
E v o l D i r

November 1, 2005

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.

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ArizonaStateUTempe SMBE May24-28

*** Please take note that the deadline for proposals for symposia at the 2006 SMBE Conference in Tempe, AZ is November 1, 2005. All information is below. ***

CALL FOR SYMPOSIA for 2006 Conference on Genomes, Evolution, and Bioinformatics (ANNUAL SMBE MEETING 2006)

The 2006 annual meeting of the Society for Molecular Biology and Evolution will be held from May 24-28, 2006, at the Arizona State University in Tempe. The Organizing Committee invites individuals to present their proposals for potential symposia ideas. Symposia proposals should include:

Cover sheet including symposium title and all information for point of contact Brief abstract including clear description of topic and rationale for its presentation to the society Identify up to four potential participants, affiliations, and what each may contribute

Successful proposals will be identified based on their clarity, innovation, and relevance to the theme of the 2006 meeting: Genomics, Evolution, and Bioinformatics. In addition, proposals that support an emerging field or discipline that reflects the unique and specific

interests of the SMBE will also be targeted. Both the society and the committee are especially interested in proposals that highlight diversity in science and include underrepresented groups.

Each symposium will have three or six speakers, with each speaker allotted 25 minutes (plus 5 minutes for questions). The organizers will provide support for the symposium proposer and invited speakers in the form of registration fees. In exceptional cases, the conference organizers are also prepared to provide hotel and airfare reimbursements for invited speakers. All proposals will be considered in the order submitted and proposers will be notified of the committee's decision at the latest by November 15, 2005.

All queries and the symposia proposals should be addressed to symposia@smbe.org. Proposals may be received as a Word or PDF attachment via email and must be received on or before November 1, 2005.

Organizing committee Sudhir Kumar, Jeffrey Touchman, and Brian Verrelli George Poste & Jeffrey Trent, Honorary Co-chairs www.biodesign.org/efg www.biodesign.org www.tgen.org bvc1972@yahoo.com

Atlanta Bioinformatics Nov17-19 2

UPDATE –

Per requests, we will extend the abstract submission deadline to October 14, 2005.

- Online abstract submissions open until October 14, 2005 - NIH travel grant for PhDs and postdoctoral fellows: . \$750 for foreign scholars . \$500 for scholars within US and Canada. . Nomination due: extended to October 7, 2005. - Early registration due October 14 2005 - Conference schedule available online - Check hotel information on conference website

5th Georgia Tech - ORNL International Conference on Bioinformatics, in Silico Biology

“Computational Genomics and Evolutionary Biology” November 17-19, 2005, Atlanta, Georgia, USA

Home Page: <http://opal.biology.gatech.edu/-conference/> ORGANIZED BY

Georgia Tech Oak Ridge National Lab

Selected papers will be published in a special issue of BIOINFORMATICS journal (Oxford University Press)

IMPORTANT DATES

November 17-19, 2005 - Conference time September 30, 2005 - Poster Abstract submissions due October 14, 2005 - Early Registration due

CONFIRMED INVITED SPEAKERS:

Naama Barkai, Weizmann Institute of Science Natalia Komarova, Rutgers University Michael Lynch, Indiana University, Bloomington Pierre Baldi, University of California, Irvine Philip Bourne, University of California, San Diego Volker Brendel, Iowa State University Julio Collado-Vides, UNAM, Cuernavaca, Mexico Andrew Ellington, University of Texas at Austin Dmitrij Frishman, University of Munich & Max-Planck, Germany Sorin Istrail, Brown University Alex Kondrashov, NCBI / NIH John McDonald, Georgia Tech Jeffrey Thorne, North Carolina State University

STEERING/PROGRAM COMMITTEE

- Conference Chairs: Mark Borodovsky, Georgia Tech Eugene Koonin, NCBI / NIH

- Program Chairs: Eva K. Lee, Georgia Tech and Emory University Andrey Gorin, Oak Ridge National Laboratory

Georgia Tech Conference Announcement
<conf@opal.biology.gatech.edu>

Edinburgh PopGenetics Dec2005

The web site for the Population Genetics Group meeting, in Edinburgh, December 2005 is now open for registration and payment at

<http://web.bio.ed.ac.uk/public/conferences/-PopulationGenetics2005/index.html>

It is possible to complete both parts together, or at separate times, but all accommodation bookings will be provisional until you have paid.

The deadline for both registration and payment is November 7th (see the web site for full details).

– Professor Deborah Charlesworth Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Ashworth Lab., King’s Buildings, West Mains Rd., Edinburgh EH9 3JT, UK

phone 131-650-5751 Fax: 131-650-6564
deborah.charlesworth@ed.ac.uk debo-
rah.charlesworth@ed.ac.uk

Edinburgh PopGenetics Dec2005 2

This is to remind you that the deadline is getting close for registration and payment for the Population Genetics Group meeting, in Edinburgh, December 2005

The deadline is November 7th

There will be three plenary speakers

Wolfgang Stephan (Munich) Population genetics of adaptation

Gil McVean (Oxford) The causes and consequences of human recombination hotspots

Patrice David (Montpellier) Quantitative genetics of traits controlling selfing and outcrossing in hermaphroditic snails

The web site

<http://web.bio.ed.ac.uk/public/conferences/-PopulationGenetics2005/index.html>

gives all details that are currently available (the programme will appear close to the date of the meeting). It is possible

to complete both registration and payment parts together, or at separate times, but all accommodation bookings will be provisional until you have paid.

Please note that the correct information about how to select the Pop Group in the payment site is as follows (the pdf and Word versions that are available from the web site are both correct, but an earlier version had different information, because the university changed things slightly after I had sent out the first announcement):

>After entering your email and other details as prompted, you get a >page to select the 'product' you want to pay for. From the left hand >pull-down menu, select Institute of Evolutionary Biology, and from >the right-hand menu select Conferences, and then the lower menu >shows the Pop Group.

Update of the information about arrival, computers and Poster boards. Arrival Go to the Reception desk of the James Watt Centre. They will direct you to the Registration desk, which will be open from 2pm. The building will be closed at 9pm, but there is a bell (on the left of the entrance) for the night porter (all night). The Reception desk or the night porter will give room keys.

Guests may check in to their accommodation from 1400 on the day of arrival and are asked to vacate bedrooms and return keys to reception by 1000 on the day of departure.

The registration desk for the meeting will be open in the main reception foyer just outside James Watt Centre from 1400-2200.

Computers The meeting rooms have a built-in projection system, and we will provide Macintosh computers for those who prefer them. We prefer people to bring their talks on a CD or 'data stick' and to load them onto one of the computers, at the latest in the break before their session. If you are bringing your own computer, however, for your talk, or other uses, remember that non-UK equipment will require an adaptor, because UK sockets are quite different from those elsewhere in Europe.

Poster boards The boards measure 1.2m x 1.8m and have a blue felt backing which requires posters to be affixed by using either hook velcro or pins. If you are presenting a poster, please email me whether it is to be upright or 'landscape' format.

– Professor Deborah Charlesworth Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Ashworth Lab., King's Buildings, West Mains Rd., Edinburgh EH9 3JT, UK

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debo-

KansasCity EcolGenomics Nov4-6

Please Note: Hotel reservation deadline is Friday, October 14, at midnight!

We are continuing to accept Registrations for you to attend

What? Ecological Genomics Symposium When? November 4, 5, and 6, 2005 (Friday evening, Saturday, & Sunday morning) Where? Radisson Hotel, Lenexa-Overland Park, KS (Kansas City metro area) How do I register? Click on the following links: ONLINE Registration for the conference <https://www.dce.ksu.edu/cgi-bin/conf/ecological_genomics.cgi> , and ONLINE Reservations for the Radisson Hotel <<http://www.radisson.com/ecogen>> Deadline for a guaranteed room rate of \$65 is Friday, 10/14/05. Who is speaking? You will learn about this new interdisciplinary field from leaders at the forefront of ecological and evolutionary functional genomics: Toby Bradshaw, John Kenneth Colbourne, Edward F. DeLong, Martin E. Feder, Jan Kammenga, Trudy F. C. Mackay, Thomas Mitchell-Olds, Johanna Schmitt, Jack C. Schultz, Charles W. Whitfield. (Titles of their presentations are below.) You will also learn about research of the Kansas ecological genomics initiative that comprises over 35 faculty from three universities. What is ecological genomics? Ecological Genomics is an emerging 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. Questions? Contact ECOGEN@ksu.edu <<mailto:ECOGEN@ksu.edu>> or (785) 532-3482.

A complete brochure and Symposium schedule can be downloaded by clicking on the Symposium Information website at www.ksu.edu/ecogen/symp2005.html <<http://www.ksu.edu/ecogen/symp2005.html>> . Links for online Conference Registration and Hotel Reservations are also posted on the website. On Saturday night, an optional dinner has been arranged at the Brio Tuscan Grille on the Country Club Plaza, Kansas City, Missouri. The cost is \$40 and transportation will be provided. Please share this announcement with colleagues and students who are interested in learning more about the emerging field of Ecological Genomics. Ecology in Genes, Genes in Ecology Featured Speak-

ers: Toby Bradshaw, University of Washington, The genetic basis of adaptive evolution in natural plant populations John Kenneth Colbourne, Indiana University, Finding genes linked to the ecological success of *Daphnia* Edward F. DeLong, Massachusetts Institute of Technology, Exploring the natural microbial world, from genomes to biomes Martin E. Feder, The University of Chicago, Transposition and heat-shock genes: a genomic scan for evolvability of transcription Jan Kammenga, Wageningen University, Genomical approaches for understanding life-history adaptation to temperature in natural populations of *C. elegans* Trudy F. C. Mackay, North Carolina State University, The genetic architecture of complex traits: Lessons from *Drosophila* Thomas Mitchell-Olds, Max-Planck Institute of Chemical Ecology, Functional evolutionary genomics of ecologically important variation Johanna Schmitt, Brown University, Adaptive evolution of seasonal timing in *Arabidopsis thaliana* Jack C. Schultz, Penn State University, Whole-genome microarray analysis reveals species-specific responses by *Arabidopsis* to insect herbivores Charles W. Whitfield, University of Illinois, Genomic dissection of naturally occurring behavioral maturation in the honey bee

Funding for this symposium is provided by Kansas NSF EPSCoR, The Kansas Technology Enterprise Corporation, and Kansas State University. Ecological Genomics in Kansas Project Leaders: Loretta Johnson & Mike Herman, Kansas State University; Bob Cohen & Daniel Crawford, University of Kansas

Doris Merrill Ecological Genomics, Div of Biology Kansas State University 785-532-3482, dmerrill@ksu.edu www.ksu.edu/ecogen dmerrill@ksu.edu

signed to promote interaction among researchers working on diverse aspects of this exciting inter-disciplinary field. The meeting is limited to 80 participants and so should you be interested in attending early registration is recommended.

Invited speakers include: Kathleen Donohue (Harvard University, Cambridge, MA, USA) Candace Galen (University of Missouri-Columbia, MO, USA) Angela Hodge (University of York, UK) Andre Kessler (Cornell University, Ithaca, NY, USA) Ariel Novoplansky (Ben-Gurion University of the Negev, Israel) Johanna Schmitt (Brown University, Providence, RI, USA) Jack C. Schultz (Penn State University, University Park, PA, USA) Harry Smith (University of Nottingham, UK) Fernando Valladares (CSIC Madrid, Spain) Rens Voesenek (University of Utrecht, The Netherlands) Cynthia Weinig (University of Minnesota, St Paul, MN, USA)

Further details can be found at: <http://www.newphytologist.org/eco-devo> Important dates Abstract deadline - 30 October 2005 Registration deadline - 30 November 2005

Contact Holly Slater (New Phytologist, h.slater@lancaster.ac.uk <<mailto:h.slater@lancaster.ac.uk>>)

Dr HOLLY SLATER Managing Editor, New Phytologist

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New! 2004 Impact factor 3.355

"Slater, Holly" <h.slater@lancaster.ac.uk>

London PlantEcolDev Jan23-24

SYMPOSIUM ANNOUNCEMENT

14th New Phytologist Symposium: New directions in plant ecological development The Royal Society, London, UK. 23-24 January 2006

Keynote Speaker: Professor Anthony D. Bradshaw

Organizers: Sonia Sultan (Wesleyan University, USA), David Ackerly (University of California at Berkeley, USA), Holly Slater (New Phytologist, UK)

New Phytologist is pleased to announce that our next symposium will focus on plant ecological development. This will be a discussion-based, two-day meeting de-

London PlantEcolDev Jan23-24 2

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Contact Holly Slater (New Phytologist, h.slater@lancaster.ac.uk <<mailto:h.slater@lancaster.ac.uk>>)

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New! 2004 Impact factor 3.355

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London NHM Phylogenetic Trees Nov2

CEE Workshop. "Evolutionary Inferences from Phylogenetic Trees.

Wednesday 2nd November.

Flett Theatre, Natural History Museum, Exhibition Road (Earth Galleries) Entrance.

ALL WELCOME. ENTRY IS FREE

9.30 Welcome and Introduction.

Session 1. Chair Prof Linda Partridge. Dept Biology, UCL

9.40 Mark van der Giezen. School of Biol. Sciences, Queen Mary London Degenerate mitochondria; convergent adaptations to an anaerobic lifestyle

10.20 Richard Emes. Department of Biology, UCL Genome wide detection of adaptive molecular evolution

11.00-11.30 Tea

Session 2 Chair Dr Sandy Knapp. Dept. Botany NHM.

11.30 Peter Olson, Department of Zoology, NHM Using phylogenies for diagnostics and co-evolution in parasitic flatworms

12.10 James Clarkson, Jodrell Laboratory, Kew. Molecular clocks and polyploid evolution: A case study from *Nicotiana* (Solanaceae)

12.50-2.30 Lunch

Session 3 Chair Dr Peter Olson. Dept Zoology, NHM.

2.30 James Cook. Division of Biology, Imperial College London Searching the jungles for trees: phylogenies of coevolving figs and wasps

3.10 Andrew Parker, Department of Zoology, NHM Tracing the evolution of optical reflectors in animals

3.50-4.20 Tea

Session 4 Chair Prof. Adrian Lister. Dept Biology UCL.

4.20 Mark Carine Department of Botany, NHM Relationships of Macaronesian island floras: insights from molecular phylogenetics

5.00 Cassandra Extavour. Department of Zoology, Cambridge Germline-Soma Differentiation: Can phylogeny predict molecular mechanisms of germ cell specification?

5.50 Drinks reception

– Dr Max Telford Department of Biology, University College London, Darwin Building, Gower Street, London 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> Zoonet website: <http://www.zoonet.eu.com> m.telford@ucl.ac.uk

London NHM Speciation Nov9

REMINDER

Speciation Symposium

The Natural History Museum, Cromwell Road, London
- Wednesday 9 November 2005

Everyone interested in speciation is warmly invited to attend. The symposium will be held in the Flett Lecture Theatre (use Exhibition Road entrance to the Museum and follow signs), beginning at 12.45 and ending at about 18.00. There will be an invited presentation by Patrik Nosil and 10 other talks (programme available on request).

Registration is not required and admission is free. However, if you are interested in joining us for dinner after the meeting, please let one of us know (by 27 Oct) so that we can try to book a table.

Roger Butlin (r.k.butlin@sheffield.ac.uk) and Ralph Harbach (reh@nhm.ac.uk)

Malta Mediterranean Seagrass May29-Jun3 2

Mediterranean Seagrass Workshop 2006 - Second Announcement We are pleased to announce that abstract submission is now open!

Please visit the 'abstract submission and publications' page at <http://events.um.edu.mt/msw2006/Abstracts.html> for further details. You will also be notified of registration details and forms, since this will be available soon. We take this opportunity to remind you of the following important dates: 15th October 2005: Close of abstract submission 15th December 2005: Notification of abstract acceptance 28th February 2006: Close of early registration 30th April 2006: Close of registration 30th May 3rd June 2006: MSW 2006 Please visit the web page <http://events.um.edu.mt/msw2006/index.html> for further details Thank you!

The MSW 2006 Organising Committee

gpro@szn.it

Marseilles EvolBiol10 Sep20-22

The 10th evolutionary biology meeting at marseilles will take place the 20th, 21st, 22nd of September 2006. fore more info

<http://www.up.univ-mrs.fr/evol-cgr/> – Pierre Pontarotti EA 3781 Evolution Biologique Université d'Aix Marseille I Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 <http://www.up.univ-mrs.fr/evol> We are organizing the 10th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol-cgr/> Pierre.Pontarotti@up.univ-mrs.fr

PortTownsendWA EVO-WIBO Apr21-23

This is a reminder that the 2nd Evo-WIBO meeting of Pacific Northwest evolutionary biologists has been scheduled for April 21-23 at Fort Worden State Park in Port Townsend, Washington.

Registration won't be open until January 2006, but you can get the meeting on your calendar now.

More information at <http://www.zoology.ubc.ca/-evo-wibo> Patrick C. Phillips, Associate Professor of Biology Center for Ecology and Evolutionary Biology Email: pphil@uoregon.edu Phone: (541) 346-0916 | FAX (541) 346-2364 Address: 5289 University of Oregon Eugene, OR 97403-5289 USA Web: Lab <http://www.uoregon.edu/~pphil> EvoNet <http://www.EvoNet.org> CEEB <http://evolution.uoregon.edu> IGERT <http://-evodevo.uoregon.edu> pphil@uoregon.edu

Prague EuropeanEvolDevo Aug17-19

*First announcement: Prague, 17-19 August 2006

*We are pleased to announce the first and founding meeting of the *European society for Evolutionary Developmental biology (EED) *Plenary talks-Symposia-Contributed sessions-Poster sessions

Costs will be kept as low as possible.

The aim of the society is to promote evolutionary developmental biology by regularly organizing meetings on this subject in Europe, perhaps alternating with the meetings of ESEB. The society will welcome scientists from all over the world. A second more detailed announcement regarding the Prague meeting will follow soon.

Please forward this mail to colleagues that might be interested in joining the new society. For those of you who have received this mail as forwarded message from a colleague, or via an email list, please send us your name and email address to make sure that you receive further information.

The organizing committee is looking forward to see you in Prague.

Organizing committee: Graham Budd Didier Casane Phil Donoghue Robert Cerny Dave Ferrrier Frietson Galis Jordi Garcia-Fernandez Scott Gilbert, Thomas Holstein Ivan Horacek Ann Huysseune Ronald Jenner Jukka Jernvall Chris Klingenberg Sylvie Mazan Lennart Olsson Michael Richardson Isaac Salazar-Ciudad Gerhard Schlosser Urs Schmidt-Ott Seb Shimeld Günter Theissen Tom Van Dooren Adam Wilkins Eckhard Witten Adam Wilkins

Scientific board Per Ahlberg Richard Aldrich Claudio Alonso Wallace Arthur Jaume Baguñà Patricia Beldade Paul Brakefield Mike Coates Martin Cohn Quentin Cronk Gunter Eble Barbara Gravendeel Alain Ghysen Thomas Holstein Shigeru Kuratani Bertrand Lefebvre Armand Leroi Miguel Manzanares Hans Metz Axel Meyer Alessandro Minelli Gerd Mueller Claus Nielsen Luis Puelles Mark Purnell Moya Smith Gerhard Scholtz Jean-Yves Sire Ralph Sommer Matthias Starck Diethard Tautz Miltos Tsiantis Günter Wagner

A website will be available soon For more information: frietson.galis@gmail.com

vdooren@rulsfb.leidenuniv.nl

**QueensGate London Entomology
Feb1**

Royal Entomological Society Postgraduate Forum 2006
Call for oral and poster presentations from postgraduate research students

The forum is a friendly venue where young scientists can gain experience giving presentations in a conference setting, as well as networking with other researchers. We invite students working on any aspect of entomology to join. [For university students: this is an excellent opportunity to get credit points towards your degree]. Prizes for best poster and oral presentation will be awarded.

Confirmed invited postgraduate speakers are:

Alessandra Curtotti (Queen Mary) "Host biting preferences of British *Culex p. pipiens* vs *Culex p. molestus* and the risk of West Nile Virus in Britain" and

Nehal Saleh (Queen Mary) "Scent marking and foraging behaviour in bumblebees"

The conference is FREE and will take place February 1, 2006 at 41 Queen's Gate, London. Deadline for registration and abstract submission is January 15, 2006. For more information visit: <http://www.royensoc.co.uk/> or contact Mr Eligiusz Baumgart Email:eligiusz.baumgart@imperial.ac.uk or Ms Nehal Saleh Email: n.saleh@qmul.ac.uk.

Nehal Saleh PhD Candidate School of Biological Sciences Queen Mary London E1 4NS UK

<http://www.biology.qmul.ac.uk/research/staff/-chittka/chittkalab/Team/Nehal.html> Tel: 44 (0) 207 882 5555 Ext. 4169

Interested in giving a presentation for our discussion group? Everyone welcome! For more information please visit: <http://alpha.qmul.ac.uk/~btw092/biolunch/index.htm> n.saleh@qmul.ac.uk
n.saleh@qmul.ac.uk

SouthAfrica SASSB Jul14-17

Please forward this announcement to all interested parties.

The sixth conference of the Southern African Society for Systematic Biology (SASSB VI) in association with the University of Johannesburg will be held in the Kruger National Park, South Africa from 14-17 July 2006. Registration and talk/poster submission is NOW available. Please visit <http://swarm.co.za/SASSB2006/> for all in-

formation. The webpage is a window based operating system using windows explorer.

The SASSB VI 2006 organizing committee

Michelle Van der Bank <mvdb@na.rau.ac.za>

Sussex HumanAltruism Oct11

The programme for the meeting on Human Altruism (to be held in Sussex on 11 October, 2005) is now available at www.lifesci.sussex.ac.uk/altruism .

It is still possible to accept a few late registrations. If you would like to attend the meeting, then please fill out a registration form (available on www.lifesci.sussex.ac.uk/altruism), and email it to altruism@sussex.ac.uk . Please do not pay for the meeting or travel to Sussex for the meeting until your registration is confirmed.

Yours, Joel Peck Centre for the Study of Evolution The University of Sussex

j.r.peck@sussex.ac.uk j.r.peck@sussex.ac.uk

Tucson RelatedGenomics Jan12-14

GENOMICS OF CLOSELY RELATED ORGANISMS
January 12-14, 2006 Marriott University Park Hotel,
Tucson, Arizona

The University of Arizona IGERT Program in Genomics is sponsoring an international meeting on the genomics of closely related organisms. It will bring together leading researchers on genome evolution of both prokaryotes and eukaryotes, including empirical, theoretical, and computational approaches. The meeting will take place at the Marriott University Park Hotel adjacent to the University of Arizona campus in Tucson, January 12-14, 2006. The format of the meeting will allow considerable time for informal discussion and interaction among participants. Participation by graduate students and postdoctoral fellows is strongly encouraged, and discounted rates for registration will be available. For registration and more information, please visit

www.genomics.arizona.edu/meeting2006.html Speak-

ers: Jeffrey Bennetzen, University of Georgia David Haussler, University of California Santa Cruz Philip Hugenholtz, Lawrence Berkeley Joint Genome Institute Austin Hughes, University of South Carolina Peter Keightley, University of Edinburgh Bruce Lahn, University of Chicago Manyuan Long, University of Chicago Kateryna Makova, Pennsylvania State University Nancy Moran, University of Arizona Elaine Ostrander, National Institute of Health Svante Paabo, Max Planck Institute for Evolutionary Anthropology, Leipzig Eduardo Rocha, Centre National de la Recherche Scientifique, France Joana Silva, The Institute for Genomics Research Patricia Wittkopp, University of Michigan Mariana Wolfner, Cornell University

—— Michael Nachman Professor, Department of Ecology and Evolutionary Biology Director, IGERT Program in Genomics BioSciences West Bldg. University of Arizona Tucson, AZ 85721

Phone: (520) 626-4595 (office), 626-4747 (lab) Fax: (520) 621-9190 Email: nachman@u.arizona.edu

WellesleyC NEMEB Nov5 abstract deadline

Dear Colleague,

Just a reminder that the deadline for abstracts for this year's NEMEB (New England Molecular Evolutionary Biologists) Meeting at Wellesley College on Saturday November 5th is approaching.

Please remember there is no registration fee for the meeting and that the deadline for abstract submissions is October 14th. Abstracts submitted after the 14th will be considered for poster presentations. We look forward to seeing you in Wellesley, MA on November 5, 2005.

For more information about the meeting, registration and abstract submission please visit us at <http://www.wellesley.edu/Biology/Faculty/webAndrea/-Nemeb2005/Main/main.html> . Andrea Sequeira Assistant Professor Department of Biological Sciences Wellesley College Wellesley, MA 02481

(781) 283-3376 (office and voice mail) (781) 283-3079 (lab) (781) 283-3642 (fax)

asequeir@firstclass.wellesley.edu

ase-

[queir@firstclass.wellesley.edu](mailto:asequeir@firstclass.wellesley.edu)

WellesleyC NEMEB Nov5 abstract deadline2

Dear Colleague,

The new deadline for abstract submission for this year's NEMEB (New England Molecular Evolutionary Biologists) Meeting at Wellesley College is October 25th as originally posted in the meeting website. We apologize for the discrepancy with the date in previous messages and hope this change will work better for everyone.

Please remember there is no registration fee for the meeting and that abstracts submitted after the 25th will be considered for poster presentations. We look forward to seeing you in Wellesley, MA on November 5, 2005.

For more information about the meeting, registration and abstract submission please visit us at <http://www.wellesley.edu/Biology/Faculty/webAndrea/-Nemeb2005/Main/main.html> . Andrea Sequeira Assistant Professor Department of Biological Sciences Wellesley College Wellesley, MA 02481

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queir@firstclass.wellesley.edu

WellesleyCollege NEMEB Nov5

Dear Colleague,

Just a reminder that we are hosting this year's NEMEB (New England Molecular Evolutionary Biologists) Meeting here at Wellesley College on Saturday November 5th. This is the 16th annual NEMEB and we are hoping for a good turnout. For more information about the meeting, registration and abstract submission please visit us at <http://www.wellesley.edu/Biology/Faculty/webAndrea/Nemeb2005/Main/main.html> . Please remember there is no registration fee for the meeting and that the deadline for abstract submissions is October 14th. We look forward to seeing you in Wellesley, MA

on November 5, 2005.

Andrea Sequeira Assistant Professor Department of Biological Sciences Wellesley College Wellesley, MA 02481
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YaleU Phylogenetic Nomenclature Jun29-Jul2

2nd Meeting of the International Society for Phylogenetic Nomenclature

Yale University, New Haven June 29 - July 2, 2006

We are pleased to announce the 2nd Meeting of the International Society for Phylogenetic Nomenclature (ISPN).

Venue:

The meeting and associated social gatherings will be held on Yale University's beautiful campus in New Haven, Connecticut, USA. Accommodations are being organized both on and off campus.

Scope:

This meeting will follow the format of the 1st and founding meeting of the ISPN that was held in Paris, France in 2004 by providing opportunities for formal oral and poster presentations while leaving ample time for discussions. The annual business meeting of the ISPN will also be held during this conference.

Conference Language:

English

Organizing Committee:

Nico Cellinese, Co-Chair, Yale University
Walter Joyce, Co-Chair, Program Officer, Yale University
Michael Donoghue, Co-Host, Yale University
Jacques Gauthier, Co-Host, Yale University
David Baum, University of Wisconsin
Philip Cantino, Ohio University
Michel Laurin, CNRS, Paris
Kevin de Queiroz, Smithsonian Institution

Registration:

Instructions on how to register will be provided in the second circular.

Important Dates and Deadlines:

Abstract submission deadline: April 1, 2006

Advance registration: May 1, 2006

Contact

Nico Cellinese (Logistics and general information) Walter Joyce (Program) Yale Peabody Museum 170 Whitney Avenue POB 208118 New Haven, Connecticut, 06511 USA Email: nico.cellinese@yale.edu or walter.joyce@yale.edu

nico.cellinese@yale.edu

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Biodiversity hotspots

9 Marie Curie Early-Stage PhD Researchers (PhD studentships)

Understanding and Conserving the Earth's Biodiversity hotspots

REF: Hotspots

HOURS OF WORK: Full Time

JOB STATUS: 3 years Fixed Term Appointment.

DEPARTMENT: One of Nine European Hosting Partners (UK, France, Spain, Finland, Germany, Switzerland) see <http://www.kew.org/hotspots> DETAILS:

Working within a new European consortium for training in biodiversity research and conservation, you will be enrolled in a multi-disciplinary challenging PhD programme on ?understanding and conserving the Earth's

biodiversity hotspots (HOTSPOTS)?.

The European HOTSPOTS consortium will work towards increasing the knowledge and understanding of biodiversity hotspots, including the Mediterranean Basin and some European overseas territories. Applying field, molecular and bioinformatics approaches to flagship plants and animals, HOTSPOTS will train a new generation of biologists in state-of-the-art methods of evolution, ecology, and conservation. The PhD programme will comprise individual research projects, university training modules (France, Finland, Germany) and summer schools (UK & Africa). Nine PhD positions are available within this Marie Curie Early Stage Training Network (EST), and details of the individual research projects are listed on our web site (<http://www.kew.org/hotspots>).

The European Commission provides funds to the host organisations to cover salary related costs for the Researchers (salaries depend on the country that will host the fellow. As an indication, in the UK, the fellow will receive a salary in the range of 20-23K p.a. incl. benefits).

ESSENTIALS:

You will have BSc/BA (or equivalent), with above-average grades, and excellent background knowledge in biology and/or bio-computing/statistics. You will also need to meet the eligibility criteria of the Marie Curie Actions: (1) you will be an early-stage researcher (less than 4 years of postgraduate research experience) and (2) you will not be a national of the country in which you will be appointed (trans-national mobility. Once you have checked your eligibility criteria (see <http://www.cordis.lu/mariecurie-actions> for details), chose which is(are) the hosting partner(s) you would like to be considered for, complete the application forms and rank your preferences for these hosting departments and/or institutes.

Applications are open to international competition.

CLOSING DATE: 28 October 2005

INTERVIEW DATE: to be organised during the week 28 November ? 2 December 2005

DISCLAIMER: This job offer is subject to successful completion of the contract negotiation with the European Commission

How To Apply

See application packs at <http://www.kew.org/aboutus/jobs/RefHotspots.htm> See more details about the project at <http://www.kew.org/hotspots> Dr Vincent Savolainen Molecular Systematics Section Jodrell Laboratory Royal Botanic Gardens, Kew Richmond, Surrey TW9 3DS London UK Tel +44-(0)20-8332-5366 Fax +44-(0)20-8332-5310 Email v.savolainen@kew.org

<http://www.kew.org/hotspots> Vincent Savolainen <v.savolainen@kew.org>

Fish EvolEcol

Graduate Student Research Opportunity in Stream Fish Ecology I am currently seeking graduate students at the master's or PhD level who are interested in working on the behavior, ecology, and/or evolution of stream fish populations in Kansas beginning May 2006. Possible projects could include foraging and dispersal behavior, predator-prey interactions, population dynamics, and patterns of community structure. I am especially interested in seeking students who want to use mathematical modeling and/or molecular techniques in concert with field and/or laboratory work in their studies.

Interested students should contact Dr. Garrick Skalski, Department of Ecology and Evolutionary Biology, University of Kansas. Informal inquiries are encouraged. Stipends start at ~ \$1,600/month, tuition is reduced or waived, and health insurance is available.

Required Qualifications See <http://www.ku.edu/~eeb/graduate/index.html> for information, including admission requirements, on graduate studies in the Department of Ecology and Evolutionary Biology at the University of Kansas.

Preferred Qualifications Field experience, especially with fishes Programming, mathematical, and/or statistical skills Molecular skills, especially with microsatellite loci

Contact Information Garrick T. Skalski Assistant Professor Department of Ecology and Evolutionary Biology University of Kansas skalski@ku.edu <http://people.ku.edu/~skalski/> skalski@mail.ku.edu

FordhamU EvolGenetics

One or two Graduate Research Assistantships: Molecular and evolutionary ecology

I invite applications from prospective graduate students (M.S. or Ph.D) interested in conducting research in the Laboratory of Ecological Genetics at the Louis Calder Biological Field Station of Fordham University. The lab focuses on the ecological and evolutionary genetics of arthropod- bacterial symbioses, although highly motivated students generally interested in molecular and evolutionary ecology are encouraged to apply.

Positions are available for Fall 2006. Qualified students will receive a teaching assistantship in the Department of Biological Sciences (\$24,000 annual stipend and full tuition remission). Please visit fordham.edu/biology/ for information about the department and the field station, and fordham.edu/academics/colleges_graduate_s/graduate_profession/arts_sciences/index.html for application information. The deadline for application is 4 January 2006.

Inquiries are welcome via email to Dr. Gordon Plague (plague@fordham.edu).

Gordon R. Plague Louis Calder Biological Field Station Department of Biological Sciences Fordham University Armonk, NY 10504 (914) 273-3078x20 fordham.edu/calder_center/plague

plague@fordham.edu plague@fordham.edu

Karl-FranzensUniversittGraz MolEvolEcol

Molecular Ecology PhD position - 3 years - approximately 16,000 Euro's net/year Karl-Franzens Universität Graz, Graz Austria

Coregonid Genomics

The project is a joint effort between the Institute of Zoology in Graz (Steve Weiss), and the Limnology Research Station in Mondsee (Joseph Wanzenböck). The research plan will involve extensive molecular genetic work with a wide variety of approaches (DNA sequencing, microsatellite typing, AFLP's etc); extensive ecological field work (primarily done by a second PhD), and laboratory crosses. The candidate for this position would be primarily based in Graz, under my supervision, but would also spend some time during critical experiments in Mondsee, and most likely some months in the laboratory of Louis Bernatchez, in Quebec City, Canada, who is collaborating on this project.

Some molecular genetic experience is required, the more the better. Please send a CV and/or questions to me. Starting time is negotiable, but we would prefer that the candidate begin as soon as possible.

Steven Weiss Dr. Karl-Franzens University of Graz
Institute of Zoology Universitätsplatz 2 A-8010 Graz
E-mail: steven.weiss@uni-graz.at phone: +43-316-380-5599 FAX: +43-316-380-9875

steven.weiss@uni-graz.at

LundU PlantSystematics

PhD studentship (utbildningsbidrag) in Plant Ecology and Systematics

A four-year PhD studentship, funded by the Faculty of Science, Lund University, is available at the Section for Plant Ecology and Systematics, Department of Ecology, for studies of evolutionary implications of pollen competition in a species with delayed stigma receptivity.

In recent years, increasing interest in conflicts between the sexes in relation to reproduction has led to important evolutionary insights. In plants, however, few studies have considered the potential for conflicts between sexual functions. During pollen competition, pollen traits that confer a selective advantage should be selected even when this would disfavour the interests of the female function. The proposed project will use greenhouse experiments to study evolutionary implications of pollen competition in an annual plant species with delayed stigma receptivity (*Collinsia heterophylla*). Particular attention will be given to the ability of pollen to germinate earlier than pollen from other donors, the consequences of delayed stigma receptivity for female function, and the timing of receptivity in relation to the origin of the pollen donor and recipient. The heritability of the ability of pollen to germinate early during the stigmatic phase as well as the heritability of the timing of stigma receptivity will also be quantified.

The duties of the student include (up to 10%) undergraduate teaching and a certain amount of administration.

We are seeking a candidate holding a B.Sc. degree (or equivalent) in biology or a related subject, and having a strong interest in plant ecology, evolution and genetics. Experience of field- or greenhouse work as well as of general laboratory work is an advantage. Possession of a driving-license, and social and cooperative skills are also considered important.

The application should be written using a form found at the Faculty website <http://www.naturvetenskap.lu.se/-fou/antagn.blankett_eng.pdf>http://www.naturvetenskap.lu.se/-fou/antagn.blankett_eng.pdf, marked with ref.no. 493 and sent to Registrar, Lund University, Administration Office, PO Box 118, SE-221 00 Lund, Sweden no later than 21st of November 2005. It should include a signed and witnessed CV, publication list, and witnessed copies of exam certificates.

Further information: Dr Åsa Lankinen, tel +46 46 222 9293, e-mail Asa.Lankinen<mailto:Hans_Henrik.Bruun@ekol.lu.se>[@ekol.lu.se](mailto:Asa.Lankinen@ekol.lu.se), or Docent Stefan Andersson, tel +46 46 222 8975 e-mail Stefan.Andersson@ekol.lu.se

Åsa Lankinen, PhD Department of Plant Ecology and Systematics Lund University Ecology Building 223 62 Lund Sweden Tel: +46 46 2229293 Fax: +46 46 2224423

Åsa Lankinen <asa.lankinen@ekol.lu.se>

MichiganStateU SquirrelEvol

Graduate Research Assistantship - Red Squirrels,
Michigan State University

A Graduate Research Assistantship is available for a Ph.D. student interested in investigating the interactions between food abundance and contemporary evolution in red squirrels. Field research will be performed in Kluane, Yukon, Canada and will complement a large-scale food manipulation experiment that was initiated in 2005 (see www.redsquirrel.msu.edu). Specific research questions can be tailored to the particular skills and interests of the candidate and may include topics such as: spatial variation in selection, correlated responses to selection, genotype x environment interactions, or the ecological genetics of metabolism.

This position will be funded for 8 months per year including stipend, tuition and benefits. The candidate will be expected to secure funding for fall semesters through a graduate teaching assistantship or fellowship. There are opportunities for qualified candidates to secure either of these at MSU. The student will be expected to enroll in the fall of 2006, but fieldwork and funding could start as early as March 2006.

Candidates should have experience and interests in evolutionary biology and ecological genetics as well as strong quantitative and interpersonal skills and an interest in working in a remote field location. Interested applicants should send a cover letter outlining their research interests and experience, CV and a copy of GRE scores and transcripts to: Dr. Andrew McAdam

Department of Fisheries and Wildlife

Michigan State University

East Lansing, MI

48824

Electronic materials are preferred (mcadama@msu.edu) and the deadline for receipt of materials is December 1, 2005. Members of under-represented groups are particularly encouraged to apply.

The Ecology Evolutionary Biology and Behavior (EEBB; www.msu.edu/~eebb) graduate program provides abundant opportunity for interaction and collaboration with faculty and students across several departments. The successful candidate will be expected to

enroll and actively participate in the EEBB program.

Andrew G. McAdam Ecology, Evolutionary Biology & Behavior Program, Department of Fisheries & Wildlife, Department of Zoology

13 Natural Resources Building Michigan State University East Lansing, MI 48824 tel: 517-432-0396 / fax: 517-432-1699 www.fw.msu.edu/people/McAdam/Index.htm www.redsquirrel.msu.edu
mcadama@msu.edu mcadama@msu.edu

NewZealand InsectPhylogeography

PhD student:

We are seeking a PhD student for a Royal Society of New Zealand Marsden Fund project on the comparative phylogeography of New Zealand forest insects. The project will involve a combination of field work, insect identification, DNA sequencing, and associated phylogenetic and population genetic analyses. We aim to reconstruct the response of forest insects to recent glacial advances and test hypotheses on the nature of glacial refugia. The student will join an international team of biologists and geologists working on the effects of glacial environmental change on the New Zealand biota.

The Ph.D. student will be based at Landcare Research on the Auckland University campus at Tamaki and will be enrolled at Auckland University through the Centre for Biodiversity and Biosecurity. They will receive training in field entomology, taxonomy, molecular systematics and population genetics. The student will be jointly supervised by Thomas Buckley and Richard Leschen (Landcare Research), and Allen Rodrigo (Auckland University). The student will also have the opportunity to spend time at the University of Connecticut in the laboratory of Chris Simon who will be a co-supervisor.

A 3 year stipend of \$19,000 plus NZ university fees (per annum) is provided. For general enquiries please contact Thomas Buckley at the e-mail address below. Potential candidates should submit a CV, two references, and a short statement of research interests to:

Thomas Buckley buckleyt@landcareresearch.co.nz
<http://www.landcareresearch.co.nz/> <http://www.landcareresearch.co.nz/research/biodiversity/-invertebratesprog/>

Thomas Buckley Landcare Research Private Bag 92170
Auckland New Zealand

E-mail: BuckleyT@LandcareResearch.co.nz
+64-9-5744116 Fax: +64-9-5744101

BuckleyT@landcareresearch.co.nz

Phone: Graduate studentships available in Ecology and Evolutionary Biology at the University of Kansas.

ReadingU PopulationGenetics

A PhD position is available in the School of Biological Sciences, working with Mark Beaumont. This studentship is fully funded for any applicants from the EU (fees and stipend). It is also available to applicants outside the EU, but they will need to pay for the difference between EU and non-EU fees (around 6,000 per year).

The student will be working on a project funded by a grant from the Engineering and Physical Sciences Research Council (EPSRC) in conjunction with David Balding in the Department of Epidemiology and Public Health at Imperial College, London. The student will be working closely with a postdoctoral researcher at Imperial College, funded on the same grant. The aim of the project is to develop and apply novel statistical methods (mainly based on what has come to be called 'approximate Bayesian computation', ABC) for the analysis of genetic data. The problems we are particularly interested in relate to fitting complex models of demographic history to genetic data. Training will be provided in population genetics, bioinformatics, and on the application of modern methods of computational statistics and simulation in biology.

This project would suit a biologist with an interest in mathematical modelling and programming. Further details are available from Mark Beaumont (contact information below). Ideally we would like the student to be able to start as soon as possible.

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

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

Students who are highly motivated to work on evolutionary questions are encouraged to apply to EEB at KU where there is an active group of faculty with diverse research interests. The potential for graduate positions exists in, but is by no means limited to, the following labs:

Dr. Jennifer Gleason (jgleason@ku.edu)- Behavioral evolutionary genetics of *Drosophila* <http://www.ku.edu/~eeb/faculty/gleason.html> A PhD level studentship is available to join a lab studying the genetics of courtship differences (courtship song and pheromones) between species of *Drosophila*. Students will gain experience in behavioral analyses, quantitative genetics and molecular biology techniques. Possible projects include quantitative trait loci (QTL) mapping of behaviors and preferences and microarray analysis of genes introgressed between species. Opportunities also exist for students to develop their own research ideas in behavioral genetics.

Dr. Garrick Skalski- Behavior, ecology, and/or evolution of stream fish populations in Kansas <http://www.ku.edu/~eeb/faculty/skalski.html> Possible projects could include foraging and dispersal behavior, predator-prey interactions, population dynamics, and patterns of community structure. Dr. Skalski is especially interested in seeking students who want to use mathematical modeling and/or molecular techniques in concert with field and/or laboratory work in their studies. Masters or PhD level students are encouraged to apply and work will commence in May 2006.

Dr. Pauly Cartwright (pcart@ku.edu)- Medusozoan phylogenetics <http://www.ku.edu/~eeb/faculty-cartwright.html> Opportunities for PhD level students to work on a recently NSF Cnidarian Tree of Life project. Preferred starting dates are August 2006 and 2007. These students would be part of a collaborative project on higher-level cnidarian phylogenetics, with an emphasis on medusozoan phylogeny and/or intensive concentration on a lower-level clade within medusozoans. Participation in field trips for collecting specimens may be involved. Students will be enrolled in the Ph.D. program in the Department of Ecology and Evolutionary Biology at the University of Kansas, but it is anticipated that he/she would share their time between Lawrence, KS and the National Systematics Laboratory in Washington DC. Interested applicants should contact not only the investigator listed above but also Dr. Allen Collins (Collins.Allen@nmnh.si.edu <mailto:Collins.Allen@nmnh.si.edu>) at the Smithsonian.

Dr. Lena Hileman (lhileman@ku.edu <mailto:lhileman@ku.edu>): Evo-devo and floral diversification <http://www.ku.edu/~eeb/faculty/hileman.html> The Hileman lab takes an integrative approach to study how the evolution of development contributes to floral diversification. By integrating phylogenetic, molecular evolutionary and molecular developmental research, we investigate patterns of floral evolution, the underlying genetic mechanisms leading to floral diversification, and the role of gene family evolution in morphological change. Opportunities exist for students who are highly motivated by evolutionary questions in this area.

If interested in any of the above positions, email the principle investigator to express interest and inquire about specifics.

The Department of Ecology and Evolutionary Biology at the University of Kansas guarantees 5 years of funding for PhD students (pending budgetary approval from the state and subject to yearly review of the student's performance) This support may be in the form of a combination of graduate teaching assistantships, research assistantships, curatorial assistantships, and fellowships. The support includes both a stipend and a tuition waiver. Visit the KU/EEB website (<http://www.ku.edu/~eeb/>) for more information about admission requirements, application procedures and general details about the program.

In addition, exceptional PhD students who are US citizens may be eligible for scholarships from the Self Foundation (<http://www.ku.edu/~selfpro/> <<http://www.ku.edu/~selfpro/>>). The Self Graduate Fellowship is a four-year award consisting of an annual \$23,000 stipend, full tuition and fees, and a development program.

jgleason@ku.edu jgleason@ku.edu

UKansas Phylogenetics

PH.D. OPPORTUNITIES IN MEDUSOZOAN PHYLOGENETICS RESEARCH AT THE UNIVERSITY OF KANSAS AND SMITHSONIAN INSTITUTION

The recently NSF-funded Cnidarian Tree of Life project (see announcement below) provides support for PhD candidates. Preferred starting dates are August 2006 and 2007. These students would be part of a collaborative project on higher-level cnidarian phyloge-

netics, with an emphasis on medusozoan phylogeny and/or intensive concentration on a lower-level clade within medusozoans. Participation in field trips for collecting specimens may be involved. Students will be enrolled in the Ph.D. program in the Department of Ecology and Evolutionary Biology at the University of Kansas, but it is anticipated that he/she would share their time between Lawrence, KS and the National Systematics Laboratory in Washington DC. Interested applicants should contact Allen Collins at Collins.Allen@nsmnh.si.edu and Paulyn Cartwright at pcart@ku.edu and visit the KU/EEB website <http://www.ku.edu/~eeb/admission/index.html> for application and admission requirements.

NSF-AToL Cnidarian Tree of Life Project

The NSF Assembling the Tree of Life Program has awarded five years of funding distributed amongst several principal investigators, to investigate cnidarian phylogeny. The CnidToL award allows for opportunities for collaborative research amongst members of the cnidarian community and training for graduate students and postdoctoral researchers. Of immediate interest are graduate study opportunities. The primary aim of this project is to develop new molecular markers and gather large amounts of DNA sequence data from an extensive sampling of cnidarian taxa. Other goals of this project are: build collaborations with cnidarian researchers; characterize and classify nematocysts in a comparative context; develop culture conditions for select cnidarian species in an effort to develop new model organisms; build cnidarian collections through field work, assemble a Cnidarian Tree of Life database modeled after the Hexacoral database; contribute to museum exhibits on cnidarian evolution; hold a symposium on cnidarian phylogeny. If you are interested in more information and to discuss potential collaborations and/or contributions to the project, please contact one of the following PI's listed with their particular role in the project.

Neil Blackstone (culturing new model organisms, neilb@niu.edu); Paulyn Cartwright (hydrozoan phylogeny, pcart@ku.edu), Allen Collins (medusozoan phylogeny, Collins.Allen@nsmnh.si.edu), Cliff Cunningham (molecular marker development cliff@duke.edu with research assistant Bernie Ball, bernie.ball@duke.edu), Meg Daly (anthozoan phylogeny and nematocyst morphology, daly.66@osu.edu), Daphne Fautin (database development, fautin@ku.edu) Dan Janies (data analyses, janies-1@medctr.osu.edu), Daniel Martínez (hydra phylogeny, dmartinez@pomona.edu), Cathy McFadden (octocoral phylogeny, mcfadden@hmc.edu), Sandra Romano (coral phylogeny, sromano@uvi.edu)

agc@PaleoBio.org

ULausanne EvolGeneticsSymbiosis

PhD studentship: in Molecular Genetics & Symbiosis

We are seeking a highly motivated student with a background in molecular biology to join our group working on mechanisms of evolution in symbiotic mycorrhizal fungi. These important fungi form mutualistic symbioses with plant roots. Although the fungi grow clonally, they have a highly unusual genome organization, harbouring genetically different nuclei that are passed from one generation to the next (see Hijri & Sanders, Nature 2005; Kuhn, Hijri & Sanders, Nature 2001). The goals of our research are to understand how this unusual organization of the genome affects their evolution and their adaptation to the different environments offered by the roots of different plant species. Other than their unusual genome organization, the fungi have formed symbioses with plants ever since they colonized land over 400 million years ago and are thought to be the oldest putative ancient asexuals.

The candidate should be familiar with molecular biology and have an interest in applying this knowledge to evolutionary questions. He/she should also be able to interact with the other group members working on evolution and population biology of mycorrhizal fungi (see list of recent papers on our web site).

The successful candidate will be located in the Department of Ecology and Evolution at the University of Lausanne (Switzerland). The Dept. of Ecology and Evolution in Lausanne is situated on the shores of Lake Geneva and provides a pleasant & exciting research environment and a strong PhD program. It is also one of the largest institutions in Europe for research in ecology and evolutionary biology, comprising 17 different research groups. A genomics research centre has also been recently established at the same site.

The studentship is funded by the Swiss National Science Foundation for a period of 3 years. Starting date should be as soon as possible. To apply, applicants should send a CV plus a letter of motivation by EMAIL to Ian Sanders, Dept of Ecology and Evolution, University of Lausanne, Switzerland. Email: ian.sanders@unil.ch; Tel: +41 21 692 4261. More details can be found about our group at: <http://www.unil.ch/dee/page7238.html>

Please make it clear in your application if you are applying for the PhD studentship as there is a similar

position for a postdoc currently available.

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

Tel (direct): +41 (0)21 692 4261 Tel (secretary): +41 (0)21 692 4260 Fax: +41 (0)21 692 4265 <http://www.unil.ch/dee> New email!: ian.sanders@unil.ch

Ian.Sanders@unil.ch

UMainz Lophotrochozoan phylogeny

Dear colleagues, there is an open position (phD) at the University of Mainz, Institute of Zoology, Germany:

“Phylogeny of molluscs and their relatives based on new molecular data; Phylogeny of Lophotrochozoa”

In collaboration with other scientists we are intending to create a stable and well resolved reconstruction of the Metazoa with special focus on the lophotrochozoan phylogeny by me and two other collaborators. Our analyses will mainly focus on the Phylum Mollusca and their relatives, the Sipunculida and the Entoprocta, respectively. To trace this, we will follow up two strategies: (i) we will analyze a huge set of ESTs and obtain an intersection of “new” genes which can be used to trace the “deep phylogeny” of the Lophotrochozoa as well as Ecdysozoa and deuterostomes. The second way (ii) consists of ten “known” proteins common in all metazoan phyla, which will be analyzed by RT-PCR and used as a common data set to reconstruct the phylogeny of the metazoan classes at the deep Cambrian level as it is for the first approach.

The candidate should have a strong background in molecular genetics with applicable knowledge in cDNA technology. Practical experience in RNA-/DNA-isolation, reverse transcription-PCR and cDNA library construction. A sound knowledge of sequence analysis or related bio-statistical software is advisable. The position is available for 2 year.

Interested candidates are requested to send their CV to lieb@uni-mainz.de

Dr Bernhard Lieb Hochschuldozent Johannes Gutenberg-University Insitute of Zoology Müllerweg 6 55099 Mainz Germany phone +49 (+)6131 39-23158 fax +49 (+)6131 39-24652 <http://staff.uni-mainz.de/~lieb/> lieb@uni-mainz.de

UQueensland CanineMHC

I am seeking a highly motivated student interested in pursuing graduate study at a PhD level, starting in January 2006.

Title: MHC class II haplotypes in the domestic dog

Project: The Major Histocompatibility Complex (MHC) is a multigene family with a fascinating suite of evolutionary processes creating a level of diversity that is among the highest in the genome. Its functional importance as an integral component of the immune system has attracted interest among investigators looking for associations with infectious and other immune-related diseases. This study will construct extended MHC class II haplotypes in the dog. In addition to understanding the evolutionary patterns of this important gene family, haplotypes will be used to aid the search for causative mutations in an immune-related disease, type 1 diabetes, in the domestic dog.

The School of Veterinary Science at The University of Queensland has labs fully equipped for molecular genetic analyses with state-of-the-art automated DNA sequencing equipment.

PhD entry requirements at UQ are available at http://www.uq.edu.au/study/program.html?acad_prog=7501. Information about scholarship applications is available at <http://www.uq.edu.au/study/index.html?page=1135> <<http://www.uq.edu.au/study/index.html?page35&pid23>> &pid23.

To apply, send a letter/email stating your interests and suitability for the position, a CV and contact details for two referees to:

Dr Jennifer Seddon, School of Veterinary Science, The University of Queensland, St Lucia 4072, Australia. Tel +61 7 3365 1278, Fax +61 7 3365 1255, Email j.seddon1@uq.edu.au.

J.Seddon1@uq.edu.au

UUtah HostParasite

Graduate Research: Evolutionary Ecology of Host-

Parasite Interactions, Clayton Lab, Dept. of Biology, Univ. of Utah

I am seeking one or two highly motivated Ph.D. students interested in the evolutionary ecology of host-parasite systems. Projects in my lab focus on factors governing parasite specificity, speciation, co-speciation, competition, adaptive radiation, and reciprocal selective effects between parasites and hosts. We also do taxonomic and phylogenetic work on birds, their host-specific feather lice, and the endosymbiotic bacteria within those lice. Additional information on the Clayton lab can be found at darwin.biology.utah.edu

Positions are available for fall semester 2006. Qualified students will receive an NSF Research Assistantship and/or Teaching Assistantship in the Department of Biology.

Please visit www.biology.utah.edu for departmental information, admission requirements and application information. The application deadline for Fall Semester 2006 is January 13th, 2006.

Inquiries are welcome via email to Dr. Dale Clayton (clayton@biology.utah.edu).

bush@biology.utah.edu

UUtah HostParasiteEvol

Graduate Research: Evolutionary Ecology of Host-Parasite Interactions, Clayton Lab, Dept. of Biology, Univ. of Utah

I am seeking one or two highly motivated Ph.D. students interested in the evolutionary ecology of host-parasite systems. Projects in my lab focus on factors governing parasite specificity, speciation, co-speciation, competition, adaptive radiation, and reciprocal selective effects between parasites and hosts. We also do taxonomic and phylogenetic work on birds, their host-specific feather lice, and the endosymbiotic bacteria within those lice. Additional information on the Clayton lab can be found at darwin.biology.utah.edu

Positions are available for fall semester 2006. Qualified students will receive an NSF Research Assistantship and/or Teaching Assistantship in the Department of Biology.

Please visit www.biology.utah.edu for departmental information, admission requirements and application information. The application deadline for Fall Semester

2006 is January 13th, 2006.

Inquiries are welcome via email to Dr. Dale Clayton (clayton@biology.utah.edu).

bush@biology.utah.edu bush@biology.utah.edu

UppsalaU AnimalEvolEcol

Postgraduate (PhD) position (“doktorandtjänst”) in Animal Ecology

The Department of Ecology and Evolution at the University of Uppsala seeks a PhD candidate for the project “The evolution of ornaments in *Sabethes* mosquitoes”.

Male-female coevolution of reproductive behavior, morphology and physiology is well documented in many taxa. Yet, the evolutionary processes responsible for such concerted evolution is poorly understood in most cases, and this is particularly true for the evolution of costly ornaments. In the current project, neotropical mosquitoes of the genus *Sabethes* will be used as a model system. The aquatic larvae of these insects are inconspicuous but the adults are iridescent and wear colorful ornaments on their mid-legs. The aim of this PhD project is to assess sexual selection on, and constraints on the evolution of, ornaments in this group of insects. The candidate will use a variety of different methods, such as manipulative behavioral studies and artificial selection experiments on laboratory populations of these mosquitoes as well as comparative studies and field work.

The successful candidate should have a MSc (or equivalent) in biology/ecology and a strong interest in evolutionary biology and behavioral ecology.

The candidate will join a collaborative research group, currently consisting of 3 other PhD students, 3 post-doctoral associates and one senior scientist (Göran Arnqvist). The latter will function as a supervisor (see <http://www.ebc.uu.se/zooeko/GoranA/GA.html>) and the candidate will receive her/his postgraduate training within the postgraduate school at the Evolutionary Biology Centre (see http://www.ebc.uu.se/-index_eng.htm). This position is financed by the Swedish Research Council and is for four full years, and the successful candidate will receive a postgraduate fellowship the first year (14.400 SEK/month) and a postgraduate position year 2-4 (18.700 - 20.900 SEK/month).

Applications should include (1) personal information/background, (2) complete CV (3) a description of undergraduate training, (4) an authorized copy of the undergraduate degree and (5) the names and email addresses of two-three referees. Applications should be sent to Göran Arnqvist, Dept. of Animal Ecology, EBC, Norbyv. 18D, University of Uppsala, SE-752 36 Uppsala, Sweden. Please feel free to contact Göran Arnqvist by email (Goran.Arnqvist@ebc.uu.se) or by phone (+46-18-4712645) for more information. Closing date for applications is October 28, 2005, and tentative starting date is January 1, 2006.

Associate Professor Göran Arnqvist Animal Ecology Department of Ecology and Evolution Evolutionary Biology Centre University of Uppsala Norbyvägen 18d SE - 752 36 Uppsala Sweden

Email: Goran.Arnqvist@ebc.uu.se Phone: +46-18-471 2645 Fax: +46-18-471 6484 New! Home-page with complete PDF downloads and more at: <http://www.ebc.uu.se/zooeko/GoranA/GA.html> goran.arnqvist@ebc.uu.se goran.arnqvist@ebc.uu.se

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CaliforniaStateUChico PlantPopulations

The Department of Biological Sciences at California State University, Chico invites applications for a full-time, academic year, tenure-track faculty position as an ASSISTANT PROFESSOR in PLANT POPULATION ECOLOGY to begin Fall 2006. Applicants should have a strong background in organismal ecology, and address questions in one or more of the following field research areas: experimental plant population ecology, plant-animal interactions, life-history evolution, fungal/plant interactions, pollination biology, and conservation biology. The successful candidate will be expected to have an externally funded research program involving undergraduate and Master's students, and contribute to the biology curriculum. Applicants must have a Ph.D., postdoctoral experience preferred, and a strong record of research accomplishment. Submit a letter of application, statement of teaching philosophy, curriculum vitae, complete academic transcripts (student copy acceptable), representative reprints, and three letters of reference to: Plant Population Ecologist Search, Dr. Patricia Edelmann, Biology Chair, California

State University, Chico, Chico CA 95929-0515. Review will begin 12/5/05. For full announcement: <http://csucareers.calstate.edu> <<http://csucareers.calstate.edu>>. For disability-related accommodations, 530-898-6192 or TDD 530-898-4666. I-9/EOE/AA/ADA.

Kristina A. Schierenbeck, Ph.D. Associate Professor, Herbarium Director California State University, Chico Department of Biological Sciences Chico, CA 95929-0515 email: kschierenbeck@csuchico.edu Telephone: 530-898-6410

"Schierenbeck, Kristina"
<KSchierenbeck@csuchico.edu>

CaliforniaStateUSanMarcos ComputBiol

POSITION: ASSISTANT PROFESSOR

EFFECTIVE DATE: Fall semester, 2006

MINIMUM QUALIFICATIONS: Ph.D. in the biological sciences with training and research in the area of computational biology. Candidates must be able to teach courses in computational biology and statistics

and to communicate effectively and work cooperatively with departmental colleagues and an ethnically and culturally diverse campus community. The successful candidate will have a solid record of published research commensurate with years since receiving Ph.D. and the ability to develop and sustain an independent, externally funded research program involving students that will lead to original, peer-reviewed publications. All appointees must be able to lawfully accept employment in the U.S. when the appointment begins and provide documentation of such.

DESIRED/PREFERRED QUALIFICATIONS: Post-doctoral research experience is desirable. Preference will be given to computational biologists with broad training and technical expertise in this field and its applications and who have prior successful teaching at the post secondary level.

DUTIES: The successful candidate will develop and teach courses (including those with a lab) such as computational biology, undergraduate and graduate statistics, bioinformatics, and core course instruction. In addition, this person will teach upper division and graduate courses in the area of his/her expertise, and contribute to general education. This person should demonstrate a commitment toward the overall enhancement of quantitative and computational knowledge and skills of biology majors. Develop an active, externally funded research program in computational biology that involves undergraduate and graduate (M.S.) students. Participate in activities serving the department, college, university and community.

APPLICATION: Review of applications will commence December 1, 2005. Position open until filled contingent on funding. All applications must include a letter of application, curriculum vitae, statements of teaching philosophy and research interests that address the above minimum and desired/preferred qualifications, reprints of representative publications, and copies of all transcripts that include relevant course work. Three letters of recommendation must be provided. Applications, required documentation, and/or requests for information should be addressed to:

Dr. Richard Bray, Chair Computational Biology Search Committee Department of Biological Sciences California State University San Marcos San Marcos, CA 92096-0001 Email: rbray@csusm.edu

CSU San Marcos is an Affirmative Action/Equal Opportunity/Title IX Employer. The University has a strong commitment to the principles of diversity and, in that spirit, seeks a broad spectrum of candidates including women, members of minority groups and people with disabilities.

Richard Bray, Professor Department of Biological Sciences California State University San Marcos, CA 92096-0001 (760) 750-4175

rbray@csusm.edu

CollegeWilliamMary Genetics

FACULTY POSITION IN GENETICS

The Department of Biology of the College of William and Mary (a state-supported university, and our nations second oldest institution of higher learning) announces its search for a tenure track ASSISTANT PROFESSOR in GENETICS. Research areas of particular interest include viral, archaeal, and yeast genetics, but outstanding candidates in other areas of molecular genetics are encouraged to apply. The successful candidate will be a teacher-scholar an accomplished teacher who can maintain an active research program involving both undergraduate and masters degree students, and secure extramural funding to support that research. Applicants should consider whether their research is appropriate for work in a primarily undergraduate institution with biosafety levels not to exceed BSL-2. We offer a competitive start-up package.

The Department offers a moderate teaching load (typically one course a semester) in an environment that encourages high quality research. Teaching responsibilities include an upper division course in transmission genetics with laboratory, and another course in the candidates area of expertise. Candidates must demonstrate the potential and motivation to achieve excellence in teaching. Previous experience teaching undergraduate courses would be viewed favorably, and postdoctoral research experience is expected. The first years teaching load is negotiable.

The College is committed to faculty who not only are accomplished teachers but who excel in their research. Our Department members have productive research programs and have been very successful in obtaining outside funding for their research programs (e.g. NSF, NIH, HHMI, NASA, and other federal, state, and private agencies, including 8 NSF CAREER or equivalent awards since 1994). Further information on the Department of Biology and this position may be obtained at <http://www.wm.edu/biology/>. Further information on the College may be obtained at <http://www.wm.edu/>. Review begins November 15, 2005, and will continue until an appointment is made. Interested candidates

should submit a letter of application, curriculum vitae, statements of research plans and teaching philosophy, and arrange to have three letters of reference mailed directly to Genetics Search Committee, Department of Biology, The College of William and Mary, P.O. Box 8795, Williamsburg, VA 23187-8795. The College is an EEO/AA employer.

I would be happy to discuss this position informally by email.

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

ColoradoStateU 2 Biology

Biology at Colorado State University

Two Assistant Professors

Behavioral Ecology - We seek a broadly trained animal biologist whose research addresses fundamental questions in behavioral ecology at multiple levels of inquiry.

Animal Systematics - We seek a broadly trained animal biologist who addresses fundamental questions in systematics and molecular evolution.

The successful candidate for each tenure-track position is expected to develop an externally funded research program and contribute to undergraduate and graduate education. Applicants should have a Ph.D. and record of research excellence. Postdoctoral experience is preferred. For full consideration, submit application materials for the relevant position (cover letter, C.V., statements of research & teaching interests, contact information for 3 referees, and up to 3 representative publications) on-line at www.natsci.colostate.edu/searches/Biology/ by December 2, 2005. Applicants should provide referee contact information on-line as early as possible. Detailed descriptions of each position and the department can be found at: <http://www.colostate.edu/Depts/Biology/> CSU is an AA/EO Employer. Office of Equal Opportunity and Diversity, 101 Student Services.

– Michael F. Antolin

Professor and Assistant Chair Department of Biology
 Colorado State University Fort Collins, CO 80523-1878
 U.S.A.

e-mail: Michael.Antolin@ColoState.edu Voice: (1)-970-491-1911 FAX: (1)-970-491-0649

Colorado State University Plague Project: <http://rydberg.biology.colostate.edu/plagueweb/> Short
 Grass Steppe Long Term Ecological Research
 project: <http://sgs.cnr.colostate.edu/> Program
 Integrating Mathematics, Ecology and Statistics
 (PRIMES) NSF IGERT Graduate Training
 Program <http://www.primes.colostate.edu>
michael.antolin@colostate.edu

DukeU EvolEcolBehav

Assistant Professor in Ecology or Behavior

The Biology Department at Duke University invites applications for a faculty position in Ecology or Behavior at the Assistant Professor level. Applicants working in any area of Ecology or Behavior will be considered. Areas of interest include, but are not limited to, animal behavior, microbial ecology, ecology of infectious diseases, and ecological linkages between populations, communities, and ecosystems. The successful candidate must hold a Ph.D. and demonstrate the potential to build an outstanding research program, to obtain external funding commensurate with their research specialty, and to contribute to teaching at both the undergraduate and graduate levels. To apply, please send a curriculum vitae, statements of research and teaching interests, and three representative reprints, and arrange to have three letters of recommendation sent to: Ecology/Behavior Faculty Search, Biology Department, Duke University, Box 90338, Durham, NC 27708-0338. Application materials can also be submitted electronically to ecobehavsch@duke.edu. Applications received by Nov. 15, 2005 will be guaranteed consideration.

Duke University is an Equal Opportunity /Affirmative Action employer.

GettysburgCollege 1year EvolBiol

Evolutionary Biology

Gettysburg College invites applications for a one-year sabbatical replacement position in the Biology Depart-

ment to begin fall, 2006. We are looking for an evolutionary biologist with broad training who can contribute to our first-year sequence of core courses, including Genetics, as well as teach an upper division course in his/her area of specialization. A commitment to interdisciplinary teaching in the liberal arts tradition is essential as is integrating students in an active research program. The College actively supports research involving undergraduates. Applicants must have a Ph.D. in the biological sciences at the time of application. Gettysburg College is a highly selective liberal arts college located within 90 minutes of the Washington/Baltimore metropolitan area. Established in 1832, the College has a rich history and is situated on a 220-acre campus with an enrollment of 2500 students. Gettysburg College celebrates diversity and invites applications from members of any group that has been historically underrepresented in the American academy. The College assures equal employment opportunity and prohibits discrimination on the basis of race, color, national origin, gender, religion, sexual orientation, age, and disability. Send hard copy of curriculum vitae and statement of teaching and research goals and have three letters of reference (of which at least one can speak to the candidate's teaching effectiveness) sent to: Dr. Kazuo Hiraizumi Department of Biology, Box 392, Gettysburg College, Gettysburg, PA 17325. Review of applications will begin February 1, 2006, and will continue until a successful candidate is found.

delesall@gettysburg.edu delesall@gettysburg.edu

Harvard Curatorial Assistant

Requisition Number 24512 Title Curatorial Assistant (Collection Assistant - Entomology) School / Unit Organismic and Evolutionary Biology Department Museum of Comparative Zoology

Duties And Responsibilities Reports to the Curatorial Associate in the Department in conjunction with the MCZ's Manager of Collections Operations and the Curator of Coleoptera. Characterizes and identifies specimens using molecular systematic techniques; develops protocols for DNA characterization. Incorporates DNA samples and other molecular materials into the MCZ-wide collection database, following established protocols for data formatting and security, including tracking and interface with departmental molecular databases. Oversees, prepares and maintains loans and exchanges of materials and primers. Assists with standard record

keeping and other administrative functions required for department collecting and loan activities to comply with specimen transport (e.g., import/export) laws and regulations. Serves as a principal source of specialized information on the molecular systematics facility and the collection to visiting scholars, faculty, staff, students and general public. Supervises researcher and student use of department DNA sequencer. Addresses technical problems and procedures, including preservation, developments in specimen conservation, preparation and identification techniques. Maintains and reconciles budgets, orders supplies from vendors, tracks orders, processes invoices, and performs related duties as required, including assisting with curatorial needs of the main insect collection and museum-wide initiatives.

Required Education, Experience and Skills College background in biology. Familiarity with museum collections, entomology (especially Coleoptera), sequencing and computer programs used in DNA sequence analysis and systematics, such as Sequencer and PAUP preferred. Experience and proficiency with word processing, spreadsheet and database software. Strong attention to detail, the ability to handle a variety of tasks and shifting priorities, to work independently as well as part of a team, and to coordinate tasks with multiple constituencies including faculty, managers, and staff. – Brian D. Farrell Professor of Biology Curator in Entomology Museum of Comparative Zoology 26 Oxford Street Harvard University Cambridge, MA 02138 Ph: (617) 496-1057 Fax:(617) 495-5667 http://insects.oeb.harvard.edu/farrell_lab/ “Brian D. Farrell” <bfarrell@oeb.harvard.edu>

IndianaU DaphniaGenomics

The Center for Genomics and Bioinformatics (CGB Indiana University, Bloomington) carries out research in genomics, bioinformatics and is a principle laboratory of the Daphnia Genomics Project. This project creates genomic resources for a developing model organism in ecological and evolutionary genomics research. These resources include a 9-fold sequence coverage of the genome that was produced by the U.S. Department of Energys Joint Genome Institute in collaboration with the Daphnia Genomics Consortium. As a result, Daphnia will soon have the best characterized genome among Crustacea and will ultimately be used to address issues relating to the genome structure of the arthropods.

The CGB has an immediate opening for a Research Fellow to help create and implement algorithms that will rigorously test and help improve the assembly of the genome sequence. The research fellow will also participate in the exploration and interpretation of the data. This position is initially funded for one year and is ideal for investigators who have recently completed their graduate studies in the field of computer science / bioinformatics, or who are in the final stages of completing their dissertations. However, all candidates with expertise in computer programming and prior experience with genome sequencing projects are encouraged to apply, including visiting scientists. We offer a competitive salary (\$57,000 plus benefits) and access to state of the art facilities.

Specifically, this project aims to improve the assembly of the Daphnia genome by developing two computational methods for detecting misassembled regions, one based on pattern statistics and another based on clone coverage statistics. These independent algorithms are already proven to accurately detect false assemblies in microbial genome sequencing projects. These two algorithms will be refined and combined to provide a probabilistic support index for scaffold junctions and will function on much larger and more complex eukaryotic genomes, including Daphnia. A significant outcome is the creation and implementation of a support index along localized regions of genome sequence assemblies to indicate regions of high and low confidence.

Applications will be accepted until October 31, 2005. Interested candidates may contact John Colbourne for further information (by sending email to jobs@cgb.indiana.edu). Please submit a CV and a description of your background and interests, and have three (3) letters of recommendation sent directly to the address below. Be sure to refer to Research Fellow CGB-008 within your cover letter.

Position #CGB-008 Attn: Research Fellow Center for Genomics and Bioinformatics Indiana University 1001 E. 3rd St. Bloomington IN 47405-3700

Indiana University is an affirmative action equal opportunity employer.

Center for Genomics and Bioinformatics, Indiana University 915 East Third Street, Bloomington, Indiana USA 47405-7107 Office Phone (812) 856-0966 - Lab Phone (812) 856-0418 Daphnia Genomics Consortium - <http://daphnia.cgb.indiana.edu/> jcolbour@cgb.indiana.edu jcolbour@cgb.indiana.edu

London Parttime AssistProjectManager

ASSISTANT PROJECT MANAGER PART-TIME
UNDERSTANDING AND CONSERVING THE
EARTH'S BIODIVERSITY HOTSPOTS

REF: APM

HOURS OF WORK: part-time 18 hours per week

JOB STATUS: 3.5 years, Fixed Term Appointment

SALARY PER ANNUM: £18,030 per annum, pro rata

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

JOB DETAILS: In this role, you will assist the Project Manager with the day-to-day management of the EC funded Marie Curie Early-Stage Training Network "HOTSPOTS", an important project in understanding and conserving the Earth's biodiversity hotspots. Your duties will include writing reports, collecting/collating personal career development plans of early-stage researchers and organising courses and timetables, amongst other administrative duties. You will also manage and update the "HOTSPOTS" website and compile biodiversity and genetic data for the "HOTSPOTS" database.

ESSENTIALS:

Relevant degree or equivalent, ideally in Biology and Conservation, together with project management experience and good computer skills, including Word, Excel and web design. You will also have excellent organisational and communication skills, with proven team working experience.

CLOSING DATE: Friday 18 November 2005

Applications packs: <http://www.kew.org/aboutus/-jobs/RefAPM.htm> Further details on the project: <http://www.kew.org/hotspots> Dr Vincent Savolainen Molecular Systematics Section Jodrell Laboratory Royal Botanic Gardens, Kew Richmond, Surrey TW9 3DS London UK Tel +44-(0)20-8332-5366 Fax +44-(0)20-8332-5310 Email v.savolainen@kew.org

<http://www.kew.org/hotspots> v.savolainen@kew.org

MNHN Paris 9 SystematicsEvol

Professorship at the Museum National d'Histoire Naturelle, Paris

In spring 2006, nine positions of assistant professor and full professor will be opened in the Systematics & Evolution Department of the Paris Museum. These positions will be in the following fields :

1. Maitres de conférences (tenured assistant professor)
 1a. Genomique des populations et biostatistiques 1b. Evolution et biogeographie comparee des Mammiferes entre les continents africain et asiatique 1c. Centres de richesse, points-chauds et crise de la biodiversite : modeles arthropodes 1d. Systematique des algues 1e. Phylogenie et adaptations

2y. Professor 2a. Biologie evolutive et conservation des amphibiens et reptiles 2b. Evolution et phylogenie 2c. Systematique 2d. Rythmes et modalites de l'evolution des insectes

These positions will be opened in February or March 2006. Note however that the application process involves two steps, the first of which should be completed by the 19 October 2005. In this first step, applicants must register for evaluation by a national committee to have their names put on a qualification list. This can be made by filling out a form at <http://www.education.gouv.fr>, In this webpage, choose "personnels enseignants du superieur", then "enseignants chercheurs", then : "ANTARES". Be careful to register for the Museum, as the list is different from that for universities. The relevant section of the committee can be either 67 (biodiversity) or 68 (biology of organisms), or both. Registering must be completed by the 19 October 2005. You will then receive a letter asking for your CV and publication list. This first round of evaluation is necessary before you can apply for tenure anywhere. When applying, you will be interviewed. Fluency in French is not mandatory, but is very helpful.

The opening of positions in 2006 will be announced on evol.dir. However, potential applicants having registered for qualification can send us their CV and publication list for information.

Information : veuille@mnhn.fr

Michel Veuille <veuille@mnhn.fr>

MRC Harwell UK SystemsBiol

Systems Biology in the Laboratory Mouse - MRC Harwell

We are looking for someone with a strong mathematical biology or mathematical science background to initiate a programme of research on systems modelling and analysis in the laboratory mouse.

The research will be carried out in the bioinformatics group at the MRC's Mammalian Genetics Unit at Harwell, the UK's leading mouse genetics institute, and will form part of the Enfin EU-funded Network of Excellence.

The project will involve developing models of molecular systems being studied by one or more experimental groups at the MGU with the aim of furthering understanding of human disease, using mouse as a model. There will be considerable freedom to develop new lines of research within this general framework.

The position, which will run from November 2005 or as soon as possible thereafter to November 2008, would suit someone who has recently completed a PhD in a relevant area or someone with comparable research experience. For further details contact John Hancock (J.Hancock@har.mrc.ac.uk).

MGU web site: <http://www.mgu.har.mrc.ac.uk/>
 Bioinformatics group web site: <http://informatics.har.mrc.ac.uk/> Dr John M. Hancock
 Head of Bioinformatics, MRC Mammalian Genetics Unit, Harwell, Oxfordshire OX11 0RD, U.K.

E-mail: J.Hancock@har.mrc.ac.uk Telephone: +44 (0)1235 84 1014 Fax: +44 (0) 1235 84 1210
 WWW: <http://informatics.har.mrc.ac.uk/> Personal Page: <http://informatics.har.mrc.ac.uk/jmhwww/-johnhancock.html>

MichiganStateU PopGenet

Population Geneticist (Assistant or Associate Level)

The Graduate Program in Ecology, Evolutionary Biology and Behavior (EEBB) at Michigan State University

invites applications for a 9-month, tenure-system position in Population Genetics at the Assistant or Associate Professor level. The successful candidate will join strong interdisciplinary campus-wide programs in areas of molecular, quantitative, ecological and evolutionary genetics. Departmental affiliation is open, and will be based upon the candidate's training and research interests.

Applicants should have a PhD and post-doctoral experience in biological science, with appropriate training in theoretical and/or empirical approaches to Population Genetics in animal, plant, or microbial systems. The successful candidate will teach graduate and undergraduate courses in genetics and population genetics, establish a graduate training program, develop a strong externally funded research program, and serve on faculty committees. Collaboration with empirical EEBB faculty and students across campus will be expected and encouraged.

Review of applications will begin October 28, 2005 and continue until a suitable candidate is found. Applicants should submit a CV, statements of research interests and teaching philosophy, and 3-4 reprints, and should arrange for 3 letters of recommendation to be sent to: Chair-Population Genetics Search Committee, c/o Ecology, Evolutionary Biology and Behavior Program Office, 103 Giltner Hall, Michigan State University, East Lansing, MI 48824-1222. Tel: (517)-353-3288, Fax (517)-432-1699, e-mail: eebb@msu.edu; EEBB web site: <http://www.msu.edu/~eebb>. Michigan State University is an equal opportunity/affirmative action employer.

scribe3@msu.edu

NSF Director Environmental Biol

National Science Foundation Senior Executive Service Vacancy

ANNOUNCEMENT NUMBER: S20060002 OPEN: 10/11/2005 CLOSE: 11/14/2005

POSITION VACANT: Director, Division of Environmental Biology (DEB), Directorate for Biological Sciences

LOCATION: Arlington, Virginia

The National Science Foundation Directorate for Biological Sciences (BIO) is seeking qualified candidates for the position of Director, Division of Environmental

Biology (DEB). DEB supports fundamental research on populations, species, communities, and ecosystems. The Division is structured in four clusters - Ecological Biology that supports research on natural and managed ecological systems, primarily in terrestrial, wetland, and freshwater habitats; Ecosystems Science that supports research on natural, managed, and disturbed ecosystems, including those in terrestrial, freshwater, and wetland (including salt marsh) environments; Population & Evolutionary Processes that focuses on population properties that lead to variation within and among populations; Systematic Biology and Biodiversity Inventories that support the general science of systematics, whose three main missions are: to discover, describe, and inventory global species diversity; and analyze and organize the information.

Position will be filled on a one to three year Senior Executive Service (SES Limited Term appointment or on an Intergovernmental Personnel Act (IPA) assignment basis).

Senior Executive Service (SES) Limited Term Appointment The Senior Executive Service (SES) covers managerial positions above GS-15 in the Federal Service. The Federal pay range for Senior Executive Service positions is \$107,550 to \$149,200 per annum. Persons appointed to the SES are eligible for health benefits, life insurance, social security, Federal retirement and thrift savings plan coverage, and participate in the Federal leave system. Competitive status is not required, veteran's preference does not apply and there are no grade restrictions.

Intergovernmental Personnel Act (IPA) Assignment Individuals eligible for an IPA assignment with a Federal agency include employees of State and local government agencies or institutions of higher education, Indian tribal governments, and other eligible organizations in instances where such assignments would be of mutual benefit to the organizations involved. Initial assignments under IPA may be made for a period of up to two years. The individual remains an employee of the home institution and cost-sharing arrangements are generally negotiated between NSF and the home institution.

STATEMENT OF DUTIES: Provides leadership and direction for the Division of Environmental Biology (DEB) and serves as the Foundation's spokesperson in the areas of ecological, population, and systematic biology; ecosystem science; and long-term research in environmental biology. Assesses needs and trends in research and education related to the Division's programs, implements overall strategic planning and policy setting, provides leadership and guidance to Division

staff members, determines funding requirements, prepares and justifies budget estimates, balances program needs, allocates resources, oversees the evaluation of proposals and recommendations for awards and declinations, and represents NSF to relevant external groups. Fosters partnerships with other Divisions, Directorates, Federal agencies, scientific organizations and the relevant community.

QUALIFICATIONS REQUIREMENTS EXECUTIVE/MANAGERIAL Essential 1. Leading Change. Demonstrated ability to develop and implement an organizational vision that integrates key national science and engineering research and education goals. Includes understanding of the relative roles and relationships of Federal, academic and private organizations involved in the development and support of programs to improve the status of science and engineering research and education. Includes the ability to formulate effective program strategies consistent with the overall goals of the organization.

2. **Leading People.** Demonstrated ability to achieve organizational objectives by creatively managing and motivating staff. Includes the knowledge and ability to promote quality through the effective use of performance standards and assessment. Includes leveraging diversity and other differences, promoting developmental opportunities for staff, fostering commitment and team spirit, and constructively resolving conflicts.

3. **Results Driven Leadership.** Demonstrated knowledge and ability in planning, prioritizing, and coordinating large, complex programs. Includes the ability to make timely and effective decisions and to produce results through strategic planning, and the implementation and evaluation of programs and policies. Includes the ability to address

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

NewYorkU
ComparativeFuncGenomics

FACULTY POSITIONS

Center for Comparative Functional Genomics Department of Biology New York University

As part of a multi-year hiring plan, New York University's Center for Comparative Functional Genomics in the Department of Biology invites applications for multiple faculty positions (rank open) to begin September 1, 2006, or as negotiated, pending administrative approval. Candidates using high throughput approaches and/or computational methods to investigate biological regulatory mechanisms and their evolution at the level of systems and networks are especially encouraged to apply. Candidates will be expected to have or develop active, externally funded research programs and to participate in the department's teaching activities at both the undergraduate and graduate levels. The Center and the Department (<http://www.nyu.edu/fas/dept/biology>) offer an outstanding and collegial research environment and opportunities for active collaborations with other related divisions within the university including the NYU Courant Institute's Departments of Math and Computer Science and with genomic consortia formed with other New York institutions.

Applications should include cover letter, research statement, curriculum vitae, and three letters of reference. Electronic applications as PDF files may be sent to biology.recruitment@nyu.edu

Chair of the Search Committee Center for Comparative Functional Genomics Department of Biology New York University 1009 Silver Center 100 Washington Square East New York, N.Y. 10003

Selection of initial candidates will begin on Nov 15, and proceed on a rolling basis thereafter.

NYU is an Equal Opportunity/Affirmative Action Employer.

NOTE: for official correspondence related to this search, please do not email me directly (use biology.recruitment@nyu.edu)

Regards, Mark

Mark L. Siegal Assistant Professor Center for Comparative Functional Genomics Department of Biology New York University 100 Washington Square East New York, NY 10003 mark.siegal@nyu.edu

NewZealand EvolPlantMarineBiol

Lecturer/Senior Lecturer Plant Biology (1 position) (Ref SA0555B) & Marine Biology (2 positions) (Ref SA0556B) School of Biological Sciences Victoria Uni-

versity of Wellington, New Zealand

Victoria University of Wellington is a dynamic, rapidly growing university in the capital city of New Zealand. The School of Biological Sciences (www.sbs.science.vuw.ac.nz) seeks to make one appointment in Plant Biology and two appointments in Marine Biology.

The School of Biological Sciences provides a friendly, collegial and supportive working environment for about 80 academic, research, and general staff, and about 100 research students. The present appointments arise from growth of the School in response to successes in both teaching and research. The School maintains a Marine Laboratory on Wellington's Cook Strait coast. Wellington is an important centre for Marine Biology, and Victoria University has strong links to government research and management agencies.

We seek productive researchers who can contribute to our teaching in Ecology & Biodiversity, Marine Biology, and Conservation Biology. The ideal candidates will be active researchers who use theory to inform empirical research. Demonstrated strengths in experimental and/or quantitative approaches will be advantageous. For the Plant Biology position, we seek a researcher with expertise in integrated plant structure & function (especially ecophysiology) or in plant evolutionary ecology. For the two Marine Biology positions, we seek expertise in hard shore and/or soft shore coastal ecology; fisheries & aquaculture; marine pollution; or marine conservation.

Applications close 28 October 2005. For more information about these positions, see the website: www.nzjobs.co.nz/vuw <<http://www.nzjobs.co.nz/vuw>> An application pack is available from the Human Resources Officer, Faculties of Science, Architecture and Design, email: science-appoint@vuw.ac.nz, telephone ++64 4 463 5100, fax ++64 4 463 5122. Please quote the relevant reference number on all correspondence.

Peter Ritchie <Peter.Ritchie@vuw.ac.nz>

Paris PopGenetics

Professorship in population genomics.

In spring 2006, a tenured position of professor in molecular population genetics will be open at the Ecole Pratique des Hautes Etudes in Paris. Applicants should

have the publishing record of a professor, and have the ability to supervise a research group including Ph.D. students. Teaching duties are low. Teaching in English is possible, but fluency in French is appreciated. The successful applicant will collaborate with the research group of Michel Veuille at the Paris Museum. The position is mostly for research, either for empirical studies in population genomics or for theoretical work. In recent years, this research group has been mostly interested in characterizing selective sweeps in the drosophila genome.

Information : veuille@mnhn.fr

Michel Veuille <veuille@mnhn.fr>

PrincetonU EvolBiol

job posting ASSISTANT PROFESSOR ECOLOGY, EVOLUTION AND/OR BEHAVIOR

Princeton University's Department of Ecology and Evolutionary Biology invites applications for a tenure-track Assistant Professorship. We are interested in broad thinkers who will integrate research on environmental and organismal biology across ecology and evolution, including behavior, physiology, conservation biology, and biogeochemistry. Applicants should have a well-developed conceptual basis to their research and a strong commitment to teaching. A vision statement describing how specific research interests act to advance biology, a curriculum vitae, three reprints and three letters of recommendation should be sent to: Dr. Lars Hedin, Department of Ecology & Evolutionary Biology, Guyot Hall, Princeton University, Princeton, NJ 08544-1003. Screening of applications will begin 1 November 2005. Princeton University is an Affirmative Action/ Equal Opportunity Employer. For information about applying to Princeton and how to self identify, please link to <http://web.princeton.edu/sites/dof/ApplicantsInfo.htm> . Laura Landweber <llf@Princeton.EDU>

SanFranciscoStateU EcolEvol

BEHAVIORAL ECOLOGY/EVOLUTION San Francisco State University Department of Biology

The Department of Biology invites applications for a tenure-track faculty position at the Assistant Professor level. We seek an Evolutionary Biologist/Ecologist focusing on behavior. Relevant areas of research interest include, but are not limited to: evolution of behavior, behavioral ecology, and quantitative/evolutionary genetics of behavior. We prefer scientists with research programs that complement current faculty research interests and will contribute to building a strong and interactive evolution/ecology group. The successful candidate will establish an externally funded research program involving undergraduate and Master's students, and contribute to the Biology curriculum, including the teaching of an undergraduate course in Animal Behavior. Applicants must have a Ph.D. degree, a strong record of research accomplishment, and postdoctoral training.

A curriculum vitae, separate statements of research and teaching interests, representative reprints, and 3 letters of reference should be sent to: Chair, Behavioral Ecology/Evolution Search Committee, Department of Biology, San Francisco State University, 1600 Holloway Ave. San Francisco, CA 94132. Review of applications will begin December 1, 2005. Additional information about the department can be found on the Biology Department web page: <http://www.sfsu.edu/~biology>. The California State University is an Equal Opportunity/Affirmative Action Employer.

Eric Routman, Professor Department of Biology San Francisco State University 1600 Holloway Ave. San Francisco, California 94132 Phone: 415/338-1196 FAX: 415/338-2295

routman@sfsu.edu

Smithsonian GeneticsLabManager

Genetics Laboratory Manager, Smithsonian Institution
We are recruiting for a Laboratory Manager [Biological Science Laboratory Technician (Molecular Biology)] position for the Genetics Program of the Smithsonian Institution in Washington, DC. The Genetics Program conducts research and service for both the National Zoological Park and the National Museum of Natural History in the fields of population and conservation genetics, and molecular evolution, systematics and ecology. Starting salary is a GS-9, \$43,365 per annum, with promotion potential to GS-11. (Salary is subject to salary level increase pending FY06 Fed-

eral budget allocation) The position entails laboratory management and research, and the ideal applicant will have had experience managing a genetics laboratory (i.e., maintenance of laboratory equipment, facilities and frozen tissue collections, and purchasing of supplies and equipment) and conducting and training students and technicians in various molecular genetic methods (including, for example, PCR, DNA sequencing using capillary sequencers, construction of genomic libraries, development of microsatellite and SNP markers, ancient and non-invasive DNA extraction, and microarray procedures). Reference specific application procedures in actual announcement * see www.sihl.si.edu or contact Audrey Davis at 202-275-1005. Announcement will open October 24, 2005. Applications must be received by November 18, 2005, and must reference announcement number 05AD-1307. All applications will be notified by email or phone when their application is received. The Smithsonian Institution is an Equal Opportunity Employer. For more detailed information about the position please contact Rob Fleischer (fleischer@si.edu).

Robert C. Fleischer Genetics Program National Museum of Natural History National Zoological Park Smithsonian Institution 3001 Connecticut Ave., NW Washington, DC 20008-0551, USA phone 202-633-4190; fax 202-673-0040 fleischer@si.edu USE STREET ADDRESS

Fleischer.Robert@NMNH.SI.EDU

TexasAnMU ComparativeGenomics

JOB ADVERTISEMENT

Department of Wildlife and Fisheries Sciences Faculty of Ecology and Evolutionary Biology Genomics Signature Program at Texas A&M University

We seek a tenure-track assistant professor with research expertise in comparative genomics and/or quantitative genetics of vertebrates as applied to systematics, evolution, conservation, and management of natural populations. The candidate must establish an independently funded graduate research program, and teach in his/her area of expertise. Submit CV, statement of research and teaching interests, relevant reprints, and have three letters of reference sent to: Dr. John W. Bickham, Department of Wildlife and Fisheries Sciences, 210 Nagle Hall, Texas A&M University, College Station, Texas 77843-2258, telephone (979) 845-5777,

email j-bickham@tamu.edu. Reviews of applications will begin January 1, 2006; start date is expected to be September 1, 2006.

rhoneycutt@neo.tamu.edu

UAlabama Systematic Botany

The Department of Biological Sciences at The University of Alabama invites applications for a tenure-track Assistant Professor position in Systematic Botany to begin August 2006. We seek candidates with a Ph.D. and postdoctoral experience whose research integrates modern molecular approaches to study the systematics, biogeography, and evolution of vascular plants. Candidates should also provide evidence of curatorial experience and/or abilities. The successful applicant will be expected to interact with and strengthen existing research groups in molecular systematics, museum collections, aquatic biology, biodiversity, and evolution. We are especially interested in candidates that have the ability to explore evolutionary and molecular systematic questions relating to aquatic vascular plants.

The successful candidate will be expected to: * Develop an active, externally-funded research program * Actively curate and direct the University of Alabama Herbarium (UNA) * Collaborate with other faculty in Ecology, Systematics and Evolutionary Biology * Advise and direct undergraduate and graduate research * Develop quality instruction at the undergraduate and graduate levels

The Department of Biological Sciences is a vibrant, research-active department dedicated the development of teaching scholars. Our Howard Hughes Medical Institute Undergraduate Science Education Program grant and our NSF IGERT graduate training grant are examples of our philosophy of combined excellence in teaching and research. The University of Alabama Herbarium is an active participant in the Alabama Checklist of Vascular Plants Project. The Center for Freshwater Studies and The Alabama Museum of Natural History provide faculty opportunities for interdepartmental collaborations.

To apply, send curriculum vitae and a letter of application that includes research goals, evidence of curatorial experience, teaching philosophy and proposed courses, and have at least three letters of reference sent to: Plant Systematist Search, Department of Biological Sciences, Box 870344, The University of Alabama, Tuscaloosa,

AL 35487-0344. Review of applications will begin on December 16, 2005 and continue until the position is filled.

Further information on facilities and research opportunities at the University of Alabama can be found through the following links: * UA Herbarium, Johnson Molecular Systematics Lab and other biological collections at UA (<http://www.as.ua.edu/biology/scf/Collections&Facilities.html>) * Aquatic Biology Program (www.as.ua.edu/aquatic_biology) * University Arboretum (www.bama.ua.edu/~arboretum/) * Center for Freshwater Studies (www.as.ua.edu/cfs) * University of Alabama (www.ua.edu)

The University of Alabama is an Equal Opportunity/Affirmative Action employer and welcomes applications from women and members of minority groups.

Phillip M. Harris, Ph.D. Assistant Professor and Curator of Fishes Dept. of Biological Sciences Box 870345 The University of Alabama Tuscaloosa, AL 35487-0345

Phone: 205-348-1831 FAX: 205-348-6460

pharris@bama.ua.edu

<http://bama.ua.edu/~pharris/lab> Phillip Harris
<pharris@bama.ua.edu>

UAlgarve Comparative Endocrinology

Research scientist (Investigador auxiliar) in Comparative Endocrinology Commencing date: As soon as possible, after the closing date Place of work: Centre of Marine Sciences, Univeristy of Algarve, Campus de Gambelas, 8005-139 Faro, Portugal

Job description: To integrate into a Comparative and Molecular Endocrinology group which investigates the evolution and function of hormones in development, adaptation and reproduction. The group uses fish as primary models and combine classical endocrinological and physiological methods with molecular and genomics approaches. Some current projects focus on the role of parathyroid hormone and PTH-related peptide in calcium regulation and skeletal development, the role of thyroid hormones and binding proteins in early development and metabolism, the mechanisms of sex determination, endocrinology of stress, including endocrine disruption.

Qualifications and experience: Candidates must hold

a Ph D, a minimum of 3 years of postdoctoral experience preferably, but not necessarily, in the fields of endocrinology, biochemistry and or molecular biology.

Further information can be obtained from prof. Adelino Canário: <mailto:acanario@ualg.pt>acanario@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 with the possibility of renewal.

Closing date: 10 December 2005.

To apply for this position, candidates should submit a detailed CV with a concise description of research experience, a 2-3 page outline of a research proposal in the research area of the group and the names and addresses of at least two referees, quoting ref. CIMAR / 10 / 2005 to: <mailto:secretariado@cimar.org>secretariado@cimar.org

Centro Interdisciplinar de Investigação Marinha e Ambiental, Rua dos Bragas, n 289 4050 - 123 Porto, Portugal

Fax: +351 223 390 608 E-mail: <mailto:secretariado@cimar.org>secretariado@cimar.org

<http://www.ualg.pt/ccmar/investigador.htm> Adelino V.M. Canario Centro de Ciencias do Mar, Universidade do Algarve, Campus de Gambelas, 8005 - 139 FARO, Portugal Tel:(+351)289-800925, Fax:(+351)289-818353
<http://w3.ualg.pt/~acanario>

acanario@ualg.pt

UCBerkeley EvolEcol

UNIVERSITY OF CALIFORNIA, BERKELEY
ECOLOGIST

The Department of Integrative Biology, University of California, Berkeley invites applications to a faculty position in Ecology at the Assistant Professor level. We are searching broadly, without regard to taxon or system, for individuals who integrate experimental field studies with theory. We will consider exceptional ecologists in all areas, but are particularly interested in those working on species interactions, biological invasions, the community-ecosystem interface, and other areas that complement current faculty strengths on campus. UCB provides outstanding access to field sites, including the UC Natural Reserve System.

Applicants must have a Ph.D., productive postdoctoral

experience, and a demonstrated record of research excellence. Candidates must be strongly committed to developing an externally funded, internationally recognized, research program, and contributing significantly to both the undergraduate and graduate curricula through teaching and mentorship.

Submit a CV, statements of research and teaching interests, and the names and addresses of three references to Chair, Ecology Search Committee, Dept. of Integrative Biology, 3060 Valley Life Sciences Bldg. #3140, University of California, Berkeley, CA 94720-3140 USA. The deadline for receipt of applications is December 16, 2005. The University of California is an Equal Opportunity Employer committed to excellence through diversity.

– Sean Versoza Academic Personnel Associate Department of Integrative Biology University of California, Berkeley 3060 Valley Life Science Building #3140 Berkeley, CA 94720-3140 Phone (510) 642-2740 Fax (510) 643-6264

Sean Versoza <sversoza@berkeley.edu>

UCaliforniaIrvine 3 EvolGenetics

EVOLUTIONARY GENETICS: THREE FACULTY POSITIONS UNIVERSITY OF CALIFORNIA, IRVINE

The Department of Ecology and Evolutionary Biology seeks to fill three assistant professor tenure-track positions in the area of Evolutionary Genetics. Possible areas of specialization include population genetics and molecular evolution, broadly defined. Applicants interested in theory and modeling, as well as those conducting experimental, laboratory or natural population studies will be considered. Each successful candidate will be expected to teach in undergraduate and graduate courses in evolutionary genetics. Applications will be accepted until the positions are filled, but will be considered starting on December 1, 2005.

Please submit letter of application, curriculum vitae, a sample of relevant publications and arrange to have three letters of recommendation sent to Evolutionary Genetics Search Committee, Department of Ecology and Evolutionary Biology, 321 Steinhaus Hall, University of California, Irvine, CA 92697-2525. Information about the Department can be obtained at <http://ecoevo.bio.uci.edu/>. The University of California,

Irvine has an active career partner program, is an equal opportunity employer committed to excellence through diversity, and has a National Science Foundation Advance Gender Equity Program.

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

“Francisco J. Ayala” <fjayala@uci.edu>

UCaliforniaMerced MarineGenomicsTech

Laboratory Assistant on Marine Genomics. University of California, Merced

Description: The University of California is creating a dynamic new university campus and campus community in Merced, California, which opened in August 2005 as the tenth campus of the University of California and the first American research university built in the 21st century. The campus is located at the base of the Sierra Nevada foothills, near Yosemite and the San Francisco Bay Area. A full-time Laboratory Assistant position is available as part of an ongoing NSF-funded biocomplexity project to look at the functional genomics of coral-zooxanthellae symbiosis in two Caribbean coral species. The exact position, level of expectation and responsibility will depend upon previous education and experience. The successful candidate will be part of a multidisciplinary research team and a member of the Quantitative Systems Biology Group in the School of Natural Sciences.

Duties: Duties include but are not limited to: cDNA library construction, sequencing, gene expression microarray analyses, reverse transcriptase and real-time quantitative PCR. Participation in fieldwork in the Florida Keys and Puerto Rico during spawning season. Potential for scientific diving. Questions regarding the exact duties and responsibilities may be addressed to: mmedina@ucmerced.edu. Additional information about the School of Natural Sciences and the University of California at Merced can be found at <http://www.ucmerced.edu>. Conditions: The position is available immediately. Salary negotiable based on experi-

ence. Continuation is contingent on performance and available funds. The position includes generous benefits. The University of California at Merced is an affirmative action/equal opportunity employer with a strong institutional commitment to the achievement of diversity among its faculty, staff, and students.

Education: B.A or M.S. in Biology. Previous research experience in molecular biology, gene expression analysis/functional genomics, or a related field is required. Additional desired skills include computational biology (DNA sequence and microarray data management) and microarray statistics.

Instructions: Applicants should submit a cover letter, curriculum vitae or resume, and a list of three or more references including telephone numbers and email address to: Mónica Medina mmedina@ucmerced.edu. Online add at: http://paws.ucmerced.edu/~view_staff_position.faces?positionId16

Deadline: Until a suitable candidate is identified.

Monica Medina Assistant Professor School of Natural Sciences University of California, Merced P.O. Box 2039 Merced CA 95344 tel: 209-381-7863 fax: 209-812-1857 mmedina@ucmerced.edu

Monica Medina <mmedina@ucmerced.edu>

UCaliforniaSantaCruz PlantEvolBiol

UNIVERSITY OF CALIFORNIA, SANTA CRUZ PLANT EVOLUTIONARY BIOLOGY Assistant Professor The Ecology & Evolutionary Biology Department of the University of California, Santa Cruz, invites applications for a tenure-track position in Plant Evolutionary Biology, including, but not limited to, plant systematics or physiology. The successful candidate is expected to build a strong research group, supervise graduate students, teach modern terrestrial or marine plant systematics, as well as other courses at the undergraduate and graduate levels, and interact strongly with other faculty. The campus is especially interested in candidates who can contribute to the diversity and excellence of the academic community through their research, teaching, and/or service. RANK: Assistant Professor SALARY: Commensurate with qualifications and experience POSITION AVAILABLE: Fall 2006 MINIMUM QUALIFICATIONS: A Ph.D. in a relevant field; postdoctoral or equivalent research experience; a demonstrated record of research excellence;

and demonstrated potential for teaching at the university level-both undergraduates and graduates. APPLY TO: Please send a curriculum vitae and a statement of research and teaching interests to the address below. Candidates should also arrange for three or more letters of reference evaluating the candidate's scholarly contributions, teaching, and other professional accomplishments to be sent directly to this address. Electronic submissions are preferred. All letters will be treated as confidential (please direct your references to UCSC's confidentiality statement at <http://www2.ucsc.edu/-ahr/policies/confstm.htm>). Susan Thuringer Department of Ecology & Evolutionary Biology University of California, Santa Cruz 1156 High Street Santa Cruz, California 95064 Please refer to position #799-06 in all correspondence. Send electronic submissions, including letters of reference, to susan@biology.ucsc.edu CLOSING DATE: Position is opened until filled. For full consideration, applications must be received by December 5, 2005. UC Santa Cruz overlooks the Monterey Bay National Marine Sanctuary, about 70 miles south of San Francisco. The successful candidate will have access to multiple core facilities of the university, including the Molecular Ecology and Evolutionary Genetics laboratory, Long Marine Lab, Arboretum, Greenhouses (with reference collections), and Stable Isotope Laboratory, as well as a diverse range of local habitats and access to the University of California's Natural Reserve System. Information about the EEB Department is available at <http://www.biology.ucsc.edu>. UCSC IS AN AFFIRMATIVE ACTION/EQUAL EMPLOYMENT OPPORTUNITY EMPLOYER WOMEN AND MINORITIES ARE ENCOURAGED TO APPLY Inquiries regarding the University's equal employment opportunity policies may be directed to: Equal Employment Opportunity/Affirmative Action Office at, University of California, Santa Cruz, CA 95064; (831) 459-2686. Under Federal law, the University of California may employ only individuals who are legally able to work in the United States as established by providing documents as specified in the Immigration Reform and Control Act of 1986. If you need assistance due to a disability please contact the Academic Human Resources Office at 350 McHenry Library (831) 459-4300. This position description is available in alternate formats, which may be requested from Academic Human Resources at (831) 459-4300. VISIT THE AHR WEB SITE AT <http://www2.ucsc.edu/-ahr/employment/> 10/05/05

- Susan Thuringer Department Manager Ecology & Evolutionary Biology A308 Earth & Marine Sciences University of California Santa Cruz, CA 95064 (831) 459-4715 / Fax: (831) 459-

5353 <http://www.biology.ucsc.edu> Susan Thuringer <susan@biology.ucsc.edu>

UCentralFlorida FishConservation

POSITION: OPEN RANK TENURE-TRACK

DESCRIPTION: The Department of Biology at the University of Central Florida invites applications for an OPEN RANK TENURE-TRACK FACULTY POSITION in fish conservation biology. Candidates must have a Ph.D. and a demonstrated ability to establish and maintain a vigorous, extramurally-funded research program in fish conservation biology. This individual will contribute to our Ph.D. program in Conservation Biology and M.S. program in Biology, and teach a graduate course in ichthyology and other undergraduate and graduate courses. Preference will be given to innovative and productive scientists whose expertise complements those of our active and growing faculty. See <http://www.cas.ucf.edu/biology/> for department details.

Applicants should send a letter of intent, curriculum vitae, one-page statements of research plans and teaching philosophy, and arrange for three letters of recommendation to be sent directly to:

Dr. John E. Fauth, Chair, Fish Conservation Search Committee, Department of Biology, University of Central Florida, Orlando, FL 32816-2368.

Review of applications will begin November 15, 2005, with an anticipated start date of August 2006.

The University of Central Florida is the 7th largest university in the USA and the 2nd largest in the state of Florida. The University of Central Florida is an Affirmative Action/Equal Opportunity Employer. Search documents may be viewed by the public upon request in accordance with Florida statute.

Eric A. Hoffman Department of Biology University of Central Florida Orlando, FL 32816 407-823-4007

eahoffma@mail.ucf.edu eahoffma@mail.ucf.edu

UConnecticut NeurosporaFuncGenomics Res Asst

Research Assistant Position Open

An additional research assistant position is available at the University of Connecticut in the Townsend Laboratory to work in the field of the functional genomics of *Neurospora*. Responsibilities will include the printing and use of whole-genome microarrays for the purpose of assaying genome-wide gene expression. A B.A. or B.S. in biology with previous laboratory experience is required, but potential applicants with Master's degrees or Ph.D.s are encouraged to apply, as salary will be commensurate with education and experience. Funding is potentially available for multiple years, depending on performance. Storrs is located in a beautiful community in the heart of New England, close to Hartford, New Haven, Providence, and Boston.

The Townsend lab integrates theory and experiment to study population genetics, functional genomics, and evolutionary biology. Ongoing research includes experimental work on the population genetics and functional genomics of the model fungi *Saccharomyces cerevisiae* (wine yeast) and *Neurospora crassa* (bread mold), bioinformatics and statistics for the analysis of DNA microarrays, and population genetic theory on horizontal gene transfer in microbial populations.

For full consideration please apply by November 1, 2005. Starting date is as soon as possible.

To apply, please send a CV or resume and contact information for three academic references to Jeffrey.Townsend@UConn.edu.

Jeffrey P. Townsend, Ph.D.

Assistant Professor Molecular and Cell Biology Department
354 Mansfield Road U-2131 University of Connecticut Storrs, CT 06269

<http://web.uconn.edu/townsend> (860) 486-1899

Jeffrey Townsend <Jeffrey.Townsend@uconn.edu>

UFlorida Director Biotechnology

POSITION ANNOUNCEMENT

TITLE: DIRECTOR, INTERDISCIPLINARY CENTER FOR BIOTECHNOLOGY RESEARCH LOCATION: UNIVERSITY OF FLORIDA, GAINESVILLE, FLORIDA SALARY: COMMENSURATE WITH QUALIFICATIONS AND EXPERIENCE CLOSING DATE: Formal review of applications will begin on

November 15, 2005 and will continue until the position is filled.

DUTIES AND RESPONSIBILITIES: The mission of the Interdisciplinary Center for Biotechnology Research (ICBR) is to support the growth of the life science research program of the University of Florida and that of researchers throughout the state, by making widely available the needed facilities, technologies, training, and competent personnel. ICBR is a service-oriented organization. The Director will manage the personnel and core facilities in support of the research faculty across all the colleges and departments of the University of Florida and in major research centers such as the UF Shands Cancer Center (www.ufscc.ufl.edu), the Genetics Institute (www.ufscc.ufl.edu), and the McKnight Brain Institute (www.mbi.ufl.edu). The funding for ICBR is a mix of state appropriated funds and fees for services.

The Director will have a full-time position reporting to the University of Florida Vice President for Research with an initial appointment for a specified and negotiable period. The Director has a highly visible position as a key advocate for biotechnology, both within the University community and to those outside. The duties require leadership in several important functions:

- Promoting the use of emerging biotechnology advances in sponsored research.
- Utilizing staff efficiently with fluid reallocation across Core Facility boundaries.
- Working successfully with university leaders to leverage institutional financial resources and obtain the external funding to meet the research infrastructure goals.
- Develop new ICBR Core services, periodically review existing services and, when found necessary, eliminate obsolete services and enhance underdeveloped services.
- Seek opportunities for external collaboration and cooperation with other academic and industrial partners.
- Encourage and enable the staff to improve their technical skills and scientific knowledge to benefit the ICBR mission.
- Establish a formal advisory structure, drawing from within and without the University of Florida with representation from leading academic and industrial programs.

QUALIFICATIONS: Candidates must possess an earned doctorate. The Director must have demonstrated successful leadership and administrative abilities; recognized excellence in research, teaching, outreach, and related scholarly activities; an exemplary funding record, and proven ability to foster cooperative

relations within a university and among stakeholders at the state, national, and international levels. Excellent communication skills will be necessary for interacting with the public and policy makers and for actively participating in interdisciplinary research and education programs. Candidates must also have a commitment to UF's core values of excellence, diversity, global involvement, and accountability.

BACKGROUND INFORMATION: The ICBR currently provides the following Core services: Genomics, Microarrays, Genetic Analysis, Custom DNA Sequencing, Proteomics, Electron Microscopy, Flow Cytometry, Hybridoma, Biological Computing, Education and Training. A complete description of the services and personnel can be found at www.biotech.ufl.edu. The University of Florida, the state's Land Grant institution, with a student population of 47,000, is located in Gainesville, a city of 110,000 residents in north-central Florida. A member of the prestigious American Association of Universities, the University conducts research, instruction, and outreach programs on campus and across the state. The 111 masters and 70 doctoral programs of the Graduate School rank the University of Florida as one of the nation's most comprehensive major universities.

APPLICATION: Applicants should submit a file including: 1) a curriculum vitae, 2) a letter of application describing experience, philosophy, and qualifications related to this position, and 3) the names, addresses, and phone numbers of three professional references to the Search and Screen Committee on or before November 15, 2005. Formal review of applications will begin on this date and will continue until the position is filled. Nomination of candidates is encouraged. Women and minorities are encouraged to apply.

ADDRESS CORRESPONDENCE TO: Search and Screen Committee Chair, 223 Grinter Hall, University of Florida, Gainesville, Florida 3211.

The University of Florida is an equal opportunity, equal access, affirmative action employer. The "government in the sunshine" laws of

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

UFlorida EvolMorphologist

The following job advertisement will appear in the Oct. 7 issue of Science.

*ASSISTANT or ASSOCIATE PROFESSOR IN EVOLUTIONARY MORPHOLOGY

The Department of Zoology at the University of Florida seeks an evolutionary morphologist broadly defined as one who studies morphology in an evolutionary context, from the functional, comparative or developmental perspectives. Candidates will be evaluated on innovation as well as productivity. The successful candidate will join a vibrant and collegial research community that integrates behavior, development, ecology, genetics, morphology and physiology with evolutionary principles. The Department enjoys strong ties with the Florida Museum of Natural History, UF Genetics Institute and multiple University centers in biomedical, veterinary, environmental and agricultural sciences, making it central to a University-wide expansion in the life sciences. The new hire will be expected to develop an internationally recognized research program and to excel in teaching. Teaching requirement includes comparative/functional vertebrate morphology. Please submit curriculum vitae, a maximum of three reprints, and statements of research interests and teaching philosophy, both as hard copy and in PDF format on a CD, and have three letters of reference sent to Evolutionary Morphology Search Committee, Department of Zoology, PO Box 118525, University of Florida, Gainesville, FL 32611-8525. Applications must be received by November 4, 2005. For more information, contact evomorphsearch@zoo.ufl.edu or visit <http://www.zoo.ufl.edu/evomorphsearch>. Our department is committed to diversity as a component of excellence. Women, minorities and members of other under-represented groups are particularly encouraged to apply. The University of Florida is an equal opportunity institution.

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

Phone: 352-392-3550 Fax: 352-392-3704 Email: cbaer@zoo.ufl.edu Web: <http://www.zoo.ufl.edu/faculty/baer.html>

UGeorgia EvolBiol

The following ad will appear in the Sept. 16 issue of Science.

Systematic and Evolutionary Biology

The Plant Biology Department at the University of Georgia has an opening for an Assistant or Associate Professor in Systematic and Evolutionary Biology. We seek a systematic biologist who uses innovative approaches to address fundamental questions about plants, algae or fungi in areas such as phylogenetics, molecular evolution, speciation or genome evolution. The successful candidate is expected to develop a vigorous, externally-funded research program and to teach and train undergraduate and graduate students in systematics. Cover letter, curriculum vitae, short statements of research interests and teaching philosophy and no more than five reprints should be assembled into a single pdf file and submitted online at <http://www.plantbio.uga.edu/positions.html>. Candidates should request four referees to submit letters of recommendation to the same site or by mail to Systematic and Evolutionary Biology Search Committee, Plant Biology Department, University of Georgia, Athens, GA USA 30602-7271. Applications received by November 4, 2005 are assured full consideration. The Franklin College of Arts and Sciences is committed to increasing the diversity of its faculty and strongly encourages applications from individuals in under-represented groups. UGA is an Equal Opportunity Employer.

Shu-Mei Chang Plant Biology Department 2502 Miller Plant Sciences Bldg University of Georgia Athens, GA 30602 <http://www.plantbio.uga.edu/~chang/-chang.html>

chang@plantbio.uga.edu

UIllinoisChicago EcolEvol

Colleagues:

Ecology/Evolution Faculty Position University of Illinois at Chicago

The Department of Biological Sciences at the University of Illinois at Chicago (UIC) invites applications for an Assistant Professor position. This is a tenure-track faculty position starting August 16, 2006. We seek outstanding candidates to establish a vigorous, extramurally funded research program in an area that complements the existing strengths of the ecology and evolution program. Potential research areas include, but are not limited to, theoretical or empirical studies of evolutionary genetics, ecosystem processes, or landscape ecology. The successful candidate will contribute to the departments undergraduate and graduate teaching efforts. Candidates must have a Ph.D. in ecological and/or evolutionary biology or a related science field and significant postdoctoral experience. UIC is among the top 50 national universities in federal research funding, and is located in downtown Chicago. Visit our website: <http://www.uic.edu/depts/bios>. For fullest consideration, please send curriculum vitae, a brief summary of research plans, and at least three letters of recommendation to: JOB ID #15608, Ms. Stephanie Davis, UIC, Dept. of Biological Sciences, MC 066, 845 W. Taylor St., Chicago, IL, 60607 or e-mail: sydavis@uic.edu. Review of applications will begin 11/15/05. UIC is an AA/EOE employer.

Please feel free to contact me with questions about this position.

Sincerely, Mary Ashley

– Mary V. Ashley Professor Faculty Coordinator, Ecology and Evolution University of Illinois at Chicago 845 W. Taylor St., M/C 066 Chicago, IL 60607

<http://www.uic.edu/depts/bios/ecoevo/ashley.htm>

Phone: (312) 413-9700 FAX: (312) 996-9462 E-mail: ashley@uic.edu

UIowa MathBiol

THE UNIVERSITY OF IOWA

The Department of Mathematics at the University of Iowa invites applications for a tenure-track assistant professorship, starting in August 2005, in the area, broadly defined, of computational and mathematical biology. The University of Iowa has many excellent programs in the biological and medical sciences, with a University-wide bioscience initiative. The Department of Mathematics is in the midst of a multi-year expansion of its mathematical biology research group. Selec-

tion will be based on evidence of outstanding research accomplishments or potential and excellent teaching.

A Ph.D. or equivalent is required. Screening of applications will begin December 1, 2005. Applications will be accepted until the position is filled. To apply, send a letter of application, a completed AMS cover sheet, a complete vita, a research statement and a statement of teaching philosophy. Also have three letters of recommendation sent. Please indicate in your application the position for which you are applying. Materials should be sent to:

Professor David Manderscheid, Chair Department of Mathematics The University of Iowa Iowa City, Iowa 52242-1419

The University of Iowa is an Equal Opportunity/Affirmative Action Employer. Applications from women and minorities are strongly encouraged. For further information about the Department see www.math.uiowa.edu. Professor Herbert W. Hethcote Department of Mathematics University of Iowa 14 MacLean Hall Iowa City, Iowa 52242 USA Tel:(319)335-0790 FAX:(319)335-0627 <http://www.math.uiowa.edu/~hethcote/> Herbert Hethcote hethcote@math.uiowa.edu

ative Genomics. The Center is fully equipped for robotically driven high throughput DNA sequencing and functional genomics. More about the Departments and the Center for Comparative Genomics may be found at www.uiowa.edu/~anthro, www.biology.uiowa.edu, and www.biology.uiowa.edu. Candidates must have post-doctoral experience and a recognized record of accomplishment, including publications in leading journals. Successful candidates will be expected to establish and maintain an extramurally-funded research program and participate in teaching at the undergraduate and graduate level. Newly renovated space and a competitive start-up package will be available. Applicants should send a curriculum vita, statement of research objectives, selected reprints, a description of teaching interests, and the names of three references to: Biological Anthropology Search Committee, c/o Becky Birch, Department of Biological Sciences, 143 Biology Building, The University of Iowa, Iowa City, IA 52242-1324. Review of applications will begin November 1, 2005 and continue until the position is filled. The University of Iowa is an affirmative action/equal opportunity employer. Women and minority candidates are especially encouraged to apply.

becky-birch@uiowa.edu

UIowa PrimateGenomics

Job: ANTHROPOLOGICAL GENETICS/PRIMATE GENOMICS

The Departments of Anthropology and Biological Sciences In conjunction with the Roy J. Carver Center for Comparative Genomics at The University of Iowa

Applications are invited for a tenure-track position at the Assistant Professor level. Successful candidates are expected to have an internationally visible research program that focuses on anthropological genetics and primate genomics. Some representative areas of research are: the developmental genetics of complex morphological traits; the genetic basis for unique character traits such as language; the comparative genomics of primates; and the use and analysis of molecular genetic markers in living populations to infer historic and pre-historic population demography. The Departments of Anthropology and Biological Sciences are committed to expanding their respective programs to reflect modern genomic approaches to primate and human evolution in association with the Roy J. Carver Center for Compar-

UKansas SystematicOrnithology

The following job advertisement will appear in the October 7th issue of Science

The University of Kansas: Assistant Professor/Assistant Curator - Systematic Ornithology

The Department of Ecology and Evolutionary Biology and the Natural History Museum and Biodiversity Research Center at the University of Kansas invite applications for a tenure-track position as Assistant Professor/Assistant Curator in the area of systematic ornithology beginning 18 August 2006. The ideal candidate will have a systematic and phylogenetic focus on questions regarding the evolution of avian diversity, using specimen-based research methods. Required qualifications: Ph.D. (by date of appointment); active research program in systematics of birds; commitment to ornithological research collections; commitment to teaching and mentoring undergraduate and graduate students; ability to teach courses in ornithology, organismal biology, and area of expertise. Preferred qualifications: postdoctoral research experience;

ability to secure extramural funding; curatorial experience; well-developed research program involving detailed, specimen-based field work; teaching experience and a candidate who will contribute to the climate of diversity in the College, including a diversity of scholarly approaches.

TO APPLY: send curriculum vitae (with e-mail address), reprints of key papers, statements of current and future research plans, teaching philosophy that includes course-development interests, and have at least three letters of recommendation sent to: Dorothy Johanning (email: jdorothy@ku.edu), University of Kansas, Department of Ecology and Evolutionary Biology, 1200 Sunnyside Avenue, Rm 2041, Lawrence, KS 66045-7534. Review of applications will begin 11 November 2005, and continue until position is filled. Both positions include a competitive start-up package. For more information visit <http://www.ku.edu/~eeb>. Paid for by KU. The University of Kansas is an EO/ AA Employer.

lhileman@ku.edu lhileman@ku.edu

UKansas TheoSystematist

The following job advertisement will appear in the October 7th issue of Science

The University of Kansas: Assistant Professor - Theoretical Systematist

The Department of Ecology and Evolutionary Biology at the University of Kansas invites applications for a tenure-track position as Assistant Professor in the area of theoretical systematics. We encourage applications from outstanding candidates with research interests in all areas of theoretical systematics. These may include, but are not limited to, theoretical phylogenetics, computational phylogenetics, or development of new methods within the broad framework of evolutionary biology. The successful candidate is expected to pursue an active research program and to teach at undergraduate and graduate levels. Required qualifications: Ph.D. (by date of appointment) with expertise in systematics, computational phylogenetics or a related field; commitment to excellence in research, service and undergraduate/graduate education; ability to teach courses in undergraduate biology and area of expertise; and commitment to seeking extramural funding. Preferred qualifications: postdoctoral experience, demonstrated ability to secure extramural funding, teaching experience, and

interest in collaborative research and a candidate who will contribute to the climate of diversity in the College, including a diversity of scholarly approaches.

TO APPLY: send curriculum vitae (with e-mail address), reprints of key papers, statements of current and future research plans, teaching philosophy that includes course-development interests, and have at least three letters of recommendation sent to: Dorothy Johanning (email: jdorothy@ku.edu), University of Kansas, Department of Ecology and Evolutionary Biology, 1200 Sunnyside Avenue, Rm 2041, Lawrence, KS 66045-7534. Review of applications will begin 11 November 2005, and continue until position is filled. Both positions include a competitive start-up package. For more information visit <http://www.ku.edu/~eeb>. Paid for by KU. The University of Kansas is an EO/ AA Employer.

lhileman@ku.edu lhileman@ku.edu

UMarylandBC MolEvol

Positions in Neurobiology and Molecular Evolution University of Maryland Baltimore County, UMBC?

The Department of Biological Sciences seeks to recruit two tenure-track assistant professors. One appointment will be in neurobiology. The second will be in molecular evolution. Successful applicants will have a doctoral degree in biology or a related field and post-doctoral experience, and will be expected to establish a vigorous, extramurally funded research program.? Other obligations include mentoring Ph.D. students and teaching?at the graduate and undergraduate levels.? ? UMBC is a medium-sized research university in the Baltimore-Washington area with a tradition of combining excellence in research with outstanding educational programs.?The Department of 25 faculty has strengths in the areas of neuroscience, evolutionary biology and bioinformatics, as well as in molecular, cellular and developmental biology.

Applicants should send a cover letter, summary of current research, curriculum vitae, concise summary of future research plans, statement of teaching interests, and three letters of reference to: Search Committee, Department of Biological Sciences, University of Maryland Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250. Email applications will not be accepted.? Review of applications will begin immediately and highest priority will be given to completed applications received

by December 1, 2005.

Information about the Department and its graduate programs can be found at <http://www.umbc.edu/biosci/>.? The University of Maryland Baltimore County is an Affirmative Action/Equal Opportunity Employer.? UMBC values gender, ethnic, and racial diversity; women, members of ethnic minority groups and individuals with disabilities are strongly encouraged to apply.?

– Kevin Omland, Ph.D. Assistant Professor Dept. of Biological Sciences University of Maryland, Baltimore County 1000 Hilltop Circle Baltimore, MD 21250 410-455-2243 (phone) 410-455-3875 (fax) <http://www.umbc.edu/biosci/Faculty/omland.html> Kevin Omland <omland@umbc.edu>

UMassAmherst EvolGenomics

As seen in the 07 October issue of Science: Evolutionary Genomics

Department of Biology University of Massachusetts Amherst

The Department of Biology at UMass Amherst invites applications for an Open Rank, Tenure-Track Faculty Position in the area of Evolutionary Genomics. We seek candidates whose research and teaching expertise addresses questions in the areas of evolutionary development, systematics, molecular evolution or population genetics using comparative genomics and related methodologies. The successful candidate is expected to establish an externally funded research program and to be actively committed to teaching at both the undergraduate and graduate levels. Competitive salary and startup package

Applicants should mail a curriculum vitae, statement of research plans and teaching philosophy, and arrange for three letters of reference to be sent to: Evolutionary Genomics Search #R23811, c/o Ms. Karen Nelson, Department of Biology, University of Massachusetts, Amherst, MA 01003. Review of applications will begin November 14, 2005 and continue until the position is filled

The University of Massachusetts is an Affirmative Action Equal Opportunity Employer. Women and members of minority groups are encouraged to apply

Regards,

Peg

– Dr. Margaret (Peg) Riley Professor, Department of Biology Director, Massachusetts Museum of Natural History Director, Organismic and Evolutionary Biology Graduate Program University of Massachusetts Amherst Amherst, MA 01003

413-545-2132 riley@bio.umass.edu

Peg Riley <riley@bio.umass.edu>

UMassachusettsAmherst EcolEvol

Evolutionary Ecology The Biology Department at the University of Massachusetts Amherst invites applications for a tenure-track position at the Assistant Professor level. We seek a field-oriented biologist whose research addresses fundamental questions in ecology and evolutionary biology. Specific areas of interest include, but are not limited to, population genetics, adaptation, speciation, and the evolution of species interactions. We expect this individual to develop an internationally recognized, externally funded research program, to have a strong commitment to research and to undergraduate and graduate education. Competitive salary and startup package.

Applicants should mail a curriculum vitae, statement of research plans and teaching philosophy, and arrange for three letters of reference to be sent to: Evolutionary Ecology Search #R23805, c/o Ms. Karen Nelson, Biology Department, University of Massachusetts, Amherst, MA 01003-9297. Review of applications will begin November 14, 2005 and continue until the position is filled.

The University of Massachusetts is an Affirmative Action Equal Opportunity Employer. Women and members of minority groups are encouraged to apply.

Jeff Podos <jpodos@bio.umass.edu>

UMemphis ChairBiol

The University of Memphis Chair, Department of Biology

Applications and nominations are invited for the po-

sition of Chair of the Department of Biology at The University of Memphis. Applicants should have the academic rank of Professor or be near to achieving such rank. They must have an established research program, a commitment to academic excellence, and strong interpersonal and administrative skills. The Department is seeking candidates possessing a successful history of research, extramural grant support, and teaching in any of the basic areas of the biological sciences. Candidates with backgrounds in integrative biology are encouraged to apply. The starting date is flexible with an anticipated start date on or after August 2006.

The University of Memphis is a comprehensive state university with an enrollment of approximately 21,000 students. The Department of Biology offers B.S., M.S., and Ph.D. degrees in Biology. There are approximately 30 faculty, 14 staff, 50 full-time graduate students, and 700 majors in the department. The department administers the Meeman Biological Field Station and the Ecological Research Center, and is closely affiliated with the Integrated Microscopy Center and the W. Harry Feinstone Center for Genomic Research.

Additional information: Departmental information (<http://biology.memphis.edu>), University information (<http://www.memphis.edu>), or contact Dr. Joan T. Schmelz at (901) 678-2419 or jtschmelz@memphis.edu.

Applicants should submit a letter of application, separate statements of research and teaching interests, a statement of administrative philosophy, and a complete curriculum vitae including a list of five references to: Chair, Search Committee, Department of Biology, The University of Memphis, Memphis, TN 38152. Review of applicants will begin November 1, 2005, and may continue until the position is filled. Women and minority candidates are encouraged to apply. The University of Memphis is an Affirmative Action/Equal Opportunity Employer.

mbeck@memphis.edu

UMinnesota Bioinformatics

The Department of Computer Science & Engineering at the University of Minnesota is accepting applications for a tenure-track position in Bioinformatics. Complete application information about this position can be found at <http://www.cs.umn.edu/-employment/faculty.php> For full consideration, applications should be received by January 9, 2006.

Liz Freppert Department of Computer Science University of Minnesota and Engineering 4-192 EE/CSci Bldg. freppert@cs.umn.edu 200 Union St SE Phone: (612) 625-1890 Minneapolis MN 55455 Fax: (612) 625-0572

Liz Freppert <freppert@cs.umn.edu>

UMinnesota PlantSystematics

POSITION ANNOUNCEMENT

Plant Systematist University of Minnesota, Twin Cities

The Department of Plant Biology and the Bell Museum of Natural History at the University of Minnesota announce a 9-month tenure-track position for an assistant or associate professor and herbarium curator in the area of non-flowering plant systematics and/or mycology. Candidates are required to have experience in collections-based research involving non-flowering plants and/or fungi including lichens. The successful applicant is expected to develop an externally funded research program; contribute to teaching and advising in organismal biology and systematics; curate sections of the herbarium including lichens; and contribute to public outreach through the Bell Museum. Tenure will reside in the Department of Plant Biology. The successful applicant is also expected to foster collaboration with biologists in other fields including phylogenetics, molecular evolution, genomics, development, ecology, and/or conservation biology. A Ph.D. degree and herbarium experience is required; post-doctoral experience is preferred. Please send a curriculum vitae; up to five selected reprints; a statement of research, teaching, and curatorial interests and experience; and three letters of reference to Dr. George Weiblen, Search Committee Chair, Department of Plant Biology, 250 Biological Sciences Center, 1445 Gortner Avenue, University of Minnesota, St. Paul, Minnesota, 55108, USA. The committee will meet to begin consideration of complete applications on 1 December 2005. For further information visit the Department of Plant Biology (<http://www.cbs.umn.edu/plantbio/>), the Bell Museum of Natural History (<http://bellmuseum.org>), or contact the search chair by email (gweiblen@umn.edu). The University of Minnesota is an equal opportunity educator and employer.

George Weiblen

Assistant Professor, Department of Plant Biology Curator of Flowering Plants, Bell Museum of Natural His-

tory University of Minnesota 250 Biological Sciences
1445 Gortner Avenue Saint Paul, MN 55108 USA

Office: 612-624-3461 Lab: 612-625-8749 Fax: 612-
625-1738 Email: gweiblen@umn.edu Web: [http://-
geo.cbs.umn.edu](http://-
geo.cbs.umn.edu) [gweiblen <gweiblen@umn.edu>](mailto:gweiblen@umn.edu)

UNebraska Tech

FIELD and LABORATORY TECHNICIAN – Univer-
sity of Nebraska-Lincoln – for a project examining the
potential ecological effects of the escape of a transgene
for virus resistance from cultivated squash into wild
squash populations.

This project, recently funded by the USDA Biotechnol-
ogy Risk Assessment Program, will involve surveying
wild squash populations for virus infection and the pres-
ence of transgenes derived from transgenic cultivated
squash, experiments to quantify factors controlling the
dynamics of wild squash populations (including the ef-
fect of virus infection), and the development of stochas-
tic demographic models to evaluate the potential effect
of transgenic virus resistance on the dynamics of wild
squash populations.

The technician's duties will include using PCR and RT-
PCR to detect transgenic resistance to viral infection
and identify virus-infected plants, general lab mainte-
nance, data entry, and database management. During
the field season (~4 months each year) the technician
will work under the supervision of a graduate student
at a field site in Mississippi (housing provided) estab-
lishing field experiments and collecting field data.

Previous experience using plant molecular techniques is
preferred and a willingness to do field work and travel
in the summer required. This would be an excellent
job for a recent college graduate interested in gradu-
ate school in a couple of years. Excellent benefits in-
cluding health insurance and staff/dependent scholar-
ship program. We will begin screening applications on
10/10/2005. To apply send letter of interest, CV, and
names of three references to Dr. Diana Pilson at School
of Biological Sciences, 348 Manter Hall, University of
Nebraska, Lincoln NE 68588-0118. Applications must
also be completed online through the University's em-
ployment site: [<http://employment.unl.edu/>](http://employment.unl.edu/)[http://-
/employment.unl.edu](http://-
/employment.unl.edu). If you require an accommoda-
tion, please call (402) 472-2120. UNL is an equal op-
portunity employer, and encourages applications from
women and minorities.

dpilson1@unl.edu dpilson1@unl.edu

UPoitiers EvoEco

A Full Professorship in EVOLUTIONARY ECOLOGY
will be available at the University of Poitiers, starting
September 2006.

We seek to fill a permanent position of Professor in
Evolutionary Ecology (senior researcher) in the joint
research unit (UMR) GBPC (Population Biology and
Genetics of Crustaceans, D. Bouchon) of the University
of Poitiers (France).

There is flexibility concerning the specific research area.
The ideal candidate works in the field of evolutionary
ecology of host-parasite interactions and genetic con-
flicts. The successful candidate will be expected to
interact broadly with collaborators at the CNRS Re-
search Unit which is mostly interested in investigating
the arthropod-symbiont interactions.

Teaching responsibilities entail introductory courses for
1st year students and specialized courses in our grad-
uate and master program in ecology and evolutionary
biology. Introductory courses must be taught in French.

Cautionary Note : Due to the administrative pro-
cedures of the French system, the candidates need
to register for a 'liste de qualification' before OC-
TOBER 19, 2005 (before 5pm Paris time) to be
allowed to apply for the position in spring 2006. The
applications will be assessed by disciplinary commit-
tees at the national level. Note that the relevant
committee in the case of ecology and evolution is
the so called CNU section 67 (Population Biology
and Ecology). For further information and online
application see ([http://www.education.gouv.fr/-
personnel/enseignant_superieur/](http://www.education.gouv.fr/-
personnel/enseignant_superieur/)
en-
seignant_chercheur/antares.htm).

Candidates should send their CV, a list of publications
and grant income to date, and a research plan to:

Pr. Didier Bouchon Universite de Poitiers Gene-
tique et Biologie des Populations de Crustaces UMR
CNRS 6556 40 avenue du Recteur Pineau F-86022
POITIERS Cedex tel : +33 (0)5 49 45 38 95 fax : +33
(0)5 49 45 40 15 <http://labo.univ-poitiers.fr/umr6556>
<mailto:didier.bouchon@univ-poitiers.fr>

Further enquiries about the position may be made to
Prof. Brigitte Crouau-Roy, tel +33 561 55 6259, email
bcrouau@cict.fr

Prof B. CROUAU-ROY Université Paul Sabatier UMR CNRS 5174 "Evolution et Diversité Biologique" EDB Bat. IV R3 b2 31062- Toulouse cédex 9 FRANCE Tel (33)5 61 55 62 59 (direct) 73 28 (secretariat) Fax:(33)5 61 55 73 27 <http://www.edb.ups-tlse.fr> bcrouau@cict.fr – Pr. D. Bouchon

Universite de Poitiers Genetique et Biologie des Populations de Crustaces, UMR CNRS 6556 40 avenue du Recteur Pineau F-86022 POITIERS Cedex tel : +33 (0)5 49 45 38 95 fax : +33 (0)5 49 45 40 15 <http://labo.univ-poitiers.fr/umr6556> mailto:didier.bouchon@univ-poitiers.fr

USouthCarolina Bioinformatics

FACULTY POSITION BIOINFORMATICS/QUANTITATIVE MOLECULAR BIOLOGY

The College of Arts and Sciences at the University of South Carolina (USC) is seeking to fill a tenure-track position at the assistant professor level, beginning Fall 2006, in the area of quantitative analysis of molecular biological data. Potential research areas include genomics (microarray) and/or proteomics data analysis, systems biology, statistical modeling, population genetics, the genetics of complex traits, and molecular evolution. Candidates whose research interests overlap with existing areas of research strength at USC will be given preferential consideration. This is a joint search involving the Departments of Biological Sciences, Mathematics, and Statistics. The successful candidate will have a primary appointment in one of the three departments, with the possibility of a secondary appointment in one of the other departments.

For further information, contact Austin L. Hughes (Biological Sciences) austin@biol.sc.edu; Dan Dix (Mathematics) dix@math.sc.edu; or Walt Piegorsch (Statistics) piegorsch@stat.sc.edu. To apply, go to <http://uscjobs.sc.edu> or send curriculum vitae, reprints of three representative publications, a statement of current and future research interests, graduate transcripts, and a brief description of teaching interests; and arrange to have three letters of recommendation sent to: Dr. Austin L. Hughes, Chair, Bioinformatics Search Committee, Department of Biological Sciences, University of South Carolina, Columbia SC 29208. Review of applications will begin December 1st, 2005, and continue until the position is filled. The University of South Carolina is an Affirmative Action/Equal Oppor-

tunity Employer.

"Austin L. Hughes" <austin@biol.sc.edu>

UTennessee CompGenomics

This position will be in the laboratory of Dr. Julia Krushkal (jkrushka@utmem.edu) or Dr. Ronald Adkins (radkins1@utmem.edu) at the University of Tennessee Health Science Center in Memphis.

Job Title: DATA ANALYST PIN Number: #18049

JOB SUMMARY: The Data Analyst will be responsible for the handling and analysis of genetic data from a collaborative research study studying the genome potential of environmentally important microorganisms, species of *Geobacter*. The duties including management and manipulation of large data sets that include genome sequences, microarray data, and proteomics data; writing computer programs to handle the data; running available public and commercial bioinformatics software to analyze the data; statistical analysis; and preparation of results for scientific publication. The Data Analyst will provide automated support of genetic analysis and data handling, as well as assist with data analysis for the *Geobacter* project. This position will also provide technical assistance to study staff on genome data handling, analysis, and formatting, and on information systems, and will be responsible for conducting literature reviews and assisting in manuscript and grant proposal preparation and publication of study results. **REQUIREMENTS:** Bachelor's Degree in Biology, Biostatistics, Genetics, Epidemiology, Microbiology, Computer Science, Engineering, or other technical or biomedical discipline; three (3) years experience in data analysis with a knowledge of programming or bioinformatics or biostatistics; fluent in one or more computer programming and statistical languages on personal computer platforms or workstations: C, C++, Perl, Fortran, Java, Unix Shell Scripting, SAS, SPSS, Splus. Must be familiar with common database applications or with tools of genome or microarray analysis, computer skills and excellent written and verbal communication skills. OR Master's Degree in above fields and one (1) year of data experience and above mentioned knowledge and job skills. OR a combination of college coursework in above fields and work experience in data analysis. **TRANSCRIPT REQUIRED IF EDUCATION IS USED TO QUALIFY FOR THIS POSITION.**

Interested individuals should apply through the University of Tennessee Human Resources. The application form and the instructions on how to apply can be obtained from the UT Human Resources web site at <http://www.utmem.edu/humanresources/HowToApply.htm> Applicants should refer to the position number 18049

UToronto KofflerReserveDirector

Director, Koffler Scientific Reserve The Department of Botany and the Department of Zoology at the University of Toronto invite applications for a tenured or tenure track position as Director of the Koffler Scientific Reserve, effective July 1, 2006. The rank of the position is open (Assistant, Associate, Full Professor) and the area of specialization includes all areas of ecology and evolution. Special opportunities exist for applicants with strong field components in their research and teaching programs. Opportunities exist for collaboration with aquatic and terrestrial biologists on all three campuses of the University of Toronto: St. George (downtown), UTM (Mississauga) and UTSC (Scarborough). The Departments of Botany and Zoology have both made recent hires in the areas of ecology and evolution and more are expected with physical geographers, foresters, chemists and physicists interested in environmental issues.

The successful applicant will have a PhD, post-doctoral or relevant experience, an outstanding academic record and evidence of potential for excellence in teaching. The appointee will be expected to build an active, externally funded and internationally recognized research program and to contribute to the education and training of undergraduate and graduate students. Salary will be commensurate with qualifications and experience. The appointee will be cross-appointed to the Department of Botany (<http://arachnid.botany.utoronto.ca/newBotany/index.cfm>) and Zoology (<http://www.zoo.utoronto.ca>).

Both departments offer a broad spectrum of programs where field biology is an integral component, and the directorship is an exciting opportunity to fully develop a unique field station that will attract researchers from other institutions. The successful candidate will serve a five-year term (renewable) as director and will live on site in a very attractive home. Responsibilities as director include all administrative aspects of the Reserve, including coordinating the research and teaching station,

database management, grant writing, advancement activities, liaison with the local community and supervising administrative and technical staff. The director is expected to allocate approximately 50% of their time to these duties. Details on the Reserve can be found at (<http://www.zoo.utoronto.ca/jokershill/jh.html>).

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

Applications will be accepted until December 15, 2005. Applicants should provide a curriculum vitae, statement of teaching philosophy and interests, an outline of their proposed research, and should arrange to have three confidential letters of recommendation sent on their behalf to: Professor Robert L. Baker, Chair, Department of Zoology, University of Toronto, Toronto, Ontario, Canada M5S 3G5.

Diana Powell <dianap@zoo.utoronto.ca>

UToronto PlantEvolEcol

The Department of Botany at the University of Toronto invites applications for a tenure-track faculty position at the Assistant Professor level in the area of Plant Ecology to begin July 1, 2006. Specialists in all areas of plant ecology are encouraged to apply. Applicants who are using, or will develop, experimental approaches to understanding ecological pattern and process will be given priority.

The successful candidate will have demonstrated excellence in teaching and research and will be expected to participate in undergraduate and graduate teaching of ecology, plant biology and field courses at the University of Toronto. She or he would also be expected to interact with faculty across campus working in related fields. Salary to be commensurate with qualifications and experience.

Applicants should arrange to have four reference letters sent directly to the address below. In addi-

tion, applicants should forward their curriculum vitae, copies of significant publications, and statements of research and teaching interests to the Chair, Plant Ecology Search Committee, Department of Botany, University of Toronto, 25 Willcocks Street, Toronto, ON M5S 3B2 Canada before October 24, 2005. Inquiries should be directed to Dr. Rowan Sage at Rsage@botany.utoronto.ca.

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

—

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/>

UWindsor MolEvolEcol

Great Lakes Institute for Environmental Research (GLIER) Tenure-Track Position in Molecular Ecology

The University of Windsor invites applications for a tenure-track position in Molecular Ecology for the Great Lakes Institute for Environmental Research (GLIER) at the rank of Assistant Professor commencing July 1, 2006. This position is subject to final budgetary approval.

The Great Lakes Institute for Environmental Research (GLIER) of the University of Windsor is a multidisciplinary research team focused on studying the impact of multiple stressors on aquatic ecosystems. It is dedicated to the management of the earth's resources to protect and maintain human and environmental health. GLIER is located in world-class facilities on the Detroit River at the University of Windsor. These facilities consist of fully equipped state of the art analyti-

cal laboratories for both trace organics and metals, an applied molecular genetics analysis facility, a toxicology laboratory specializing in in vitro assays, an ecology laboratory with a full-service aqua-research center and an environmental modeling facility. For further details about GLIER visit our website at: <http://www.uwindsor.ca/glier>. The successful candidate will be cross-appointed to a relevant Department within the University of Windsor, and will contribute to teaching in GLIER's graduate program as well as undergraduate instruction. The successful candidate must have a Ph.D. and postdoctoral experience is an asset. S/he is expected to develop vibrant, individual and collaborative research programs. We seek faculty whose interests integrate with existing strengths of GLIER in the areas of conservation genetics, geochemistry, aquatic toxicology, invasive species, and lake productivity. The Molecular Ecologist should utilize molecular tools to address ecological problems with applications to large lakes, including adaptation to environmental stressors.

Applications should include: a letter of application, including a statement of citizenship/immigration status; a detailed curriculum vitae; a research statement outlining research interests and potential for scholarly achievement; a teaching dossier or evidence of teaching effectiveness that might include sample course syllabi/outlines, teaching evaluations and a statement of teaching philosophy and interests; samples of scholarly work; and three current letters of reference forwarded directly to the Department by the referees.

To ensure full consideration, complete applications and letters of reference should be submitted by November 15, 2005 to:

Dr. Brian J. Fryer, Director Great Lakes Institute for Environmental Research University of Windsor, Windsor, ON N9B 3P4 Phone: 519.253.3000, ext 2732, Fax: 519.971.3616 E-mail: bfryer@uwindsor.ca

Applications may still be received after the deadline date. If you are unable to submit the application by the deadline date, you should contact the Department Head to alert him that you intend to submit an application after the deadline date. If you are viewing the advertisement after the deadline date, you should contact the Department Head to find out the status of the search and discuss the possibility of submitting an application.

The University of Windsor is committed to equity in its academic policies, practices, and programs; supports diversity in its teaching, learning, and work environments; and ensures that applications from members of traditionally marginalized groups are seriously considered under its employment equity policy. Those who

would contribute to the further diversification of our faculty and its scholarship include, but are not limited to, women, Aboriginal peoples, persons with disabilities, members of visible minorities, and members of sexual minority groups. The University of Windsor invites you to apply to our welcoming community and to self-identify in your letter of application. Priority will be given to Canadians and permanent residents of Canada.

dheath@uwindsor.ca

UWisconsinEauClaire EvolGenetics

University of Wisconsin-Eau Claire

Department of Biology

POSITION: Geneticist We have an opening for a probationary tenure track faculty position in Genetics in the Department of Biology at the rank of Assistant Professor beginning August 21, 2006. We are particularly interested in candidates who are committed to undergraduate instruction and faculty-student collaborative research and would bring diverse perspectives and experience to the position.

QUALIFICATIONS: - Ph.D. degree by August 21, 2006. - must have demonstrated teaching ability at post-secondary level and commitment to developing an active research program **RESPONSIBILITIES:** Applicants will be expected to participate in the teaching of Genetics and Essentials of Cell Biology and Genetics as well as in upper level course(s) in his/her specialty. The teaching load is approximately 12 contact hrs. with 1-2 preps/semester. The successful candidate will develop an active research program involving undergraduate students. The department desires a broadly-trained candidate whose uses molecular approaches in their research and whose expertise would complement existing faculty and student interests. Possible specializations include but are not limited to evolutionary biology, developmental biology, conservation biology or genomics. The position is also expected to provide academic advising to students and engage in service to the department, college, university and/or community. Salary will be commensurate with teaching and research experience. **DEPARTMENT:** The Department of Biology currently has 25 faculty and academic staff and approximately 500 majors. Faculty are collegial, dedicated to teaching and are actively involved in research with students as demonstrated by co-authored presentations

and publications. Our interests span from molecular biology to ecosystem ecology. Departmental facilities include a variety of teaching and research laboratories, three greenhouses, an animal care facility, the James Newman Clark Bird Museum, a departmental field bus for travel to field sites, shared access to transmission and scanning electron microscopes, molecular biology instrumentation and a Geographic Information System lab. We have easy access to a variety of terrestrial and freshwater communities and are affiliated with the Gulf Coast Research Lab in Mississippi and field stations in the Bahamas. Research is supported by both external and internal grants, and we participate in the Ronald McNair Post-baccalaureate Achievement Program. Internal funds are also available to support faculty and student travel to professional meetings.

UNIVERSITY & EAU CLAIRE COMMUNITY: The University of Wisconsin-Eau Claire campus community consists of 10,500 students and 700 faculty and administrative/professional staff. As the UW System's only Center of Excellence for Faculty-Undergraduate Student Collaborative Research, faculty and students regularly work side-by-side on original research. 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 imbedded in a rural landscape and 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/research interests (specifically addressing ability to teach introductory level biology and Genetics), experience, and future plans as well as a curriculum vitae, copies of all undergraduate and graduate transcripts, copies of recent publications (up to 3) and three letters of reference (responsibility of applicant) to: Geneticist Search Committee Department of Biology University of Wisconsin Eau Claire, Wisconsin 54702-4004 To ensure consideration, complete applications must be received by November 7, 2005. However, screening may continue until the position is filled. 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. NOTE: We have several searches open on campus including one for a vertebrate biologist in biology and a biochemist in Chemistry.

To learn more about us and the position, please visit our web

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

UWisconsinEauClaire VertEvol

University of Wisconsin-Eau Claire

Department of Biology

POSITION: Vertebrate Biologist We have an opening for a probationary tenure track faculty position in the Department of Biology at the rank of Assistant Professor beginning August 21, 2006. We are particularly interested in candidates who are committed to undergraduate instruction and faculty-student collaborative research and would bring diverse perspectives and experience to the position.

QUALIFICATIONS: - Ph.D. degree by August 21, 2006. - must have demonstrated teaching ability at post-secondary level and commitment to developing an active research program **RESPONSIBILITIES:** Applicants will be expected to participate in the teaching of Comparative Vertebrate Anatomy, Animal Physiology and Human Anatomy and Physiology as well as introductory level courses such as Organismal Form and Function or General Biology. The successful candidate may also have an opportunity to teach upper level course(s) in his/her specialty. The teaching load is approximately 12 contact hrs. with 1-2 preps/semester. The successful candidate will develop an active research program involving undergraduate students. The department desires a candidate whose research interests include but are not limited to evolutionary biology, developmental biology, comparative physiology and anatomy, or other specialty that would complement existing faculty and student interests in vertebrate structure and function. The position is also ex-

pected to provide academic advising to students and engage in service to the department, college, university and/or community. Salary will be commensurate with teaching and research experience. **DEPARTMENT:** The Department of Biology currently has 25 faculty and academic staff and approximately 500 majors. Faculty are collegial, dedicated to teaching and are actively involved in research with students as demonstrated by co-authored presentations and publications. Our interests span from molecular biology to ecosystem ecology. Departmental facilities include a variety of teaching and research laboratories, three greenhouses, an animal care facility, the James Newman Clark Bird Museum, a departmental field bus for travel to field sites, shared access to transmission and scanning electron microscopes, molecular biology instrumentation and a Geographic Information System lab. We have easy access to a variety of terrestrial and freshwater communities and are affiliated with the Gulf Coast Research Lab in Mississippi and field stations in the Bahamas. Research is supported by both external and internal grants, and we participate in the Ronald McNair Post-baccalaureate Achievement Program. Internal funds are also available to support faculty and student travel to professional meetings.

UNIVERSITY & EAU CLAIRE COMMUNITY: The University of Wisconsin-Eau Claire campus community consists of 10,500 students and 700 faculty and administrative/professional staff. As the UW System's only Center of Excellence for Faculty-Undergraduate Student Collaborative Research, faculty and students regularly work side-by-side on original research. 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 imbedded in a rural landscape and 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/research interests (specifically addressing ability to teach introductory level biology, Comparative Vertebrate Anatomy and Human A&P), experience, and future plans as well

as a curriculum vitae, copies of all undergraduate and graduate transcripts, copies of recent publications (up to 3) and three letters of reference (responsibility of applicant) to: Vertebrate Biologist Search Committee Department of Biology University of Wisconsin Eau Claire, Wisconsin 54702-4004 To ensure consideration, complete applications must be received by November 7, 2005. However, screening may continue until the position is filled. 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.

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

UWyoming Tech

The Nucleic Acid Exploration Facility at the University of Wyoming seeks an Academic Professional Research Scientist (position number 4811) at the MS or PhD level to run and manage a high throughput DNA sequencing and genotyping core service and preparation/training facility. Responsibilities include preparing and running samples on two AB 3130xl genetic analyzers and an AB 7500 Real-Time PCR System; interfacing with the director, personnel and scientists; and managing the purchasing, accounting and invoicing. In addition, the individual will work with faculty, graduate and advanced undergraduate students in the techniques of nucleic acid extraction, amplification and primer and genetic marker development; help train users and oversee use of equipment in the training/preparation portion of the facility; and help trouble-shoot problems with equipment and analyses. The candidate must have documented experience in managing DNA sequencing and genotyping apparatus, have documented experience in PCR, DNA sequencing and genotyping, primer and marker development, and have documented skills in teaching. Preference will be given to candidates with experience in running and maintaining AB 3100 series genetic analyzers and AB 7500 Real-Time PCR Systems.

Interested applicants should send PDF files of application materials, including letter of application and CV

(to include experience and skills) and arrange for three letters of recommendation, also in PDF format (with contact information) to: Dr. Steven L. Miller, Director of the Nucleic Acid Exploration Facility, Department of Botany, 3165, 1000 E. University Ave., Laramie, WY 82071; email fungi@uwyo.edu. Review of applications will begin in October 2005. Starting date is 1 November, 2005. The University of Wyoming is a Carnegie Foundation Research Extensive Institution, and is an AA/EEO employer.

Universidad de los Andes Human Geneticist

GENETISTA HUMANO

El Departamento de Ciencias Biológicas, Universidad de los Andes (Bogotá) requiere profesor de planta de tiempo completo en GENETICA HUMANA. Los aspirantes deben poseer título de Ph.D., preferiblemente con experiencia postdoctoral así como en docencia e investigación y disposición a proponer y gestionar proyectos de investigación en el campo de la genética humana. Son especialmente bienvenidos candidatos con experiencia previa en biología molecular, mutagénesis ambiental, genética de poblaciones humanas, epidemiología molecular del cáncer, manejo de cultivos celulares y/o citogenética.

Se espera del candidato seleccionado que interactúe como profesor y orientador de estudiantes de pregrado y postgrado del Departamento de Ciencias Biológicas y que realice docencia a nivel de pre y postgrado en cada semestre. Enviar hoja de vida, copia de publicaciones, una breve descripción del programa de investigación y docencia, y dos cartas de recomendación antes del 30 de noviembre de 2005 a:

Comité de Contrataciones Profesorales Atención: Svetlana de Arteaga svde@uniandes.edu.co Departamento de Ciencias Biológicas Universidad de Los Andes Carrera 1 No. 18A-70 P.O.Box 4976 Bogotá, Colombia

HUMAN GENETICIST

The Department of Biological Sciences, Universidad de los Andes (Bogotá) seeks to fill a position in Human Genetics. The applicants must possess Ph. D. title, preferably with research, teaching and postdoctoral experience, and disposition to propose and manage research projects in the field of the Human Genetics. It is desirable that the applicants have previous experi-

ence in molecular biology, environmental mutagenesis, human population genetics, cancer molecular epidemiology, cellular cultures and/or cytogenetics.

It is expected that the chosen candidate will interact as advisor of undergraduate and postgraduate students at our Department. Send curriculum vitae, copies of recent publications, a brief description of research and teaching program, and two letters of recommendation before November 30, 2005 to:

Faculty Search Committee Attention: Svetlana de Arteaga svde@uniandes.edu.co Departamento de Ciencias Biológicas Universidad de Los Andes Carrera 1 No. 18A-70 P.O.Box 4976 Bogotá, Colombia

samadrin@uniandes.edu.co

WashingtonU ComputationalBiol

Computational Biology and Genome Analysis Faculty Positions

Department of Genetics Washington University School of Medicine

Applications for these positions are invited at all levels, from Assistant Professor to Full Professor. The Department currently has strengths in the areas of algorithms for sequence analysis and modeling of regulatory

networks. Applicants working in these areas as well as in other areas that would complement our current strengths are encouraged to apply. The Department is also the home to many outstanding laboratories involved in basic research in model organisms and human genetics.

Washington University provides an excellent environment for Computational Biology and Genomics research. The interdepartmental Graduate Program in Computational Biology includes faculty with expertise in many areas. The Washington University Genome Sequencing Center has long been at the forefront of large scale DNA sequencing. The Center for Computational Biology and the Center for Genome Sciences bring together faculty from multiple departments with shared interests in Computational Biology and Genome Science.

We will consider applications beginning Sept. 15, 2005 and until the positions are filled. Applicants should send, either by email or regular mail, a current CV, a statement of research interests, and arrange to have three letters of recommendation sent to:

Dr. Gary Stormo Professor, Department of Genetics Director, Computational Biology Program Washington University Medical School 4444 Forest Park Ave, CAMP BOX 8510 ST. LOUIS, MO 63108-8510

email: stormo@genetics.wustl.edu

Women and members of minority groups are encouraged to apply. Washington University is an Affirmative Action Employer.

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ABI3100 for sale

ABI PRISM 3100-Avant Genetic Analyzer For Sale
Current Home: Yale University, New Haven, CT. Contact: dnanalysis@yale.edu

The ABI 3100 gives you sophisticated automation and superior performance. Keep pace with your throughput needs with this 16 capillary array. Reduce labor with automated polymer and sample loading and easy-to-use tools to visualize data analysis. Perform all your sequencing and genotyping applications quickly, accurately, and reliably on a single instrument. The Ideal Genetic Analyzer for Low- to Mid-Throughput Labs The 16-capillary system will increase your daily throughput.

Consistent, Hands-Off Runs The 3100 increases your run-to-run consistency and saves you time and labor by automating everything from polymer loading to data analysis. It automatically injects your samples into the sixteen capillary arrays – and unlike slab-gel systems, you only need minimal amounts of DNA for accurate

analysis. Add this to new application-specific analysis software and proven sequencing and fragment analysis chemistries, and you have a complete system for all your sequencing needs.

Analyze Hundreds of Samples in a Single Day Simply set up your sample and data, then sit back and watch as the analyzer sequences up to 72,000 bases or provides thousands of genotypes in only 24 hours.

Integrated Data Analysis Tools Reduce Time-to-Results The 3100 Genetic Analyzer software suite allows you to generate more meaningful data with less work.

This software suite includes: Data Collection Software (supplied with the instrument) Manages your instrument Sequencing Analysis Software Designed to base-call; assign quality values; trim, display, edit and print DNA sequencing data using the KB basecaller software. Seqscape Software Provides everything you need to perform resequencing applications such as VariantSeqr Resequencing System. GeneMapper Software Provides configurable, automated allele calling – a plus for high-throughput genotyping. The closely related GeneMapper ID Software is specifically designed for human-identity applications. Current Home: Yale University, New Haven Connecticut. Contact: dnanalysis@yale.edu

sis@yale.edu In the subject line: ABI For Sale
 carol.mariani@yale.edu carol.mariani@yale.edu

Ambiguous Alignments

Hi everybody, I have a question concerning ambiguously alignable regions in aligned nucleotide sequence data for phylogenetic analyses. Instead of omitting those sites entirely, I thought it might be a good idea to keep those taxa, that are unambiguously alignable within such regions, and only recode the respective nucleotides of those taxa that cannot be aligned unambiguously to the other taxa, as missing data. The idea is to keep as much phylogenetic information as possible while minimizing the risk of alignment artefacts. In my case, this concerns primarily outgroup taxa that cannot be aligned to the ingroup. I am analyzing my data with model-based approaches of phylogenetic inference (Bayesian, to be specific). The question now is, if these additional amounts of missing data (especially of missing outgroup information) in some regions of the alignment can have any biasing effects on the outcome of the analysis. At least in my case, there seems to be no significant effect on the topology. The only effect I observed was a decrease in a few clade support values. Does anybody have any general recommendations or theoretical considerations for this problem?

Cheers, Martin

Martin Dohrmann Department of Geobiology Geoscience Center Göttingen (GZG) Georg-August-Universität Göttingen Goldschmidtstr. 3 37077 Göttingen Germany mdohrma1@gwdg.de

AntiID petition mistake

Dear Colleagues,

Why stoop to the level of the Discovery Institute to sign a petition that is (1) not entirely accurate (it actually is fact-based and empirical) and (2) misses the broader message we should be developing:

That is, ID spreads a lie about evolution, which is why ID SHOULD be mentioned and discussed in classrooms.

This lie is clearly stated in the Discovery Institute petition: IDists portray evolution by natural selection as a “random process”. It is not. It is obvious to every scientist and lay person that life cannot have formed through a random process. As long as people perceive evolution as “random”, evolution and evolutionists will be perceived as biased idiots.

Moreover, ID presents an insidious lie about religion. IDists promote the assumption that, if evolution were true, it would directly imply that there is no God. This is only “true” if God’s only role is as designer/creator/intervener. Apparently, the public needs reminding that this limited view is degrading and demeaning to Christianity, Judaism, and Islam, at least. Those of us who are part of those communities need to continually speak out, not only to support a positive public perception of evolution, but to preserve the power and beauty of the world’s great religious philosophies. Those great philosophies and traditions should not be subjugated to a simplistic, materialist, and ultimately empty search for “evidence” to prove the existence of some designer.

With regard to signing petitions for or against one theory or another, we scientists should not hold to the mistaken notion that scientific truth is based on some kind of vote or consensus. That the lawyers and theologians and pols of the Discovery Institute think science is driven by consensus belies their very great misunderstanding of the scientific process. We do not need to follow their lead on this at all.

Finally, it simply counter-productive to disallow discussion of ideas in our classrooms, particularly the misguided ones! Instead, we need to train our students how to distinguish testable hypotheses from non-testable ones, like ID. We need to train our students how to discriminate between testable hypotheses, like Lamarckian evolution, some forms of special creation, and descent with modification. Just because we know the world is a sphere, that there is global warming, and that we breathe oxygen doesn’t mean we should fail to teach our students HOW we know these things—i.e., HOW we know the other ideas are wrong. Without that discussion, students and the public will continue to regard the scientific community as elitist, anti-religion, and narrow-minded.

I propose an alternative: Let’s demand that ID be allowed for discussion in public schools, with the proviso that discussion include the following: (1) evolution by natural selection is a very non-random process, and (2) even if evolution were true (or false), that is no test for or against the existence of God.

(I suppose another alternative might be to sue the Dis-

covery Institute in court because it is slandering evolution and evolutionists...but we already have problems finding funding for evolution!)

Dave Fitch

~ ~ ~ ~ ~ David
H. A. Fitch ~ \ / / / ~ Associate Professor ~ \ / / / ~
Department of Biology ~ \ / / ~ New York University
~ [] / / ~ Main Building, Room 1009 ~ \ / / ~ 100
Washington Square East ~ \ / / ~ New York, NY 10003
~ \ / ~ U S A ~ \ / ~ Tel.: (212) 998-8254 ~ \ ~ Fax:
(212) 995-4015 ~ \ ~ e-mail: david.fitch@nyu.edu ~ \

<http://www.nyu.edu/projects/fitch/> "David H. A. Fitch" <david.fitch@nyu.edu>

Arlequin responses

Here is a list of all the responses I got in regards to my question about Arlequin. Thanks for all your help!

Arlequin will implicitly recognize that you have shared alleles if you tell him to infer haplotype from distance matrix in the "Polymorphism control" tab. There is now a discussion Forum for Arlequin on <http://www.rannala.org/phpBB2/> Laurent Excoffier

If you are simply listing the haplotypes after you have entered them into Arlequin, I think it will only list them as you entered them. However, when you perform analyses (e.g., AMOVA), then Arlequin will automatically search for haplotypes shared among populations. Mike Taylor

I had the same problem that with the new version it did not recognise the shared haplotypes whereas the old version did. But I did not succeed in solve the problem. Sabine Wornick

Combine all your populations into a single large population and you will get the information you want. Jan McDowell

Try to write unic name for each haplotype. When Arlequin run will give you a lot of WARNING!, but you must forget it. In the text you will see what haplotype shares with each other from the different populations. Joaquin

– NON,AMY L University of Florida 352-359-6529

"NON,AMY L" <anon@ufl.edu>

Bead DNA extraction

I am interested in advice regarding magnetic bead based extraction methods, kits, etc. I recall that there had been a post recently (last 6 months?), but cannot find it in the archives. If anyone saved the posts, would you please forward them to me?

If not, i am interested in pursuing the magnetic bead system, and would greatly appreciate any suggestions for non-robotic microtube or 96well-format, especially as regards costs, simplicity and downstream applications (ie. sequencing product cleanup). Furthermore, do you have a protocol for reusing the beads, or making your own extraction buffers?

many thanks, ~amy

– 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)

Bead extraction answers

Many thanks to everyone who responded; the general sense seems to be that it works best if you spend a little more, but sometimes a stripped-down kitchen sink approach is good too... ahh, science!

cheers, ~amy

***** We recently published an article that included a comparison of 96-well DNA extraction protocols. In it, we tested one commercially available magnetic bead based kit (Invitrogen's CST kit) against four others. In short, we found the CST kit to be quick, easy, moderately expensive, effective for extracting from fresh vertebrate tissue, not effective for extracting from fresh or archival moth tissue, and sensitive to contamination. The reference is below.

Hajibabaei, M., deWaard, J.R., Ivanova, N.V., Ratnasingham, S., Dooh, R., Kirk, S.L., Mackie, P.M., and Hebert, P.D.N. (2005) Critical factors for the high volume assembly of DNA barcodes. *Philosophical Transactions: Biological Sciences* 362:1959-1967.

***** I have no experience myself on this topic, but if I remember well what other people were used to do where I was before, magnetic beads ARE re-useable.

***** I worked closely with invitrogen & eppendorf to develop a beads-based robotic protocol for plant genomic DNA isolation (attached). The comparisons of invitrogen vers promega beads demonstrated that DNA yield from invitrogen beads is ~5times higher.

***** We are using Magnesil Blue from Promega with robot and non-robot protocols. Instead of the suggested buffers, we are performing two ethanol washing steps and elude the DNA simply with ddH2O. It works well for further fragment as well as sequencing analyses.

***** A year ago my lab tried Qiagen's MagAttract-96 kit for various plant tissue (needles, leaves, megagametophytes) with no success. A small percentage of the species produced hi yields, but most yielded DNA in concentrations less than 5 ng/uL. I tested this procedure both on the benchtop and on a robot, but found that the system was suseptible to "gumming up," even when extremely small amounts of tissue was used. We returned to the column-plate kits since the increase in cost per sample is offset by knowing we will get good DNA every time. Qiagen maintains that other labs use the MagAttract kit on plant material to great success, though.

***** (the relevant previous post) Have you thought about magnetic beads extractions? They are designed for automated use but can also be used for manual extractions. You just need a magnetic plate (AGOVA box). See at Quiagen or Promega. Product name at Promega is Magnesil. There are different types of beads, depending what kind of DNA. We perform extractions with a much simpler protocol than provided by the producer, just using Magnesil Blue, ethanol and distilled water. No extra solutions included in the kit are really necessary. We use this protocol on various animal, although it is originally designed for plant tissue or plasmids. Like this we could lower the costs very much.

– 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> masmith@nature.berkeley.edu masmith@nature.berkeley.edu

CAIC vs Nexus

Dear Evoldir members, I have some problems with phylogeny translation: I would like to run Compare with 6112 bird taxa, and Compare only accepts Nexus files. I've written my phylogenetic codes in a CAIC fashion, as I'm used to (and it's so easy...), and tried to run TreeEdit to convert these codes into Nexus codes. But it doesn't work, I suppose it's because there are too many taxa. In the worst case scenario, I thought about cutting my CAIC codes, translating the several files in Nexus, but how can I paste them together then? Otherwise, is there a program that could for example translate CAIC codes into Newick codes and then Newick codes into Nexus codes? Please, does anybody have any idea? Many thanks for any help or advice. All the best,

Marine

Marine DANEK-GONTARD - Centre d'Etudes Biologiques de Chizé CNRS UPR 1934 Villiers-en-Bois 79360 Beauvoir-sur-Niort Cedex France Phone: (33 1) 05 49 09 78 38 Fax.: (33 1) 05 49 09 65 26 Email: danek@cebc.cnrs.fr

Canadian Society EcolEvol

For information only / À titre indicatif seulement:

NSERC recently hosted a meeting of representatives of the Canadian evolution and ecology community to discuss its future directions. This meeting was arranged following discussions which arose during the NSERC Evolution and Ecology Grant Selection Committee deliberations in February 2005. NSERC considers it to be part of its responsibility to facilitate this type of undertaking for disciplines which fall under our mandate.

The outcome of the recent meeting was a resolution to create a new national society for evolution and ecology. Attached below is the formal announcement of this society, provisionally titled 'The Canadian Society for Ecology and Evolution', and a call for membership.

Le CRSNG a récemment tenu une réunion des représentants du milieu canadien de l'évolution et de

l'écologie pour discuter de son orientation future. Cette réunion découle des discussions soulevées au cours des délibérations de février 2005 du Comité de sélection des subventions en évolution et en écologie du CRSNG. Le CRSNG considère qu'il lui incombe de faciliter ce type d'initiative pour les disciplines qui relèvent de son mandat.

Cette récente réunion a donné lieu à une résolution visant la création d'une société nationale dans le domaine de l'évolution et de l'écologie. Vous trouverez ci-joint l'annonce officielle de cette société, qui s'intitule provisoirement «La Société Canadienne d'Écologie et d'Évolution», ainsi qu'un appel de mises en candidature.

Announcement: 18 October 2005

FORMATION OF THE CANADIAN SOCIETY FOR ECOLOGY AND EVOLUTION

Canada is a world leader in ecological and evolutionary research, with the highest ranking per grant dollar in terms of number of publications and citations (Peters et al. 1996 *Can J Fish Aquat Sci* 53, 670). This research contributes to the social and economic wellbeing of Canadians in many ways. For example, it has given us better predictions of the consequences of global climate change, revealed the scope of ecosystem change within the Arctic, monitored the spread of invasive species, improved control measures for diseases, and furthered our understanding of the basic mechanisms by which biodiversity evolves and is maintained.

Nevertheless, there is a need for us to come together as a group to communicate our findings to the public and to participate in the development of government policies relevant to our fields. Furthermore, we need a voice to advocate our need for research funding. Ecology and evolution is one of the fastest growing disciplines supported by NSERC (GSC18), yet it received the largest cut in the last reallocations process. A small planning group mandated by the GSC18 panel to review the situation and suggest possible remedies met 7-8 September at NSERC headquarters in Ottawa. With the encouragement of NSERC, we have founded a national society for ecology and evolution, provisionally titled The Canadian Society for Ecology and Evolution, and have drafted a constitution (www.ecoevo.ca).

The purposes of the society shall be (1) to promote the study of ecology and evolution in Canada, (2) to raise public awareness of the importance of ecology and evolution to Canadian society, (3) to facilitate communication between members of the Society and decision-makers in the public, private and non-governmental sectors, and (4) to act as a liaison with Federal and Provin-

cial funding agencies to support and promote ecological and evolutionary research in Canada.

The inaugural meeting of the society will be held in Montreal in April 2006, when a constitution will be approved and officers elected (information and registration will be available at www.ecoevo.ca). In the meantime, the business of the society will be conducted by a temporary council comprising Graham Bell (McGill, acting President), Douglas Morris (Lakehead, acting Vice-President), Sally Otto (UBC, acting Secretary), Louis Bernatchez (Laval, acting Treasurer) and council members Douglas Haffner (Windsor), Jeff Hutchings (Dalhousie), Kathy Martin (UBC), Denis Réale (UQAM) and Locke Rowe (Toronto).

To achieve our goals, we need your membership. We believe that the society is vital to ensure the future of our discipline in Canada, and we aim for the broadest possible membership. If you support our objectives, we urge you to become a member and to circulate this announcement among your students and personnel. The application form can be found on our website (www.ecoevo.ca). Membership dues will be used to cover the costs of establishing the society, running meetings, supporting targeted workshops, and publishing policy statements and other documents to improve the communication of our work. Please join us and improve the voice of ecology

— / —

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>

Clonal Structure Statistics

Hello,

I am a graduate student at Iowa State University and am working with multiflora rose, an invasive plant that reproduces clonally and by seeds. I used genetic markers (allozymes) to analyze clonal structure within small and large patches of this plants an am now trying to calculate the power of my data to distinguish clones.

In particular, I was interested in calculating for each patch the average probability that ramets with identical allozyme patterns belong to the same genet (as in Aspinwall & Christian 1992 *Am. J. Bot.* 294-299)

Does anyone know of a computer program that calcu-

lates this statistic and other measures related to the analysis of clonal structure?

Thanks in advance, Laura Jesse

Laura Jesse Extension Associate Iowa State University Department of Entomology 109 Insectary Ames, IA 50011 515/294-BUGS

lrahnsen@iastate.edu lrahnsen@iastate.edu

Convert to PDB

I have taken these data from a research paper and I am wondering if you knew what format these atomic coordinates are in and how I can convert them into PDB format. Thank you

N(21) 9345 (4) 8207 (3) 424 (2)
 N(22) 6886 (4) 7120 (3) -656 (2)
 N(23) 5248 (4) 6913 (3) 794 (2)
 N(24) 7733 (4) 8084 (3) 1896 (2)
 C(1) 10322 (5) 8734 (4) 1055 (3)
 C(2) 11588 (5) 9039 (4) 676 (3)
 C(21) 12936 (5) 9580 (5) 1153 (3)
 C(3) 11296 (5) 8732 (4) -185 (3)
 C(31) 12197 (5) 8859 (5) -843 (3)
 C(32) 13347 (6) 9570 (6) -821 (4)
 C(4) 9873 (5) 8195 (4) -348 (3)
 C(5) 9142 (5) 7771 (4) -1112 (3)
 C(6) 7738 (5) 7271 (4) -1273 (3)
 C(7) 7050 (5) 6865 (4) -2101 (3)
 C(71) 7665 (5) 6941 (5) -2924 (3)
 C(8) 5737 (5) 6436 (4) -1985 (3)
 C(81) 4547 (5) 5911 (5) -2653 (3)
 C(82) 3698 (6) 6928 (6) -2884 (3)
 C(9) 5651 (5) 6597 (4) -1087 (3)
 C(10) 4463 (5) 6269 (4) -705 (3)
 C(11) 4266 (5) 6392 (4) 139 (3)
 C(12) 3036 (5) 6051 (4) 504 (3)
 C(121) 1723 (5) 5454 (5) 12 (3)
 C(13) 3315 (5) 6382 (4) 1374 (3)

C(131) 2358 (5) 6249 (4) 2028 (3)
 C(132) 73 (5) 5597 (5) 2294 (3)
 C(14) 4725 (5) 6929 (4) 1551 (3)
 C(15) 5462 (5) 7422 (4) 2326 (3)
 C(16) 6808 (5) 7957 (4) 2481 (3)
 C(17) 7444 (5) 8484 (5) 3373 (3)
 C(171) 7551 (6) 7440 (5) 3940 (3)
 C(172) 8009 (6) 7989 (6) 4853 (3)
 C(173) 6937 (7) 8637 (6) 5269 (3)
 C(174) 6522 (8) 10288 (7) 6301 (4)
 C(18) 8835 (5) 9177 (5) 3212 (3)
 C(181) 8901 (6) 10627 (5) 3367 (4)
 C(19) 8923 (5) 8711 (4) 2289 (3)
 C(20) 10121 (5) 8968 (4) 1907 (3)
 0(1) 1103 (3) 5725 (3) 1704 (2)
 0(2) 2646 (4) 6586 (4) 2766 (2)
 0(3) 5714 (5) 8361 (5) 5114 (3)
 0(4) 7471 (4) 9607 (4) 5853 (3)

Yahoo! for Good Click here to donate to the Hurricane Katrina relief effort.

Anaiseh Hashemi <aniss20042000@yahoo.com>

DNA Barcoding

EvolDir members might be interested in the latest issue of Systematic Biology, which carries papers that came out of a debate between Kip Will and Paul Herbert, convened by Vince Smith PEET V. For links to the issue, and video and PowerPoint presentations please visit <http://systematicbiology.org> . Regards

Rod

Professor Roderic D. M. Page Editor, Systematic Biology DEEB, IBLS Graham Kerr Building University of Glasgow Glasgow G12 8QP United Kingdom

Phone: +44 141 330 4778 Fax: +44 141 330 2792 email: r.page@bio.gla.ac.uk web: <http://-taxonomy.zoology.gla.ac.uk/rod/rod.html> reprints: <http://taxonomy.zoology.gla.ac.uk/rod/pubs.html>

Join Systematic Biology through the Soci-

ety of Systematic Biologists Website: <http://-systematicbiology.org> Search for taxon names at <http://darwin.zoology.gla.ac.uk/~rpage/portal/>
r.page@bio.gla.ac.uk

DNA from feces

Hello all,

Do you have any trick that may help to extract DNA from very dry feces?

cat.

Catarina Moreira <catinm@netcabo.pt>

Drosophila AChE strains

Hi all, I am interested in obtaining *D.melanogaster* strains that show either strong reduction or increase in the activity of AChE (acetyl choline esterase). I would greatly appreciate any suggestions, help.

thanks ahead, Yael

ysalzman@stanford.edu

Drosophila psuedoobscura balancer

Does anyone have (or know of someone who has) a *Drosophila pseudoobscura* balancer strain for the second chromosome (Muller's E; homologous to *D. melanogaster* 3R)? I believe there was a balancer floating around the community a few years back that carried the Ba mutation as a marker, but it was rumored to not fully suppress recombination. There are no *D. pseudoobscura* balancers available from the Tucson stock center. Any help would be greatly appreciated.

Thanks, rich

Rich Meisel meisel@psu.edu

Drosophila strains

I am a PhD student at Stanford and need old strains of *D.melanogaster* (M strains) for my current study. Please let me know if you can contribute strains from your stocks

Thanks in advance, Yael

ysalzman@stanford.edu

Echinoderm samples

Dear Mr or Mrs, I'm just beginning my PhD at the oceanologic center of Marseille, at the diversity, evolution and functional marine ecology laboratory (DIMAR). My work deals with the irregular urchins and more particularly with the heart urchin *Echinocardium cordatum* for which we are studying phylogeography and population genetics. So, I'm looking for specimens of different populations of the world, and I'm wondering if you could send me some in order to integrate them in my study. About 30 specimens by location would be ideal for population genetics, but just a few are enough for a phylogeography study. As I work on DNA, the specimens must have been conserved in alcohol or frozen. I would be very obliged if you could help me or if you know somebody that could help me, and I'm open to new collaborations. I'm very impatient to read your replay, thank you for your help.

Cordially

Emilie EGEEA, PhD student Centre d'Océanologie de Marseille UMR DIMAR, Station Marine d'Endoume Rue de la Batterie des Lions 13007 Marseille, France
e-mail egea@com.univ-mrs.fr

egea@com.univ-mrs.fr

Evol bibliography

A few years ago I introduced a big downloadable bibliography of about 10,000 references on evolutionary biology, ecological genetics and population genetics. It has accumulated over many years as an aid to research, and to help a book on frequency-dependent selection for the Oxford University Press. It struck me that others might find the bibliography useful.

I have now updated it (to about 12,000 references). The bibliography is potentially valuable to others because it includes many references to papers written before computer searches became established. The files have the advantage over the Web of Science (or Google Scholar) in that they go back before the 1980s, they are much faster to obtain, and they have already been winnowed for their evolutionary interest. Many of the recent references have abstracts attached.

Please note that the bibliography contains errors and duplications, and offers no guarantees of accuracy. You should always check any reference against the original publication before quoting it.

The bibliography can be downloaded at <http://www.nottingham.ac.uk/biology/contact/academics/-clarke/special.phtml?from=peg&G=&R=1&T=&P=1&S=The+Big+Bibliography&St=&m1=&m2=-&ID=32>

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Bryan Clarke <bryan.clarke@nottingham.ac.uk>

Evolution Artwork UMichigan

A&DLife in conjunction with the University of Michigan School of Art & Design would like to announce a call for submissions to its upcoming exhibition of contemporary art, ENDLESS FORMS: ENGAGING EVOLUTION. ? www.endlessforms.net Now more than ever, the concepts, practices, and influences of evolutionary biology spotlight the aestheticised experiences of contemporary life and culture.? The aim of this show is to explore the diversity of forms that communicate, comment on, and engage the science of evolutionary biology and mechanisms of evolutionary change.??

A&DLife presents this exhibition during the Exploring Evolution theme semester at the University of Michigan. ?From February 24th to March 24th, 2006, the

WORK exhibition space in bustling Ann Arbor, Michigan will be transformed to engage evolution and its endless forms.

The theme of the show will revolve around the five commonly observed forces or mechanisms of organic biological evolution. ?? Works should focus on one or more of the following: NATURAL SELECTION The processes of nature by which the presence of heritable genetic variation in traits leads to differential reproduction. ?Advantageous traits that influence survival and reproduction are transferred from the parents to the offspring and result in a disproportionate representation of traits in the next generation. ?But don't forget the environment!?! What's good today may be gone tomorrow!?

SEXUAL SELECTION Because traits involved in sexual displays for attracting mates are often visually compelling, no exploration of contemporary art and evolutionary biology would be complete without including mechanisms of sexual selection.?Sexual selection is driven by competition for mates and is often characterized by its elaborate displays.

MUTATION Changes in the DNA sequence within a gene or chromosome of an organism possibly resulting in the creation of a new trait not found in the parental type.

MIGRATION The act or an instance of migrating that leads to changes in the gene frequencies within populations (Also referred to as gene flow).

GENETIC DRIFT Random fluctuations in the frequency of a gene in a small population, presumably owing to chance rather than natural selection and often results in a reduction of genetic variation.

We seek works that build upon the confluence of contemporary art and design along with biological evolution as object and/or as process. We have a particular interest in works that examine the history and philosophy of evolutionary biology, competing ideas or hypotheses that have contributed to our current understanding of evolution, the role of sex and recombination in shaping genetic diversity, and the burgeoning emphasis we place on organismal development in our conceptions of genetic evolution.

All submissions should be in the form of a url where images of works and media are displayed. ?

Submissions should include 2-3 images for each work or a link to online video if time-based work is to be considered. The category or categories that the work falls into should be specified along with its dimensions, and medium(s). Each entry should also include contact

information for the artist.

Consideration for inclusion in this special exhibition, associated venues, its companion web exhibition, and accompanying catalogue will be given to all work submitted before the deadlines. Shipping arrangements will be made by contacting the artists upon acceptance.

Open call submissions due: November 21th, 2005.

University of Michigan School of Art & Design community submissions due: January 20th, 2006

Please use our convenient online form to send your links: <http://www.endlessforms.net> Contact us for more information at info@endlessforms.net

Gabriel Harp <gharp@umich.edu>

Evolution Videos

Hi,

I am teaching evolution in a Brazilian university and I would like to know if there is some kind of video or applet in the web about constructing cladograms. Could you help me please ?

Thanks !!!

Voltolini

Prof. Dr. J. C. VOLTOLINI Grupo de Estudos em Ecologia de Mamíferos (ECOMAM) Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010. E-Mail: jcvoltol@uol.com.br Website do ECOMAM: <http://jcvoltol.sites.uol.com.br/> Fotos de Cursos: <http://jcvoltol.fotoblog.uol.com.br/> Currículo Lattes: <http://lattes.cnpq.br/buscaoperacional/> Fotos Artísticas: <http://voltolini.fotos.net.br/texturas> “Siamo tutti angeli con un’ala e possiamo volare soltanto se ciabbracciamo”

VOLTOLINI <jcvoltol@uol.com.br>

Extraction kits answers

Here are the comments I got on cheap and easy to use extraction kits (for automated use!): hope that it would be helpful for someone else too

Martin

ich empfehle einen Blick auf das EZNA Tissue Kit von Peqlab (www.peqlab.de). Ich habe damit sehr gute Erfahrungen gemacht. Es ist insbesondere viel günstiger als Qiagen und Macherey-Nagel Kits.

Have you thought about magnetic beads extractions? They are designed for automated use but can also be used for manual extractions. You just need a magnetic plate (AGOVA box). See at Quiagen or Promega. Product name at Promega is Magnesil. There are different types of beads, depending what kind of DNA. We perform extractions with a much simpler protocol than provided by the producer, just using Magnesil Blue, ethanol and distilled water. No extra solutions included in the kit are really necessary. We use this protocol on various animal, although it is originally designed for plant tissue or plasmids. Like this we could lower the costs very much.

– Mag. Koch Martin Department of Zoology Universitiy of Graz Universitätsplatz 2 8010 Graz Tel.: +43 0316 8756

martin.koch@uni-graz.at martin.koch@uni-graz.at

Fluorescent micro answers

Below are the answers to my recent request:

“ We are hoping to run some minisatellites but do not have radioactivity facilities. I would be grateful if anyone could advise on any alternative methods of visualising minisatellites that are available, and where I might find details of the protocols for these.”

>>> “Jake Clarke (EMR)” <Jake.Clarke@emr.ac.uk> 2005/09/13 08:53 AM How about using DIG labelling from Roche. We used this successfully for RFLP mapping although it is quite long winded. We often size PCR fragments up to 2kb with our capillary sequencer although unfortunately this will be no help to you. I suppose you maybe able to tweak the protocols and use a non denaturing system used for SSCP but unfortunately I have never tried this.

“santos alonso” <santos.alonso@ehu.es> Regarding your question, I remember that Cellmark Diagnostics use to sell non-radioactive probes, for using in combination with CPD (I think that was the name of the substrate. This was both for fingerprinting (Jeffreys 33.15 and 33.6) and single locus probes. The probes were attached to an alkaline phosphatase. But this was

some years ago, may be they have something new now, with fluorochromes or so, but I doubt that if the minisatellite bands are big you will be able to size them in an ABI machine (or the like). If you cannot purchase probes with an attached alkaline phosphatase, you can label them yourself or have them made for you (ask any of the companies that synthesize oligos).

“Tim Sharbel” <sharbel@ipk-gatersleben.de> We do lots of AFLPs and microsatellites with PAGE in my lab, and for many of our experiments we silver stain the gels with very good success. The following web page has an AFLP method, and if you scroll to the bottom you’ll see a good and simple protocol for silver staining: <http://www.msu.edu/user/hazensam/aflp-AFLPprotocolMSU.html>

“Becher, Anette” <anette.becher@agresearch.co.nz> You could always try digoxigenin labelling. It is probably now considered an older technique, but has been used successfully with minisatellites. I have done quite a lot of dig labelling in plants in the past, basically whenever I needed to visualise DNA immobilised on a membrane (colony lifts, scoring RFLPs etc). We just followed the manufacturer’s protocol at the time (Boehringer Mannheim, I think - seems to be patented by Roche now : <http://www.roche-applied-science.com/prodinfo.fst.htm?/-DIG/dig-why.htm>), but there is probably lots on the web. I found this protocol here, which rings a bell, but is a lot shorter (due to fewer washes) than what I used to do. <http://www.cimmyt.org/-ABC/Protocols/CheckingActivity.PDF> There is some literature on comparison of non-radioactive labelling techniques at the NCBI, here are a couple that a quick query pulled out: http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=58965&dopt=abstract http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&list_uids=514067&dopt=abstract I found the DIG technique easy to use with basic equipment, it was a lot more sensitive than radiolabelling, but it was slower because of the umpteen washes (but this seems to have improved if above protocol is representative).

Thanks to you all for your suggestions and advice. Tee
Dr Tiawanna Taylor School of Biological and Conservation Sciences University of KwaZulu-Natal South Africa
Email: taylorlort@ukzn.ac.za

Genepop P-values

Hi EvolDir

I’m trying to test the significance of correlation coefficients between pairwise $F_{st}(1-F_{st})$ values and \ln dist. I’ve compared three population genetics programmes: Genepop ver. 3.4, Fstat ver. 2.9.3.2, and Spagedi ver. 1.2. Fstat (Mantel option) and SPAGeDi give similar P-values for the R^2 by permuting population locations among populations, but the P-values from Genepop (ISOLDE option) are very different. I guess that Genepop is doing a different randomization test, but I’m not clear what the randomization procedure is. Can anyone explain and advise on which test is better?

Thanks Sarah

Dr S Rendell Department of Plant Sciences University of Oxford South Parks Road Oxford OX1 3RB UK

T: +44 (0) 1865 275130 F: +44 (0) 1865 275074 E: sarah.rendell@plants.ox.ac.uk W: www.plants.ox.ac.uk/Sarah-Rendell Sarah Rendell <sarah.rendell@plants.ox.ac.uk>

Genepop randomization

Hi EvolDir

I’m trying to test the significance of correlation coefficients between pairwise $F_{st}(1-F_{st})$ values and \ln dist. I’ve compared three population genetics programmes: Genepop ver. 3.4, Fstat ver. 2.9.3.2, and Spagedi ver. 1.2. Fstat (Mantel option) and SPAGeDi give similar P-values for the R^2 by permuting population locations among populations, but the P-values from Genepop (ISOLDE option) are very different. I guess that Genepop is doing a different randomization test, but I’m not clear what the randomization procedure is. Can anyone explain and advise on which test is better?

Thanks Sarah

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www.plants.ox.ac.uk/Sarah.Rendell Sarah Rendell
 <sarah.rendell@plants.ox.ac.uk>

Guinness ID

This seems to be definitive!

http://www.framestore-cfc.com/press/05pr/-051003noitulove/amv_gune339_050_qt.mov
 schaffer

-henry

diversity databases? I am interested in collating information on global human genetic diversity in both neutral genetic markers such as microsatellites and in classical genetic markers such as blood group polymorphisms.

Any suggestions or comments relating to this issue are gratefully accepted,

Yours sincerely, Noreen von Cramon

- Noreen von Cramon-Taubadel PhD Candidate Leverhulme Centre for Human Evolutionary Studies Department of Biological Anthropology University of Cambridge Downing street Cambridge CB2 3DZ Phone: +44 1223 335648
<http://www.human-evol.cam.ac.uk/voncramon.htm>
 nv226@hermes.cam.ac.uk nv226@hermes.cam.ac.uk

Host for SEEC2006

Greetings Everyone,

We are still looking for a host for the 2006 Southeastern Ecology and Evolution Conference (SEEC). The past two years have been a great success (www.uga.edu/-seec) but we need a student and a school to run it for next year. We would still be shooting for an March/April time-frame but the date is ultimately up to the host. The host would not be starting from scratch as we have some money and materials available to ensure that the next SEEC will be a success.

Please contact Tom Luhring at luhring@srel.edu for further information.

Thanks again for all of your support and participation over the last couple of years.

Sincerely,

Tom Luhring

Jeffrey Ross-Ibarra <rossibarra@gmail.com>

Human genetic databases

Dear Evoldir readers,

I am wondering whether anyone is aware of the availability of electronic or online human population genetic

ID petition

This invitation to sign a petition expressing support for the teaching of evolution in public schools and against the inclusion of Intelligent Design just came over the campus Evolution Group email list. For those of you who missed Ed Larson's talk on the teaching evolution controversy last Friday (at the University of Wisconsin), the Discovery Institute is a pro-ID think-tank that pimps ID around by saying that "400 scientists support it - so there!" Larson pointed out that there are over 1 million scientists in the United States, and the Discover Institute could only find *400* willing to say they support ID (and it took them 4 years to find them). Furthermore, fewer than 70 of those 400 are biologists.

http://shovelbums.org/component/-option,com_mospetition/Itemid,506/ - Tom Isenbarger PhD isen@plantpath.wisc.edu 608.265.0850

Thomas Isenbarger <isen@plantpath.wisc.edu>

ID petition 2

Hello All:

There is a link below to a web site gathering signatures - specifically from those with relevant expertise - for a petition against teaching "Intelligent Design".

Perhaps you would like to look at this petition and/or pass this message along to colleagues. The list of signatories is growing at an impressive rate.

Time is of the essence for reasons explained there.

Richard Lenski East Lansing, Michigan

http://shovelbums.org/component/-option,com_mospetition/Itemid,506/

“Richard E. Lenski” <lenski@msu.edu>

Megabace Question

EvolDir Folk-

I would greatly appreciate informed opinions about the MegaBace sequencing platform. Due to the purchase of MJ Research by Bio-Rad and associated fallout, we are retiring out MJR BaseStation. We now have access to an ABI machine that is used nearly non-stop for microsatellite genotyping. Without the cash on hand to purchase a more high-throughput ABI sequencing platform, I've been considering buying a used MegaBace with the idea of devoting it entirely to sequencing for SAGE. 96 capillary machines can be bought for about \$20K, and I've been told that these machines provide high quality sequence data. On the other hand, commercial sequencing labs are getting cheaper all the time. I've seen ads for \$2.50/sample.

So.. If you have a MegaBace, I'd like to know whether you like it or not (and why) and whether or not, despite the low purchase price for a used machine, the consumables and time required to run one of these machines, and reliability would make this cost-effective relative to outsourcing the sequencing for our upcoming SAGE work.

Please reply directly off-list as I am sure the whole group is not interested in this issue.

Best-

Mark D. Camara USDA/ARS Shellfish Genetics OSU - Hatfield Marine Science Center 2030 SE Marine Science Dr. Newport, OR 97365

Office: 541-867-0296 Fax: 541-867-0138 Mailto: Mark.Camara@oregonstate.edu

Mark Camara <Mark.Camara@oregonstate.edu>

MolecularClocks answers

Dear Colleagues,

Thank you, to all of you who responded to my query about Maximum Likelihood and Bayesian methods for inferring divergence times. It was very helpful to hear your perspectives, and I was happy to learn that so many of you share my interest in this topic. Because a great many people requested that I post the replies, I have compiled them here (following my signature line). I hope you will find this helpful.

Best,

Chris Smith.

Christopher Irwin Smith, Ph.D.

Post Doctoral Research Fellow University of Idaho Department of Biological Sciences Moscow, Idaho 83844

ph: (lab) 208 885.8860 (office) 208 885 4229

<http://www.webpages.uidaho.edu/~csmith/ChrisSmith.htm> Here are the answers:

Under ideal conditions, the general effect of overspecification should be reduction of statistical power (flattening of the likelihood surface), while underspecification can indeed lead to odd artifacts (being misled). Also, the cost of overspecification in a Bayesian context should be less than in an ML context because nuisance parameters (for which the data may be only weakly informative) are integrated out. You might look at the Lemmon and Moriarty paper in Sys Bio a few years ago, which specifically investigates the practical consequences of model over and underspecification on simulated data, in a Bayesian context.

Hope that helps, D Derrick Zwickl <zwickl@mail.utexas.edu>

Hi Chris,

Is there a way to combine information from multiple genes with different mutation rates in R8's?

As far as I know this cannot be done with r8s right now. But this can be done with MULTIDIVTIME

Similarly, I am interested in the effect of model parameters on the behavior of MULTIDIVTIME. The release notes suggest that the most complicated model that can be implemented is F84+gamma. Does anyone have experience using this program for data sets where

more complicated models - say, GTR+I+G for example - are justified? What are the consequences of using the simpler model if the data depart significantly from the expectations of F84+gamma?

I would guess that there is not too much of a problem with this kind of model misspecification. However, how much of a problem it creates will be related to how divergent your sequences are, with larger divergences (corrected distances of 0.5-1+) being most drastically affected. In my opinion, the most important thing is to have a rates across sites process, like gamma, in the model. Even if I+G fits better than G alone, I don't think this will matter too much because the invariable sites end up getting accounted for in the lowest rate category for the gamma.

Keep in mind I've never done the test myself. I would suggest testing things out by simulating data under GTR+I+G using Seq-Gen and see how well ESTBRANCHES/MULTIDIVTIME does at recovering branchlengths etc using the F84+g model. This is probably the only decent way to really get an idea of how bad things could be.

Finally, I strongly suggest you do not use the additive penalty for r8s. We have good evidence that it causes serious biases in divergence times.

Sincerely Andrew J. Roger Associate Professor Dept. of Biochem/Mol. Biol. Dalhousie University Halifax, N.S. Canada

Dear Chris,

Sorry, I haven't got an answer to your question, although I am familiar with MULTIDIVTIME. I'd also be very interested in finding out whether there is a way to specify a more complex model than F84+gamma. When too simple a model is specified, Bayesian analyses (e.g. MrBayes) tend to come up with spurious results, whereas overspecification is usually not a problem. So that isn't likely to be any different in MULTIDIVTIME. Based on a recent paper in Systematic Biology (particularly at the figures on pages 909 and 910 -model underspecification vs. overspecification). According to this, MULTIDIVTIME should ideally include the GTR+I+G model, just to be on the safe side. I'd very much appreciate if you could keep me updated if anyone can suggest away how to do this.

Best wishes, Peter "Dr. Peter R. Teske"
<P.Teske@ru.ac.za>

hello Chris, I've used multidivtime and it easily does multiple genes, different position partitions. Go ahead and send Thorne an email, he responds very quickly and thoughtfully. Curious to see what you hear back,

Chris Christopher West Wheat <cww10@psu.edu>

Well, Multidivtime is a bugger to run, but once you've done it once or a couple of times it is more-or-less straightforward. When we ran both Multidivtime and r8s we got fairly different results for mean divergence times for a single data set. I'm attaching a pre-print (in press - syst biol) which briefly outlines the discrepancies. In future we won't be using Multidivtime (at least with its current model implementations) since the F84 model is clearly contradicted by some of our partitions

— / —

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>

Moller case

Dear Colleagues,

Below are links to recent developments in the case against Anders Moller. The first link is a recent essay by Moller concerning his view of the ordeal. The second is a link to the French CNRS (Moller's employer) report conducted by an independent board of inquiry that clears Moller. In essence, the conclusion of the impartial committee was that there was no evidence to support accusations of intellectual dishonesty.

http://cricket.biol.sc.edu/dedication/-moller/Moller_ISBE_Newsletter.pdf http://cricket.biol.sc.edu/dedication/moller/-CNRS_Decision.pdf Best wishes,

Tim

Dr. Timothy A. Mousseau Professor of Biological Sciences

Dept of Biological Sciences University of South Carolina Columbia, SC 29208 USA tel: 803-777-8047 fax: 803-777-4002 <mailto:mousseau@sc.edu>

Tim Mousseau <mousseau@sc.edu>

Moller criticism follow-up

In response to Mousseau and Moller, and perhaps oth-

ers who might think that Moller's reply and unpublished MS provide a satisfactory explanation, I repeat my question regarding Moller's published data. It has yet to be answered, so I hope the question is clearer this time.

Why, are symmetrical (or nearly symmetrical) individuals ABSENT among shorter-tailed male barn swallows (<100mm tail length; shaded areas in the graphs) in two early studies by Moller (1990, 1992), yet PRESENT in two subsequent graphs in a later paper by Moller (1999) for the same population? For actual graphs, see:

<http://www2.biology.ualberta.ca/palmer/pubs/-05MollerComm/MollerDataIrreg.pdf> In the former two studies, the absence of symmetrical (or nearly symmetrical) individuals among shorter-tailed individuals yielded graphs showing a tidy decrease of asymmetry with increasing tail size, which was a 'predicted' outcome in both papers. In the latter paper, symmetrical (or nearly symmetrical) individuals were expected to be most common at all tail lengths (not just longer ones) and were found to be so, in sharp contrast to the earlier studies.

This crucial point is not addressed in Moller's reply to Mousseau, nor Moller's unpublished MS submitted to Evolution:

<http://cricket.biol.sc.edu/dedication/moller/moller-FA-year.pdf> both of which deal with change in average FA, and overall size-dependence of FA, over time, not with the apparently 'missing' symmetrical individuals at small tail lengths in the 1990 and 1992 studies.

One possible resolution to this debate would be for Moller to post publicly (for example, on Mousseau's web site) his raw data on the lengths of the right and left outer tail feathers of male barn swallows from his well-studied Kraghede population, for each year, for the years 1988 - 2004. Perhaps the patterns exhibited in the 1988 and 1990 sampling years were simply flukes. This possibility cannot be judged merely by examining summary statistics like those in Moller's unpublished MS.

As for public discussion, a public clarification will go further towards putting the community's concerns to rest than private re-assurances.

Regards, Rich Palmer

PS. To my chagrin, when double checking Moller's original 1992 paper, I discovered a graphing error in the figure I posted earlier (two extraneous points in panel 1b – the uppermost two). I have now corrected the posted file. If anything, the discrepancy between the early and

later Moller data sets is now even stronger. I apologize for this careless oversight. –

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 rich.palmer@ualberta.ca

Moller data

Further to the recent developments in the case regarding data fabrication by A.P. Moller posted to this list by Tim Mousseau, I offer the following. A commentary I prepared on another – more compelling – example of questionable data published by A.P. Moller was rejected editorially (without review) by Nature (Mar. 24, 2004), TREE (May 12, 2004) and Evolution (Oct. 24, 2004). It was also submitted (Mar. 30, 2004) to the CNRS committee that evaluated Moller's 'conviction' by the Danish Committee on Scientific Dishonesty, but the CNRS committee ignored it and chose to focus solely on the data at issue in the now infamous and withdrawn Oikos paper. A careful reading of the decision by the CNRS "committee of wise men" reveals that no clear conclusion was possible – either guilty or innocent – regarding scientific misconduct in the Oikos incident: "Lacking the material evidence necessary to establish innocence, the committee was equally unable to reach this conclusion . . . [so] the presumption of innocence must be applied". As peer-reviewed journals and CNRS seem unwilling to consider additional evidence regarding suspicious irregularities in data published by A.P. Moller, I make these data publicly available. In a nutshell, scatterplots of data from two early papers by Moller, reporting an association between size and asymmetry in barn swallow outer tail feathers, appear strongly inconsistent with similar data from a later paper that wished to draw a different conclusion. A plausible explanation for the patterns exhibited in these scatterplots would be welcome.

A pdf copy of this commentary, including scatterplots of the suspect data, may be downloaded from:

<http://www2.biology.ualberta.ca/palmer/pubs/->

05MollerComm/MollerDataIrreg.pdf Judge for yourself whether these published data are questionable or not.

Regards, Rich Palmer

—
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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 sec-
tion, Canadian Society of Zoologists. For info.
see: <http://www.biology.ualberta.ca/CMD/home.htm>
Rich Palmer <rich.palmer@ualberta.ca>

Moller debate offline

Moller's detailed response to my last posting (including some curious comments on saintliness, godliness, and university enrollments) may be viewed on the EvolDir web site:

<http://evol.mcmaster.ca/brian/evoldir.html> or at

<http://www2.biology.ualberta.ca/palmer/pubs/-05MollerComm/MollerExchange.htm> On the latter site, it is accompanied by the entire unedited exchange that unfolded on EvolDir, as well as my responses to salient points in Moller's 'saintliness/godliness' essay above.

My apologies to those who feel EvolDir is an inappropriate venue for this exchange. Further debate regarding Moller's swallow tail feather asymmetry data – should it arise – will be posted at the above link on my web site, or some other more appropriate venue.

Regards, Rich Palmer –

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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 sec-
tion, Canadian Society of Zoologists. For info.
see: <http://www.biology.ualberta.ca/CMD/home.htm>
rich.palmer@ualberta.ca rich.palmer@ualberta.ca

Moller enough

Boys,

this has been going on for a sufficient number of years, posts, counter-posts, claims and counterclaims. I really think you should go in the courtyard and settle it as real men would... :-)

Cheers, Massimo Pigliucci

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Massimo

Pigliucci

[www.genotypebyenvironment.org](http://www.genotypebyenvironment.org)

[www.rationallyspeaking.org](http://www.rationallyspeaking.org)

[http://-](http://www.rationallyspeaking.blogspot.com)

[www.rationallyspeaking.blogspot.com](http://www.rationallyspeaking.blogspot.com)

“It is better to be a human being dissatisfied than a pig satisfied; better to be Socrates dissatisfied than a fool satisfied.”  
-John Stuart Mill

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

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### Moller enough 2

Dear Massimo and others,

In response to Massimo Pigliucci's letter: Do you really mean what you say? Should we settle an important scientific dispute in court? The case is not just about M's personal conduct. It is also about the validity of many scientific claims and results. Palmer's criticism concerns published scientific results, many of which have had considerable impact on the field. It is more than a little embarrassing that leading scientific journals are so unwilling to publish serious criticisms of published research. Those of us who care about scientific truth certainly would like to know whether and what we should believe from M's papers, and this is true regardless of whether the problems are due to fraud or to more or less innocent carelessness. I think Palmer deserves our respect for being willing to put his criticisms forward. As for M, the best he could do for both science and for his reputation would be to provide a serious to-the-point explanation that addresses the essence of Palmer's criticism.

Real men may prefer settling disputes in courtyards, but real scientists prefer to settle them in open debate.

Sincerely

Thomas F. Hansen

Thomas Hansen <thomas.hansen@bio.uio.no>

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### Moller more

Dear Colleagues,

For those of you who are not interested in this PUBLIC discussion, I apologize for continuing it longer. I can assure you that I have no interest in perpetuating this debate, or mediating it in any way. However, in the face of ongoing and unjustified PUBLIC criticisms of my colleague, Anders Moller, whose behavior I have found to be above reproach and certainly not worthy of unsubstantiated attacks, I offer the following response to Rich Palmer's recent posting:

Rich has insinuated that changes in tail length FA distributions among three Moller papers (Moller 1990, 1992, 1999) reflects selective use of data (or worse).

See <http://www2.biology.ualberta.ca/palmer/-pubs/05MollerComm/MollerDataIrreg.pdf> <sup>f</sup>  
<http://www2.biology.ualberta.ca/palmer/pubs/-05MollerComm/MollerDataIrreg.pdf> for details.

As far as I know, Rich has not asked Moller directly for clarification concerning possible biological explanations. Thus, for my own benefit, and that of this group, I have asked Moller myself. His response:

+

Dear Tim,

I have recorded asymmetry in barn swallows annually since the 1980's. Concomitant with a dramatic increase in tail length in males (Moller & Szép 2005) there has been a dramatic decrease in mean and variance in asymmetry. Furthermore, the relationship between unsigned asymmetry and character size has changed from significantly negative to completely flat, with this temporal effect being present in males, but not in females. All this information is contained in a manuscript that was submitted to *Evolution*, but rejected because it was not "novel". I would be happy to share this manuscript with Palmer or anybody else. Perhaps Palmer's emotional attitude prevented him from looking for a biological explanation and from contacting a colleague before making public accusations.

All the best,

Anders

M, A. P. and Szép, T. 2005. Rapid evolutionary change in a secondary sexual character linked to climatic change. *J. Evol. Biol.* 18:481-495.

++

A copy of Moller's rejected paper showing changes in FA through time can be viewed at:

<<http://cricket.biol.sc.edu/dedication/moller/moller-FA-year.pdf>> <http://cricket.biol.sc.edu/dedication/-moller/moller-FA-year.pdf>

Another paper that may interest those following this discussion:

Direct and indirect tests for publication bias: Asymmetry and sexual selection. - *Anim. Behav.* 70:497-506, 2005 (authors A. P. M, R. Thornhill and S. W. Gangestad).

Sincerely,

Tim Mousseau

Dr. Timothy A. Mousseau Professor of Biological Sciences

Dept of Biological Sciences University of South Carolina Columbia, SC 29208 USA tel: 803-777-8047 fax: 803-777-4002 <mailto:mousseau@sc.edu>

Tim Mousseau <[mousseau@sc.edu](mailto:mousseau@sc.edu)>

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### Multidivtime calibration point

Dear EvolDir members,

Does anybody know if the node used as calibration point in the relaxed molecular clock program Multidivtime needs to be within the main phylogeny we're interested in? We have no clade that could be used for calibration in our crustacean COI phylogeny, only one from a different crustacean family. The program runs fine as long as the outgroup specified is basal (e.g. from a different Order), but how reliable are the results from such an analysis likely to be? Or is there an alternative method?

Many thanks for any help or advice! Cheers, Peter – Dr. Peter R. Teske Postdoctoral Researcher Molecular Ecology and Systematics Group Department of Botany Rhodes University 6041 Grahamstown South Africa [P.Teske@ru.ac.za](mailto:P.Teske@ru.ac.za) [http://www.ru.ac.za/-academic/departments/botany\\_research/Peter/](http://www.ru.ac.za/-academic/departments/botany_research/Peter/) “Dr.



Peter R. Teske" <P.Teske@ru.ac.za>

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### NineWellPlates source

Dear all,

for gene expression work we need 9-well glass plates with well volume about 1 ml and we can not find a company selling them. If you know where we can order those plates, please contact us.

Thanks,

Suzanne Saenko.

s.v.saenko.2@umail.leidenuniv.nl

Institute Biology Leiden.

suzanna saenko <ssaenko@hotmail.com>

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### PCR cleanup

Colleagues:

Because of problems with competitive uptake of salts, unincorporated primers and dNTPs during capillary electrophoresis, we are looking for a high-throughput method to remove these from PCR reactions prior to analysis on a CEQ8000. Most kits remove salts and DNA <100 base pairs, but we have informative fragments between 60 and 100 bp so we need a method that will retain DNA >60 bp but remove both salts and DNA <60 bp. Does anyone know of a method or kit that will do this?

Yours, Keith Hopper

Keith R. Hopper, PhD USDA-ARS-BIIR, 501 South Chapel St., Newark, DE 19713; phone 302-731-7330 x238; fax 302-737-6780; email khopper@udel.edu

khopper@udel.edu

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### Peromyscus Newsletter

In an attempt to disseminate this information multiple list-servs have been utilized. My apologies for cross-postings.

Peromyscus Newsletter, a non-refereed publication dedicated to disseminating the latest information and research on all members of the genus, *Peromyscus*, is going on-line. *Peromyscus*, or white-footed and deer mice as they are commonly known, is the most thoroughly studied genus of native mice in North America. *Peromyscus* offers special potential as a model for studying the genetics of speciation and habitat adaptation, as well as the genetics and biology of host-pathogen interaction, behavior, and genomic imprinting. Currently, efforts by the *Peromyscus* Genetic Stock Center are underway to produce an intermediate-density genomic map to promote research in these areas. *Peromyscus* Newsletter attempts to keep researchers abreast of the latest developments in all these areas in the hopes of inspiring future research opportunities and collaborations.

Anyone interested in receiving *Peromyscus* Newsletter should send an e-mail to:

PeromyscusNewsletter@biol.sc.edu (please do not email the editor)

We will add your address to the mailing list and you will receive issues twice per year. Copies will also be posted on our website. For those interested in learning more about the *Peromyscus* Genetic Stock Center, its activities, and resources, please visit us at: <http://stkctr.biol.sc.edu/> Hope to have you on our mailing list!

Julie Weston, Ph.D. Editor, *Peromyscus* Newsletter

Wally Dawson, Ph.D. Editor Emeritus, *Peromyscus* Newsletter

– Julie Weston Post-Doctoral Researcher *Peromyscus* Genetic Stock Center Department of Biological Sciences University of South Carolina Columbia, SC 29208 Phone: (803) 576-5775 FAX: (803) 576-5780 E-mail: weston@biol.sc.edu

peromyscusnewsletter@biol.sc.edu

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### Phenylalanine decarboxylase source

Basically i need to locate somebody somewhere on the planet who has some Phenylalanine decarboxylase. I am desperate for this enzyme so that i can finish processing

my samples, and ultimately finish my Ph.D. I can find nobody who makes this anymore, so i was hoping somebody may have some in the darkest corners of their lab freezer and would be willing to let me buy it off them. Please reply to [stephen\\_mccleary@yahoo.co.uk](mailto:stephen_mccleary@yahoo.co.uk) if you can help thanks – S.J.McCleary [bsu642@bangor.ac.uk](mailto:bsu642@bangor.ac.uk)

“S.J.McCleary” <[bsu642@bangor.ac.uk](mailto:bsu642@bangor.ac.uk)>

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## Phylogenetic congruence

Hello all,

I am just looking for a software other than Paup implementing ILD test (also known as “partition homogeneity test for phylogenetic congruence”). The aim is to test whether or not three chloroplastic genes could be concatenated and used as a single one to reconstruct a phylogeny. If you have an idea of another test, any advice are welcome!

Many thanks

Stephane

[stephane.fenart@ed.univ-lille1.fr](mailto:stephane.fenart@ed.univ-lille1.fr)

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## Phylogenetic congruence answers

Cher Stéphane,

Une question similaire a déjà été posée sur Evoldir il y a quelques mois. Voici les réponses:

Dear all,

A few days ago, I posted the following query:

“I often use the Partition Homogeneity Test (= ILD) in PAUP\* to test data homogeneity for pylogenetic analyses, but as the number of taxa increases, this rapidly becomes impossible to use. This is related to the use of parsimony in this test, even if the principle of PHT should allow the use of other (and faster to compute) optimality criteria. Unfortunately, PAUP requires the use of parsimony in PHT. Is anyone aware of another (good) method to test data homogeneity, with an associate software or PAUP routine?”

Many people seem to have the same problem. Here are

the putative solutions I received:

- See attachment [Zelwer M and Daubin V; 2004. Detecting phylogenetic incongruence using BioNJ: an improvement of the ILD test. *Mol Phyl Evol* 33: 687-693].

Rob Cruickshank

- The test was made for and justified based on the parsimony criterion, of course. To make it tractable for a large dataset, you can use an abbreviated heuristic search to speed up the analysis of the random partitions if necessary (i.e., limit the number of trees swapped using `nchuck` command, for instance, or use a smaller number of repetitions using the `nrep=5` command, or even using the parsimony ratchet, though implementing that might be a chore). This app[roach risks not finding the very best tree for each random replicate, which would have the effect of increasing the variance of your p-value from its “true” value that you would find using exact searches. However, this approach shouldn’t introduce a strong bias that would drive the p-value strongly up or down, because the failure to find the best tree would be equally likely to affect the partitioned and unpartitioned length estimates for each replicate, giving the ILD for each replicate a more-or-less equal chance of increasing or decreasing.

You should not use an abbreviated search for your test partition, however, since the accuracy of this length difference is critical. You want this estimate to be as precise as possible.

As for switching to other criteria, the ILD concept could be adapted to likelihood, but this would be much more time consuming, so it wouldn’t help you. Huelsenbeck and Bull have their likelihood-based nonparametric bootstrap for incongruence, but it is far more computationally intensive than the parsimony ILD. I don’t know of a clear justification for using an ILD-like test in a distance context, and I would be very wary of such an approach. The ILD measures conflict between and within data subsets, which has a direct relationship to length difference. I don’t know if we can assume that differences in total branch lengths (for minimum evolution criterion) or least-squares-fit or other such distance measures should be distributed in a similar way under the null hypothesis of no incongruence, which is what is required for the ILD test to be valid.

Joe Thornton

- Did you try Winclada + Nona (<http://www.cladistics.com/>)? These programs are faster than PAUP.

Sophie Quérrouil

[My translation]

- 1. I don't know of a faster optimality criterion than parsimony. If you're thinking of neighbor-joining, that method doesn't have an optimality criterion, and therefore the test can't be performed on it. I suppose you could construct a neighbor-joining tree and then evaluate the topology under some optimality criterion, either least squares or parsimony. Parsimony would still be the fastest to compute.

2. Are you aware of recent literature showing that the ILD isn't a reliable test? In particular, I'm thinking of Barker, F. K., and F. M. Lutzoni. 2002. Spurious rejection of phylogenetic congruence by the ILD test: A simulation study. *Syst. Biol.* 51:625-637. But there are other similar papers.

John Harshman

- The attached paper by Waddell, Kishino and Ota [2000. Rapid Evaluation of the Phylogenetic Congruence of Sequence Data Using Likelihood Ratio Tests. *Mol Biol Evol* 17(12): 1988-1992] describes a homogeneity test that can use RELL. RELL is, in this sort of application, very fast. The required parts are available in PAUP (the site likelihoods or probabilities of data patterns) but an R script would be best to put it all together.

Peter Waddell

I sincerely thank all those who answered (with or without proposal!).

Yves

Sophie Qu erouil Instituto do Mar (IMAR) da Universidade dos Aores Cais Santa Cruz 9901-862 Horta - Portugal Tel / fax: +351 292 200 439 / 411

Sophie Querouil <squerouil@notes.horta.uac.pt>

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## Pistachio SSR markers

Dear Researcher, I'm Leila Pazouki. I'm a biotechnologist. I'm doing my project about "Analysis of genetic diversity in Iranian wild and cultivated pistachio genotypes using morphological traits and molecular markers (AFLPs and SSRs)" I need 14 SSR primers based on Ahmad riaz 2003, but it's not enough i need more.

I hope you can help me

thanks Leila

leila pazouki <pazouki712@yahoo.com>

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## PopGenetics podcast

Dear All,

The first population genetics podcast is now online at

[http://www.philippwesche.org/popgen\\_radio/-popgen.rss](http://www.philippwesche.org/popgen_radio/-popgen.rss) The direct link to the mp3 file is

[http://www.philippwesche.org/popgen\\_radio/-popgen01.mp3](http://www.philippwesche.org/popgen_radio/-popgen01.mp3) It has also been submitted to the iTunes podcast directory and is awaiting review.

Topics covered in this programme are

- recent conferences in Bordeaux and Krakov - centenary of Conrad Hal Waddington's birth - conference listings until December

I look forward to your comments.

Philipp

- Philipp Wesche Institute of Evolutionary Biology University of Edinburgh Tel.: 0131 650 8659 (office) <http://www.philippwesche.org/>

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## Protein Science paper out

Further to Mike Lynch's earlier message that his paper in response to the ID spokespersons Behe & Snoke in 'Protein Science' was accepted by that journal, his paper has now appeared. A reply to that reply, by Behe & Snoke, is in the same issue.

Ross Crozier -

Ross H Crozier FAA

Professor of Evolutionary Genetics School of Tropical Biology James Cook University Townsville, Queensland 4811 AUSTRALIA

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<http://medusa.jcu.edu.au/crozier/croziergroup/home/>  
ross.crozier@jcu.edu.au

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## Qiagen DNeasy recipes

Hello,

Does anyone know the recipe for the buffers that come with the QIAGEN DNeasy tissue kits? I have some of the tubes/filters left, but the buffers are three years old. I'm assuming the buffers would be expired by now? Also, if the proteinase K was kept in the fridge, should it still be OK?

Erika

erika.crispo@mail.mcgill.ca erika.crispo@mail.mcgill.ca

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## Removing PCR inhibition

Dear Colleagues

I am currently trying to isolate DNA from parasite eggs in feces and am having considerable difficulty in getting good DNA and good PCR products. The parasites in question are Eimeria, Nematodes and Cestodes found in birds that eat both plant matter and insects. I can get weak signals after PCR when the sample contains thousands of Oocysts, for example, but the results are not consistent.

I was wondering if anyone had managed to do this in birds that have low parasite numbers, or if anyone had tips on additions to the PCR, or steps in the extraction procedure, that may nullify effects of inhibitors present in feces, insect digests, or plant digests. I currently use a standard Phenol chloroform extraction, with a glycogen carrier to aid DNA precipitation. I use a CTAB stage in the extractions, which seems to improve the yield of DNA. I have also tried using several spin columns, but the recovery of DNA from this method is low. I have the appropriate positive control DNA which works well at the PCR stage.

Thanks

Iain Barr, UEA, Norwich, UK.

i.barr@uea.ac.uk i.barr@uea.ac.uk

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## SSCP band reamplification answers

Dear all,

I've to apologise for my delay. Thanks to the helpful comments regarding the recovery of SSCP bands. What seemed to work best for me is to simply excise the band and let it soak for a couple of hours in some 20µl of water.

-Basti

Here are the answers I got:

I put the excised bands directly into 60ul 1xTBE, incubated at 70c for two hours, then left in the fridge overnight. I was subsequently able to successfully reamplify 25 of 26 bands. I've not done any sequencing to assess the quality of what I've reamplified as I've literally just run the PCR out on agarose, but this method appears to be working well so far as I can tell.

I simply excise the bands from the gel with a wide-bore (tips cut down) 200 ul pipette tip. I suspend the gel plug in 50-100 ul of H<sub>2</sub>O overnight. I use the water directly for re-amplification. A little BSA in the re-amplification reaction might help. The only problem I have encountered is cross-contamination from other SSCP bands, in this case you have to end up cloning the PCR products.

We have success with most templates cutting dsDNA or ssDNA bands from dried non-denaturing and denaturing acrylamide gels and allowing some DNA to elute from the band for a few hours at room temperature in TE (1mM EDTA, 10mM Tris, pH8). 1 ul of the eluate is good as PCR template. It can be worth removing the backing paper after the gel has rehydrated and is easily peeled off.

The way that I extract PCR amplified fragments from MDE gels (usually 0.4X or 0.5X gels) or any polyacrylamide gels in that matter, is by using QIAGEN Gel Extraction Kit. I use the exact same protocol as for extracting fragments from agarose gels, except I add a minimum of 6 volumes of QG buffer to one volume of gel and then incubate it for 16 h at 55 C. After the final step (i.e., eluting DNA), you can either re-PCR the purified fragments and then clean the PCR product (recommended) or directly use the eluted DNA for cloning.

I have amplified many SSCP bands from acrylamide gels - usually radiolabelled on dried acrylamide. I place the excized band - often with paper attached - into 12 - 25 ul of water or 0.1x TE (volume dependent on how well the product amplified), centrifuged for a few seconds, then left the bands soaking for a couple of hours at room temp. Then used 1ul of this as template in a 20ul pcr. This never fails. I'm not sure how MDE differs from standard poly acrylamide. I'm guessing that the ethanol precipitation step in your protocol #1 is where you lost your product - there is very little product rescued from a gel slice, only enough to use a pcr template. It is likely the TBE inhibited your pcr reaction, try using the Water or TE and avoid any acrylamide in the reaction.

b\_bentlage@gmx.net

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## Second Hand Equipment

Other, Dear all, I am in need of a spectrophotometer, a dissolved oxygen meter, a conductivity meter, pH meter and an echo souder torch which are second hand and still working, for affordable prices. once found, please don't hesitate to contact me via my e-mail adress (mbalassa2003@yahoo.fr) or on my mobile phone +256 078554316.

kind regrads, yours sincerely, Mbalassa  
mbalassa2003@yahoo.fr

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## Sequencing problem

To all memebers,

I wish to thank all those who have responded to my previous question regarding my sequencing difficulties. I will post the responses I received within the next week. However, a few of you said that maybe my primer is not appropriate for sequencing. Can you please elaborate?

I have discussed this with others and a few thoughts have arisen, but no concrete reason was given. I was wondering if anyone has discovered reasons for why a primer would work well in PCR but does not work for sequencing.

Thank you.

Respectively, Lucia Iachetta Graduate Researcher  
Lakehead University liachett@lakeheadu.ca

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## Sequencing problems

To all members,

I was wondering if anyone could help me with my sequencing problems. I have been attempting to retrieve a sequence from a PCR product but have had minimal success. I always seem to get similar sequencing results and have tried numerous alterations in protocol to overcome this. I have altered the denaturation temperature and annealing temperature, increased and decreased the amount of template added to the reaction, increased and decreased the number of cycles, I have even attempted a reaction with additives and still no success. My sequences are usually unreadable and seem to consist mainly of Gs and As. However, the gene fragment to be sequenced does not contain large G or A stretches.

If anyone could provide me with some advice, it would be greatly appreciated.

Thank you.

Respectively, Lucia Iachetta Graduate Researcher  
Lakehead University Thunder Bay, ON Canada liachett@lakeheadu.ca

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## Sequencing problems answers

Thank you to all that have responded to my question regarding sequencing primers. Here are the responses that I have received. I appologize for the delay in posting.

Respectively, Lucia Iachetta

(1) My understanding of the issue with sequencing vs. PCR primers (which may not be completely correct) is that the best PCR primers have the strongest affinity to their target sequence in the 5' portion of the primer, while the best sequencing primers must bind strongly at the 3' end. A large determinant of this is the GC content in different portions of the primer. The presumed

reason is that in PCR the most important thing is target specificity, or only getting amplification when the entire sequence matches the target. This can be assured by only getting extension (which requires a perfect 3' end match) when the entire primer has annealed to the target sequence. Perfect efficiency in amplification is not important, as exponential amplification should still generate plenty of product if enough cycles are used.

With sequencing primers, on the other hand, there is a much more limited number of possible target sites (e.g. just the PCR product or plasmid that is being sequenced), and amplification is linear, so efficient generation of products is the most important criterion. This requires a strong 3' match, and one rule of thumb is that the last several bases of the primer should be at least 50% G+C. I should point out that I have not tested this empirically but try to keep it in mind when designing sequencing primers or deciding whether my PCR primers are likely to be useful for sequencing. David

(2) It depends what you mean by "does not work for sequencing": Do you have no sequence at all? or do you have several overlapping sequences?

My guess is that in the first case, the PCR product can fold in such a way that the primer's pairing (or the polymerase's work) is just not possible, it was possible with the DNA template that could not fold the same way. (Of course, PCR and sequencing do not necessarily share reaction conditions and may have an effect to DNA folding too, but if I remember well your previous e-mail, you already "played" with these parameters.)

In the second case, my guess is that the other primer used for the PCR was the one that allow a product amplification, when the first primer (the "bad one" !) was able to pair in different regions. When you use the first for sequencing, it will pair in different regions too, and then generate a sequence from each different region, the result will be "overlapping sequences", not readable at all. Marie-Pierre

(3) I have often experienced sequencing problem with long primers ( $\geq 30$  bp) that were working fine for PCR amplification. Just shortening the primer length (to 20-25 bp) usually solved the problem. Patrick

liachett@lakeheadu.ca liachett@lakeheadu.ca

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## Software AllelesInSpace

Dear EvolDir readers:

A new computer program for spatial analyses of genetic data is available from <http://www.marksgeneticsoftware.net>. The program, called "Alleles In Space (AIS)", is designed to facilitate statistical analyses of inter-individual spatial and genetic information that may be obtained during the course of performing phylogeographical analyses or analyses of local spatial genetic structure. AIS performs a variety of different procedures including Mantel tests, spatial autocorrelation analyses, allelic aggregation index analyses, Monmonier's algorithm, and "Genetic Landscape Shape" interpolations. Analyses can be performed using codominant marker systems (such as microsats or allozymes), dominant marker systems (such as AFLPs or RAPDs), or DNA sequence data.

The program is designed to run under any 32-bit Windows operating system. However, given that the program is inherently graphical in nature, a fast Pentium III machine with at least 128MB of RAM is suggested. Detailed instructions for using the program (in the form of a conventional "Help" file and a 29-page PDF manual) and some sample data sets are installed with the software.

Thanks for looking,

-Mark

Mark P. Miller Department of Biology 5305 Old Main Hill Utah State University Logan, Utah 84322-5305 USA <http://www.marksgeneticsoftware.net/> mp-musu@cc.usu.edu

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## Software Arlequin 3 0

A new version of Arlequin (a free and integrated software package for population genetics data analysis) is now available for WinXP on

<http://cmpg.unibe.ch/software/arlequin3> Compared to version 2, Arlequin 3.0 introduces a completely new graphical interface and a much more robust semantic analysis of input files.

Other main changes include:

1. Correction of many small bugs.
2. Incorporation of 2 new methods to estimate gametic phase and haplotype frequencies.
3. Estimation of the parameters of an instantaneous spatial expansion from DNA sequence diversity within samples.
4. Estimation of

bootstrap confidence intervals for F-statistics. 5. Updated user manual (<http://cmpg.unibe.ch/software/-arlequin3/arlequin3.pdf>) 6. Updated java-script routines, making output files fully compatible with Mozilla and Firefox web browsers.

Note that the Genetic Software Forum (GSF) (<http://www.rannala.org/phpBB2>) hosts a discussion forum on Arlequin, where people can report bugs, and post their questions and comments (positive ones are also welcome).

– Laurent Excoffier Computational and Molecular Population Genetics (CMPG) Zoological Institute, University of Bern 6, Baltzerstrasse, CH-3012 Bern, Switzerland Tel: +41 31 631 30 31 Fax: +41 31 631 48 88 Email: [laurent.excoffier@zoo.unibe.ch](mailto:laurent.excoffier@zoo.unibe.ch) URL: <http://cmpg.unibe.ch/people/excoffier.htm> [laurent.excoffier@zoo.unibe.ch](mailto:laurent.excoffier@zoo.unibe.ch)

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## Software Clann 3 0

We wish to announce the release of Clann version 3.0. This version has some significant advances (as described below). See the website at: <http://bioinf.nuim.ie/software/clann/> For those that don't know Clann. Clann is a free software tool licenced under GPL for combining phylogenetic information. Primarily its focus is on supertrees but it also carries out consensus analyses. Clann allows the user to analyse their data using 5 different supertree techniques as well as consensus approaches. The focus of the software is to allow the user to explore their data, so Clann comes equipped with many ways of exploring signal within a dataset.

Advances in this version: - The need for the installation of readline for Mac OS X has been eliminated. - Fixed Several bugs - New Criterion added: Average Consensus. Missing Data estimated using either an ultrametric or 4 point condition estimate. - NJ tree can be created using the command 'nj'. This is a neighbor-joining tree of an average consensus distance matrix of the data. - Neighbor-joining tree can be used as a starting tree for heuristic searches. - 'Showtrees' command added. This allows the user to view selections of the sourcetrees as ascii trees on the screen. The user can select the trees to be displayed according to their size, taxa compliment, score against the best supertree or according to the name of the trees. The selection can be saved to file. - Specific weights can be assigned to individual source trees. - 'Excudetrees' and 'Include-

trees' commands added. This allows the user to either exclude or include trees from the analysis according to the size of the tree, the taxa compliment, the score of the tree against a predefined supertree or according to the name given to the tree. - 'Deletetaxa' command added. This allows the user to select a taxon for deletion from the dataset. This has the effect of pruning the taxa from each of the source trees in which it appears. Source trees that have fewer than 4 taxa after any taxa are deleted are removed from the dataset. - 'Generate-trees' command added. This allows the user to generate random supertrees and assess them against the source tree data (or against randomised or idealised versions of the source trees). The results from the generation of supertrees are displayed as a histogram. Statistics about the distribution are also calculated. This command also allows the user to create (and save to file) randomised or idealised version of their data. - 'Consensus' command added. This allows Clann to carry out a consensus analysis of all the universally distributed trees (those trees that have all the taxa) in the source tree dataset. The user can choose from doing a majority-rule, or strict consensus. The results are displayed to screen in a graphical ascii format. This means that clann can now be used for the summary of bootstrap proportions from phylogenetic analyses. - Clann now also calculates a consensus tree from any bootstrap analyses it carries out. - Robinson-foulds distances can now be calculated from the sourcetrees dataset using the command 'rfdists'. For each comparison between two source trees, taxa are pruned from both trees until only the taxa that are shared by both trees remain. The results of these calculations are saved to file. The user has the choice of matrix or vector format. - Clann now reads nexus format files. The file may contain translation tables or not and this also allows the inclusion of a 'clann block'. This is a set of commands that are to be carried out on the data in the file. Clann will ignore any data blocks that are not relevant to it. - When a dataset is executed (loaded into memory) Clann will now also display a summary of the distribution of sizes of trees. - Clann will now "catch" ctrl-c signals so that a search of tree-space may be aborted early. Clann will display the best supertree found before the ctrl-c signal was sent.

Dr. Christopher J. Creevey Bioinformatics and Pharmacogenomics Laboratory, Department of Biology, National University of Ireland, Maynooth Co. Kildare Eire.

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f: + 353 1 708 3845 w: <http://bioinf.may.ie/>  
[chris.creevey@nuim.ie](mailto:chris.creevey@nuim.ie)

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## Software DNASlider

DNA Slider is a program for identifying statistically significant variation in the polymorphism-to-divergence ratio within a gene. It may be useful for detecting peaks of polymorphism caused by balancing selection and areas of low polymorphism caused by selective sweeps. Almost a third of the *Drosophila* data sets analyzed with the program in the original publication had significant heterogeneity (McDonald, J.H. 1998. Improved tests for heterogeneity across a region of DNA sequence in the ratio of polymorphism to divergence. *Molecular Biology and Evolution* 15: 377-384.)

The previous version of the program was only available for Mac OS 7, 8, and 9; I have now written versions for Windows and Mac OS X. The program, its source code, and an example data set, are available from <http://udel.edu/~mcdonald/aboutdnaslider.html>. John H. McDonald Department of Biological Sciences University of Delaware Newark, Delaware 19716 USA mcdonald@udel.edu

mcdonald@UDel.Edu

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## Software RNA-treefinder

One more unpaid TREEFINDER version at:

<http://www.treefinder.de> See what free work can achieve!

TREEFINDER is a computer program to compute phylogenetic trees from molecular sequences.

New features: empirical rRNA models with secondary structure, PMB protein model, SH test for user-supplied topologies, faster computation of edge support, improved manual.

I still have no position in Munich. Nobody feels responsible to support my TREEFINDER project. They say they cannot pay me a fair salary because others might want a fair salary, too. They say they cannot let me do my own project because others might want their own projects, too. They say they cannot let me work at home because others might want to work at home,

too. But if everybody dislikes the system - why don't we change it? We are living in a democracy.

Did you know that a patent attorney in Germany gets a starting salary of 6000 Euros per month? Ironically, the patent attorney has not spent more effort in his or her education than a post-doc in biology: University studies in a natural science or technology, plus three more years of internships and a special course in laws. There are good and long-term perspectives for patent attorneys in Germany.

Did you know that low wages and short-term contracts make people feel less responsible for their work? If a project is unsuccessful - who cares. Write an article about it! Apply for the next job, no matter how uninteresting it is, no matter where it is - it is just for a short time. Start some cooperations, have a nice time traveling to conferences, visiting other discontent scientists until the contract is over. And after all, it was somebody else's project, somebody else's money.

Did you know that paying fair salaries could be cheaper than trying to cheat?

Too few people define the goals and directions in science, decide about funding regulations, projects, careers - exquisite experts sharing public money among themselves, trying to get as much as possible for their own fields. The others are welcome to work, but not to compete. Tax-payers are welcome to pay, but not to propose. If scientists were elected into positions by a broad community I would not be unemployed. If funding was based on a democratic decision I would earn a fair wage for my work. Academic research would be less biased by various interest groups, but would be more focussed on what people really want. There would be less research on consumer behavior and gene foods without any taste, but more research on renewable energies, on developing cars that are clean and faint. We need more democracy in science. We need a scientific system that acts in the interest of science, in the interest of society, and not just in the interests of those few who have managed to become professors by having served other professors. We need a political system that acts in the interest of all people and saves our planet, that is robust against mass stupidification, lobbyism, corruption - someone should invent that, do research on that!

I am still collecting opinions about the ridiculous employment situation in science and, more importantly, ideas to improve it. I am interested in examples where good research has been abandoned due to stupid regulations, or because competent people did no longer accept the miserable payment and the lack of perspectives and left. Give me examples of incompetent people who are now consuming much more tax money for less use-



ful work than properly paid competent people would. Write me of people in the mid-thirties who are still being treated like students because they are excluded from getting their own funding. Write me of cases where professors have unexpectedly forced their employees to move to foreign cities, about professors putting their names on other's work. Write me everything that can be used against the system. I will put your comments on the web so that everybody can read what scientists think about science. I will not publish anybody's name so that nobody must fear any sanctions.

Saying 'yes' all the time is definitely not a good strategy, it is the cause of bad treatment. Become politically active and spread your opinion. Otherwise, the oppressors' opinion will dominate. Write a few extra lines in your papers, say a few extra words in your talks, make a nice website. Join or found a political party. Spread your opinion until it comes to the right ears. Ridicule the system, reveal its incompetence. Be creative and numerous and it will fall!

Gangolf Jobb

Gangolf Jobb <gangolf@treefinder.de>

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### Species DNA markers

Hi

I am looking for a marker to detect variation at a species/sub-species level aimed at identifying birds (I will be looking at a parrot species) within the different sub-species and hopefully to identify hybrids

Can anyone please recommend a nuclear marker that has been useful at this level.

Cheers Kerry Pillay

kerryopil@yahoo.com

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### Symmetry response

A. R. Palmer - a divine guardian of good scientific practice, or just another human being?

Palmer has in his recent posting on evoldir stated that my responses to his questions do not address the issues

about why there was an absence of symmetric males among short-tailed males in early samples, but many such symmetric males in recent samples of barn swallows from my study population in Denmark. However, I will reiterate once more for Palmer in an attempt to convey the message. I have show in the manuscript posted on the website of Prof. T. A. Mousseau by honestly listing all available information that (i) tail length of males has increased by over 1.2 standard deviations during the last 20 years; (ii) asymmetry in tail and wing length has decreased dramatically during the same period; and (iii) the relationship between asymmetry and tail length in males, but not in females has changed from being significantly negative to being flat during that period. This addresses exactly Palmer's question because it shows that since short-tailed males (at least by the standards of the 1980's) are absent or rare in recent years, this fraction of the population does no longer contribute to the distribution of asymmetry. Therefore, there is no deficiency of symmetric short-tailed males any more, because there are hardly any short-tailed males in the population any more. Finally, any differences in individual data points among publications, as identified by the detective work of Palmer, are due to differences in selection criteria for inclusion of observations in specific analyses.

Having read the recent postings by A. P. Palmer on EvolDir between my other required activities, I have started to wonder what is the problem at stake. Since when has a professor at a small university in western Canada been appointed the universal oracle of all matters related to asymmetry? Recently, A. R. Palmer has listed on the web a number of different findings from his analyses of some of my papers. He has in addition posted a number of questions that he apparently imagined that I had to answer in public on the internet until he some future day felt satisfied with the replies. This entire procedure seems utterly absurd to me because as far as I know Palmer has never been elected overseer in these or any other matters. He has no legal or moral obligation or right to pursue what he is doing. At worst, his behavior reminds me more of prosecutions in certain medieval societies, or in certain parts of North America a couple of hundred years ago when the same person was acting as sheriff, judge and guard of the local prison.

If A. R. Palmer had a saintly or godly behavior that made him a superior of others, I might be able to understand his ways. However, that appears not to be the case. When Palmer wrote a piece for the newsletter of the International Society for Behavioral Ecology a couple of years ago, the president of the society, Prof. N. B. Davies, wrote in the subsequent issue that all fu-

ture contributions to the newsletter would be required to reach certain minimum standards in terms of normal collegial behavior. Furthermore, Palmer has as the senior author of a paper published in *Evolution* in 1997 reproduced four figures from four other papers without requesting permission to reproduce these from the copyright holders. That was done against the advice of at least one referee who recommended that he not proceed with this illegal behavior. Hence, Palmer clearly has no rights based on a higher moral standing to pursue what he is doing.

I would be happy to share data sets with others, as I have done hundreds of times including with Palmer himself. However, I do not subscribe to the idea that a single person should be allowed to conduct personal vendettas under the disguise of promoting a fair society of scientists devoid of dishonesty and fraud. When such activities are left in the hands of single individuals they often become tools to meet the desires of that individual rather than a fair and open-minded inquiry, as I have already explained in detail in my recent article in the newsletter of the International Society for Behavioral Ecology. We are all best left without such unsolicited actions by parties directly or indirectly involved in a case.

Perhaps A. R. Palmer should focus on his teaching, research or some other activity and stop harassing people by posting his thoughts and beliefs in public on the internet. Then I and other persons being scrutinized in public could be left on their own to pursue their everyday life at work and at home together with colleagues and families.

Finally, I would like to invite Palmer or anybody else interested to personally inspect all data sheets in my office at their own expense to erase any doubt about the existence of the authentic data. I have all my notes since October 1969 neatly ordered so they are readily accessible. In

— / —

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

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### Thought diversity

Dear Brian and All,

Since the ID discussion on EvolDir has taken a bit of a satirical direction (e.g., recent “Other: Guinness’ answer”), I’d like to offer my two cents. If Brian feels that it’s too off-topic, and chooses not to post it, I won’t mind. It does have a serious component, though. I, too, chose not to sign the recent anti-ID petition, but for a different reason, than Dave Fitch and Nathan Pearson. I think that responding to ID’s 400 signatures with our 4000 or 40000 defies the main point we are trying to make: ID is outside of the realm of science. Why take the discussion down to their level? Scientific questions are not answered by vote count. After all, when Wegener came up with the continental drift or Belousov discovered what became known as Belousov-Zhabotinsky reaction, the vote count was one to everyone else. Instead of taking part in a petition signing contest, we should point out that creationists of any creed are, by and large, ridiculous, nearly as much as flat-Earth proponents would have been today. Hence, I propose another petition to sign and distribute:

Support alternative points of view in our schools! Stop the monopoly of the irrational pi theory in school curricula!

For years on end our children are presented with only one point of view on the value of the number pi. They are told by their math teachers that this number equals, approximately, 3.1415926. Note the word approximately! Despite centuries of work, there is no agreement among scientists on the exact value of this number. We asked 100 respected mathematicians from leading universities the same two questions: Do you know the exact value of pi? Does anyone know? All 100, with not a single exception, answered NO to both questions! Thus, the figure 3.1415926, which is presented as a scientific fact in our textbooks, from elementary schools to colleges, is based on nothing but theory, with no solid evidence behind it and with no agreement among this theory’s most ardent supporters on what the precise value of pi is!

Meanwhile there is an alternative, very unequivocal point of view. It comes from the Scripture itself. Open 1 Kings and read verse 7:23: “And he [King Solomon] made a molten sea, ten cubits from one brim to the other: it was round all about, and his height was five cubits: and a line of thirty cubits did compass it round about?”. If a perfectly round object (?round all about?) has the diameter of 10 cubits and the circumference of 30 cubits, then the value of pi is precisely 3. No mess, no uncertainty, no irrationality. King Solomon knew what he was doing. We believe that it’s time to end the monopoly of the so called irrational theory of pi on the heads of our children. The two theories must be presented as equal points of view and given the same

amount of time in classroom.

Let the kids decide!

–

Lev Yampolsky

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439-4359 Fax 423-439-5958

Lev Yampolsky <yampolsk@etsu.edu>

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## Transilluminators

Hi All

Transilluminators We are looking at purchasing a transilluminator - for quite basic use reading bands and taking photos - no cutting/cloning etc. We will be using it in a dark room.

Currently we use a UV transilluminator and Ethidium Bromide staining and it has been suggested that we might consider switching to one of the Dark Reader transilluminators (e.g. Clare Chemical Research DR88M Transilluminator to avoid the UV light etc.

I would be grateful to hear from people who have experience with this type of transilluminator.

Is the resulting visualisation comparable with that of UV transilluminators - I understand it may not be as useful with Ethidium Bromide...

Digital Cameras We are also looking at the possibility of obtaining a good commercial digital camera (aimed at public rather than lab work) to use with this set up (as opposed to a gel documentation system) and would be grateful for any advice from people operation this type of system.

Thanks Tiawanna

Dr Tiawanna Taylor School of Biological and Conservation Sciences University of KwaZulu-Natal Private Bag X01 Scottsville 3209 KwaZulu Natal South Africa

Email: taylor@ukzn.ac.za

Tiawanna Taylor <TaylorT@ukzn.ac.za>

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## White Tern samples

Hello evoldir people,

I am doing a phylogeny and population structure project on the white tern, sub-species *Gygis alba candida* and *Gygis microrhynca*. I would need some samples for these particular sub-species, as well as others (*Gygis alba leucopes* and *Gygis alba alba*) as outgroups. These birds live in the South Pacific (i.e., Marquesas), South Atlantic Ocean (from islands off coast of Brazil eastward to Ascension and St. Helena Is.), and Indian Ocean, (i.e., Seychelles, Chagos Archipelago, and Cocos Is.). If you can help me, please contact me at this email address: nyeung@hawaii.edu

Thanks,

Norine Yeung University of Hawaii at Manoa Honolulu, HI

Norine Wing Yeung <nyeung@hawaii.edu>

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## antiID petition mistake 1

On Oct 3, 2005, at 10:16 PM, David H. A. Fitch wrote:

> Why stoop to the level of the Discovery Institute to sign a > petition that is (1) not entirely accurate (it actually is fact-based > and empirical) and (2) misses the broader message we should be > developing: > > That is, ID spreads a lie about evolution, which is why ID SHOULD > be mentioned and discussed in classrooms. [snip]

I must admit that I was not drawn to sign the petition based on some of the rhetoric used to attract potential signers like myself, but I did sign it when I finally read the statement, which was very brief and to the point. Obviously, I disagree with what David wrote above. We often do, and probably should more often, introduce students to alternative scientific hypotheses and models, explanations at all levels, in the classroom. Throwing ID into the mix would appear to students to validate this agenda-driven sociopolitical claim as similar enough in kind to other scientific explanations to merit a similar level of consideration by scientists. This

is not only misleading, but it can potentially result in serious damage to our goal of raising the standards of scientific literacy among the general public. I am certain that the proponents of ID see no chance that so-called “ID theory” (a misleading rhetorical trick of a term, which no scientist or journalist should EVER concede to use) will ever infiltrate the mainstream of the scientific community. They don’t care. Their main objective is for science teachers to do exactly what David is recommending. It won’t matter to the students the Discovery Institute wants to capture politically if the teacher argues that ID is a poor alternative explanation. The Discovery Institute will have already won the hearts and minds of those students as soon as ID is anointed as a legitimate alternative idea. Regardless of how well the teacher then argues that ID is a poor alternative, the politically relevant set of students will then be ready to exercise what they perceive as critical thinking to disagree with the teacher regarding the relative quality of the alternatives.

IMHO, we would be playing into the hands of the Discovery Institute if we include ID in any list of alternative scientific ideas. I would only bring up ID in the classroom as an example of sociological pressures that can be brought to bear on scientists to abandon scientific principles when science advocates ideas that are uncomfortable to the scientifically ignorant.

Regards,

Guy Hoelzer Department of Biology University of Nevada Reno Reno, NV 89557

Phone: 775-784-4860 Fax: 775-784-1302

“Guy A. Hoelzer” <hoelzer@unr.edu>

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### antiID petition mistake 2

Hello Evol-Dir:

I must say that I’ve followed the whole ID / Evolution discussion with great interest. I agree with Dr. Fitch that we have gotten to a point where we can no longer advocate that ID should not even be mentioned in Biology classes. We have to teach students why this new version of creationism is basically flawed. I think Prof. Dawkins and Dr. Coyne were quite right when stating, at the end of their article in a British newspaper, that “it would only take about 10 mins to exhaust the case for ID”. We also have to teach students how to differentiate between scientific hypotheses and those that

clearly do not follow the scientific method. I think our discussion has also missed one crucial point. Intelligent Design and “pols” from the Discovery Institute are not only targeting Evolutionary theory but also scientific materialism which is the basis of the scientific method, of all science! As scientists all our work must be based on scientific materialism, there is no room for metaphysics in scientific theories. I think any discussion about Metaphysics does not belong in a science class. From a purely scientific point of view we would require evidence to prove the existence of some designer! But that is not our field of expertise and frankly it has nothing to do with science. Religious beliefs are a personal matter.

Sincerely,

Alejandro.

“Those who do not stop asking silly questions become scientists.” -Leon Ledermen, physicist

Alejandro Gonzalez Voyer Estudiante de Doctorado Laboratorio de Conducta Instituto de Ecologia Circuito Exterior S/N Ciudad Universitaria UNAM Mexico, D.F. 04510

Tel: (52-55) 5622-9041 E-mail: aglez@miranda.ecologia.unam.mx

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### antiID petition mistake 3

All,

Like Dave Fitch, I declined to sign the anti-ID petition (posted on shovelbums.org). His missing signature on that petition spoke much louder than mine, but I think it’s worthwhile to convey my reasons for not signing – especially since some of them run directly counter to reasons invoked by Fitch. While I agree with Dave that the petition did nothing to counter IDers’ strategic inattention to non-random evolutionary processes, I was most dismayed that the petition (at least the draft I read) bent over backwards to reassure religious folks, and by extension the well-entrenched societal institutions that they represent, that they and their ancient ideologies had nothing to fear from evolutionary biology. The religion/science never-the-twain-need-conflict tack is hackeneyed, craven, and, worse, false. We err in assuming that we can simply close our eyes to bald incompatibilities between modern scientific understanding of the world and many of the detailed, empirical, and patently silly cosmological claims that are integral

to much religious dogma.

ID, of course, falls in squarely with the latter. As was noted in a prior EvolDir thread, the core claims of ID are anything but metaphysical; rather, they are explicit claims about physics, positing that the material 'complexity' (however one measures the latter) that we observe implies that some quite -real- (if yet undetected) and – here's the rub – even more complex designer really exists. Even as a fanciful tidbit to be chewed over in a philosophy course, ID has a, well, damning logical flaw at its core: the spontaneous manifestation of a sufficiently complex 'designer' would violate the theory's own key claim about how complexity can arise. Moreover, key proponents of ID have famously resorted to sleight-of-math (e.g. Dembski's curiously crucial omission of a log term in ostensibly invoking Claude Shannon's definition of information) and have appealed to nonsense like accepting 'microevolution' but rejecting 'macroevolution' (as if the two are rigorously qualitatively distinct); positing that any new fossil discovery just adds another 'missing link' that evolutionists must answer for; &c.

The petition we were asked to sign, in its eagerness to appease potential allies in relatively liberal religious institutions, glossed over inescapable conflict between modern scientific cosmology its fossilized, but still well-entrenched antecedents. Moreover, the petition neglected to even allude to the specific logical flaw(s) inherent in ID that render it a ludicrous theory to spend time on even in a philosophy course; to grant ID signif-

icant airtime even in a 'non-science' curriculum seems like a disservice to public school students, and ultimately to our own interests as beneficiaries of voters' largesse. It's disappointing that such a big, coordinated response from the scientific community would end up being this sort of intellectually soft-pedaled, needlessly apologetic statement. Perhaps a more forthright communal position statement on the matter is in order.

Nathan Pearson

Nathan Pearson <n-pearson@uchicago.edu>

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## g1 phylogeny statistics

Dear all,

I am actually analysing MtDNA sequences and looking for methods to test for phylogenetic signal, apart from the resampling analyses (bootstrap). Several papers referred to the g1 statistics, but I could not find the way to calculate this value and the associated p values. I would be very grateful to get some advices.

Many thanks

S everine Roques Estaci on Biologica de Do ana Molecular Ecology Lab Avda Maria-Luisa Sevilla, 41013

severineroques@hotmail.com

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## PostDocs

|                                            |    |                                                 |    |
|--------------------------------------------|----|-------------------------------------------------|----|
| AtlanticSalmon ConservationGenet .....     | 78 | SanDiegoZoo GorillaGenetics .....               | 83 |
| CNRS Paris MathModelEvol .....             | 79 | SanFranciscoStateU MarineEcolEvolGenetics ..... | 83 |
| Dunedin NZ EvolBiol .....                  | 79 | Sydney Genetics .....                           | 84 |
| Harvard Avian craniofacial evolution ..... | 80 | TexasAMU MolPopGenet .....                      | 84 |
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## AtlanticSalmon ConservationGenet

Postdoc and Ph.D. positions in Atlantic Salmon Conservation genetics: Positions are available for two postdoctoral fellows and two Ph.D. students at to work on the conservation genetics of wild Atlantic salmon. The postdoctoral fellowship positions begin in April 1, 2006 and are funded for two years. The Ph.D. positions begin in January or May 2006 and are initially funded for three years.

The project is lead by Dr. Elizabeth Boulding (U. Guelph) with co-investigators Dr. Ian Fleming (Memorial University of Newfoundland) and Dr. Patricia Schulte (U.B.C.). We are collaborating with Drs. Patrick O'Reilly and Brian Glebe of the Department of Fisheries and Oceans, Canada (DFO), Dr. Fred G. Whoriskey, Atlantic Salmon Federation (ASF), Dr. Keng Pee Ang of Marine Harvest, and Dr. Paloma Moran from the University of Vigo, Spain. This project involves looking for correlations between gene expression polymorphisms and morphological, behavioural, life history, and physiological traits in Atlantic salmon, and determining the extent to which these correlations have an underlying genetic basis. Atlantic salmon of the inner Bay of Fundy (iBoF), including the Upper Salmon River run, are listed by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC) and thus have been the subject of a breeding program by DFO. Researchers at DFO have used molecular markers to demonstrate that approximately 10% of the smolts obtained from the Upper Salmon River (located in Fundy National Park), are F1 hybrids between European aquaculture and North American (likely native Upper salmon fish). In the first part of our project the F1 "Trans Atlantic" individuals he identified will be backcrossed back to one of the parental populations to create two large full sib research families that will be segregating for the alleles that are unique to each of the original parental strains.

The Fleming Ph.D. student will then compare the morphometric, life history, and behavioural traits of the

backcrossed strains with those of each of the pure strains raised at constant density at the Mactaquac Biodiversity Centre near Fredericton, New Brunswick. This will allow us to identify functional candidate genes that are correlated with the differences in complex growth and behaviour (aggressiveness/dominance, risk aversion, boldness) and life history (early parr maturity) traits previously shown by Fleming et al. to exist between domesticated and wild Atlantic salmon. The Fleming Ph.D. student will also quantify functional trait differences, and outbreeding depression by rearing crosses from three iBoF populations at the Mactaquac Biodiversity Centre. In addition, wild native salmon with known pedigrees and with different levels of cumulative domestication, will be crossed within populations, reared in captivity and released into the wild. Survival, growth and other characteristics will be and monitored over time in captivity and in the wild to study the effects of captive rearing and breeding on salmon.

The Schulte postdoc, working at UBC, will use Genome Canada's GRASP microarray, which contains 16,000 different genes from salmonid fishes, to document differences in mRNA levels in tissues of fish of the same age from iBoF salmon populations reared in a common environment. Our use of microarrays is unique because our segregating backcross families will enable us to use a statistically powerful method to identify candidate genes whose expression level polymorphisms (ELPs) are strongly correlated with particular values of morphological, behavioural, physiological and life history traits for individuals within each of our full sib families.

In the third part of our project, the Boulding postdoc (working at Guelph) will determine which of these correlations between ELPs and the complex traits have a genetic basis. This will be done by comparing the DNA sequences of the candidate gene and look for SNPs (single nucleotide polymorphisms) that vary in sequence between the North American and European parental populations. In collaboration with O'Reilly, the Boulding Ph.D. student will then use our most promising SNP markers to genotype fin clips from the backcrossed wild Atlantic salmon families. We will also genotype these SNPs in families from backcrossed North American and

European aquacultural strains which will be held in a common hatchery tanks at St. Andrews Biological Station under the supervision of Brian Glebe. This will enable us to document statistical associations between SNPs in candidate genes and genetic differences in complex traits among these endangered salmon populations which, may assist in their conservation. Development of these SNP genetic markers will eventually enable the aquaculture industry to practice marker-assisted selection for complex traits within the St. John's Aquaculture strain that is authorized for use in New Brunswick.

Please apply for the postdoctoral positions with Dr. Boulding

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

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### CNRS Paris MathModelEvol

Dear colleagues, I would very much appreciate it if you could pass this information around. Thank you very much for your help Franck

Mathematical model in economics and ecology

A postdoctoral associate is sought to join a young research team at the Ecology, Systematics and Evolution Lab, a CNRS laboratory at the University of Paris-XI, 30km south of Paris, France. The University hosts 27000 students (2500 PhD) and 127 research labs, our Lab hosting 100+ staff. The position is for one year and may be renewed another year. The salary is 1830 euros (~2200 US \$) per month, plus health insurance. We are seeking a motivated postdoctoral fellow to construct and analyse a mathematical model at the interface of economics and animal or plant population dynamics. The ideal candidate would have an experience in mathematical modelling, ecological economics and conservation biology. However, candidates with less optimal profiles will be considered provided their motivation, work power and skills allow them to adapt rapidly to the project. Interested candidates should send a curriculum vitae, a brief summary of research experience and interests, and at least two references to

Franck Courchamp

Lab ESE. UMR CNRS 8079 [franck.courchamp@ese.u-psud.fr](mailto:franck.courchamp@ese.u-psud.fr) Batiment 362 Tel 0033 1 69 15 56 85 Univer-

sité Paris-Sud XI Fax 0033 1 69 15 56 96 F-91405 Orsay Cedex France <http://www.ese.u-psud.fr/epc/-conservation/pages/Franck.html> –

Franck Courchamp Universite Paris-Sud XI Tel (0033/0) 1 69 15 56 85 Batiment 362 Fax (0033/0) 1 69 15 56 96 F-91405 Orsay Cedex FRANCE <http://www.ese.u-psud.fr/epc/conservation/pages/-Franck.html> [franck.courchamp@ese.u-psud.fr](mailto:franck.courchamp@ese.u-psud.fr)

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### Dunedin NZ EvolBiol

UNIVERSITY OF OTAGO Te Whare Wananga o Otago

Dunedin, New Zealand

Postdoctoral Fellow in Evolutionary Biology (Fixed-term)

DEPARTMENT OF ZOOLOGY

Applications are invited from suitably qualified persons for the full-time position of Postdoctoral Fellow in Evolutionary Biology within the Department of Zoology. This position in the laboratory of Associate Professor Hamish G Spencer is funded by the Marsden Fund of the Royal Society of New Zealand and is available for three years.

The research project entitled “Modelling the Evolutionary Genetics of Parental Effects” will involve the construction and mathematical analysis as well as computer simulations of models of various types of parental effects, both genetic and epigenetic, in an investigation of how such effects may influence the evolution of natural populations. Some experience with mathematical population genetics would be desirable, but researchers with mathematical expertise in any area of evolutionary biology are strongly encouraged to apply.

Applicants must have been awarded the degree of Doctor of Philosophy before taking up this position.

We wish to fill this position by January 2006 or as soon as possible thereafter.

Specific enquiries may be directed to Associate Professor Hamish G Spencer, Department of Zoology, Tel +64-3- 479 7981, Email [h.spencer@otago.ac.nz](mailto:h.spencer@otago.ac.nz)

Reference Number: A05/154. Closing Date: Friday 25 November 2005.

APPLICATION INFORMATION

With each application you must include an application form, an EEO Information Statement, a covering letter, contact details for three referees and one copy of your full curriculum vitae. For an application form, EEO Information Statement and a full job description go to: <http://www.otago.ac.nz/jobs> [www.otago.ac.nz/jobs](http://www.otago.ac.nz/jobs) Alternatively, contact the Human Resources Division, Tel 03 479 8269, Fax 03 479 8279, Email karen.sutherland<mailto:ling.chong@stonebow.otago.ac.nz>@stonebow.otago.ac.nz

Equal opportunity in employment is University policy.

E tautoko ana Te Whare Wananga o Otago i te kaupapa whakaorite whiwhinga mahi.

Assoc. Prof. Hamish G. Spencer Allan Wilson Centre for Molecular Ecology and Evolution Department of Zoology University of Otago P.O. Box 56 Dunedin New Zealand

Phone: +64-3-479 7981 Fax: +64-3-479 7584 Email: h.spencer@otago.ac.nz Courier: 340 Great King Street, Dunedin, New Zealand

Departmental Website: <http://www.otago.ac.nz/zoology/staff/academic/spencer.html> AWC Website: <http://awcmee.massey.ac.nz/> Mollusca Website: <http://www.molluscs.otago.ac.nz/>

hamish.spencer@stonebow.otago.ac.nz

ogy in other avian groups. We will use the data obtained from Darwins Finches to formulate and test hypothesis pertaining the diversity of avian craniofacial structures.

The post-doc fellow will lead/participate in abovementioned and related project(s).

Starting Date: beginning of 2006

Duration: 24 months

Salary: suggested HMS/HSDM level based on experience

Hosting Laboratory: Abzhanov Lab, Department of Developmental Biology, Harvard School of Dental Medicine

Requirements: Molecular evolution, molecular biology and/or bioinformatics

Contact Persons: Arkhat Abzhanov, PhD 188 Longwood Avenue Department of Developmental Biology Harvard School of Dental Medicine Boston, MA 02115 Email: aabzhano@genetics.med.harvard.edu Phone: 617-432-5772 Fax: 617-432-5867 Website: <http://www.hsdm.harvard.edu/faculty/faculty-abzhanov.html> aabzhano@genetics.med.harvard.edu

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## Harvard Avian craniofacial evolution

Please Post:

Post-doctoral position in craniofacial evolution and development in avians

Research Topic: We are mainly interested in precise links between developmental genes and evolution of craniofacial structures in vertebrates, particularly avians and related groups.

Main research projects: - Molecular and genetic mechanisms of evolution of beak morphology in Darwins Finches. Darwins Finches are a classic example of morphological adaptive evolution in a group of closely related species. - Genomic analysis of regulatory changes during evolution of key craniofacial genes found to be important in beak evolution. For example, we previously found that regulation of expression of Bmp4 signaling molecule correlated with morphological change in Darwins Finches. We will search for specific genomic alterations in this gene to find the exact causes for morphological change. - Evolution of craniofacial morphol-

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## HarvardU EvolEnvir

Attention recent doctorate recipients in the evolutionary biology field:

The Harvard University Center for the Environment has just created the Environmental Fellows Program to enable you to use and expand Harvard's extraordinary resources to tackle complex environmental problems. The Environmental Fellows will work for two years with Harvard faculty members in ANY school or department to create new knowledge while also strengthening connections across the university's academic disciplines.

The fellowship will provide an annual salary of \$50,000 plus health insurance, other benefits, and a \$5,000 allowance for travel and professional expenses. Applications and all letters of reference must be received by the Center for the Environment by January 15, 2006.

Harvard University is an Affirmative Action/Equal Opportunity Employer.

To find out more - visit <http://www.environment.harvard.edu/navigation2/funding.htm> David Havelick



<david.havelick@gmail.com>

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## Honeycreepers PopGenet

University of Kent Post Doctoral Research Associate  
University of Kent and University of Sheffield Durrell  
Institute of Conservation and Ecology  
POST DOCTORAL RESEARCH ASSOCIATE  
R06/04

RA1A, up to point 6: £19,460 - £21,640 pa depending  
on experience Fixed term for 12 months from 1 February  
2006 This post will be mainly based at the NERC  
facility at the University of Sheffield

### POPULATION GENETICS OF HAWAIIAN HONEY- CREEPERS

The post-holder will apply microsatellite DNA tech-  
niques to construct historical genetic profiles for several  
species of Hawaiian forest birds, using ancient DNA  
and material from museum specimens. This NERC-  
funded project aims to measure temporal levels of ge-  
netic diversity within extinct and extant bird popula-  
tions, to examine the role of genetic inbreeding in recent  
extinction events on Hawaii. The appointee will form  
part of the conservation genetics research group of Dr.  
Jim Groombridge, although the majority of the genetic  
work will be carried out at the NERC molecular genet-  
ics facility at the University of Sheffield.

The appointee will have a recent PhD or DPhil with  
experience in microsatellite DNA methods, ideally in-  
cluding genotyping of museum-aged material.

Informal enquiries may be made to:

Dr. Jim Groombridge, Tel: 01227 824097,  
Fax: 01227 827289, email, J.Groombridge@kent.ac.uk;  
Website [http://www.kent.ac.uk/anthropology/staff/-  
jimG.html](http://www.kent.ac.uk/anthropology/staff/-jimG.html) Further particulars are available from  
the Personnel Office on 01227 827837 (24 hours)  
or from our website [http://www.kent.ac.uk/registry/-  
personnel/vacancies.htm](http://www.kent.ac.uk/registry/-personnel/vacancies.htm) Text phone users please tele-  
phone 01227 824145. Please quote the reference number

Closing date for receipt of completed applications: Fri-  
day 4 November 2005

Interviews are likely to be held: Late November 2005

We actively promote equal opportunity in education  
and employment and welcome applicants from all sec-  
tions of the community.

Dr. Jim Groombridge Lecturer in Biodiversity Con-  
servation Durrell Institute of Conservation and Ecol-  
ogy Room 161, Marlowe Building, University of Kent,  
Canterbury CT2 7NZ, Kent, UNITED KINGDOM  
Tel. -44 (01227) 824097 Fax. -44 (01227) 827289  
Email: J.Groombridge@kent.ac.uk Work page: [http://  
www.ukc.ac.uk/anthropology/staff/jimG.html](http://www.ukc.ac.uk/anthropology/staff/jimG.html)

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## IndianaU EvolBactInteractions

Department of Biology Indiana University, Blooming-  
ton IN

Postdoctoral / Research Associate Position in the Evo-  
lution of Bacterial Interactions

We are seeking a motivated individual with ex-  
pertise in microbiology for a new project evaluat-  
ing the role of pathogen relatedness on host ex-  
ploitation and virulence evolution. This project  
is a collaboration between Curt Lively and Farrah  
Bashey ([http://www.bio.indiana.edu/facultyresearch/-  
faculty/Lively.html/](http://www.bio.indiana.edu/facultyresearch/-faculty/Lively.html/)) that integrates strategic model-  
ing with laboratory experimentation.

Steinernema carpocapsae is an insect-parasitic nema-  
tode that has a mutualistic relationship with the bac-  
terium *Xenorhabdus nematophila*. For the last year, we  
have been using an experimental evolution approach to  
test the effect of parasite relatedness on the evolution  
of host exploitation. To date, we have been focusing  
on the evolutionary responses of the nematode; how-  
ever, in the next year we will expand our work to assess  
the evolutionary responses of the bacteria. The im-  
mediate aims involve testing our experimental strains  
as well as all available *Xenorhabdus* strains for  
variation in sensitivity and production of bacteriocins.  
The candidate would be responsible for setting up  
our laboratory to run these assays; consequently, the  
position suits candidates with a strong background  
in microbiology that have good organizational and  
trouble-shooting abilities. Additionally, we are  
hoping for a candidate with skills in molecular  
biology that have the creativity to be involved  
in future experiments focusing on the dynamics  
of virulence evolution.

This position provides an exciting opportunity to  
join a highly interactive lab and to train in evolu-  
tionary biology. The research environment at IUB  
is outstanding (<http://www.bio.indiana.edu/>) and the successful  
candidate will be able to participate in all the  
scholarly activities of the Department as well as  
attend confer-

ences, prepare manuscripts and contribute to grant applications.

The position is currently funded for one year starting January 1, 2006. We are primarily interested in candidates with a Ph.D. degree in microbiology with an interest in evolutionary biology; however, we will consider experienced applicants without a Ph.D. Salary is \$32 K (plus benefits). If you are interested, please email the Personnel Manager (malockha@indiana.edu) with a CV, statement of research interests, and the names, phone numbers and email addresses of three references. Please direct all inquiries about the position to Curt Lively (clively@indiana.edu). Women and minorities are particularly encouraged to apply. We will begin reviewing applications as soon as they are received and will continue to do so until the position is filled.

Indiana University is an Equal Opportunity / Affirmative Action Employer.

fbasheyv@indiana.edu fbasheyv@indiana.edu

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### LundU GenomicEcol

Postdoctoral Research Fellow in Genomic Ecology (Lund, SWEDEN)

Lund University announces a position for Postdoctoral Research Fellow (reference no.4794) that will be affiliated with a newly started Centre for Genomic Ecology ([www.biol.lu.se/ekologi/CGE/](http://www.biol.lu.se/ekologi/CGE/)). A key ambition within the research programme of the centre is to improve our understanding of the molecular and genetic mechanisms behind key evolutionary processes such as adaptation to environmental change, evolutionary differentiation and speciation. Such mechanisms could be manifested at different levels of biological organization from molecules and cells to organisms and populations.

The applicant's should have a strong empirical and/or theoretical research background in areas related to the research programme of the Centre and could include, but are not limited to fields like experimental evolution, developmental biology, theoretical evolutionary biology, molecular ecology, evolutionary ecology, evolutionary genomics/genetics and population biology. Guidelines for applications are found at <<http://www.naturvetenskap.lu.se/utlysningar>><http://www.naturvetenskap.lu.se/utlysningar> Applications should be received no later than November 24, 2005.

Erik Svensson <erik.svensson@zoekol.lu.se>

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### PennStateU EvolInfectiousDiseases

Post doctoral position available in the Center for Infectious Disease dynamics (CIDD) [www.cidd.psu.edu](http://www.cidd.psu.edu) <<http://www.cidd.psu.edu/>> at Penn State University, USA from February 2006 for up to 5 years.

We seek to appoint an ecologist with an understanding of parasitology and an interest in community structure to start work with a large team on an exciting new grant from NSF studying the parasite community dynamics of small mammals (Grant abstract: <http://www.nsf.gov/awardsearch/showAward.do?AwardNumber=0520468>). This project will investigate how a community of parasites is shaped at the level of the individual host and the consequences this has for the dynamics of parasitic infections at the population level using a mixture of field and lab experiments coupled with mathematical modeling.

The post-doc will be expected to carry out field and lab experiments and ideally should have experience of both, with the greater emphasis on fieldwork.

Desirable skills include:

- Field organisation skills, especially familiarity with small mammal systems
- Knowledge of experimental design
- Good statistical knowledge, e.g. GLM's and repeated measures analyses
- Database management and team work

Research projects within CIDD have a strong emphasis on inter-disciplinary collaboration and interactions with other CIDD researchers are strongly encouraged.

The proposed start date is February 2006 and the position will remain advertised until filled. Applicants should send (email preferred) a CV, cover letter, and list of publications to:

Peter Hudson - [pjh18@psu.edu](mailto:pjh18@psu.edu)

Peter Hudson Center for Infectious Disease Dynamics  
208 Mueller Penn State University State College PA 16803, USA

Penn State is committed to affirmative action, equal opportunity, and the diversity of its workforce

[sep18@psu.edu](mailto:sep18@psu.edu)

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## RutgersU MolEvol

Postdoctoral Position Available: Molecular evolution of Hox genes in the ray-finned fishes.

An NSF-funded postdoctoral position is available immediately in the Department of Genetics, Rutgers University, NJ, USA. The position is initially funded for two years. The lab investigates Hox cluster regulation and evolution in the ray-finned fishes, with focus on basal lineages such as the bichir (*Polypterus*). The work is carried out in an evo-devo framework. Representative publications from the lab include (Chiu, C-H. et al. 2004. Bichir HoxA cluster sequence reveals surprising trends in ray-finned fish genomic evolution. *Genome Research*, 14: 11-17 and Chiu, C-H. et al. 2002. Molecular evolution of the HoxA cluster in the three major gnathostome lineages. *Proc Natl Acad Sci USA* 99: 5492-5497).

The ideal candidate will have demonstrated experience in molecular biology. Experience in working with animal models (e.g. zebrafish) and/or comparative sequence analysis is highly desirable.

To apply, please send a CV, up to 3 relevant manuscripts, and contact information for three references. Please send applications (either electronically or via post) to

Chi-hua Chiu Department of Genetics HGI, Rm. 222 Rutgers University 145 Bevier Road Piscataway, NJ 08854 [chiu@biology.rutgers.edu](mailto:chiu@biology.rutgers.edu)

“Chiu, Chi-hua” <[Chiu@nel-exchange.Rutgers.Edu](mailto:Chiu@nel-exchange.Rutgers.Edu)>

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## SanDiegoZoo GorillaGenetics

Job: CRES/San Diego Zoo - postdoc in gorilla genetics The Zoological Society of San Diego's Conservation and Research for Endangered Species (CRES) program is seeking a Postdoctoral Fellow to work on genetics of captive and wild gorilla populations. The successful applicant will work with the Genetics Division at CRES for a minimum of two years. An increased understanding of mitochondrial and nuclear genetic variation at the DNA sequence level will contribute to health

assessments, population biology, behavioral ecology, a broader understanding of the evolutionary diversification of apes, and conservation management of captive and wild populations of gorillas. We seek a candidate skilled in techniques of molecular genetic analysis including methods of genome bioinformatics who is interested in and capable of forming productive relationships with in-country scientists in gorilla range states. An extensive collection of cell cultures from captive gorillas and samples obtained through noninvasive methods from wild populations of gorillas are immediately available in support of project objectives.

Please submit a letter of interest, the names of three references, and a c.v. to Human Resources, San Diego Wild Animal Park, 15500 San Pasqual Valley Road Escondido, CA 92027-7017 Fax: (760) 796-5614 Job Line Information: (760) 738-5006.

for more information: visit [www.sandiegozoo.org](http://www.sandiegozoo.org) and click through for job openings also see [www.conservationandscience.org](http://www.conservationandscience.org) for details of the location and facilities

[oryder@ucsd.edu](mailto:oryder@ucsd.edu) [oryder@ucsd.edu](mailto:oryder@ucsd.edu)

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## SanFranciscoStateU MarineEcolEvolGenetics

Research associate/post-doc: San Francisco State University, Romberg Tiburon Center Marine Ecological and evolutionary genetics

Position in a marine population biology/genetics and molecular evolution lab at the Romberg Tiburon Center for Environmental Studies (<http://rtc.sfsu.edu/>) of SFSU (<http://rtc.sfsu.edu/>). The lab uses molecular techniques to characterize patterns and investigate mechanisms of population differentiation. An additional focus is on mechanisms of immune system evolution using genomic resources.

Projects in the lab currently include immunogenetic (Mhc) and detoxification genetic variation in estuarine fish, connectivity between onshore and offshore invertebrate populations, population structure and restoration genetics of seagrasses in SF Bay, and invasion biology and evolution of allorecognition in colonial tunicates. We are additionally interested in the genetic architecture of the Mhc in fish.

Must be interested in some mentoring of students. Must have a car and be able to travel to the main

campus in SF occasionally. Familiarity with capillary sequencing and sizing would be a plus. Good organizational and communication skills are essential.

Please contact Dr. Sarah Cohen by email and include a statement of interest and CV, and contact info for 3 references.

Salary approximately \$34,000 annually. The position includes full benefits. EOE/AA

Email resume and cover letter (MS word or pdf attachments) to: <mailto:sarahcoh@sfsu.edu>sarahcoh@sfsu.edu

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

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

This is a full-time, non-exempt, benefited position. This position is administered by the San Francisco State University Foundation, Inc., (SFSUFI), and said employment for this position is with SFSUFI. This is a non-State of California, non-University position. SFSUFI is an EOE/AA employer.

sarahcoh@sfsu.edu sarahcoh@sfsu.edu

ods. Experience with manipulation of proteins including western and 2D-gel analysis. General computer literacy. High degree of competence in the use of bioinformatics. Demonstrated highly developed organisational skills. Demonstrated well developed interpersonal skills and capacity to work as part of a team. Excellent oral and written communication skills.

Desirable: Specific experience with culture and manipulation of human neuronal cells. Experience in the development of quasi-functional assays including gel-shift and promoter assays. Experience with ChIP analysis. Experience with manipulation and analysis of mouse derived tissue samples. Practical experience with microarray technology. Previous experience in the supervision of junior research staff and students. Experience with grant writing.

Details: Position description is available <http://www.chw.edu.au/about/jobs/vacancies/#RR8006.0326.05> Previous applicants need not re-apply.

Enquiries: Professor John Christodoulou on (02) 9845 3452, via the Hospital switchboard on (02) 9845 0000 and page 6053 or email [johnc@chw.edu.au](mailto:johnc@chw.edu.au).

Closes: 21/10/05.

John Christodoulou <[JohnC@chw.edu.au](mailto:JohnC@chw.edu.au)>

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## Sydney Genetics

Ian Thorpe Charity Research Fellow The Western Sydney Genetics Program Temporary Full-time 12 mths (renewable) Position No. RR8006/0326/05

The Research Officer is responsible, in consultation with the Head of Unit, for conceiving, planning and executing research projects in the area of molecular and functional (including gene expression) studies relevant to the neurodevelopmental disorder Rett syndrome. The Research Officer will be expected to work collaboratively with other Research Officers within the Unit, and when delegated by the Unit Head, may also act as supervisor to the research assistants and students working in the laboratory.

Essential: PhD with extensive experience in Molecular Biology. Experience in the preparation and analysis of RNA and DNA. Experience with various mutational screening strategies. Substantial experience with mammalian cell culture and manipulation. Substantial practical experience with recombinant DNA meth-

POSTDOCTORAL RESEARCH SCIENTIST - MOLECULAR POPULATION GENETICS:

Department of Wildlife and Fisheries Sciences Texas A&M University College Station, Texas 77843-2258

Responsibilities: Position responsibilities involve development and assay of nuclear-encoded microsatellites and of mitochondrial DNA sequences for projects involving population genetics and molecular ecology of marine fishes. Primary responsibilities include data acquisition and analysis, and preparation of reports and publications.

Qualifications: Dissertation or postdoctoral work in molecular population genetics and/or molecular ecology is required, as is experience with microsatellite and/or mtDNA data acquisition and analysis. Experience with major software programs (e.g., ARLEQUIN, GENEPOP etc.) also is required.

Salary: Salary will depend on experience. Benefits are

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## TexasAMU MolPopGenet

included. Position is for 12-24 months.

Closing date: Position will remain open until filled.

Contact: Send curriculum vitae, description of research experience, and names, addresses, phone numbers, and e-mail of three references to: Dr. John R. Gold, Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, Texas 77843-2258. Electronic submissions are acceptable: goldfish@tamu.edu. International applicants will be considered if they hold the correct visa(s). Texas A&M University is an Equal Opportunity/Affirmative Action/Equal Access Employer.

John Gold <goldfish@tamu.edu>

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### UAlbany ExpProteinViralEvol

Postdoc: Experimental protein and viral genome evolution

An NIH-funded postdoctoral position is available immediately at the Department of Biological Sciences at the State University of New York at Albany.

The lab is interested in using bacteria and bacteriophages as a model system to study the evolution of proteins, viral life history traits, and viral genomes. Both experimental and comparative approaches are used.

Individuals having experience in molecular techniques are preferred. Experience in working with bacteria and bacteriophages is highly desirable.

To apply, please send a CV and contact information for three references. Please send applications (either electronically or via post) to

Ing-Nang Wang Assistant Professor Dept. of Biological Sciences University at Albany State University of New York 1400 Washington Ave. Albany, NY 12222

Phone: (518) 591-8844 (O) (518) 591-8845 (L) Fax: (518) 442-4767 email: ingnang@albany.edu

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### UAlgarve FunctionalGenomics

Post doc position "Functional genomics of Fish environmental Adaptation"

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: This project is developed within the framework of the Network of Excellence Marine Genomics Europe, which implies collaboration and coordination between several laboratories aimed at developing and applying cDNA and oligo microarrays. The research objectives are to identify genes and gene networks involved in the adaptation of fish to changing environmental conditions.

Qualifications and experience: Candidates must hold a Ph D and have experience in microarray analysis.

Further information can be obtained from prof. Adelino V. M. Canário: <mailto:acanario@ualg.pt>acanario@ualg.pt

Contractual conditions: Initial 2-year contract, in accordance with current fellowship legislation and for the implementation of the project.

Closing date: 10 November 2005.

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. CCMAR /BPD/0025/2005 <mailto:to:ccmar@ualg.pt>to:ccmar@ualg.pt Centro de Ciências do Mar, Universidade do Algarve, Campus de Gambelas 8005-139 Faro, Portugal Fax: +351 289 818 353 E-mail: <mailto:ccmar@ualg.pt>ccmar@ualg.pt

<http://www.ualg.pt/ccmar/postdocs.htm> Adelino V.M. Canario Centro de Ciencias do Mar, Universidade do Algarve, Campus de Gambelas, 8005 - 139 FARO, Portugal Tel:(+351)289-800925, Fax:(+351)289-818353 <http://w3.ualg.pt/~acanario>

acanario@ualg.pt

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### UCaliforniaRiverside SexualSelection

Post-doctoral opportunity available

I am searching for an individual to participate in a range of research activities examining how insects balance reproductive traits against immune defense and parasitoid avoidance. Currently we have two projects

underway: 1) An examination of immunity in the context of sexual selection in the ground cricket, *Allonemobius socius*; and 2) Evolution of signaling and reproductive behavior in the field cricket *Teleogryllus oceanicus*, which is subject to an acoustically-orienting parasitoid. The successful candidate will supervise undergraduate assistants and maintain the day-to-day operation of the lab, but will also be independent in the design and execution of related research in line with the candidate's own interests. Experience with laboratory work (molecular genetic, physiological, or epidemiological) is desirable. Position is for two years, starting as soon as possible but ideally no later than January 2006. Salary is approximately \$US 33,000 per year plus full benefits. To apply, send or email a cv, statement of research interests and goals, and the names and addresses of two references by November 1 to: Marlene Zuk, Department of Biology, University of California, Riverside, CA 92521 USA, email [marlene.zuk@ucr.edu](mailto:marlene.zuk@ucr.edu)

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

Marlene Zuk Department of Biology University of California Riverside, CA 92521 USA email: [marlene.zuk@ucr.edu](mailto:marlene.zuk@ucr.edu) phone: 951-827-3952 fax: 951-827-4286 Sexual Selections: what we can and can't learn about sex from animals University of California Press 2002 <<http://www.ucpress.edu/books/pages/-9600.html>>

Marlene Zuk <[marlene.zuk@ucr.edu](mailto:marlene.zuk@ucr.edu)>

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## UConnecticut EvolBioFuncGenomics

### Postdoctoral Position Open

An additional post-doctoral position is available at the University of Connecticut in the Townsend Laboratory to work in the field of evolutionary biology and/or functional genomics, particularly the functional genomics of *Saccharomyces* or *Neurospora*. The precise project is flexible, but possible projects may include experimental, theoretical, or computational studies on the evolution of gene expression or the functional genomics of interspecies infertility.

This position will require an independent and motivated individual, preferably with laboratory experience with *Saccharomyces* or *Neurospora*. All applicants should have received their Ph.D. prior to taking up the

appointment.

Funding is available for multiple years, depending on performance. The salary is greater than the NIH guidelines, and commensurate with experience and expertise. Storrs is located in a beautiful community in the heart of New England, close to Hartford, New Haven, Providence, and Boston.

For full consideration please apply by November 20, 2005. Starting date is flexible; the position will remain open until filled.

To apply, please email a CV, a brief statement of research interests and contact information for three academic references to [Jeffrey.Townsend@UConn.edu](mailto:Jeffrey.Townsend@UConn.edu).

Jeffrey P. Townsend Molecular and Cell Biology Department 354 Mansfield Road U-2131 University of Connecticut Storrs, CT 06269

<http://web.uconn.edu/townsend> (860) 486-1899

Jeffrey Townsend <[Jeffrey.Townsend@uconn.edu](mailto:Jeffrey.Townsend@uconn.edu)>

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## UFribourg EvolPlantEcol

POSTDOCTORAL POSITION IN EVOLUTIONARY PLANT ECOLOGY Department of Biology, University of Fribourg, Fribourg (Switzerland)

Rationale: The European knapweed *Centaurea maculosa*, introduced from Central Europe into North America during the late 19th century, where it covers now an area larger than Switzerland, has become a model for research on the ecological and evolutionary causes and consequences of invasions. We aim to explore the role of rapid evolutionary processes in the invasion success of *C. maculosa*. This involves the analysis of selection exerted by herbivorous insects (biocontrol agents) on plant life-histories in different environments and the study of genetic factors (especially polyploidisation) underlying evolutionary change in the exotic range.

We seek a highly motivated person to conduct quantitative genetic experiments in the field and greenhouse, and various lab studies (molecular markers, flow cytometry) using seed material collected in Europe and North America. Surveys of cpDNA sequence variation and cytotype distributions are currently under way. New ideas and complementary studies are of course highly invited.

Requirements: - doctoral degree in experimental plant ecology or evolution, or related disciplines; - knowledge

of, and experience in one or several of the following areas of research is highly desirable: population ecology, ecological genetics, plant-herbivore interactions, experimental design and statistics.

Salary and conditions: Salary dependent on age and status (gross salary in the first year about CHF 67'000). Start date: preferentially on 1 March 2006. The position will also include support of research activities of our group. The position is for 2 years, but may be extended depending on funding.

Applications: Applicants should send their CV, including the publication list, a short summary of research experience and interests, and the names of two professional referees to the address below (preferably by e-mail). Deadline is 1 December 2005.

For further information, please contact: Prof. Dr. Heinz Mueller-Schaerer Département de Biologie, Unité Ecologie et Evolution Université de Fribourg Chemin du Musée 10 CH-1700 Fribourg, SWITZERLAND. tel: + (41) (0) 26-300 88 35 direct, ++ 50 secr., fax: + (41) (0) 26-300 96 98; e-mail: heinz.mueller@UNIFR.CH; <http://www.unifr.ch/biol/ecology/> This is a joint position between H. Müller-Schärer, Thomas Steinger (Uni Fribourg) and Urs Schaffner (CABI Bioscience, Delémont) within the National Centre of Competence in Research (NCCR) Plant Survival, funded by the Swiss National Science Foundation.

thomas.steinger@unifr.ch thomas.steinger@unifr.ch

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## UGlasgow MolEvolEcol

POST-DOCTORAL RESEARCHER IN BEHAVIOURAL AND MOLECULAR ECOLOGY at the University of Glasgow, UK (£20,044 - £30,002 p.a.)

A postdoctoral research assistant is required for a project entitled 'Life history consequences of growth variation', funded by a NERC grant to Pat Monaghan, Neil Metcalfe and Lubna Nasir. This project will use novel techniques (e.g. analysis of telomeres, and of ethane in breath samples) to examine the links amongst early nutrition, growth, oxidative stress and senescence within a life-history framework, using zebra finches as a model system. The post is available for up to 3 years. Further particulars can be found at: <http://www.gla.ac.uk/ibls/news/posts.html>. Letters of application, including two CVs, the names, postal and e-mail

addresses and fax numbers of two academic referees, should be sent to: Lesley Frew, IBLS, West Medical Building, University of Glasgow, Glasgow, G12 8QQ, UK, quoting reference number 11629/DPL/A3. Closing Date: 4 November 2005.

Division of Environmental & Evolutionary Biology Graham Kerr Building Glasgow University Glasgow G12 8QQ U.K.

Phone: (0)141 330 5968 (N. Metcalfe direct line) (0)141 330 6640 (P. Monaghan direct line) (0)141 339 8855 ext.5506 (messages) Fax: (0)141 330 5971 Omit zero if outside the UK

Web page: <http://www.gla.ac.uk/Acad/IBLS/-DEEB/> - Dr. Barbara Mable NERC Advanced Research Fellow Rm 404, Graham Kerr Bldg Division of Environmental and Evolutionary Biology University of Glasgow Glasgow, Scotland U.K. G12 8QQ Phone: +44 (0)141 330 3532 Mobile: +44 (0)791 083 3819 Fax: +44 (0)141 330 5971 email: b.mable@bio.gla.ac.uk website: <http://www.gla.ac.uk:443/ibls/staff/staff.php?who=PQdGnd> b.mable@bio.gla.ac.uk

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## UHertfordshire BioComputation

University of Hertfordshire

Post Doctoral Research Fellow in Biocomputation

Biological & Neural Computation and Adaptive Systems Research Groups Science and Technology Research Institute (STRI)

(Ref: L6211AC)

Salary: Up to 25k (British pounds).

A post-doctoral research position (Researcher B) is available to support further development of an interactive tool for visualizing and simulating the behaviour of multi-cellular biochemical networks. The successful candidate will assist in developing tools for the computational modelling of multicellular biochemical networks. The post will support ongoing work on a project funded by the Wellcome Trust. Details of the research in the Biological & Neural Computation and Adaptive Systems Research Groups are featured on the STRI website, <http://perseus.herts.ac.uk/uinfo/-research/stri/>, and information on the computational tools that are being developed is found on <http://strc.herts.ac.uk/bio/maria/NetBuilder/>. The post will

be available for at least two years from January 2006. A successful candidate will have a background in Biochemistry/Molecular Biology and/or Computer Science, a PhD or equivalent experience in an appropriate field, as well as strong programming skills and experience with at least one of the following languages: Python, C++, Java, XSLT. Advantageous would be previous experience with mathematical modelling of biochemical systems, bioinformatics, software design, and web development, or a further background in theoretical/evolutionary biology and systems biology/artificial life.

We seek someone who can, as part of a team, think and work independently, who is committed to doing high-quality research, and can demonstrate excellent communication and scientific writing skills in English.

For informal enquiries contact Dr. Maria J. Schilstra, m.j.l.schilstra@herts.ac.uk.

Further information and an Application Form can be obtained from:

Personnel Department University of Hertfordshire College Lane Hatfield Herts AL10 9AB United Kingdom

Tel: +44-1707 284802 (24 hour voicemail). Please quote reference: L6211. You can apply on-line at <http://recruitment.herts.ac.uk/recruit/> Closing date: 7 November 2005

— Prof. Dr. Chrystopher L. Nehaniv Research Professor of Mathematical & Evolutionary Computer Sciences

Adaptive Systems & Algorithms Research Groups School of Computer Science University of Hertfordshire College Lane Hatfield, Hertfordshire AL10 9AB United Kingdom e-mail: C.L.Nehaniv@herts.ac.uk phone: +44-1707-284-470 fax: +44-1707-284-303 URL: <http://homepages.feis.herts.ac.uk/~nehaniv/welcome.html> Director, EPSRC Network on Evolvability in Biological & Software Systems Associate Editor, BioSystems Associate Editor, Interaction Studies

C.L.Nehaniv@herts.ac.uk

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## UIowa TheoEvol

A postdoctoral position is available for a period of one or two years to study theoretical questions in evolution in the department of Biological Sciences at the University of Iowa.

Current research in my lab concentrates on the evolution of variation-generating mechanisms (recombination, mutation, dispersal, alternative splicing), with emphasis on the plasticity of such mechanisms and the evolution of stress responses. Other topics include adaptive landscapes and variation and selection within the organism. The postdoctoral fellow will be encouraged to pursue independent research.

Desired skills are a strong background in mathematics and computer programming, and knowledge in evolutionary biology.

Please send CV, a letter of research interests, and contacts of three references to:

Lilach Hadany Department of Biological Sciences University of Iowa Iowa city, IA 52242 Lilach-hadany@uiowa.edu

The position is available immediately and will stay open until filled. Informal enquiries welcome.

The Evolution group at the University of Iowa is diverse, dynamic, and collegial, and offers plenty of interactions. Iowa City is a charming university town with a lively cultural scene, excellent school system, and low cost of living.

The University of Iowa is an Affirmative Action/Equal Opportunity Employer. Women and minorities are encouraged to apply.

Relevant links Evolution group: <http://www.biology.uiowa.edu/research.php?area=2> Genetics group: <http://www.biology.uiowa.edu/research.php?area=5> Center for Comparative Genomics: <http://www.biology.uiowa.edu/ccg/> "Hadany, Lilach" <lilach-hadany@uiowa.edu>

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## ULausanne EvolGeneticsSymbiosis

Postdoc position: Molecular Genetics & Symbiosis We are seeking a highly motivated postdoc with a strong background in molecular biology to join our group working on mechanisms of evolution in symbiotic mycorrhizal fungi. These important fungi form mutualistic symbioses with plant roots. Although the fungi grow clonally, they have a highly unusual genome organization, harbouring genetically different nuclei that are passed from one generation to the next (see Hijri & Sanders, Nature 2005; Kuhn, Hijri & Sanders, Nature 2001). The goals of our research are to un-



derstand how this unusual organization of the genome affects their evolution and their adaptation to the different environments offered by the roots of different plant species. Other than their unusual genome organization, the fungi have formed symbioses with plants ever since they colonized land over 400 million years ago and are thought to be the oldest putative ancient asexuals.

The candidate should should have a good knowledge of molecular biology and molecular genetics and have an interest in applying this knowledge to evolutionary questions. He/she should also be able to interact with the other group members working on evolution and population biology of mycorrhizal fungi (see list of recent papers on our web site).

The successful candidate will be located in the Department of Ecology and Evolution at the University of Lausanne (Switzerland). The Dept. of Ecology and Evolution in Lausanne is situated on the shores of Lake Geneva and provides a pleasant & exciting research environment and a strong PhD program. It is also one of the largest institutions in Europe for research in ecology and evolutionary biology, comprising 17 different research groups. A genomics research centre has also been recently established at the same site.

The position is funded by the Swiss National Science Foundation initially for a period of 1.5 years, with possibility of extension. Starting date should be as soon as possible. To apply, applicants should send a CV plus a letter of motivation and a list of publications by EMAIL to Ian Sanders, Dept of Ecology and Evolution, University of Lausanne, Switzerland. Email: [ian.sanders@unil.ch](mailto:ian.sanders@unil.ch); Tel: +41 21 692 4261. More details can be found about our group at: <http://www.unil.ch/dee/page7238.html> Please make it clear in your application if you are applying for the Post-doc position as there is a similar position for a PhD studentship currently available in our group as well.

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

Tel (direct): +41 (0)21 692 4261 Tel (secretary): +41 (0)21 692 4260 Fax: +41 (0)21 692 4265 <http://www.unil.ch/dee> New email!: [ian.sanders@unil.ch](mailto:ian.sanders@unil.ch)

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

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## UNebraska Arachnids

Post-doctoral Fellowship to study Amblypygids (Class Arachnida, Order Amblypygi)

I am looking for a neuroethologist with a strong background in invertebrate electrophysiology to join a research project exploring the neural basis of complex behavior in amblypygids. Research will involve some combination of extracuticular recordings, behavioral trials in conjunction with neural ablations, neuroanatomy, and behavioral trials investigating the potential for amblypygid learning, memory and spatial orientation. The project will likely involve a field component. Funding is currently available for 2 years. Applicants should have received their PhD and be available as early as January 2006.

Amblypygids are bizarre and unique arachnids with a sensory system unlike any other in the animal kingdom. Not only do they possess giant interneurons with peripheral cell bodies in their antenniform legs, but they also boast the largest relative mushroom body of any arthropod. My experience with these fascinating animals has been one of continual discovery and interested applicants should be adventurous, patient, and creative.

For specific information or to apply please contact Eileen Hebets ( <http://www.biosci.unl.edu/-faculty/FacPages/hebets.asp>); 402-472-2571; [ehebets2@unlnotes.unl.edu](mailto:ehebets2@unlnotes.unl.edu); applicants will need to send a current C.V. and 3 letters of recommendation. Applications will be accepted until the position is filled.

Dr. Eileen A. Hebets Assistant Professor School of Biological Sciences University of Nebraska Lincoln, NE 68588 (402) 472-2571 [ehebets@unlnotes.unl.edu](mailto:ehebets@unlnotes.unl.edu) <http://www.biosci.unl.edu/faculty/FacPages/hebets.asp>  
Eileen A Hebets <[ehebets2@unlnotes.unl.edu](mailto:ehebets2@unlnotes.unl.edu)>

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## UOxford 2 MathGenetics

UNIVERSITY OF OXFORD Mathematical and Physical Sciences Division

DEPARTMENT OF STATISTICS

Postdoctoral Research Assistant(s): 2 Positions:

(1) Statistical Methods for the Analysis of Genome-Wide Association Studies (3 years) (2) Statistical Methods for Geographical Population Structure in Genetic Studies (4 years)

Academic-related Research Staff Grade 1A: Salary £20,044 to £30,002 (bar) per annum

Two fixed-term research positions, both funded by the Wellcome Trust, are available to work in the research group of Professor Peter Donnelly, on statistical issues in modern genetic studies. The posts would commence on January 1, 2006, or at a different time by arrangement. Well-qualified successful applicants are likely to be appointed at or near the top of the salary scale given above.

The first post relates to the development, study, and application of novel statistical methods for genome-wide association studies for human diseases. Although the focus of the post is on methodological development, it is associated with the Wellcome Trust Case Control Consortium, a UK-wide collaboration which will perform large genome-wide association studies on eight common human diseases, and represents an exciting opportunity to be involved in one of the largest studies of its type internationally. Professor Donnelly chairs the consortium.

The second post concerns the development of statistical methods for inferring geographical population structure on the basis of genetic data, and how best to account for structure in genetic association studies. Again, the primary focus of the post is methodological, but it is associated with a large Wellcome Trust-funded study which will sample and genotype around 3,000 individuals to assess UK population structure empirically. There will be close involvement with the data generated by this project.

For the first post, candidates should have a strong background in modern statistics and its application. For the second post, a background in either modern statistics or statistical population genetics is necessary. Good computational skills are essential for both posts, and candidates should have, or expect soon to have, a doctorate. An existing background in genetics applications would be an advantage for both posts, but candidates wishing to move into the genetics field are also welcome to apply. The Department of Statistics in Oxford is one of the largest and strongest in the UK, and a world leader in statistical genetics.

Informal enquiries should be directed to donnelly@stats.ox.ac.uk. Further particulars are available from <http://www.stats.ox.ac.uk>, or the address below.

Applications should comprise a curriculum vitae and a list of publications together with the names, addresses, telephone, fax and e-mail details of three referees. Applicants should make clear for which of the posts they are applying, or whether they wish to be considered for

both posts.

Applications (7 copies, one copy for candidates outside the UK) should be submitted to Personnel Administration, Department of Statistics, 1 South Parks Road, Oxford, OX1 3TG. Applications faxed to +44 1865 272595 or e-mailed to jobs@stats.ox.ac.uk are acceptable as long as they are followed by hard copy. Please always quote reference number: AM-05-012.

The closing date for applications is 8 November, 2005.

donnelly@stats.ox.ac.uk donnelly@stats.ox.ac.uk

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## UOxford Bioinformatics

Mathematical and Physical Sciences Division Department of Statistics UNIVERSITY OF OXFORD

Postdoctoral Research Assistant: Academic-related Research Staff Grade 1A

Salary: £20,044 to £30,002 (bar) p.a.

A postdoctoral research position of up to two years and two months (26 months) duration in Bioinformatics funded by BBSRC is available for working in the Bioinformatics Group headed by Jotun Hein. This project will focus on models of sequence evolution that includes a process of insertion-deletion of nucleotides and their implementation. The work will include algorithm development, statistical modelling, software development and large scale comparative analysis of genomes.

The Research Project: Practical Statistical Alignment

Although bioinformatics is perceived as a new discipline, certain parts have a long history and could be viewed as classical bioinformatics. For example, application of string comparison algorithms to sequence alignment has a history spanning the last three decades. The present project will develop, implement and simultaneously apply methods including insertion-deletions of nucleotides/amino acids to give a full model of sequence evolution.

The key goals of this project are:

- i. Software package: A central aim of the project is to develop a package doing Bayesian statistical alignment for many sequences and performs a series of essential associated analyses: hypothesis testing for molecular clock, phylogeny, mutation rate, selection estimation, assessing ancestral sequences, and structure prediction.
- ii. Development of better biological models and cor-

responding algorithms: The TKF91 model allows only single insertions and deletions which is biologically irrelevant. Modelling long insertions and deletions is necessary to make statistical alignment practical.

iii. Structure prediction: Most of the comparative structure prediction methods are based on alignments, which might be misleading when the alignment is wrong. Statistical alignment will improve this.

iv. Comparative genomics: Since statistical alignment is based on a general model of molecular evolution including both insertions and deletions, issues related to the nature of these events can be addressed and parameterized.

Applications for the PDRA post are invited from researchers interested in working on this high-impact project. Candidates should have a relevant background and research experience in computer science, mathematics, statistical modelling and computational biology. A PhD, or equivalent research experience, would be required.

#### Application Procedure

Informal enquiries should be directed to [hein@stats.ox.ac.uk](mailto:hein@stats.ox.ac.uk). Further particulars are available from [jobs@stats.ox.ac.uk](mailto:jobs@stats.ox.ac.uk), or <http://www.stats.ox.ac.uk>. Applications should address the selection criteria, and also include a curriculum vitae and a list of publications together with the names, addresses, telephone, fax and e-mail details of two referees.

Applications should be submitted to Personnel Administration, Department of Statistics, 1 South Parks Road, Oxford OX1 3TG. Applications faxed to +44 1865 272595 or e-mailed to [jobs@stats.ox.ac.uk](mailto:jobs@stats.ox.ac.uk) are acceptable. Please always quote reference number: AM-05-011.

The closing date for applications is 12 noon, Friday, 4 November 2005.

Andrea Rocco <[rocco@stats.ox.ac.uk](mailto:rocco@stats.ox.ac.uk)>

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## USouthCarolina Bioinformatics

### POSTDOCTORAL POSITION IN BIOINFORMATICS

A postdoctoral position in bioinformatics is available immediately in the Department of Biological Sciences at the University of South Carolina (USC). The responsibilities of the position involve: (1) assisting the Bioinformatics

Core of the South Carolina INBRE (IDeA Networks of Biomedical Research Excellence) program in training and assisting South Carolina Researchers in using bioinformatics tools in their research; and (2) collaboration with Dr. Austin Hughes (<http://www.biol.sc.edu/faculty/hughes.html>) in bioinformatics research. INBRE is a 5-year NIH-funded program to enhance biomedical research in the state of South Carolina. For further information and to apply, contact Dr. Hughes at [austin@biol.sc.edu](mailto:austin@biol.sc.edu). The University of South Carolina is an Affirmative Action/Equal Opportunity Employer.

“Austin L. Hughes” <[austin@biol.sc.edu](mailto:austin@biol.sc.edu)>

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## UStellenbosch Genetics

Post Doctoral position available in the Department of Genetics, University Stellenbosch, South Africa (10 Okt 2005)

A Post Doctoral position in biotechnology is available in the Aquaculture Division, Department of Genetics, Stellenbosch University with the project title “Genetic improvement of the abalone *Haliotis midae*.”

*Haliotis midae*, known locally as ‘perlemoen’, occurs along the Western, Southern and Eastern shores of South Africa and is the only one of the six species that occurs in South Africa that is commercially exploited. *H. midae* displays a very slow growth rate, taking two to five years to reach market size. This is an obstacle in the profitable farming and global competitiveness of this species. In order to increase the productivity and the profitability of the commercial activity, a research program has been designed that makes use of the modern technology currently applied to other aquaculture species. The research program consists of three main parts: a) establishment of breeding programs with the assistance of genetic markers, b) generation of linkage maps and QTL identification, c) and the application of gene transfer technology.

The successful candidate will be primarily responsible for establishing gene transfer technology in the perlemoen, *Haliotis midae*. This is an extremely exciting new project that will establish a biotechnology platform for abalone in southern Africa. This will be the first biotechnology application to a species used for commercial application in Africa. Applicable knowledge in gene transfer system, especially in aquatic species (fish or shellfish) will be a strong recommendation. The

position is available for 2 years

Interested researchers are requested to send their CV to Dr. Rouvay Roodt-Wilding at roodt@sun.ac.za

Closing date: 7 November 2005.

Dr. Rouvay Roodt-Wilding Aquaculture Division Department of Genetics JC Smuts Building Room 213 University of Stellenbosch Private Bag X1 Matieland SOUTH AFRICA 7602 Tel: +27 (0) 21 808 5831 Fax: +27 (0) 21 808 5833

I'm not afraid of storms, for I'm learning to sail my ship. Louisa May Alcott

roodt@sun.ac.za

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## UWyoming LineageSpecificEvol

From December, 2005, the Liberles Research Group will have moved from University of Bergen (Norway) to University of Wyoming (USA). The research group works on detecting and characterizing lineage-specific evolution using a combination of experimental and computational approaches. The computational approaches include modeling, comparative sequence analysis, methods development, and database generation. The experimental approaches involve sequencing rapidly evolving genes from groups of closely related species, phylogenetic analysis including ancestral sequence reconstruction, and ultimately functional assays involving either cell culture or protein expression. A postdoctoral position is available for someone interested in computational or experimental evolutionary comparative genomics (broadly defined). If you are interested, please send me a cover letter, your c.v., contact information for two references, and your two favorite papers that you have published.

email: liberles@cbu.uib.no current group website: <http://www.cbu.uib.no/liberles/> David Liberles <David.Liberles@bccs.uib.no>

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## YaleU Morphologist

Two-year postdoctoral opportunity at for an evolutionary morphologist to study heretofore undescribed clades of the Phylum Placozoa with Leo Buss' group at the Department of Ecology & Evolutionary Biology and the Peabody Museum, Yale University, New Haven CT USA.

The Phylum Placozoa, the simplest and probably the basal-most extant metazoan, was once thought to be a monotypic taxon, comprised of the single species *Trichoplax adhaerens*. In recent years, it has become clear that the phylum is comprised of at least four different widely divergent clades.

The wide divergence is known, however, only from sequence and mt genome structure data. Differences in their morphology & ultrastructure, while surely present, have yet to be characterized. My lab has collected placozoan material from several localities and established multiple representatives of each of the known clades in laboratory culture. Thus, the material is on hand to address the problem.

While the post-doctoral position is intended for a morphologist, my lab group is also involved in ongoing field work and molecular work on aspects of placozoan diversity and candidates that might wish to add these areas of competence to that background in morphology are welcome to apply.

The position is expected to be funded by an internal Yale fellowship, which has an application (2 page) deadline of 9 December 2005. Applications to this deadline typically have a start date of 7/06 - 9/06, although some flexibility is possible in this regard. The salary is \$40K and comes with a \$2K contingency fund and with full medical benefits.

Candidates with prior SEM and fine structure experience are urged to contact [leo.buss@yale.edu](mailto:leo.buss@yale.edu) with their CV's.

[leo.buss@yale.edu](mailto:leo.buss@yale.edu)

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## WorkshopsCourses

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### Finland AdaptiveDynamics Jan10-14

CALL FOR PARTICIPATION Adaptive dynamics workshop, Tvärminne zoological station, Finland, January 10-14, 2006.

Adaptive dynamics is a mathematical framework for modelling evolutionary change by natural selection in complex nonlinear ecological systems. An ESF funded Adaptive dynamics workshop will be held in the Tvärminne zoological station, Finland, January 10-14, 2006. The grant from the European Science Foundation allows us to cover all local costs, including accommodation, meals, and transportation from Helsinki to Tvärminne and back. Due to limited resources, we cannot cover the airplane tickets for participants. Each participant is invited to give a talk in the workshop. The length of most talks will be 25 minutes and 5 minutes for discussion (30 minutes in total).

There are a few places (approximately 8) available to participate in the workshop. The participation of young scientist is encouraged. In case you are interested to participate, please send your contact details to [kalle.parvinen@utu.fi](mailto:kalle.parvinen@utu.fi), along with a few words about what you are doing and whether you would be ready to give a talk (and the topic of the talk). Decisions on participation will begin in the end of October and end when all places are filled.

For more details, see the workshop homepage: <http://www.math.utu.fi/research/bio/workshops/-addyn2006/> Best wishes,

Kalle Parvinen, Mats Gyllenberg, Eva Kisdi, and Stefan Geritz

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### Helsinki EcolResponseToClimateChange Nov3-4

#### FINAL ANNOUNCEMENT

Please distribute this advert freely within your institution.

WORKSHOP ADVERT: The Spatial Ecology programme, Department of Biological and Environmental Sciences (University of Helsinki), in conjunction with the EcoClim Project (Nordic Centre of Excellence), and the Department of Geology (University of Helsinki), is organising a workshop on the Ecological Responses to Climate Change at the Viikki Campus, southern Finland, on November 3 to 4, 2005.

Website: <http://www.helsinki.fi/bioscience/-spatialecology/workshop8.html> The goal of the meeting is to review climate related changes in Earths biota as they have been observed at different spatial, temporal, and ecological scales and to discuss the nature of the underlying processes, in particular the biological and technical reasons for scale-dependence (or lack thereof). Within this framework, main focal points are spatial patterns and rates of change. The meeting is organised around three scaling levels: coarse (global to subcontinental,  $10^4$  -  $10^7$  a, biomes, provinces), intermediate (regional,  $10^2$  -  $10^3$  a, ecosystems, communities) and fine (local, annual to decennial, populations).

Programme Thursday, November 3 08.30 - 09.00 Coffee 09.00 - 09.15 Opening words: ESA RANTA 09.15 - 09.55 RAY BRADLEY: Temporal and spatial scales of climate change in the Quaternary paleoclimatic record 09.55 - 10.35 ARNE MICHEELS: Simulating climatic effects of palaeovegetation changes in the Late Miocene using climate models 10.35 - 10.55 Coffee 10.55 - 11.35 TONY BARNOSKY: The problem of scale in detecting mammalian response to climate change in the fos-

sil record 11.35 - 12.15 FLAGSTAD: Environmental change and evolutionary events: Mammalian radiation over the past 20 million years 12.15 - 13.15 Lunch 13.15 - 13.55 MIKAEL FORTELIUS ET AL.: Temporal clustering of small versus large fossil mammal taxa at the continental scale 13.55 - 14.35 PASQUALE RAI: The 4th dimension of Bergmann's rule. The effect of Quaternary climate changes on the evolution of mammal body size 14.35 - 15.15 DAVID POLLY: Palaeophylogeography: the spatial and temporal scales of phenotypic adaptation 15.15 - 15.35 Coffee 15.35 - 16.15 JOHN WILLIAMS: Vegetational responses to novel climate regimes 16.15 - 16.55 HILARY BIRKS: Biological responses to rapid climate change at the last glacial - interglacial transition - patterns and processes 16.55 - 17.35 JOHN BIRKS: Biological responses to rapid climate change at the last glacial - interglacial transition - dynamics, turnover and rates of change

Friday, November 4 08.30 - 09.15 Coffee 09.15 - 09.55 OUTI SAVOLAINEN: Local adaptation during climate change 09.55 - 10.35 ELIZABETH HADLY: Genetic, morphologic and population responses of mammals to climatic change over hundreds to thousands of years 10.35 - 10.55 Coffee 10.55 - 11.35 BOB HOLT: Theoretical perspectives on evolutionary responses to climate change 11.35 - 12.15 PER LUND-

BERG: A general theory of population responses to climate change 12.15 - 13.15 Lunch 13.15 - 13.55 JOËL DURANT: Match-mismatch and food threshold in recruitment 13.55 - 14.35 KATJA ENBERG: Sustainable harvesting in variable environments 14.35 - 15.15 MIKE FOWLER: Estimating interspecific interaction strengths from noisy data series: empirical tests of classic theories 15.15 - 15.35 Coffee 15.35 - 16.15 NILS CHRISTIAN STENSETH: The dynamics of the Canadian lynx under climatically varying conditions 16.15 - 16.55 CHRIS THOMAS: Distribution responses to rapid climate change in the past 40 years 16.55 - 17.35 ANDREW ALLEN: The role of metabolic processes in long-term population dynamics 18.00 - late Workshop Dinner

Please contact Johan Kotze ([johan.kotze@helsinki.fi](mailto:johan.kotze@helsinki.fi)) if you want to attend this meeting. Attendance is free.

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Editor-in-Chief, Journal of Negative Results - EEB ([www.jnr-eeb.org](http://www.jnr-eeb.org)) <http://www.helsinki.fi/bioscience/-spatialecology/spatialecology.html> [www.helsinki.fi/science/globenet/](http://www.helsinki.fi/science/globenet/)

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## Instructions

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

To be removed from the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto: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](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as L<sup>A</sup>T<sub>E</sub>X files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

## 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  $\text{\LaTeX}$  do not try to embed  $\text{\LaTeX}$  or  $\text{\TeX}$  in your message (or other formats) since my program will strip these from the message.