to the X chromosome and prevent the production of Y-bearing sperm. The loss of Y sperm is related to the inability of the Y chromosome sister-chromatids to separate properly during the second meiotic division (1). The trait was recently mapped to two small regions located about 150kb apart on the X chromosome of *Drosophila simulans*. Each of them contains an element required for /sex-ratio/ drive (2). Several approaches should be used to identify the distorter elements: (i) search for differences in gene organization and DNA sequence between /sex-ratio/ and wild-type X chromosomes, (ii) search for qualitative or quantitative differences in testis expression of genes between /sex-ratio /and wild-type males, (iii) use of transgenes, to determine whether the putative candidate(s) do induce segregation distortion. The laboratory is well equipped with PCR and sequencing facilities.

The applicant must have a strong background in genetics and molecular biology, including a real expertise in studying gene expression. A solid knowledge of the genetic control of meiosis or technical skills in transgenesis will be appreciated.

References: (1) Cazemajor M., D. Joly, and C. Montchamp-Moreau, 2000/. / Genetics 154 :229-236. (2) Montchamp-Moreau C., D. Ogereau, N. Chaminate, A. Colard and S. Aulard, 2005. Genetics* *Ahead of Print: December 30. 10.1534/genetics.105.051755.

The application file can be loaded at <http://www.cnrs.fr/> Applicants should submit a curriculum vita, a brief statement of research interests, copies of relevant publications and/or manuscripts, and the name, address and phone number of two references to the email or postal address below. Application must be

received by june 30, 2006.

Catherine.Montchamp@legs.cnrs-gif.fr
<mailto:Catherine.Montchamp@legs.cnrs-gif.fr>

Catherine Montchamp-Moreau UPR 9034 Laboratoire Evolution, Génomes et Spéciation CNRS Avenue de la Terrasse 91198 Gif sur Yvette Cedex Tel: 01 69 82 37 20 Fax: 01 69 82 37 36 <http://www.legs.cnrs-gif.fr/>

Catherine.Montchamp@legs.cnrs-gif.fr

INRAVersailles PlantBiodiversity

Dear Sir, I would be very thankful if you could poste this announcement for a postdoc position on the EVOLDIR web site. Thank you very much

MA Grandbastien

Postdoctoral position/Transposons and Plant Biodiversity

A 21-month postdoctoral position is available at the Laboratoire de Biologie Cellulaire, Institut Jean-Pierre Bourgin, INRA- Versailles, France (<http://www-ijpb.versailles.inra.fr/>). The work will be performed in the team "Host-Transposon Interactions and Plant biodiversity", in the frame of the ANR project "Effect of polyploidy on plant genome biodiversity and evolution".

The work will focus on analyzing the consequences of interspecific hybridization on the distribution of transposable elements, and on their impact on the evolutionary history of the genus *Nicotiana* as a principal model. A major tool will be the use of the SSAP strategy to monitor insertion polymorphisms of various transposable element families. Expertize and training background in evolutionary biology, population genetics, molecular phylogenetics and systematics are required.

The starting date will be around november 2006. Requirement: no previous CDD (> 1 year) at INRA

Send CV and two recommandations contacts to:

Dr Marie-Angèle GRANDBASTIEN Laboratoire de Biologie Cellulaire Institut Jean-Pierre Bourgin INRA-Centre de Versailles 78026 Versailles cedex, France gbastien@versailles.inra.fr tel: 33 1 30 83 30 24 fax: 33 1 30 83 30 99

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Marie-Angèle GRANDBASTIEN Laboratoire de Biologie Cellulaire Institut Jean-Pierre Bourgin INRA - Centre de Versailles 78026 Versailles, France Tel: 33 (1) 30 83 30 24 Fax: 33 (1) 30 83 30 99 Email: gbastien@versailles.inra.fr

Marie-Angèle.Grandbastien@versailles.inra.fr

IndianaU DiseaseGenetics

Post-Doctoral Position in the Ecology and Ecological Genetics of Disease

Indiana University, Bloomington

A post-doctoral position in disease ecology is available August 1, 2006 at Indiana University. We are especially interested in recruiting a theoretician working on (or willing to work on) interactions among microbes inhabiting the same host. The project would be part of a larger NSF-funded study on microbial interactions within ticks, working with Keith Clay, Clay Fuqua, Curt Lively and Mike Wade (see <http://www.bio.indiana.edu/gradprograms/EEB/faculty.html> for faculty research in Evolution, Ecology and Behavior at Indiana University).

The successful candidate will have the opportunity to develop new lines of thinking regarding microbial interactions within hosts. The applicants' graduate work should be in a relevant area and a PhD is required before the start date. The salary is \$32,000 per year and includes a comprehensive benefits program. The position is for one year, renewable for a second year.

For more information contact Keith Clay (clay@indiana.edu, 812-855-8158), Curt Lively (clively@indiana.edu, 812-855-1842), or Mike Wade (mjwade@indiana.edu, 812-856-4680). All applications, including curriculum vitae, statement of research interests and experience, and contact information for three potential referees should be sent via email to malockha@indiana.edu, enter Microbial Interactions Postdoc position in the subject line. Applications will be accepted immediately and until the position is filled.

Indiana University is an Equal Opportunity, Affirmative Action Employer and is committed to achieving excellence through cultural diversity.

Curt Lively <clively@indiana.edu>

LyonFrance Genetics

A one-year Post-doctoral position in Genetics, sponsored by the Centre National de la Recherche Scientifique, is available at the Laboratoire de Biométrie et Biologie Evolutive (UMR CNRS 5558), at Lyon, France. It should start before January 2007. The successful applicant will join the group of Frédéric Fleury, working on host-parasitoid-microparasite interactions.

see http://www.k-projects.com/-cnrs_postdocs/public/departement_details.php?IdDpt&Dep=SDV&NumOffre&Langue=en for details

Title: Genetic and phenotypic consequences of a vertically and horizontally transmitted virus infection on its parasitoid insect hosts : a functional approach.

Julien Varaldi <varaldi@biomserv.univ-lyon1.fr>

QueensU MathEvolEpidemiology

Postdoctoral Fellowship in Mathematical Evolutionary Epidemiology.

Applications are sought from outstanding researchers for a 2 year postdoctoral position in mathematical evolutionary epidemiology in the labs of Dr. Peter Taylor and/or Dr. Troy Day in the Department of Mathematics and Statistics at Queen's University. There is considerable flexibility in research projects, but possibilities include developing theory for the effects of kin interactions on host /parasite (co)evolution, the effects of host/parasite plasticity on their (co)evolution, the evolutionary consequences of public health interventions, and the evolutionary biology of immunopathology. Successful applicants will be free to conduct research in any of these or other related areas of interest. Ideally the position would be taken up by Sept. 1, 2006 but there is some flexibility in start date. Duties will include the teaching of two one-semester courses per year. Salary will be \$38,000 per year.

For more information on research in our labs see: www.mast.queensu.ca/~tday and

www.mast.queensu.ca/~peter. Information about the Department of Mathematics and Statistics and Queen's University can be found at www.mast.queensu.ca and www.mast.queensu.ca respectively.

To apply, send a current CV and a statement of research interests, and arrange to have at least two letters of reference, one of which should comment on the candidate's teaching, sent by email to Dr. Troy Day (tday@mast.queensu.ca). We will continue to accept applications until the position is filled but anticipate making a decision by May 30, 2006.

tday@mast.queensu.ca

UArizona Phylogenetics

POSITION AVAILABLE: Postdoc in phylogenetics/phyloinformatics/computational biology. Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ 85721

SALARY/TERMS: Salary between \$40,000 and \$45,000, commensurate with experience and skills, benefits included. Position renewable for a second year conditional on performance. Start date negotiable after November 1, 2006.

QUALIFICATIONS: Ph.D in biology or computer science. Proficiency in phylogenetic methods, phyloinformatics, bioinformatics, or computational comparative genomics; demonstrated ability to program in PERL, C, C++ or equivalent. Training or experience in computational biology and/or algorithms desirable. However, candidates with a strong empirical background in the phylogenetics of a particular taxon will also be considered. Strong personal skills and willingness to work in an interdisciplinary collaboration essential.

RESPONSIBILITIES: Postdoc will work with PI Mike Sanderson at the University of Arizona on a collaborative NSF-funded AToL (Assembling the tree of life) project developing software tools and algorithms to mine sequence databases for phylogenetic inference. Postdoc will also be involved in testing software tools and evaluating their performance on real sequence data sets. Collaborators include Junhyong Kim (U Penn) and Oliver Eulenstein and David-Fernandez-Baca (Iowa State, Computer Science).

APPLICATION PROCESS: Position is open until filled; application review will begin immediately. Interested applicants should submit: 1) a letter outlining

their research interests and specific qualifications as described above; 2) curriculum vitae; and 3) the names and addresses of three references in an online application to the University of Arizona Human Resources web site (<http://www.hr.arizona.edu>). Please address questions about the position directly to:

Dr. Mike Sanderson Section of Evolution and Ecology University of California Davis, CA 95616 mjsanderson@ucdavis.edu

Please note that my new address after July 31, 2006 will be

Department of Ecology and Evolutionary Biology University of Arizona, Tucson, AZ 85721

mjsanderson@ucdavis.edu mjsanderson@ucdavis.edu

UBern TheoEvolEcol

Postdoc Position in Theoretical Evolutionary Ecology at Dept. Behavioural Ecology, University of Berne; chair: Michael Taborsky

RESEARCH AIMS: Evolutionary mechanisms of conflict and cooperation, with particular emphasis on reciprocity. Ideal candidates will have a PhD in theoretical biology, mathematics or economy and should be experienced in modelling (e.g. game theory, agent-based simulation models, dynamic programming), preferably with a sound background in theoretical issues in evolutionary biology. The position is initially for three years and can be prolonged.

Closing date: Open until filled, but all application materials, including CV, a summary of research experience, copies of relevant published or in-press papers, and two letters of recommendation should be received by 31 May 2006 to ensure full consideration. The position will start at the earliest possible date. Candidates should indicate in a cover letter when they could take up the position. Please send all application material to the secretary's office, c/o Marlis Gerteis, Dept. Behavioural Ecology, University of Bern, Wohlenschtrasse 50A, CH- 3032 Bern, Switzerland; or as e-mail attachments to marlis.gerteis@esh.unibe.ch. For inquiries please contact michael.taborsky@esh.unibe.ch. Please see also <http://www.zoology.unibe.ch/behav/-jobs.d.php> Prof. Michael Taborsky University of Bern Dept. Behavioural Ecology, Institute of Zoology, Wohlenschtr. 50a, CH-3032 Hinterkappelen/Bern Switzerland

Phone: +41-(0)31 631 9156 Secret: +41-(0)31 631 9111 Fax: +41-(0)31 631 9141 e-mail: Michael.Taborsky@esh.unibe.ch <http://zoology.unibe.ch/behav/> Michael Taborsky <michael.taborsky@esh.unibe.ch>

UBerne 2 PopGenetics

The Aquatic/Fish Ecology and Evolution department of Ole Seehausen and the Aquatic Ecology Department of Jukka Jokela at EAWAG/University of Berne, and EAWAG/ETH respectively, are seeking to fill two 3-year Postdoc positions to work at the interface between population genetics, biodiversity theory and conservation biology.

We wish to investigate the relationships between environmental heterogeneity, neutral genetic, and adaptive diversity using the evolutionary melting pot aquatic biota of perialpine drainages.

We are looking (1) for a computational population ecologist/geneticist to develop theoretical models for investigating the relationships between the environment, genetic variation and adaptive diversity, including the emergence of functional polymorphisms and speciation. The ideal candidate will have a PhD in theoretical biology, computational population genetics or a related field, and will have extensive modeling experience in metapopulation ecology and/or evolutionary genetics.

(2) for an ecologist or population geneticist to conduct molecular genetic analyses using AFLPs, and ecological analyses using stable isotopes and morphometrics on different kinds of aquatic organisms, and to guide PhD students. The ideal candidate will have a PhD in population genetics or ecology with extensive experience in molecular genetic lab techniques and handling of large data sets for statistical hypothesis testing.

The two Postdocs are expected to interact closely with each other and with several PhD students. Details about the departments and their research programs are available at <http://www.fishecology.ch/> and http://www.eawag.ch/research_e/lim/e_index.html.

For specific information please contact Ole Seehausen (ole.seehausen@eawag.ch) and Jukka Jokela (jukka.jokela@eawag.ch). Send application letter, CV and publication list, and contact details of three referees by email to sandra.isenring@eawag.ch, Personnel Department.

Deadline is 30 June 2006, but applications will be considered until the posts are filled.

Eawag is the Swiss Federal Institute for Aquatic Science and Technology, a Swiss-based and internationally operating aquatic research institute within the ETH domain.

Prof Ole Seehausen Aquatic Ecology & Evolution

Institute of Zoology University of Bern Baltzerstr. 6, CH-3012 Bern Phone +41 31 631 31 31 FAX +41 31 631 30 08 and EAWAG Ecology Research Center Seestrasse 79 CH-6047 Kastanienbaum Phone +41 (0)41 349 21 21 Fax +41 (0)41 349 21 68

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

UBritishColumbia ConiferGenomics

Population and Evolutionary Genomics

Post-doctoral fellowship Genome B.C./ Genome Canada University of British Columbia Vancouver, Canada

A post-doctoral position in the area of population and evolutionary genomics is available immediately, for a duration of two years. You will be part of an interactive group in a large genomics project working on the comparative genomics of conifers, with a focus on spruce, and a focus on insect defense mechanisms and chemical ecology. (This project is a continuation of the one described at www.treenomix.ca). Activities may include: (1) Large scale sequence alignments and evolutionary comparisons between spruce and pine, and with angiosperms; (2) Prioritization of genes for SNP discovery based upon in-silico analyses; (3) Analysis of patterns of nucleotide diversity in candidate genes; (4) Analysis of microarray data and eQTLs. Other possibilities exist depending on your interest and abilities, including the new development of approaches for data interpretation and analysis.

Contact Kermit Ritland kermit.ritland@ubc.ca

Kermit Ritland <kritland@interchange.ubc.ca>

UCBerkeley EvoGenomics

POSTDOCTORAL POSITIONS IN COMPUTATIONAL EVOLUTIONARY DEVELOPMENTAL BIOLOGY IN THE EISEN LAB AT THE UNIVERSITY OF CALIFORNIA BERKELEY

I am seeking two talented computational postdoctoral fellows with experience and deep interest in evolution to use the now twelve sequenced *Drosophila* genomes, and a wealth of experimental data we are generating, to study the evolution of gene expression and gene regulation. The members of my lab have been employing a combination of computational and experimental genomics techniques to characterize gene regulation in developing *Drosophila melanogaster* embryos. We are systematically generating in vivo (ChIP-chip) and in vitro (SELEX) binding data on all of the transcription factors involved in early (pre-gastrulation) pattern formation. We are also producing a three-dimensional atlas of gene expression patterns in the embryo that will include the protein and RNA expression patterns of these factors and their targets. All of these methods are now being extended to the other *Drosophila* species to generate the ideal dataset for a detailed, quantitative study of the evolution of gene expression and regulation. These positions are fully funded by grants from the National Institutes of Health and are open to citizens of any country.

Send questions/applications (letter/CV and references) to MBEISEN@BERKELEY.EDU

mbeisen@lbl.gov mbeisen@lbl.gov

UCIrvine SocialInsectEvol

POSTDOCTORAL SCHOLAR Genetics and Behavior of Social Insects

The Department of Ecology & Evolutionary Biology at UC Irvine is currently seeking one or more Postdoctoral Scholar(s) in the laboratory of Dr. Neil Tsutsui.

We are seeking Postdoctoral Scholar(s) to study the genetics, behavior and social structure of social insects. Previous work has focused on the charming, yet in-

vasive, Argentine ant (*Linepithema humile*). In this species, genetic changes during introduction have altered individual behavior and, in turn, the social organization of introduced populations. These changes have contributed to the Argentine ant's invasive success by promoting the formation of massive "super-colonies" in the introduced range. Publications from previous research can be downloaded from: <http://tsutsuilab.bio.uci.edu/>. The Postdoctoral Scholar(s) will have opportunities to contribute to ongoing genetic, behavioral and biochemical research on Argentine ants, as well as work on other projects related to the lab's core interests in behavioral, molecular and chemical ecology.

The successful applicant(s) must have a strong background in molecular techniques, population genetics and data analysis, and previous experience in behavioral ecology is desired. Salary will be commensurate with experience; generous benefits are included.

Applicants should submit a curriculum vita, a brief statement of research interests, copies of relevant publications and/or manuscripts, and the name, address and phone number of two references to the email or postal address below. Review of candidates and applications will begin May 22, 2006

Dr. Neil D. Tsutsui Department of Ecology and Evolutionary Biology 321 Steinhaus Hall University of California, Irvine Irvine, CA 92697-2525 ntsutsui@uci.edu

UC Irvine is located in coastal Southern California, between Los Angeles and San Diego. The Department of Ecology & Evolutionary Biology at UCI includes a faculty of >40 professors, and includes particularly strong groups in the areas of Evolutionary Genetics (<http://evogen.bio.uci.edu/>) and Global Change Ecology (<http://globalchange.bio.uci.edu/>).

The University of California, Irvine is an equal opportunity employer committed to excellence through diversity. –

Neil D. Tsutsui, Ph.D. Assistant Professor Department of Ecology and Evolutionary Biology University of California, Irvine 321 Steinhaus Hall Irvine, CA 92697-2525 tsutsuilab.bio.uci.edu ntsutsui@uci.edu (949) 824-7525 (office)

Neil Tsutsui <ntsutsui@uci.edu>

UCLA PlantPopGenet

POSTDOC: plant molecular ecology/population genetics at UCLA

A postdoctoral position is available in Fall 2006 to study/model contemporary seed dispersal in the laboratory of Victoria Sork, University of California, Los Angeles. The post-doc position, which is part of an NSF-collaborative project between Sork and Peter Smouse (Rutgers), will involve a combination of field work, laboratory work, and statistical modeling to develop new approaches to the study of gene movement through seeds, using valley oak as its model system. The nature of the exact project will depend on the expertise and interests of the candidate. In addition, this person can establish a related project addresses complementary questions. Candidates must have strong molecular and/or statistical modeling skills, and background in population genetics.

Please email a statement of interest in the position highlighting your areas of expertise and research interests, with names and electronic addresses of three references to vlsork@ucla.edu. Please attach a CV, and 2-3 publications or manuscripts (Word or pdf format). Applications are accepted starting May 31 and reviewed upon receipt until the position is filled. Ideal starting date is September 2006.

UCLA University is an equal opportunity employer.

Victoria Sork Professor and Chair, Dept of Ecol & Evol Biology Professor, Institute of the Environment

phone: 310-825-7755 Fax: 310-206-0484

Victoria Sork <vlsork@ucla.edu>

UChicago EvolTranscriptRegulation

POSTDOCTORAL POSITION anticipated to be available 1 September 2006 for 1 year (renewable contingent on funding and satisfactory performance) to investigate the microevolution of transcriptional regulation via transposable elements. The research uses heat-shock genes/proteins in *Drosophila* as a model system, and will follow up on: Shilova, V., D. Garbuz, E. Myasyankina, B. Chen, M. Evgen'ev, M.E. Feder, and O. Zatssepina. 2006. Remarkable site specificity of local transposition into the Hsp70 promoter of *Drosophila melanogaster*. *Genetics*, Published Articles Ahead of Print: April 2, 2006, doi:10.1534/genetics.105.053959 Lerman, D.N., P. Michalak, A.B. Helin, B.R. Bettencourt, and M.E. Feder. 2003. Modification of heat-

shock gene expression in *Drosophila melanogaster* populations via transposable elements. *Molecular Biology and Evolution* 20: 135-144. Lerman DN, Feder ME. 2005. Naturally occurring transposable elements disrupt hsp70 promoter function in *Drosophila melanogaster*. *Mol. Biol. Evol.* 22:776-783.

Proposed research would test hypotheses of adaptive significance of such transposable elements via laboratory evolution.

Techniques will include PCR, cloning-sequencing, bioinformatics, transposon-mediated transformation, luciferase reporter assays, quantitative RT-PCR, laboratory evolution, and *Drosophila* procedures. The ideal candidate will have a Ph.D., expertise in the above techniques, and interest in the project and cognate areas.

To be considered for the position, submit curriculum vitae, names/phone#/email of 3 references, preferably electronically, to: Dr. Martin Feder m-feder@uchicago.edu Department of Organismal Biology and Anatomy The University of Chicago 1027 East 57th Street Chicago, IL 60637 USA Phone: 773-702-8096 Fax: 773- 702-0037

Applications received by 1 June 2006 will be assured full consideration. An Affirmative Action/Equal Opportunity Employer.

m-feder@uchicago.edu m-feder@uchicago.edu

UKonstanz MolEvol

Two Postdoc positions in molecular evolutionary biology are available in the lab of Axel Meyer in the Department of Biology at the University of Konstanz, in Germany. The evolutionary biology group is an international group of students and postdocs that consists of about 20 people from 10 different countries. The language in the lab is English.

We are looking for energetic postdocs who are interested in speciation, molecular evolution, bioinformatics/genomics and/or evolutionary developmental biology. The specific research projects involve research on the patterns of relationships and population genetics of cichlid fishes as well as the discovery and functional characterization of genes underlying the diversification of cichlids in Africa and in Nicaragua.

The great lakes in East Africa house some of the worlds most diverse freshwater ecosystems. Lakes Victoria, Malawi and Tanganyika are particularly well-known

for their adaptive radiations of hundreds of endemic species of cichlid fishes. We are interested in understanding speciation, phylogeography, molecular evolution and molecular phylogenetics of these cichlid fish assemblages. We also want to identify and characterize the function of genes that are involved in the phenotypic diversification and presumably speciation of cichlid fishes. Several molecular biological, "devo-evo" and genomic approaches, including candidate gene approaches, DNA-chip technology, characterization of ESTs, in situ hybridization in cichlids and transgenics in zebrafish are used to address these questions. We are also interested in evolutionary genomic questions and the evolution of novel gene functions after gene and genome duplications.

Some recent publications of the lab include: Verheyen et al. (2003). The origin of the superflock of cichlid fishes from Lake Victoria, East Africa. *Science* 300: 325-329. Salzburger et al. (2005). Out of Tanganyika: Genesis, explosive speciation, key-innovations and phylogeography of the haplochromine cichlid fishes. *BMC Evolutionary Biology* 5: 17. Barluenga et al. (2006). Sympatric speciation in Nicaraguan crater lake cichlid fish. *Nature* 439: 719-23 Braasch et al. (2006). Asymmetric evolution in two fish-specifically duplicated receptor tyrosine kinase paralogs involved in teleost coloration. *Molecular Biology and Evolution* 23:1192-1202.

Funding is available for at least 2 years. Postdoc salaries (BATII/a pay scale) are approximately 45 to 50,000 Euros annually, (depending on marital status, age, etc.) before deductions for taxes, health insurance and retirement contributions.

The positions are open immediately. The review and invitation of applicants will begin at the end of June 2006 and will continue until these positions are filled. To apply, please email a curriculum vitae, including a list of publications, a statement of research interests, and the names and email addresses of two references to axel.meyer@uni-konstanz.de.

Prof. Axel Meyer, Ph.D. Department of Biology Konstanz University 78457 Konstanz, Germany Email: axel.meyer@uni-konstanz.de

For more information visit <http://www.evolutionsbiologie.uni-konstanz.de/-index.php?section=10>

Axel Meyer <axel.meyer@uni-konstanz.de>

ULondon PoxVirusEvol

Postdocal position studying the evolution of chicken pox virus.

Centre for Infectious Disease, Barts and The London, Queen Mary's School of Medicine and Dentistry, University of London

salary RA1.6 - £24,500 plus on costs

We are recruiting a postdoc interested in one of two areas.

- 1) A study analyzing multiple samples taken from an outbreak of chickenpox. We will search for evidence of selection on viral genotype, and will use genetic markers to characterize the patterns of transmission. The successful candidate would have an interest in epidemiology and the effect of viral genotype on transmission and virulence. This project would require some statistical ability, along with basic lab skills (PCR & sequencing).
- 2) A study following-up preliminary evidence that naturally occurring genetic variation an origin of replication (oriS) affects viral fitness. The successful candidate would be able to set up in-vitro assays and make different viral constructs. A background in virology would be useful.

We require a rapid expression of interest. Please send a short CV to r.a.nichols@qmul.ac.uk. Any additional information should be limited to 150 words or less in the body of the email.

Closing date: midnight (London time) Weds 10th May.

You should be available for telephone interview on Thursday 11th May or Friday 12th (please include the appropriate telephone number and times [please convert to London time])

This position is for a year in the first instance, although an application to extend the funding will be made.

Ideally the successful candidate will be able to work for some time with the current postdoc during the month of June, but could start full-time at a slightly later date.

Richard Nichols Professor of Evolutionary Genetics <http://www.sbcs.qmul.ac.uk/people> Judy Breuer Professor of Virology <http://www.icms.qmul.ac.uk/-Profiles/InfectDis/Breuer%20Judy.htm> Richard Nichols <r.a.nichols@qmul.ac.uk>

UOklahoma EvolBiol

Please see the attached (below) postdoctoral fellow listing. Thanks!

POSTDOCTORAL FELLOW - THE UNIVERSITY OF OKLAHOMA BIOLOGICAL STATION (UOBS). The University of Oklahoma (OU), Norman, Oklahoma, invites applications for a Postdoctoral Fellowship in Ecology and Evolutionary Biology to be a resident research scientist based at the university's Biological Station (UOBS) on Lake Texoma (Texas-Oklahoma border; 2-hr drive from campus). This is a 12-month (0.75 FTE; equivalent to 9 mo) appointment with benefits (i.e. medical, dental), renewable on an annual basis for up to three years. The fellow will be responsible for developing a research program in conjunction with UOBS faculty and assisting with the educational outreach program at the station via occasional presentations to visiting groups. In addition, the fellow will be given the opportunity to teach a two-week long (3 cr. hr.) course at the Station during summer for extra compensation. The targeted starting date is September 1, 2006, but is flexible. More information on UOBS and UOBS faculty research interests can be found at <http://www.ou.edu/uobs>. Applicants should include a curriculum vitae, reprints of representative publications, a detailed 3-5 page outline of the research to be conducted at UOBS and arrange to have three letters of recommendation sent on the applicant's behalf. Applicants are encouraged to contact one or more UOBS faculty prior to submitting application. All materials should be sent electronically to Lawrence J. Weider, Director, UOBS (ljweider@ou.edu). Applicant review will begin 1 June 2006 and continue until the position is filled. The University of Oklahoma encourages diversity in the workplace. The University of Oklahoma is an Affirmative Action/Equal Opportunity employer.

Lawrence J. Weider Director, The University of Oklahoma Biological Station HC-71, Box 205 Kingston, OK 73439 phone: 1-405-325-7438 FAX: 1-580-564-2479 ljweider@ou.edu <<mailto:ljweider@ou.edu>>

and

Professor Department of Zoology University of Oklahoma Norman, OK 73019-6121 phone: 1-405-325-4766 FAX: 1-405-325-0835

ljweider@ou.edu

USheffield SpermDiversity

THE UNIVERSITY OF SHEFFIELD

Department of Animal and Plant Sciences

Postdoctoral Research Associate

Ref: PR2419 Closing Date: 16/06/06 Grade: 7 Salary: £23,457 per annum

The post holder will work with Prof Tim Birkhead on a Leverhulme- funded project designed to establish the evolutionary causes and consequences of sperm diversity in birds. The post holder should possess a current ringing (banding) licence, be prepared to spend time making image analysis measurements of sperm using a microscope and spend time abroad conducting field work. This post is available from October 2006 for 2 years.

For full post details / application pack please visit www.sheffield.ac.uk/jobs or email: jobs@sheffield.ac.uk / tel + 44 (0)114 222 1631 (24 hr). Please quote Ref. PR2419 in all enquiries.

Jennie Brookes (Miss) HR Assistant (Staff Recruitment) Staff Recruitment Service Department of Human Resources University of Sheffield

Located at: 340 Glossop Road, Sheffield, S10 2TN
Postal Address: Firth Court, Western Bank, Sheffield, S10 2TN

E-mail Address: J.M.Brookes@Sheffield.ac.uk Telephone: 0114 222 1614 (21614 internal) Fax: 0114 222 1475

For details of current vacancies at the University of Sheffield visit: www.shef.ac.uk/-jobs
J.M.Brookes@sheffield.ac.uk
J.M.Brookes@sheffield.ac.uk

USouthDakota PlantPhylogeography

The Department of Biology at University of South Dakota is currently seeking a Postdoctoral Scholar to join the laboratory of Dr. Molly Nepokroeff.

I am seeking a post-doctoral scholar to participate in an NSF funded research project on phylogeography of Hawaiian *Schiedea*. Successful applicant will have experience in one or more of the following areas: 1) use of nuclear markers for phylogeny and/or genealogy reconstruction; 2) statistical phylogeography methods; 3) paleomodelling and developing GIS-based habitat suitability models; 4) evolutionary dynamics of hybrid zones. Experience or interest in mentoring undergraduates in a research setting and in automated sequencer operation are also desirable.

Applicants should have a recent Ph.D. in plant evolutionary biology or related field prior to start of this two-year position. The position is expected to begin approximately August 1, 2006. To apply, send a cover letter with a full CV and contact information for three references to Dr. Molly Nepokroeff, mnepokro@usd.edu. University of South Dakota is committed to affirmative action, equal opportunity and the diversity of its workforce.

Molly.Nepokroeff@usd.edu Molly.Nepokroeff@usd.edu

UWesternOntario Drosophila larval cold adaptation

POST-DOCTORAL FELLOW INSECT CRYOPRESERVATION

Department of Biology, University of Western Ontario, London, ON, Canada.

An 18 month position is available from Fall 2006 for comparative physiological work on cold tolerance of drosophilid larvae with a view to developing a cryopreservation protocol for *Drosophila melanogaster*. This NIH-funded project is in collaboration with researchers in the USA and Europe, and will require the gathering, integration and interpretation of data on cold survival of *Drosophila* larvae at scales from sub-organismal to evolutionary. This position would suit motivated applicants with an interest in evolutionary physiology, cryobiology or biophysics. Applicants must have good communication skills and a PhD in Biological Sciences or a related field, previous experience with *Drosophila* is not essential.

Please send a CV, a cover letter describing research experience, interests and career goals and the contact information of three referees to Dr Brent Sinclair at celatoblatta@yahoo.co.uk. Informal email queries to

Dr Sinclair are welcome and encouraged. Remuneration will be on the NIH postdoctoral pay scale. Review of applications will begin 1 July 2006 and continue until the position is filled.

Brent Sinclair, PhD Postdoctoral Scholar Department of Biological Sciences University of Nevada Las Vegas, NV 89154-4004

Office: 702-895-5917 Cell: 702-379-4598 fax: 702-895-3956
 celatoblatta@yahoo.co.uk (primary);
 brent.sinclair@unlv.edu <http://www.unlv.edu/faculty/roberts/sinclairb.htm>
 Brent Sinclair
 <celatoblatta@yahoo.co.uk>

WSL SwissInst PopGenet

The Swiss Federal Research Institute WSL and its 500 staff members are committed to contribute to a landscape of high quality and to the protection of humans from natural hazards. The department Ecological Genetics investigates multi-species diversity in forest ecosystems. For a 5-month engagement, starting July 1, 2006, we are offering the position of a

PostDoc in population genetics

Embedded in the EC-supported Network of Excellence Evoltree, you will be carrying out a literature study on the relationship between genetic diversity in host

tree species and the diversity in associated organisms (insects, ectomycorrhizal fungi). You will compile the published data which serves as the basis for a meta-analysis to be published as a review. This analysis will describe the state of the art in the field and identify key research gaps which later will be addressed in a jointly executed research activity within the Evoltree network.

Your qualifications: PhD in biology or environmental sciences, a strong background in population genetics of plants, insects, or mycorrhizal fungi and experience in statistical analyses and in publishing. You should be committed and work independently in close interaction both within the WSL team and with specialists of research teams involved in the network activities.

Our institute offers a stimulating research environment and an excellent logistic support.

Interested? Please send your complete, written application including photo, under Reference Number 440 to Mrs. Monika Huber, Swiss Federal Research Institute WSL, Personnel department, Zuercherstrasse 111, CH8903 Birmensdorf, Switzerland. Further information can be obtained from Dr. Felix Gugerli, tel. +41-(0)44-739 25 90.

Felix Gugerli Biologist / Senior Scientist Swiss Federal Research Institute WSL Ecological Genetics Zuercherstrasse 111 CH-8903 Birmensdorf

SWITZERLAND

phone: +41-(0)44-739-2590 fax: +41-(0)44-739-2215
<http://www.wsl.ch/staff/felix.gugerli/>

felix.gugerli@wsl.ch

WorkshopsCourses

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Berlin EvolGenomics Aug29-Sep8

We are happy to announce the

Otto Warburg International Summer School and Workshop on Evolutionary Genomics

August 29 to September 8, 2006

Berlin, Germany

The aim of this program is to bring together researchers and students from different backgrounds (including molecular biology, bioinformatics, biological physics) to discuss a topic of high current interest. We plan an integrated program, which is focused on high-level training during the first days and leads to topical research seminars in the second part. The schedule will leave sufficient time for discussion and interaction among students and lecturers.

Invited speakers:

Casey Bergman - Manchester Laurent Duret - Lyon Arndt von Haeseler - Vienna Jerzy Jurka - Mountain View Martin Lercher - Heidelberg Michael Lynch - Bloomington Tobias Müller - Würzburg

Scientific Coordinators:

Peter Arndt - Berlin Michael Lässig - Cologne Martin Vingron - Berlin

The deadline for applications is June 16, 2006. The registration fee of 600 EUR includes costs for accommodation and meals. The registration fee for PhD and Masters students is 400 EUR (or 100 EUR without accommodation).

Application forms can be filled in online on the workshop's website at

<http://ows.molgen.mpg.de> The announcement as a printable poster is available from

<http://ows.molgen.mpg.de/2006/poster06.pdf> For further questions please contact

Hannes Luz c/o Max Planck Institute for Molecular Genetics Computational Molecular Biology Ihnestrasse 73 D-14195 Berlin, Germany Tel: +49 30 8413 - 1154 Fax: +49 30 8413 - 1152 Email: luz@molgen.mpg.de

Best regards,

the Otto Warburg Summer School team

[hannes.luz <luz@molgen.mpg.de>](mailto:hannes.luz@molgen.mpg.de)

EMBO where EvoDevo when

EMBO Practical Course on "Molecular approaches to Evolution and Development" http://www-db.embl.de/jss/EmblGroupsOrg/conf_45 in cooperation with ZOONET (Marie Curie Research Training Network) <http://www.zoonet.eu.com/> This course is aimed at PhD students and postdoctoral fellows working in the field of Evolution of Development (Evo Devo). The major focus of the course will be on recent progress in techniques that facilitate the analysis of gene expression and function in non-conventional model organisms, with teachers that have been spearheading technical developments.

Post-transcriptional gene silencing (RNA interference, RNAi) is a reverse genetics approach that allows the fast functional analysis of a given gene. RNAi experiments will be conducted in beetles, crustaceans, and spiders, but also in other ecdysozoan and lophotrochozoan models. During the course participants are encouraged to transfer available RNAi techniques to their animal model of choice.

The recent establishment of broadly applicable genetic transformation systems has been the second major breakthrough for functional analysis in a variety of non-conventional animal models. Transgenesis allows stage and site-specific expression of promoter constructs to express fluorescent proteins, or for gain- or loss-of-function analysis. Heterologous transformation into various species allows the comparative study of cis-regulatory elements. We will teach these techniques in order to facilitate transfer into additional animal models, giving an up-to-date survey of vectors and integration techniques currently available.

Single and double wholemount in situ hybridisation techniques are prerequisite for various aspects of Evo-Devo research, for example the comparison of cell types. We will focus on recent technical improvements such as double fluorescent in situ hybridisation protocols to be tried in different organisms. Again, participants are encouraged to transfer techniques to their model of choice.

A second focus of the course will be on practical and theoretical aspects of analysis and interpretation of the phylogenies and of fossil data. This part of the course will impart practical knowledge of molecular phylogeny reconstruction and the uses to which this can be put. We will also cover the fundamentals of palaeontology

with the aim of integrating fossil data into comparative evolutionary studies.

Topics

sea urchins, polychaetes, crustaceans, spiders, beetles
technique transfer to new emerging models injection,
transgenesis, RNA interference, morpholino-mediated
gene knockdown wholemount in situ hybridisation phy-
logeny reconstruction palaeontology confocal and elec-
tronic microscopy sea fauna collecting trip

Teachers

Michael Akam, Museum of Zoology, University of Cam-
bridge, United Kingdom Detlev Arendt, EMBL Hei-
delberg, Germany Maria Ina Arnone, Stazione Zoolog-
ica Anton Dohrn, Naples, Italy Michalis Averof, Inst.
Molecular Biology and Biotechnology (IMBB), Crete,
Greece Gregor Bucher, Dept. of Developmental Bi-
ology, University Göttingen, Germany Graham Budd,
Department of Earth Sciences, Palaeobiology, Uppsala,
Sweden Richard Copley, Wellcome Trust Centre for Hu-
man Genetics, United Kingdom Wim Damen, Insti-
tute for Genetics, University of Cologne, Germany
Anastasios Pavlopoulos, University Museum of Zool-
ogy, United Kingdom Niko Prpic, Dept Biology, Uni-
versity College London, United Kingdom Max Telford,
Dept Biology, University College London, United King-
dom Kristin Tessmar-Raible, EMBL Heidelberg, Ger-
many Ernst Wimmer, Dept. of Developmental Biology,
University Göttingen, Germany

Registration

Please register online.

<http://www-db.embl.de/jss/EmblGroupsOrg/conf.45>
Deadline for registration is 31 May 2006. Online regis-
tration ONLY Applications should contain a short CV,
a statement on current research and a justification of
interest in the course. A travel grant of EUR 250,- will
be offered to TWO non-Zoonet students (this decision
will be taken by the scientific organisers once they have
viewed all applications) The number of participants is
limited to 16.

– Dr Max Telford Department of Biology, University
College London, Darwin Building, Gower Street, Lon-
don WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 Fax:
+44 (0)20 7679 7096

[http://www.ucl.ac.uk/biology/academic-staff/-
telford/telford.html](http://www.ucl.ac.uk/biology/academic-staff/-telford/telford.html) Zoonet website: [http://-
www.zoonet.eu.com](http://-
www.zoonet.eu.com) m.telford@ucl.ac.uk

FaroPortugal EvolEcol Sep11-15 2

ADVANCED COURSE ON DESIGN AND ANALYSIS
OF ECOLOGICAL EXPERIMENTS September 11-15
2006, at the University of Algarve, Faro, Portugal

Presented by: Professor A.J. Underwood and Dr M.G.
Chapman Centre for Research on Ecological Impacts of
Coastal Cities, University of Sydney, NSW 2006, Aus-
tralia

Registration (with payment) deadline: June 2, 2006
Cost: 500 euros, includes course materials and coffee
breaks (accommodation and meals not included)

Site for registration and information on lodging: [http://
www.ualg.pt/ccmar/maree/education.php](http://www.ualg.pt/ccmar/maree/education.php) Course
outline:

1. Revision and Development of Alternative Designs for
Complex Experiments of Fixed and Random Factors
Typical biological experiments; Revision of The Gen-
eral Linear Model; Calculations of Sums of Squares;
Multiple comparisons; Cornfield Tukey Rules; Multi-
ple comparisons; Post-hoc pooling Practical Exercises
Evaluation of alternative designs to test complex hy-
potheses
2. Correlations and Regressions Revision of regression
and correlation Partial linear regressions One-Factor
Analysis of Covariance (a sequence of 3 linear models)
Practical Exercises Partial/multiple regression Analy-
ses of Covariance, comparisons across more than 2 sam-
ples
3. Asymmetrical analyses of variance and Environ-
mental Monitoring Asymmetrical analyses of variance
Environmental monitoring: BACI (Before/After, Con-
trol/Impact designs) Beyond BACI designs to iden-
tify pulse and press disturbances How to deal with no
³Before data² Practical Exercises Asymmetrical analy-
ses of variance for tests of fixed effects in experimen-
tal manipulations; How to construct ³Beyond_BACI
analyses² from analyses of variance tables Problem
solving with/without ³Before data²
4. Analyses of variances Identification of hypotheses
about variances; Extraction and use of components of
variation Practical Exercises Tests of hypotheses using
components of variation
5. Power in experimental design Power analysis: Fixed
and random factors Practical Exercises Calculating

power for fixed and random factors; effects of sample size, variance and number of levels of factors on calculations of power in different experiments

6. Additional topics (lectures and/or practical classes): Quantification of problem-solving Logics of experimental tests of hypotheses Hypotheses about multivariate measures: tests using multifactorial designs

eserrao@ualg.pt

KristinebergSweden LifeHistory Jul17-28

Marine Summer Course 2006

Analysing Biodiversity & Life History Strategies

* This course will deal with the latest methods in biodiversity research, including genomic approaches, DNA barcoding and molecular tools in developmental studies, presented by invited teachers, all internationally known experts in their fields. Hands-on experience with animals will be combined with possibilities to work with modern analytical techniques like phylogenetic analysis, sequence analysis, fluorescence and confocal laser scanning microscopy * Open to PhD students and post docs; both to members of the MGE network and to non-members * The MGE Network pays for everyone's course fee (including lunches, coffees, excursion and farewell dinner) and the accommodation for the PhD students. Everyone pay for their own travel. * July 17-28, 2006, Kristineberg Marine Research Station (www.kmf.gu.se <<http://www.kmf.gu.se/>>), Sweden * Deadline for applications extended to the 1st of May, 2006 * Information and application forms can be found at the MGE website (www.marine-genomics-europe.org <<http://www.marine-genomics-europe.org/>> , go to Training & Education).

Ulrika Hjelm Training and Education Programme Manager

NoE Marine Genomics Europe

Kristineberg Marine Research Station S-450 34 Fiskeb?ckskil Sweden Phone: ++46 (0) 523 18548 Fax: ++46 (0) 523 18502 Mobil: ++46 (0) 70 344 2371 E-mail: <blocked::mailto:ulrika.hjelm@kmf.gu.se> ulrika.hjelm@kmf.gu.se

Matthias Obst <matthias.obst@kmf.gu.se>

Madrid TreePopGenet Oct4

This is the first call for participation in a workshop on SIMULATION MODELS OF TREE POPULATION GENETICS

October 4th, 2006. Alcalá de Henares (Madrid, Spain)

This workshop is included in the IUFRO conference "Population Genetics and Genomics of Forest Trees: from Gene Function to Evolutionary Dynamics and Conservation", to be held in Alcalá de Henares, October 1-6, 2006 (<http://www.genfor2006.fgua.es>)

Attendance to this workshop requires registering to the IUFRO conference.

Attendants are encouraged to present their work on simulation models of tree population genetics in this 4-hour workshop, which is aimed at offering a practical overview of the role and technical features of up-to-date simulation models in tree population genetic analyses. Talks (15-20 min + 10-15 min for discussion) should deal with topics not easily addressable via experimental or analytical approaches, should stress methodological aspects, and should be structured in a didactic way.

Suggested topics include:

* Spatio-temporal demographic stochasticity and population genetic processes * Mating system evolution, hybridization and speciation * Implementation of quantitative traits under selection in individual-based models * Interaction between gene flow and selective processes (in a changing environment) * Selective consequences of the genetic architecture on inbreeding depression and adaptive variation in trees * Impact of linkage among adaptive genes and/or with neutral markers. Modelling of hitchhiking * Transgene escape risk assessment * Predictive models in forest management and conservation genetics

Priority will be given to contributions combining demographic, reproductive and selective processes in spatially explicit context, accounting realistically for life history traits of trees.

Contributors should submit an abstract before May 31 through the IUFRO conference website (<http://www.genfor2006.fgua.es>), indicating in the first line "Contribution for the Simulation Models Workshop". Please send also a copy of the abstract to Juan J. Robledo-Arnuncio (robledo@isem.univ-montp2.fr). If

some of you have already submitted an abstract for the IUFRO conference and would like it to be allocated into this workshop please contact Juan J. Robledo-Arnuncio.

Acceptance of contributions will be announced before July 1, 2006.

Workshop Organizers: Frédéric Austerlitz, John R. Pannell, Miguel Verdú and Juan J. Robledo-Arnuncio.

robledo@isem.univ-montp2.fr robledo@isem.univ-montp2.fr

PortoPt ConsGenetDataAnalysis Aug30-Sep2

THIS IS THE FINAL ANNOUNCE FOR THE COURSE TITLED

CONSERVATION GENETICS DATA ANALYSIS COURSE/WORKSHOP: Recent Approaches for Estimation of Population Size, Structure, Gene flow, Parentage, & Selection Detection

30 August to 2 September, 2006, Porto, Portugal See <http://cibio.up.pt/congen/> for the updated Program and to apply.

INSTRUCTORS/SPEAKERS: Fred Allendorf, Mark Beaumont Peter Beerli Albano Beja-Pereira Daniel Falush Adam Jones Gordon Luikart Karen Fear Martien Mark Miller Scott Mills Mike Schwartz David Tallmon Robin Waples

TOPICS: Introduction to Conservation Genetics, molecular markers, and data analysis Frequentist, Likelihood, Bayesian approaches Coalescent Non-invasive DNA sampling advantages and pitfalls Population size estimation from non-invasive DNA data Genetic monitoring Effective population size estimation and bottleneck detection Population structure, evolutionary significant units, and management units Landscape genetics and spatially explicit approaches Gene flow, dispersal and assignment tests Parentage and relatedness Population Genomics and detecting FST outliers and selection

Application costs increase after June 15 (if places are still available).

Albano Beja-Pereira <albanobp@fc.up.pt> Albano Beja-Pereira <albanobp@fc.up.pt>

ProtoPT ConsGenetDataAnalysis Aug30-Sep2

Course: Conservation Genetic Data Analysis

Second announcement: Online Registration is Open

Course: Conservation Genetics Data Analysis Recent Approaches for Estimation of Population Size, Structure, Gene flow, Parentage, & Selection Detection/ 30 August to 2 September, 2006, Porto, Portugal/**/*

* *

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genetics of natural and managed populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will mainly cover analysis of allele frequency data (not DNA sequence data), including coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 25 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students near the end of their degree program). * *

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-45 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

Instructors/Speakers: Fred Allendorf, Mark Beau-

mont, Peter Beerli, Albano Beja-Pereira, Daniel Falush, Adam Jones, Gordon Luikart, Karen Martien, Mark Miller, Scott Mills, Mike Schwartz, David Tallmon, and Robin Waples.

*Location: *The course will be held in the facilities at CIBIO (Center for Investigation of Biodiversity and Genetic Resources; <http://cibio.up.pt/>) on the Campus for Agricultural Sciences in the rural village of Vairão, just north of Porto, and a few kilometres from the Atlantic coast and the airport. Vairão is an ancient village whose origins can be traced back to the Roman Period (the Roman village Valeriani).

Registration and cost: For detailed information and registration see <http://cibio.fc.up.pt/congen> . Accommodations and meals are included in the registration fee. Cost: \$US 1,000 per person will cover all meals, lodging, transportation to and from the airport, and a visit to Gerês National Park and the World Heritage City of Porto. Up to two reduced-cost scholarships will be available for candidates with no funding.

Application and criteria for acceptance: /Deadline/ for application is */15 June/, 2006*. Applicants must provide a brief description of their research interests, career goals, and what they would like to learn from this course. Priority will be given to persons with their own data to analyze (for example graduate students near the end of their degree program). The applicants should submit a brief summary (<200 words) about the current state of their work, the hypotheses or questions addressed, the genetic markers used, and study species. To apply for scholarship support, candidates should also send their CV, a cover letter explaining why they should receive the scholarship, a cost estimate for their flight (round trip) to Porto, and a phone number where they can be reached for a brief interview. **

Albano Beja-Pereira <albanobp@fc.up.pt>

Split Croatia MedILS Jul18-22

1st MedILS Summer School “Structure and Evolution: from Bench to Terminal” 18th-22nd July 2006 Split, Croatia

We are pleased to announce that the 1st MedILS Summer School “Structure and Evolution: from Bench to Terminal” will be held at the Mediterranean Institute for Life Sciences (MedILS) in Split, Croatia from 18th-22nd July 2006.

This year’s School is intended for doctoral students interested in applying bioinformatics tools and resources in their research ranging from the investigation of structure, function and interactions of biological macromolecules to genome evolution.

The School is designed to cover basic as well as more specific topics in bioinformatics, and sensitize students to the options and solutions available. It is organized as a series of terminal-based exercises complemented by lectures and discussions in which state-of-the-art issues will be presented.

A workshop dedicated to the improvement of communication between scientists and the general public and lead by a renowned local science journalist will also make an integral part of this School.

The registration for this School will remain open until 5th June, 2006. Registration form, as well all the other information can be seen at: <<http://www.medils.hr/sschool/general.php>>www.medils.hr/sschool/general.php If you have any additional questions, you may contact us at: summerschool@medils.hr

Looking forward to meeting you in Split,

Vlatka Petrovic MedILS Summer School Organizing Committee

vpetrov@irb.hr

Vlatka Petrovic <vpetrov@irb.hr>

UBologna EukaryoteEvol Sep17-22

SUMMER SCHOOL “GENOME EVOLUTION IN EUKARYOTES (GEE)” , 17-22 September 2006

Dear EvolDir Members,

We are please to announce the first Summer School “Genome Evolution in Eukaryotes (GEE)” organized by the University of Bologna, and to be held in the University Residential Centre of Bertinoro (Ravenna - Italy) from 17th to 22nd of September 2006.

We are also pleased to inform you that the GEE website is now on line at www.gee.unibo.it . Applications are now open. Please note that the deadline is the 30th of June 2006.

Best wishes,

Dr. Marco Passamonti GEE Summer School Secretariat

Marco Passamonti Dipartimento di Biologia Evoluzionistica Sperimentale via Selmi 3 I-40126 Bologna (Italy) tel. +39/0512094162 fax +39/0512094286 mpassa@alma.unibo.it

mpassa@alma.unibo.it

UWashington MarineSpatialVariation

(apologies for cross postings)

Ecological and Evolutionary Analysis of Spatial Variation in Marine Systems Research Apprentice Course Fall Semester 2006, August 21 - December 9, 2006, 20 quarter-units at the Friday Harbor Laboratories, University of Washington Enrollment limited to 12 students Instructors: Sarah Gilman (gilmans@u.washington.edu) and Melissa Frey (mafrey@ucdavis.edu)

Applications due June 10, 2006 <http://depts.washington.edu/fhl/studentApprentice2006.html>

Live and do research for 16 weeks at Friday Harbor Laboratories, the world-renowned University of Washington marine lab on San Juan Island, 75 miles northwest of Seattle.

The Friday Harbor Labs offer intensive, full-time research training experiences to qualified undergraduates and post-baccalaureates from any college or university. Teams of students each work on one focused research problem guided by a group of faculty, postdoctoral and graduate student mentors. Students selected for participation receive financial support to defray costs for room and board at FHL and tuition charged by University of Washington.

For the first time, FHL is offering one research apprenticeship on a semester schedule, with a greater unit load to accommodate students from institutions based on a semester OR quarter system. Students will earn 20 quarter-units (approximately 13-15 semester units, de-

pending on your home institutions rules).

Course Description

Marine benthic ecosystems are notorious for exhibiting extreme environmental heterogeneity over small spatial scales. Over scales of meters to kilometers, organisms may encounter significant differences in environmental conditions, such as emersion times, wave exposure, and community composition. This heterogeneity presents a challenge to marine organisms because traits that allow an individual to succeed in one environment may be detrimental in others. Local adaptation and phenotypic plasticity are common responses to environmental heterogeneity. In turn, dispersal, which influences how frequently individuals encounter variability within or between generations, shapes these adaptive responses. In this course, apprentices will investigate how marine populations balance local adaptation, phenotypic plasticity, and dispersal to counteract the challenges of living in a spatially heterogeneous environment. A primary objective of the course is to train students in both experimental and molecular approaches to marine ecology. Through lectures, readings, and discussions, as well as field excursions and demonstration labs, students will gain hands-on knowledge of: marine ecology and the natural history of the San Juan Islands, experimental design, basic techniques in molecular ecology, and current ecological and evolutionary theory of environmental heterogeneity. The primary focus of the course will be independent research projects designed and conducted by each student

For more information check out the Research Apprentice page on the FHL website (<http://depts.washington.edu/fhl/studentApprentice2006.html>) or contact the instructors at gilmans@u.washington.edu and mafrey@ucdavis.edu

Sarah Gilman, PhD

Friday Harbor Laboratories University of Washington
620 University Rd. Friday Harbor, WA 98250

360-378-2165 gilmans@u.washington.edu
<http://faculty.washington.edu/gilmans>
gilmans@u.washington.edu gilmans@u.washington.edu

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

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

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L^AT_EX do not try to embed L^AT_EX or T_EX in your message (or other formats) since my program will strip these from the message.