
E v o l D i r

April 1, 2006

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

Forward

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

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

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Conferences

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Aarhus Bioinformatics Jun15-18

Bioinformatics Conference 2006 i Aarhus

15-18 June 2006 the SocBin Bioinformatics Conference 2006 takes place in Aarhus, hosted by Bioinformatics Research Center (BiRC), University of Aarhus. The venue of the conference is the Lakeside Lecture Theatres situated at the University campus in a beautiful, hilly park five minutes walk from downtown Aarhus.

The scientific programme covers a wide range of hot topics in bioinformatics within the following sessions: I Structure, II Transcriptional Regulation, III Cancer, IV RNA and V Genomics.

Confirmed Speakers

Session I: Structure Patsy Babbitt, University of California Nick Grishin, University of Texas Southwestern Luc Jaeger, University of California Malin Young, Sandia National Laboratories, USA

Session II: Transcriptional Regulation Nikolaus Rajewsky, New York University Gary Stormo, Washington University School of Medicine Zhiping Weng, Boston University Uwe Ohler, Duke University.

Session III: Cancer Cameron Brennan, Cornell Medical College Mattias Höglund, Lund University Daniel Rhodes, University of Michigan Pål Sætrom, Interagon, Norway

Session IV: RNA Sean Eddy, Washington University St. Louis Thomas R. Gingeras, Affymetrix Inc. John Mattick, University of Queensland

Session V: Genomics Andy Clark, Cornell University Rasmus Nielsen, University of Copenhagen Adam Siepel, Cornell University Simon Tavaré, University of Southern California

Keynote Speakers Peer Bork, EMBL Heidelberg Michael Lynch, Indiana University

Important Dates/Deadlines Deadline for early registration 15 April, 2006 Low cancellation administration fee 15 April, 2006 Deadline for submitting abstracts 1 May, 2006 Notification of acceptance of abstracts 15 May, 2006 Deadline for late registration 31 May, 2006 Conference dates 15-18 June, 2006

Further information (confirmed programme, registration, accommodation etc.) is available at <<http://www.birc.au.dk/bioinformatics2006/>> <http://www.birc.au.dk/bioinformatics2006/>

Kind Regards

Mikkel H. Schierup

Mikkel Heide Schierup <mheide@birc.dk>

BejaiaAlgeria EvolEcol Nov7-9

Dear all, Please find below an announcement for an Ecology meeting in the nice city of Bejaïa, Algeria.

The University A.MIRA of Bejaïa (Algeria), the Faculty of Nature and Life Sciences and the Laboratory of Ecology & Environment organize the first :

Mediterranean Meetings on Ecology in Bejaïa, 7- 9 november 2006

Objectives This seminar aims to assess the state of knowledge and the impact of human activities on the various ecological aspects (systematics, chorology, biogeography...) of plant and animal species, natural populations and their habitats within the diverse ecosystems (wetlands, forests, maquis, agro-ecosystems, steppes and deserts) throughout the Mediterranean geographical area. These meetings will be also an opportunity to exchange ideas and views concerning methodologies of analyses, inventories, cartographies and development of disciplines such as biogeography, conservation biology and natural spaces management. Alongside the communication sessions, workshops will be organized about the following topics: 1/ Rehabilitation of ecology, 2/ Projects of inventories, atlases and cartographies, guides, floras and faunas, 3/ Necessity of a scientific journal.

Retained topics : - Ecology of species, - Taxonomy and Phylogeny, - Population Biology and Genetics, - Modelization and management in ecology, - Conservation methods and Ecosystem planning.

Calendar 05 june 2006 : Reception of communication abstracts. 20 june 2006 : Notification to authors. 15 sept. 2006 : Reception of communication final versions (texts to be published in the Proceedings).

Presentation Abstracts of communications should be presented in at most one page using Word format and Times New Roman, characters. Abstracts should include: - Title of communication (14 bold), -Names and surnames of the authors underlining the communicating author (10 regular), - Six key words at most, - Text written in english or french (12 regular, 1.5-spaced). The final complete versions of accepted communications should not exceed 8 pages presented following the above mentioned guidelines and forwarded as diskettes or attached e-mail files.

Correspondance :

Pr. MOALI Aïssa Faculté des Sciences de la Nature et de la Vie. Université A. Mira de Béjaïa. Targa Ouzemmour. 06000 Béjaïa - Algérie. Tel : 213 34 21 47 62 213 71 72 23 08 Email : remedeco@yahoo.fr rencontreecologie06@yahoo.fr

errol.vela@free.fr

FtWarden Washington Evo-WIBO Apr21-23 2

This is a reminder that the registration deadline for the 2nd Evo- WIBO meeting of Pacific Northwest evolutionary biologists is Monday, March 13. The meeting is scheduled for the weekend of April 21-23 at Fort Worden State Park in Port Townsend, Washington.

We have had a great response thus far, with participants from Oregon, Washington, Idaho, Montana, and Alaska, but there are a few registration slots left for those who are interested.

More information and registration details 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

HalleGermany POPBIO2006 May24-27

Herewith we would like to remind you on the *deadline for submission of talks/posters and the deadline for reduced fee registration (31.3.2006)* for the

*19th Annual Meeting of the Plant Population Biology Meeting of the Ecological Society of **Germany**, **Switzerland** and **Austria** (GfOe),*

taking place in Halle, Germany, from 24 May to 27 May 2006 organized jointly by the UFZ-Centre for Environmental Research and the Geobotanical Institute of the University of Halle.

The annual meeting is being held in English and usually attended by more than one hundred people from all over Europe. Priority is given to young researchers to present results from their PhD theses. The focus of the meeting in 2006 is on interactions of plants with

other species, recognizing that plants have to cope with a large number of competitors, herbivores, pathogens and symbionts. Therefore, to understand the population biology of plants, botanist would have to broaden their scope and incorporate these interactors in their studies. Presentations from the whole field of plant population biology are welcome.

Keynote speakers include: - *Claire de Mazancourt*, Imperial College at Silwood Park - *Jacqui Shykoff*, CNRS-Paris - *Jürgen Kroymann*, Max Planck Institute for Chemical Ecology, Jena - *Amots Dafni*, University of Haifa

Please distribute this invitation freely among your colleagues ! Please visit the PopBio2006-webpage at <http://www.ufz.de/popbio2006> for further information and registration.

Looking forward seeing you,

Alexandra Erfmeier & Isabell Hensen – University of Halle

Daniel Prati, Harald Auge & Walter Durka – UFZ

email to: PopBio2006@ufz.de

InstZooLondon IslandEvol Apr26

The Centre for Ecology and Evolution in London and the Centre for Population Biology, Imperial College, are running a one day symposium, Evolution and Ecology on Islands, at the Meeting rooms, The Institute of Zoology, London, on Wednesday 26th April.

Speakers include: George Turner (Hull), Brent Emerson (UEA) Lindell Bromham (Sussex), Alfried Vogler (NHM), Sam Berry (UCL), Fred Rumsey (NHM), Ally Phillimore (Imperial), Victoria Herridge (UCL), Shai Meiri (Imperial) & Paul Pearce Kelly (Insitute of Zoology). A current programme can be found at <http://www.ucl.ac.uk/~ucbtcee/cee/events.html> The event starts at around 9:30 am and will run through to a drinks reception at 5:30. Participants are welcome to display posters at the drinks reception. A prize will be awarded to the best student poster.

Registration is not mandatory, but it would be helpful if you could register with Mark Carine on <<mailto:m.carine@nhm.ac.uk>> m.carine@nhm.ac.uk, so that we can cater appropriately for tea and coffee. Entry will either be free or at minimal cost to cover tea/coffee, and payable on the day.

If you are intending to present a poster, please also email Mark so we can book the appropriate number of boards for posters.

The meeting rooms of the Institute of Zoology are roughly opposite the main entrance to the zoo. Access to the Meeting Rooms is from the Outer Circle, Regent's Park. Nearest bus - No. 274; Underground station - Camden Town.

(Dr) Greg Hurst Reader in Evolution and Ecology Dept Biology, University College London 4 Stephenson Way London NW1 2HE UK +44 20 76795072 (t) +44 20 76795052 (f) <http://www.ucl.ac.uk/%7Eucbtghu/>

g.hurst@ucl.ac.uk g.hurst@ucl.ac.uk

Marseilles 10thEvolBiol Sep20-22

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

Deadlines Early registrations: 1st April, 2006!

We remember you that registrations and abstract submissions for the 10th Evolutionary Biology Meeting at Marseilles are on line. Also we are looking forward to receiving your submissions and registrations.

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

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

Nadège Bardiot

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 Marseilles <http://www.up.univ-mrs.fr/evol-cgr/> egee@up.univ-mrs.fr

Marseilles 10thEvolBiol Sep20-22 2

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

Deadlines Early registrations: 1st April, 2006! This is in 4 days!!

Registration form, Abstract and Payment are due before Sunday (Saturday 24:00) to be considered as early registered.

We remember you that registrations and abstract submissions for the 10th Evolutionary Biology Meeting at Marseilles are on line. Also we are looking forward to receiving your submissions and registrations.

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Montreal RECOMB ComparativeGenomics Sept24-26

CALL FOR PAPERS

Deadline: June 5, 2006

Fourth Annual RECOMB Satellite Meeting on Comparative Genomics

September 24-26, 2006, Montreal, Canada

MEETING WEBSITE: <http://www.crm.umontreal.ca/Genomics06/>

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

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

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

SUBMISSIONS:

Papers should not exceed 10 pages (all inclusive) and must be submitted via the conference website <http://www.crm.umontreal.ca/Genomics06/>. Submis-

sions must be received in electronic form by 11:59pm (Montreal local time) of June 5th, 2006.

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

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

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

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

REGISTRATION:

Registration will be available soon at the conference website <http://www.crm.umontreal.ca/Genomics06/>
PROGRAM COMMITTEE CO-CHAIRS:

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

PROGRAM COMMITTEE:

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

Nadia El-Mabrouk <mabrouk@iro.umontreal.ca>

Prague EvoDevo Aug16-19

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Third announcement:

*European Society for Evolutionary Developmental Biology *

First and founding meeting

*Prague**, 16-19 August 2006*

* *

Call to participate

You are invited to participate in, and contribute to, the First and Founding Meeting of the European Society for Evolutionary Developmental Biology in Prague, August 16-19, 2006. The scientific program will consist of plenary sessions, symposia, contributed talks and a poster session, see our website: [*http://natur.cuni.cz/evodevo/*](http://natur.cuni.cz/evodevo/) *Call for abstracts* You are invited to submit an abstract for a contributed talk or poster. Online submission is now possible. Please submit your abstract before May 1, 2006

Registration The early registration fee for students is EUR120,-, for non-students EUR200,- and for partners EUR25,-. Registration is now possible and the deadline for early registration is 1 May 2006.

Accommodation The reservation of accommodation is now possible and the deadline for reservations is June 15, 2006.

The organizing committee looks forward to seeing you in Prague!

Keynote speakers:

- Philippe Janvier /(Paris, France)/
- Pat Simpson /(Cambridge, U.K.)/
- Günter Theissen /(Jena, Germany)/
- Hervé Philippe /(Montreal, Canada)/
- Jukka Jernvall /(Helsinki, Finland)/
- Barbara Gravendeel /(Leiden, the Netherlands)/

Symposia:

- */"Evo-Devo History/*"/ (organizer: Scott Gilbert)
- */"Homeobox genes in evolution and development"/* (organizers: Dave Ferrier, Jordi Garcia Fernandez)
- */"Modularity"/* (organizer: Chris Klingenberg)
- */"*Stem groups and the integral role of paleontology in evolutionary developmental biology*"/* (organizers: Graham Budd, Phil Donoghue)
- */"Head Evo-Devo"/* (organizers: Lennart Olsson, Michael Depew)
- */"Insect Evo-Devo"/* (organizer: Urs Schmidt-Ott)
- */"Plant Evo-Devo"/* (organizer: Günter Theissen)
- */"Evolutionary Novelty"/* (organizers: Gerhard Schlosser, Shigeru Kuratani)
- */"Lamprey, shark, and vertebrate Evo-Devo"/* (organizers: Didier Casane, Sylvie Mazan)

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

- */“Late development Evo-Devo”/ *(organizers: Eckhard Witten, Ann Huysseune)

- */“Limb Evo-Devo”/* (organizer: Michael Richardson)

*Information: *

* <http://natur.cuni.cz/evodevo/> * friet-son.galis@gmail.com

vdooren@rulsfb.leidenuniv.nl

St Andrews PhDEvolBiol Sept5-8

Dear Students of Evolutionary Biology,

I write to you as the chair of this year’s committee responsible for the organisation of the 12th Annual European Meeting of PhD Students of Evolutionary Biology (EMPSEB XII).

This year the conference will be better than ever and is to be hosted in Scotland, in the historic scenic town of St Andrews. The dates of the conference are September 5th-8th, 2006, with arrival and departure on the 4th and 9th respectively.

The conference offers students the chance to present their work, it is a conference run by students for students! There will also be 7 invited expert speakers and a big meal and traditional scottish dance on the last night, with prizes for the best presentations!

We welcome all PhD students and I encourage you to spread the news to all your friends around Europe. There is a poster that can be downloaded from our website, please put a copy up in your department.

Please take a look at our website <http://www.biology.ed.ac.uk/public/conferences/evolbiol2006/> Registration opens on May 1st.

The costs are yet to be finalised. We are aiming for a total cost per delegate of £300, which will cover all your costs (accommodation, food, conference costs, and travel to and from Edinburgh airport to St Andrews). The cost however may be higher, at around £350. Details will be confirmed later. There is a newsletter which you can sign up to on the website for all the latest developments.

Cheers

Max Burton Committee Chair EMPSEB XII University of Edinburgh

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

Stockholm OriginOfLife May8-11

2ND ANNOUNCEMENT -

CONFERENCE: ORIGIN & DISTRIBUTION OF LIFE IN THE UNIVERSE - A Nordic Perspective

Royal Swedish Academy of Sciences Stockholm, Sweden May 8-11, 2006

<http://astrobiology.molbio.su.se> The Swedish Astrobiology Network is pleased to announce the 2006 Nordic Astrobiology Conference, to be held at the Royal Swedish Academy of Sciences in Stockholm May 8-11, 2006.

The conference is sponsored by the Royal Swedish Academy of Sciences, the Swedish National Space Board, the Nordic Institute for Theoretical Physics (Nordita) and the Wenner-Gren Foundations. The conference will begin with an open public lecture by Dr. Chris McKay, and sessions based around the major conference themes will begin with Keynote presentations.

Geosciences: Chris McKay, NASA Ames Research Center, USA Aivo Lepland, Geological Survey of Norway

Space Sciences: Pascale Ehrenfreund, Leiden Univ, Netherlands Hans Rickman, Uppsala Astronomical Observatory, Sweden

Biological Sciences: Eors Szathmary, Collegium Budapest, Hungary Karsten Pedersen, Gothenburg University, Sweden

In conjunction with the conference, the journal Astrobiology will produce a special issue comprising peer-reviewed contributions from participants.

If you are interested in joining us in Stockholm, please register your interest at our website:

<http://astrobiology.molbio.su.se> There is no conference fee, and we are currently accepting abstracts for both oral and poster presentations. We welcome contributions in any of the three broad areas above and look forward to seeing you in Stockholm.

Please note: The deadline for registration & abstract submission is 31 March 2006. Also, we recommend that

you book accommodation in good time. We have made a limited number of block bookings at hotels that are near the Royal Academy, but these will be filled on a first-come first-served basis.

Anthony Poole <ant@molbio.su.se>

StonyBrookU SSESSBASN2006 Jun23-27

Evolution 2006 Meeting at Stony Brook University, June 23 - 27, 2006.

“Evolution 2006,” the joint meeting of the Society for the Study of Evolution, the Society of Systematic Biologists, and the American Society of Naturalists, will be hosted by the Department of Ecology and Evolution at Stony Brook University, New York, USA from June 23 to 27, 2006. Pre-meeting events are planned for June 22 and 23, and social events will take place on the evenings of the meeting. Please visit <http://life.bio.sunysb.edu/ee/sse2006> or contact the meeting coordinator, Annie Green (sse2006@life.bio.sunysb.edu) or the co-organizers, Michael A. Bell (mabell@life.bio.sunysb.edu) and Massimo Pigliucci (Massimo@life.bio.sunysb.edu), for further information.

Michael A. Bell, Professor Department of Ecology and Evolution Stony Brook University Stony Brook, NY 11794-5245, USA

“Michael A. Bell” <mabell@life.bio.sunysb.edu>

StonyBrookU SSESSBASN2006 Jun23-27 UndergradAttendance

DIVERSITY AT SSE/SSB 2006:

Call for applications for undergraduates of diverse backgrounds to attend the 2006 meeting of the Society for the Study of Evolution/Society of Systematic Biologists

For the fourth consecutive year, the Undergraduate Diversity at SSE/SSB program, funded by the Undergraduate Mentoring in Environmental Biology (UMEB) program at NSF, will take place again at the 2006 meeting this June in Stony Brook, New York and we are now

accepting applications. The program will send 15 undergraduates from the US and Puerto Rico to attend the SSE/SSB meetings to present posters and interact with graduate student, postdoc and faculty mentors. The application deadline is April 1, 2006. Applications will consist of a title, author line and abstract of the poster to be presented by the undergraduate; a one or two paragraph (no more than 1 page) statement of academic interests and career goals and of how attending the Evolution meetings will help meet these goals; and one letter of recommendation from the undergraduate’s research advisor. The letter should indicate how inclusion of the student will increase diversity of the group participants and whether or not the student will be attending medical school. All materials should be submitted as pdf files and emailed to Rich Kliman at rmkliman@cedarcrest.edu. Applications will be accepted only from students registered or very recently graduated from U.S. institutions, including Puerto Rico (i.e., having finished classes during the winter or spring semesters before the meeting) and traveling to the meeting from within the US. Students demonstrating a need for funds to attend SSE/SSB will be given preference, and will be selected so that as a group, they will increase cultural diversity among undergraduates at Evolution meetings.

For further information, please see: <http://www.oeb.harvard.edu/faculty/edwards/community/-application.html>

Contact one of the program organizers for more information:

Scott V. Edwards, Harvard University (sedwards@fas.harvard.edu) Richard Kliman, Cedar Crest College (rmkliman@cedarcrest.edu)

Rmkliman@cedarcrest.edu Rmkliman@cedarcrest.edu

UBuffalo EGLME May6

Second announcement for the

Eastern Great Lakes Molecular Evolution Meeting University at Buffalo, May 6 2006

We are requesting that abstracts for posters or talks for the meeting be submitted until the end of this month, March 2006. This will allow us to select a number of platform presentations and allow the remainder of the participants to have enough time to prepare their work in poster format.

Below follows the first advertisement for this meeting:

The yearly Eastern Great Lakes Molecular Evolution Meeting, will be held at the Center for the Arts, University at Buffalo, on Saturday May 6, immediately after the end of the school year in both the USA and Canada.

This one-day meeting normally attracts around 100 students, postdocs, and faculty from both the US and Canada and has been held ever year in cities surrounding the great lakes. This year's meeting will be held in Buffalo, centrally located between Toronto, Guelph, McMaster, Waterloo, Cornell, Rochester, and Pittsburgh.

A number of talks will be selected from submitted abstracts, and the remaining abstracts will be presented as posters. The meeting runs all day, with the evening being dedicated to the poster session. Coffee, tea, and lunch will be provided and there will be no registration fee. Dinner is not scheduled but there are a variety of restaurants in close proximity to the meeting venue.

If you want to submit a talk or a poster please send a title and abstract (max 250 words) to one of the meeting organizers:

Dr. Antonia Monteiro (monteiro@buffalo.edu), Dr. Derek Taylor (djtaylor@buffalo.edu), and Dr. William Piel (wpiel@buffalo.edu).

Antónia Monteiro <monteiro@buffalo.edu>

UMichigan YoungScientists May6

UNIVERSITY OF MICHIGAN YOUNG SCIENTISTS SYMPOSIUM: MICROEVOLUTIONARY PROCESSES UNDERLYING BIODIVERSITY

On Saturday May 6, 2006, The Ecology and Evolutionary Biology Department at the University of Michigan will sponsor the University of Michigan Young Scientists Symposium. This one-day symposium is focused on the topic of microevolutionary processes underlying biodiversity. Eight outstanding young scientists will present current research on the genetics and evolutionary processes underlying phenotypic diversity, reproductive isolation and speciation across a wide range of plants and animals:

Hopi Hoekstra (Assistant Professor, UCSD) "Molecular basis of complex color pattern in beach mice: from QTL to QTN"

Kirsten Bomblies (Postdoctoral Fellow, Max Planck Institute) "Postzygotic reproductive isolation in *Arabidopsis thaliana*."

Scott Rifkin (Postdoctoral Fellow, Harvard) "The impact of mutation, migration, and selection on intraspecific differences in gene expression."

Matt Hahn (Assistant Professor, U. of Indiana) "Creation, extinction, and evolution of gene families in primates"

Daniel Bolnick (Assistant Professor, U of Texas - Austin) "Testing factors that promote and constrain phenotypic diversity in sticklebacks"

Briana Gross (Graduate Student, U. of Indiana) "The origin of *Helianthus deserticola*: hybridization and speciation"

Patrik Nosil (Graduate Student, Simon Fraser University) "Microevolutionary processes and the formation of new species"

Daven Presgraves (Assistant Professor, U. of Rochester) "Genetics and molecular evolution of hybrid incompatibilities in *Drosophila*"

The symposium will end with a plenary talk ("Allele frequency and the size of allelic effects") by Dr. Andrew Clark of Cornell University, a leader in the field of evolutionary genetics.

Registration is FREE and INCLUDES DINNER on Saturday night, but space is limited. To register, see <http://lessons.umm.umich.edu/2k/yss/registration> . Register early - applications will be accepted in the order in which they are received. Graduate students are invited to join speakers for lunch on Saturday and can express preferences on the registration form.

For more information, please see the Symposium website: <http://sitemaker.umich.edu/yss2006>.

Organizing committee: Jianzhi George Zhang jianzhi@umich.edu, Priscilla Tucker ptuck@umich.edu, Patricia Wittkopp wittkopp@umich.edu, Ondrej Podlaha opodlaha@umich.edu

wittkopp@umich.edu wittkopp@umich.edu

Vancouver Speciation July21-24

SECOND ANNOUNCEMENT

Genetics of Speciation

American Genetics Association Annual Symposium,
Co-sponsored by Molecular Ecology

Date: July 21-24, 2006 Location: Vancouver, British
Columbia, Canada

Website: <http://www.theaga.org/agasymposium/-index.html>
Organizer: Loren Rieseberg,
lriesebe@indiana.edu

The last decade has witnessed a transformation in our understanding of speciation genetics. This conference will attempt to synthesize what we know and to suggest promising avenues for further research. The meeting will include invited and contributed talks, as well as poster sessions to encourage greater involvement of symposium participants. The full program is now available on the meeting website.

Funds are available for student/postdoc travel and registration to promote broad participation. Travel grant applications are due April 15, 2006.

The symposium will be held at the University of British Columbia, Vancouver, which is next to the Pacific Ocean and the coastal mountains. Time will be set aside Sunday afternoon (July 22) so that symposium participants can enjoy the Vancouver area.

We hope you will join us.

Loren Rieseberg, Organizer

Invited Speakers: Allen Orr (Key Lecture) John Avise (ME Lecture) Rochester, USA Irvine, CA Richard Abbott St. Andrews, UK Keith Adams Vancouver, Canada Louis Bernatchez Quebec City, Canada Jerry Coyne Chicago, USA Salvatore Cozzolino Naples, Italy Michael Doebeli Vancouver, Canada Sergey Gavrilets Knoxville, USA Scott Hodges Santa Barbara, USA Darren Irwin Vancouver, Canada Chris Jiggins Edinburgh, UK Mark Kirkpatrick Austin, USA Leonie Moyle Bloomington, USA Mohammed Noor Durham, USA Bret Payseur Madison, USA Katie Peichel Seattle, USA Daven Presgraves Rochester, USA Dolph Schluter Vancouver, Canada Maria Servedio Chapel Hill, USA Kerry Shaw College Park, USA Willie Swanson Seattle, USA John Willis Durham, USA Chung-I Wu Chicago, USA Sara Via College Park, USA

Visit the website for more information

Loren Rieseberg <lriesebe@indiana.edu>

WoodsHoleMA EvolBehavior May27

Fourth Annual Woods Hole Behavior Symposium

Saturday, May, 27, 2006 10 AM - 6 PM

Lillie Auditorium Marine Biological Laboratory Woods Hole, MA Sponsored by the Marine Biological Laboratory and the Boston University Marine Program

Call for papers

We welcome presentation on any aspect of animal behavior. Please submit an abstract for a talk (12 min plus 3 min for questions) or for a standard-sized poster by April 30, 2006 as an attached word file to <mailto:ggerlach@mbl.edu>ggerlach@mbl.edu, (subject: Woods Hole Behavior symposium abstract).

Please indicate your name, affiliation, preference (talk or poster), title of the presentation and any special needs.

A powerpoint projector and PC laptop will be provided.

Prizes will be awarded for the best undergraduate and graduate student presentations.

Registration (at the entry): PIs: \$15 Postdocs \$10 students \$5 This will defray some costs for coffee breaks and student prizes.

For more information contact

Gabi Gerlach, MBL (<mailto:ggerlach@mbl.edu>ggerlach@mbl.edu)

Co-organizer: Hans Hofmann, Harvard

Visit <<http://www.mbl.edu/research/labs/gerlach/-index.html>> <http://www.mbl.edu/research/labs/-gerlach/index.html>> for an updated program and directions

Gabi Gerlach <ggerlach@mbl.edu>

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CEH UK EvolGenetModelling

Hi all, I have a PhD position available for someone interested in evolutionary genetics and modelling. Formal description (as advertised on www.findaphd.com) below. If you would like further details or want to discuss this PhD with me please get in touch. Unfortunately, due to the source of funding it is available only to British citizens/residents. best wishes Justin

Life-history determinants of evolvability.

This project will involve the construction of individual-based population models to explore the interaction between life-history characteristics (such as dispersal, age at first reproduction, pattern of senescence, mating system) and evolutionary potential. The work will (1) seek to establish how different life-history characteristics influence the ability of a population to adapt following an environmental change and (2) will determine whether the need for greater evolvability in a changing environment can itself drive the evolution of these life-history characteristics. A suitable candidate would have a keen interest in environmental change and evolutionary biology and have programming skills in C, C++ or Pascal. It is anticipated that the project will utilise high performance computing (parallel processing). The student will be supported by a BBSRC grant and will be based at Aberdeen starting in October 2006. Please contact Justin Travis for further details (jmjt@ceh.ac.uk).

jmjt@ceh.ac.uk jmjt@ceh.ac.uk

Copenhagen SocialEvol

PhD FELLOWSHIPS IN SOCIAL EVOLUTION, COPENHAGEN, DENMARK

The Centre for Social Evolution (CSE) at the University of Copenhagen has 2-3 vacancies for Ph.D. fellowships to study aspects of social evolution in insect societies, starting the 1st of June 2006 or as soon as possible thereafter.

CSE has six major research programs, which focus on mating system evolution, chemical communication, social parasitism, disease, invasive ants and the evolution of symbiotic interactions. Any of these topics is eligible and interdisciplinary combinations are encouraged. See <http://www.bi.ku.dk/CSE/> for further details on CSE's research, on staff and postdoctoral and Ph.D. fellows involved, and for relevant publications.

Depending on the topic concerned, successful candidates will be supervised by one or several of the senior staff of CSE: Jacobus J. Boomsma, Patrizia D'Ettore, David R. Nash and Jes S. Pedersen. Collaborative work with CSE's partner group at the Royal Veterinary and Agricultural University of Copenhagen directed by J. Eilenberg is also a possibility.

Candidates should possess a M.Sc. or equivalent degree in evolutionary biology, population biology, animal behaviour or a related field and should have demonstrated excellence in terms of one or several publications. Experience with DNA techniques, immunity assays, modelling or GC/MS will be an advantage.

Candidates who would like to be considered for one of

these posts are invited to send a CV, pdfs of published or accepted manuscripts and a one-page declaration of interest, outlining what kind of questions they would like to address and how their educational background and expertise would enable them to embark on this work in a focused and productive way, preferably by e-mail to:

Mai Valentin Nielsen Secretary, Centre for Social Evolution Department of Population Biology, Institute of Biology Universitetsparken 15, DK-2100 Copenhagen, Denmark e-mail: MVNielsen@bi.ku.dk

For informal inquiries please contact CSE's director, Professor Jacobus J. Boomsma (JJ-Boomsma@bi.ku.dk).

The deadline for receipt of documents is 24 March 2006. Declarations of interest and CV's will be reviewed by a committee of senior members of CSE by mid April to identify candidates that will be invited for interview and to submit a full Ph.D. proposal.

DRNash@bi.ku.dk

ETHZurich InsectBehaviour

We are seeking a motivated and creative PhD Student in Entomology with a Diploma degree in Biology or related University Degree. The PhD project will focus on insect behaviour and its genetic basis.

To achieve successful biological control, fitness of mass-reared and released parasitoid wasps should be high. Mechanisms leading to optimal or suboptimal sex ratios (so-called single locus complementary sex determination) shall be investigated in a parasitoid of practical relevance in vegetable farming, occurring naturally in Switzerland. Desirable is a high proportion of (diploid) females and a minimal proportion of diploid males.

Methods will include field collection, establishment and rearing of laboratory subpopulations, quantification of fitness and mate choice behaviour, as well as elucidation of genetic diversity using molecular tools (microsatellite markers). Results are expected to be relevant for basic understanding of sex allocation and mating structures in parasitoids, as well as for application in biological control.

Languages spoken in the group are mainly German and English.

Education: Diploma degree (or MSc) in Biology or re-

lated University Degree. Start: Position open until filled.

Send curriculum vitae, certificates and addresses with phone numbers of three references to:

Prof. Dr. Silvia Dorn Reference Code PhD-InsBeh
Institute of Plant Sciences/ Applied Entomology ETH
Zurich Schmelzbergstr. 9 / LFO CH - 8092 Zurich

silvia.dorn@ipw.agrl.ethz.ch

For further information contact Dr. Dominique Mazzi (dominique.mazzi@ipw.agrl.ethz.ch, phone +41 44 6323936)

Our homepage: www.em.ipw.agrl.ethz.ch

ETH Zurich HostParasite Genomics

Keyword: ETHZurich.EcolGenomics

The Institute of Integrative Biology at ETH Zurich - Experimental Ecology Group - is looking to fill the positions of a

1 PhD student Ecological Genomics of host-parasite interactions

The anticipated project uses the recently developed genomic resources for a large pollinator, the bumblebee, *Bombus terrestris*, as a technical framework for this work. Among other things, the aims are to identify further genes involved in the interaction of different *Bombus* species with their parasites, to refine methods for tracing relevant genes in populations and to eventually analyze the genetic dynamics of host-parasite interactions in the field. The ideal candidate has experience in molecular genetics, genomics, the use of data banks and bioinformatics, combined with a vivid interest in evolutionary biology, population genetics and ecology. The project will be embedded in an active research group with long-term experience of the system.

Preferred starting date is summer-autumn 2006. Please send applications (CV, Publication list, Names of referees) to Prof. P.Schmid-Hempel, ETH Zurich, Institute of Integrative Biology, ETH-Zentrum CHN, CH-8092 Zurich (by 1 May 2006 or until filled). Further information on ETH, the group, or life in Zurich can be obtained from www.eco.ethz.ch and by email (psh@env.ethz.ch).

Prof. Paul Schmid-Hempel Institute of Integrative Biology (IBZ) Experimental Ecology ETH-Zentrum

CHN, K11 CH-8092 Zurich

ph: +41 (0)44 633 6048 / 6033 fax: +41 (0)44 632 1271 psh@env.ethz.ch www.eco.ethz.ch paul.schmid-hempel@env.ethz.ch paul.schmid-hempel@env.ethz.ch

Helsinki EvolGenetics

PhD position in Evolutionary Genetics, Helsinki, Finland.

A PhD position is available in Ecological Genetics Research Unit (see <http://www.helsinki.fi/bioscience/ecology/merila.htm> for more details) at the University of Helsinki, Finland, as a part of the recently funded Finnish Centre of Excellence in Evolutionary Genetics and Physiology which also includes the research groups of Professor Craig Primmer (see <http://users.utu.fi/-primmer>) and Professor Mikko Nikinmaa (http://www.sci.utu.fi/biologia/fysiologia/nikinmaa_eng.htm).

The PhD-project will focus on inheritance, selection and evolution of quantitative traits in the Siberian jay (*Perisoreus infaustus*) on the basis of data collected during a long-term (1974-) population study of individually marked birds. All birds have been also collected for blood and genotyped for nine microsatellite loci - also this data is available for exploitation.

The project allows also interactions and collaborations with people working with development new analytical methods (e.g. <http://www.rni.helsinki.fi/~boh/>) for analyses of quantitative traits, as well as with people working with molecular population genetics, genomics and quantitative genetics in our group.

The successful applicant will be expected to have a great deal of scientific enthusiasm and at least some inclination towards numerical methods (lot of the work will be analyses conducted with 'animal model' and perhaps with Bayesian approaches).

Informal inquires and applications should be addressed to Prof. Juha Merila (juha.merila@helsinki.fi). Applications should include a full CV, a statement of previous experience as well as an outline research interests and names and contact details of two referees. Review of applications will commence at March 20 2006 with the preferred starting date prior to May 2006. The funding is guaranteed up to 4 years. The salary is settled according University of Helsinki regulations (ca. 1800 euro/month).

Juha Merila Ecological Genetics Research Unit Department of Biological and Environmental Sciences PO Box 65 (Biocenter 3, Viikinkaari 1) FIN-00014 University of Helsinki Finland

Fax: +358-9-191 57 694

juha.merila@helsinki.fi juha.merila@helsinki.fi

ImperialCollegeLondon HostParasite

Evolution in host-parasite systems

Jacob Koella (Imperial College London, Division of Biology, Silwood Park Campus, Ascot SL5 7P, UK).

A PhD fellowship is available as of October 2006 (unfortunately only for UK citizens or EU citizens that have been resident in the UK for the past 3 years)

The specifics are quite open, but any project will certainly deal with evolution in host-parasite systems. Theoretical and experimental (lab-based) work is possible. Experiments would be on the interactions between malaria and mosquitoes or would involve experimental evolution of mosquitoes and microsporidians and/or ascogregarines. Possible projects include:

Evolution of horizontal and vertical transmission Conflicts between parasites with different transmission strategies The role of multiple infections in the evolution of virulence Evolution of the mosquito's immune response against malaria Interactions between malaria and microsporidians in determining the mosquito's resistance to malaria

Please contact me at jkoella@gmail.com for more details.

- Jacob Koella

Division of Biology Imperial College London Silwood Park Campus Ascot, Berkshire SL5 7PY United Kingdom

Tel: ++44 20 7594 2254

jkoella@gmail.com

GRADUATE POSITION IN MOLECULAR ECOLOGY OF GROUSE AT KANSAS STATE UNIVERSITY. One graduate assistantship is available at Kansas State University to investigate the impacts of wind power development on Greater Prairie-chickens. Field research will involve live-trapping, behavioral observations, radio-telemetry and molecular ecology of grouse in the Flint Hills region of eastern Kansas. The emphasis of this project will be population genetics and breeding biology based on microsatellite markers. Responsibilities will include: locating suitable study sites, preparing reports, participation and coordination of field research, and working with industry partners. Applications will be accepted at a PhD level; qualified applicants should have a minimum of a Masters of Science in Biology and competitive GPA and GRE scores. Previous experience with avian field research techniques, molecular lab work, statistical software, and organization of field projects is desirable. The annual stipend for graduate positions will be \$21,000 per year including tuition. Information on graduate programs at K-State and current projects is available at www.ksu.edu/wiselylab. The start date will be August 15th, 2006. Interested individuals should send a cover letter outlining experience and research interests, a detailed curriculum vitae, unofficial copies of university transcripts and GRE scores, and contact information for three references to DR. SAMANTHA WISELY, Division of Biology, 232 Ackert Hall, Kansas State University, Manhattan, KS 66506-4901 (PH: 785-532-0978, FX: 785-532-6653, EM: wisely@ksu.edu). Applications by e-mail are welcome, and will be accepted until the position is filled.

Dr. Samantha M. Wisely Assistant Professor, Wildlife Biology Division of Biology Ackert Hall Kansas State University Manhattan, KS 66506-4901 Office:785.532.0978, Lab:785.532.6413 Fax:785.532.6653, email: wisely@ksu.edu <http://www.ksu.edu/wiselylab> wisely@ksu.edu

LeidenU EvolBirdsong

Two PhD positions available

Closing date: 30 April 2006.

Behavioural Biology, Institute of Biology, Leiden University

BIRDSONG, SPEECH AND LANGUAGE Human speech and birdsong share several striking similarities

which are such that learned birdsong is considered to be the closest animal analogue to language and both linguists and biologists have suggested that results from one field could yield hypotheses, or even answers to questions, for the other. The following two projects, for which we seek candidates, also aim to contribute to this rapidly growing field of comparative research.

1 - Bird song structure and language syntax: a comparative interdisciplinary approach.

One key feature distinguishing human language from other animal vocal communication systems concerns the presence of a rule based syntax underlying linguistic utterances. But are humans really unique in their abilities to detect and use syntactical rules, or do they share some of these properties with other species? This project will address this issue by analyzing the syntactical abilities of a songbird, the zebra finch. It will focus on two questions: 1) Are zebra finches capable of detecting and distinguishing between different types of (experimentally constructed) grammars? 2) What are the species specific grammar rules which guide zebra finch song production and development? The project will involve a bioacoustic analysis of song structure in zebra finches, different types of experiments to analyze syntactical capabilities (e.g. habituation/dishabituation tasks, operant tasks involving discrimination learning, etc.) and developmental studies on the role of experience in structuring song syntax.

2 - Bird Speech? On the production and perception of formants in bird vocalisations.

Human speech conveys language, and much research effort concerns the production and perception of acoustic features that encode linguistic meaning in speech. An important feature are formants, which are time-varying frequency bands that are emphasized in the broad-band spectrum of speech. Formant patterns result from acoustic resonances of the vocal tract, the characteristics of which are rapidly modulated using articulators such as the tongue, lips, and soft palate. Studies of birdsong have hardly addressed the role of formants, although several findings indicate their presence. The proposed project aims to provide a comprehensive analysis of formant mechanisms in birds. It will address the following questions: 1) To what extent do vocal tract resonances cause formant patterns in natural bird vocalizations, and how do vocal tract articulators modulate such patterns? 2) What are the perceptual sensitivities of birds to formant patterns in natural bird vocalizations? 3) Are formant patterns in natural bird vocalizations affected by vocal production learning? The project will involve morphological, physiological and bioacoustical analyses and experimental

studies on the vocalization systems of zebra finches and budgerigars, together with experiments on the perception of formant variants.

The projects are based in the research group Behavioural Biology. This is an active, internationally oriented research group with a strong focus on (vocal) communication in animals. The group currently consists of three tenured staff, several post-docs, PhD students and MSc-students. More information: <http://biology.leidenuniv.nl/ibl/S8/index.html>
Requirements: Candidates are expected to have an MSc (drs) degree in Biology, Linguistics (phonetics/phonology) or other relevant discipline; to have a strong interest in experimental and interdisciplinary studies, and to be interested in international collaboration (part of project 2 will be carried out in collaboration with research groups in Germany (Dr Beckers, Seewiesen) and the US).

Appointment: The appointment is for a period of 4 years and is expected to lead to completion of a dissertation. The gross monthly salary is 1.877 in the first year and increases progressively each year to 2.407 in the fourth year. Salary and fringe benefits conform to the Collective Employment Agreement for Dutch Universities. We hope to fill the vacancies as soon as possible.

Applications: Written applications (mentioning BehavBiol-PhD-1 and/or -2), including a CV with marks obtained and the names, telephone numbers and email addresses of at least two referees (who have agreed to be contacted) should be submitted to: Leiden University, Faculty of Mathematics and Natural Sciences, attn. Mr S. Brandsma, Human Resource Department, P.O. Box 9502, 2300 RA Leiden, the Netherlands, or by email: s.brandsma@science.leidenuniv.nl. Closing date: 30 April 2006.

Further information: prof dr Carel ten Cate, tencate@rulsfb.leidenuniv.nl, tel. +31-71-5275040.

tencate@rulsfb.leidenuniv.nl ten-cate@rulsfb.leidenuniv.nl

**MaxPlanckInst SexualSignals in
Birds**

PhD 'Sexual signals in purple-crowned fairy-wrens'
Graduate position offered 'Male and female sexual signals in purple-crowned fairy-wrens'

We are looking for a PhD student to work as part of a team studying multiple sexual signaling in purple-crowned fairy-wrens, *Malurus coronatus*. The PhD project is aimed at understanding the proximate and ultimate aspects of the male and female plumage ornamentation, and will combine behavioural observations of colour ringed birds with analysis of paternity, sex hormones and colour reflectance spectra. A colour-ringed study population has been established in 2005 at the Mornington Wildlife Sanctuary, Western Australia. We are looking for an ambitious, highly motivated behavioural ecologist, with good organisational skills, able to work independently as well as in a team, who would like to take this unique opportunity to combine field work in remote Western Australia with lab work at the well-equipped Max Planck Institute for Ornithology in southern Germany. Experience with molecular genetic techniques (micro-satellites for paternity determination preferably), proven ability to disseminate research results in writing, knowledge of theoretical background of sexual selection and practical experience with challenging field work under extreme tropical conditions are all highly desirable. Fluency in English is necessary, working knowledge of German is advantageous but not essential. Training in other techniques will be provided if necessary. We offer superb logistical support, both in the field and in the lab, and a body of supportive data has already been accumulated. The project is supervised by Dr. Anne Peters, Group Leader at the Vogelwarte Radolfzell, in collaboration with Dr. Michelle Hall, who addresses aspects of acoustic signaling by duetting in purple-crowned fairy-wrens. Starting date is as soon as possible. Duration of the position is for 3 years, with a six month trial-period, and an annual stipend of approximately 12.000 , depending on age and experience. Applications will be reviewed as they come in, for full consideration, please send the following details by 15 May 2005 at the latest: A full curriculum vitae, a short description of research experience and interests, 2-3 examples of written work, names and contact details (including phone number and email) of 3 referees.

Send applications and enquiries for information to:

Dr. Anne Peters peters@orn.mpg.de Behavioural Ecology of Sexual Signals Group Max Planck Institute for Ornithology Vogelwarte Radolfzell Schlossallee 2 D-78315 Radolfzell Germany

Anne Peters <peters@orn.mpg.de>

MaxPlanckInst SexualSignals in Birds 2

Graduate position offered 'Male and female sexual signals in purple-crowned fairy-wrens'

We have a position for a PhD student to work as part of a team studying multiple sexual signaling in purple-crowned fairy-wrens, *Malurus coronatus*. The PhD project is aimed at understanding the proximate and ultimate aspects of the male and female plumage ornamentation, and will combine behavioural observations of colour ringed birds with analysis of paternity, sex hormones and colour reflectance spectra. A colour-ringed study population has been established in 2005 at Mornington Wildlife Sanctuary, Western Australia.

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of 3 referees. Send applications and enquiries for information to:

Dr. Anne Peters peters@orn.mpg.de Behavioural Ecology of Sexual Signals Group Max Planck Institute for Ornithology Vogelwarte Radolfzell Schlossallee 2 D-78315 Radolfzell Germany <http://-vogelwarte.mpg.de/mitarbeiter/peterspro6.html> Anne Peters <peters@orn.mpg.de>

NorthernArizonaU GenesToEnvironment

Dear colleagues: Please distribute this information to faculty advisors and potential students.

NAU Graduate Program in Integrative Bioscience: Genes to Environment

Pending funding, we expect to offer six PhD student fellowships per year at Northern Arizona University starting in the 2006/07 academic year. The purpose of this program is to provide students with instruction and research training focused on linkages between molecular genetics and ecosystem phenomena, with special emphasis on multi-scale modeling approaches. Program graduates will have the skills to address fundamental and applied questions of genetic influences on ecosystem function and response to environmental change. Unique aspects of this program include: 1) multidisciplinary research with a special emphasis on scaling phenomena, 2) inclusion of molecular methodology and applied statistics coursework in all programs of study, 3) seminar courses covering scientific ethics, statistics and modeling, and student research, featuring guest speakers from integrative disciplines, 4) unique internships with community colleges, federal agencies, and Native American high schools to broaden the graduate experience and enhance connections between the research and the broader community. The NAU Integrative Bioscience PhD program will prepare innovative and creative scientists to become leaders in research, science outreach and communication, and environmental problem solving.

Contingent upon funding, fellowship packages will include generous, 12-month stipend support for two years, with continued support at more traditional stipend levels. Applicants must concurrently apply to, or already be accepted in, doctoral programs in the Department of Biological Sciences <http://www6.nau.edu/biology/> or the School of Forestry <http://www.for.nau.edu/cms/->

at Northern Arizona University. Application deadlines for the 2006/07 academic year will be extended for Integrative Bioscience applicants. Consideration of application packages will begin April 17th. Applications will consist of 1) standard applications required for Biology or Forestry graduate programs (including two letters of reference) and 2) a 1 page essay on how this program would address your educational and career goals. Please e-mail the essay to: Amy.Whipple@nau.edu.

Please contact us by email and phone for more information: Dr. Amy Whipple: Amy.Whipple@nau.edu, (928)523-8727 or (928) 714-0409; Dr. Maribeth Watwood, Maribeth.Watwood@nau.edu, (928)523-9322.

Amy V. Whipple Merriam-Powell Center for Environmental Research PO Box 5640 Northern Arizona University Flagstaff, AZ 86011 Fax: 928-523-8223 Phone:(w) 928-523-8727 (h) 928-714-0409 e-mail: amy.whipple@nau.edu <http://www.mpcer.nau.edu> Amy.Whipple@NAU.EDU Amy.Whipple@NAU.EDU

QMU London EvolFlowerColour

The ecology and evolution of flower colour

There is a wealth of published information on why flowers have the colours they do. Unfortunately, much of this information is flawed, since botanists rarely considered that flowers are addressed to pollinators, whose colour vision differs fundamentally from that of humans. All insect pollinators see UV light, many see the entire spectrum from UV to red, and some have colour vision systems with 5 spectral receptor types (rather than the 3 that humans have). Chittka's laboratory has, over the years, collected reflectance spectra (including the UV) from over 2000 plants species from Israel, Brazil, Italy, Germany, Austria, and Norway. The CASE collaborator, Vincent Savolainen at Kew Gardens, has the world's second most extensive database for such spectra, with over 800 species from tropical Africa, Australia and the Neotropics. Given these databases, and the extensive knowledge on pollinator vision, fundamental questions in the ecology and evolution of flower colour can now be re-addressed. We are seeking to employ a bioinformatics PhD student or a biology PhD student (ideally, but not necessarily with expertise in programming) to embark on two tasks: 1. to construct an online, open access database for floral reflectance, and 2. to use this database to explore the following questions: is there ecological divergence be-

tween flower colours of plants that flower sympatrically (i.e. in the same habitat)? To flower signals addressed to pollinators with different colour vision systems (e.g. bees and flies) differ in their colouration? Does UV reflectance differ depending on the incidence of UV radiation at different Alpine altitudes and tropical latitudes? Do flower colours (as perceived by pollinators) differ in different habitats, depending on illumination conditions and predominant background materials? Does the relatively recent increase of UV radiation in Australia have an impact on the flower colouration there, as mediated by the selection imposed through bee pollinators? These are some starting points, but the project would obviously have many degrees of freedom for a student to explore, and build the kind of scientific independence that is necessary at the outset of a scientific career. The student might also perform behavioural tests to see how bees respond to flower colours and patterns. The project will undoubtedly result in several high impact publications. The other major task would be to merge the databases from Kew and Queen Mary, to turn them into an openly accessible web based tool. Chittka & Savolainen have already worked extensively towards this goal, and have started to construct an SQL database. This is now in advanced state, but will still require fine tuning before it can go online. In addition, we hope to 1) expand the user interface in such a way that it can calculate the subjective appearance of flower colours for different taxa of pollinators; 2) Incorporate user authentication, to allow different users different levels of access - e.g. some may be able to add records to the database; a few might be able to add records on behalf of others. 3) Establish web based administration tools and backup protocols to allow the database to be maintained by a non-SQL trained administrator. The student would be trained in concepts of modern ecology and evolutionary biology, with the special perspective of the sensory ecology of pollinating insects. It is hoped the student will bring along expertise in database programming, but the bioinformatics officer at Kew Gardens is ready to help if that should be necessary. Field trips to locations in Africa and South America would also be part of the project. The student would be expected to spend at least part of the time at Kew Gardens.

Supervisors: Prof. L. Chittka (Queen Mary) and Dr. V. Savolainen (Kew Gardens) For further information please contact Lars Chittka at l.chittka@qmul.ac.uk

***Applications should be sent electronically to l.chittka@qmul.ac.uk by 21 April 2006 at the latest.
***The person hired has to be a UK citizen.

References - all available on Chittka's web page at: <http://www.biology.qmul.ac.uk/research/staff/>

chittka/chittka.htm Chittka L, Brockmann A: Perception space - The final frontier. *PloS Biology* 2005, 3:art. no.-e137. Chittka L, Wells H: Color vision in bees: mechanisms, ecology and evolution. In *Complex worlds from simpler nervous systems*. Edited by Prete F: MIT Press; 2004:165-191. Waser N, Chittka L: Bedazzled by flowers. *Nature* 1998, 394:835-836.

Dr Vincent Savolainen Jodrell Laboratory Royal Botanic Gardens, Kew Richmond TW9 3DS, London UK Tel +44-(0)20-8332-5366 Fax +44-(0)20-8332-5310 v.savolainen@kew.org

— / —

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>

QueenMaryULondon InsectImmuneEvol

Dear Evoldir people

I have a PhD studentship available. This is a three year college funded position and is open to candidates from outside the UK. Details of the project are given below. I'm looking for a good candidate who's interested in evolution, ecology, entomology and immunology (or at least some of those): if you think you fit the bill then please drop me a line! Details of the project are given below.

Cheers

Rob Knell

Email: R.Knell@qmul.ac.uk Phone +44 (0)20 7882 7720 Skype Rob Knell <http://www.qmw.ac.uk/~ugbt794> <http://www.mopane.org> "The truth is that they have no clue why the beetles had horns, it's the researchers who have sex on the brain and everything has to have a sexual explanation. And this is reasearch?!" Correspondent known as FairOpinion on Neo-Con American website discussing my research.

Cross-resistance or trade-offs in immune system evolution?

The investment that is made into an immune system is believed to be shaped by natural selection such that the costs of immunity are balanced by the benefits. Invertebrate immune systems mostly lack specific acquired immune responses, and are instead reliant on

more general defences. This raises the possibility that investment in defences against one type of parasite may also alter the host's susceptibility to other parasites by either decreasing the probability of infection, or alternatively by increasing it if the host trades-off one class of defence against another. Such changes have the potential to affect the cost: benefit balance of investment in immune defences profoundly.

The objectives of this study are to assess the extent by which resistance to particular species of parasite affects host susceptibility other parasites, and secondly to assess how any observed changes in susceptibility arise from modifications to the host's immune investment. Objective 1 will be achieved by an artificial selection experiment, in the course of which lines of host insects (*Plodia interpunctella*) resistant to three different parasites, a virus, a fungal parasite and an ichneumonid parasitoid wasp, will be created and then bioassayed against the other two species of parasite. Objective 2 will be met by assaying a variety of aspects of the immune system in each selection line. Relating these data to the results from the bioassays will allow us to assess how the selection line in question has responded to selection, and how any patterns of changed susceptibility to the other parasites have arisen.

Applications are invited from candidates with an interest in insect immunology and evolutionary ecology who have or expect to obtain an upper- second class or better honours degree in biological sciences (or overseas equivalent) in areas relevant to the project applied for. Informal enquiries about the project are welcomed, or to apply, post or email a CV, the names and contact details of two academic referees and a covering letter detailing your interest in the project to Dr Knell at the address below.

Rob Knell School of Biological Sciences Queen Mary, University of London Mile End Road, London E1 4NS, UK

R.Knell@qmul.ac.uk R.Knell@qmul.ac.uk

StockholmU Evolofaposematicdefences

PHD POSITION IN BEHAVIORAL ECOLOGY at the Department of Zoology, Stockholm University, SWEDEN

?The role of invertebrate predators in the evolution and

function of aposematic defences.?

The project involves studies on invertebrate predator behaviour towards aposematic insect prey. Much is known about the function of aposematic defences against vertebrate predators (mainly birds), yet the function of warning signals against invertebrates is relatively unexplored. However, many aposematic insects use visual warning signals also in their first larval instars, which are most likely too minute for being hunted by birds or other vertebrates. As a basis for the project, you will use the aposematic defence system of the bug *Lygaeus equestris* (Heteroptera: Lygaeidae).

For more information, please contact main supervisor Dr Gabriella Gamberale-Stille, e-mail Gabriella.Gamberale@zoologi.su.se

Preferred qualifications: MSc (or equivalent) in biology with a finished graduate project (worth 18 weeks of studies, or more, with a written report/thesis) with an ethological, ecological or evolutionary focus. Experience from entomological and behavioural studies is meriting, as is a general interest in evolutionary processes. We are looking for a PhD student who is able to take initiatives, interested in theory as much as empirical work, and who has a good analytical capacity.

The PhD studies are planned to start 1 July 2006 (or as agreed upon). For fulltime studies funding is given as a stipend for the first two years and as a position for the following two years. Normally the PhD student will do 20% teaching and supervision of undergraduates, which extends the period of PhD studies to a total of approximately five years.

The application should include: (1) a signed letter of application (no more than one A4 page) addressed to the Head of the Department of Zoology, including a personal resume and motivation for your application (2) a CV (including relevant academic degrees and former positions and a list of which university courses you have taken and the grades you were given) (3) a copy of your graduate work (4) certificates to verify the CV and (5) two reference names with contact details (phone number and e-mail address)

The application must be received no later than 28 April 2006 and should be mailed to:

PREFEKTEN Department of Zoology Stockholm University 106 91 Stockholm Sweden

— Dr Gabriella Gamberale Stille Phone: +46 (0)8 164046 Department of Zoology FAX: +46 (0)8 167715 Stockholm University 106 91 Stockholm, Sweden

Gabriella Gamberale Stille
<gabriella.gamberale@zoologi.su.se>

StockholmU Phenotypic polymorphism

PhD Position in Theoretical Evolutionary Biology
Stockholm University

The evolution of phenotypic polymorphism

A PhD position in theoretical evolutionary biology is available at the Department of Zoology, Stockholm University, Sweden. Research topics for the position include the evolution of phenotypic polymorphism and the evolution of individual variability, viewed from the perspective of modern developmental biology.

Phenotypic polymorphism is a widespread phenomenon, with examples like males and females in sexual species, alternative male mating types and winged and wingless individuals in certain insects. Variation in so-called personality between individuals of social species could also be regarded as phenotypic polymorphism. The basic issue concerns the evolution and development of alternative phenotypes, in particular, the evolution of developmental systems of phenotype determination. Such systems can implement genetically controlled polymorphisms and phenotypic plasticity, as well as stochastic (randomizing or bet-hedging) polymorphisms.

The position can be either full-time over four years or 80% over five years (with a possibility of 20% teaching assistantship), with a starting full-time yearly salary of 232800 SEK (around 24800 EUR). The starting date is flexible, but should be in the second half of 2006. Applicants should have a MSc (or equivalent background) in a field like evolution, ecology or population genetics, or possibly physics and applied mathematics. Candidates with a strong interest in evolutionary theory and good conceptual, analytical and computer programming skills are preferred. The position is open until filled, but primary consideration will be given to applications received by 15 May 2006. To apply, send a signed letter of application, containing a statement of research interests and skills, addressed to the Head of the Department of Zoology, Stockholm University, SE-106 91 Stockholm, Sweden. Attach your CV, copies of degree certificates, copies of your masters thesis (or equivalent thesis), any published or in-press papers, and contact information for two references. Informal inquiries (by email to olof.leimar@zoologi.su.se) about

the position are welcome.

Olof Leimar, Professor Department of Zoology Stockholm University SE-106 91 Stockholm Sweden

olof.leimar@zoologi.su.se <http://www.zoologi.su.se/-research/leimar/>
olof.leimar@zoologi.su.se

UBerne TheoEvolEcol

PhD-POSITIONS IN THEORETICAL AND BEHAVIOURAL ECOLOGY

Dept. Behavioural Ecology, Institute of Zoology, University of Berne, Switzerland.

1) PhD THEORETICAL ECOLOGY: We investigate how environmental conditions experienced early in life may cause ontogenetic changes on life histories through phenotypic plasticity. The successful applicant will develop and study general evolutionary models, as well as models parameterized with experimental lab and field data of African mouthbrooding cichlids. Eligible candidates will have a master's degree (or Diplom) in Biology, Mathematics, or Theoretical Physics and dispose of a sound background in theoretical and evolutionary biology. Research experience in evolutionary modeling is highly welcome. The successful candidate will work part-time at the International Institute for Applied Systems Analyses (IIASA) in Laxenburg (Austria), where the thesis project will be co-supervised by PD Dr. Ulf Dieckmann. The collaboration between IIASA and the University of Bern will provide extensive guidance in Mathematical Biology and Behavioural Ecology. Duration three years; supervisor: Barbara Taborsky.

2) PhD BEHAVIOURAL ECOLOGY: This PhD-study will investigate (i) proximate and ultimate causes of maternal effects on offspring size and (ii) physiological responses to the environment during early ontogeny, in African mouthbrooding cichlids. The study will involve experimental manipulation of ecological conditions and behavioural observations in the lab, ecological surveys and collection of samples in the field for genetic analysis. Eligible candidates will have a masters degree (or Diplom) in Biology and research experience in animal behaviour, a genuine understanding of evolutionary theory and a strong commitment to basic science. Practical skills in the work with fish, both in the lab and field and/or the measurement of physiological parameters will be very helpful. Duration three years;

supervisor: Barbara Taborsky.

The successful candidates will join an active research group consisting currently of 5 advanced research staff, 6 PhD-students and a varying number of guest scientists and masters students. Besides the Behavioural Ecology group, the ecologically oriented Zoological Institute of the University of Bern consists of research groups on Aquatic Ecology (Ole Seehausen), Conservation Biology (Raphael Arlettaz), Evolutionary Ecology (Heinz Richner), Population Genetics (Laurent Excoffier) and Synecology (Wolfgang Nentwig). Salaries will follow the schemes of the national funding organizations of Switzerland and Austria. Besides research, PhD students assist in undergraduate teaching and supervision.

Closing date: Open until filled, but all application materials, including CV, a summary of research experience, copies of any published or in-press papers, and two letters of recommendation should be received by April 15, 2006 to ensure full consideration. The positions will start at the earliest possible date. Candidates should indicate in a cover letter for which of the two positions they apply and when they could take up the position. Please send all application material to the secretarys office, c/o Marlis Gerteis, Dept. Behavioural Ecology, University of Bern, Wohlenstrasse 50A, CH-3032 Bern, Switzerland; or as e-mail attachments to marlis.gerteis@esh.unibe.ch. For inquiries please contact barbara.taborsky@esh.unibe.ch.

Please see also <http://www.zoology.unibe.ch/behav/-index.e.php> for further information on our department.

Dr. Barbara Taborsky Zoological Institute Behavioural Ecology University of Bern Wohlenstrasse 50A CH-3032 Hinterkappelen Switzerland

e-mail: barbara.taborsky@esh.unibe.ch tel: +41/ 31/ 6319 157 fax: +41/ 31/ 6319 141

barbara.taborsky@esh.unibe.ch

UGuelph RibosomalDNA

I am looking for PhD candidates who are interested in conducting research on the evolution of ribosomal DNA. Interested students should contact Teresa Crease at tcrease@uoguelph.ca. Additional information about the Zoology graduate program at the University of Guelph can be found at http://www.uoguelph.ca/ib/-graduate_zoology2.shtml. A description of my research

interests is provided below.

Ribosomal DNA (rDNA) is an important multigene family that codes for the structural RNA molecules that make up ribosomes. One unit of rDNA consists of 3 genes encoding ribosomal RNA (rRNA) separated by intergenic spacers. The spacers contain sequences that control the expression of the rRNA genes. Some regions of these genes evolve very slowly while other regions, known as expansion segments, and the intergenic spacers evolve very rapidly. Despite this rapid evolution in their sequence, they still maintain their function. In addition, it has been observed that sequence similarity among the members of this multigene family is high within species relative to similarity between copies from different species. This phenomenon is known as "concerted evolution".

Due to variation in the rate of evolution in different parts of the same repeat unit, rDNA is an excellent model system with which to study the interaction between the molecular processes that cause concerted evolution, and natural selection to maintain the structure and function of the molecule. I use freshwater crustaceans in the genus *Daphnia* as a model organism for this work as they contain unusually long expansion segments, and show variation in breeding system with some populations reproducing by cyclical and others by obligate parthenogenesis.

The current goals of my research program are to:

- 1) test the hypothesis that rates of recombination and rDNA copy number differ between *Daphnia* species, and thus cause differences in their rates of concerted evolution
- 2) test the hypothesis that natural selection is acting on rRNA gene expansion segment length variation within species
- 3) identify proteins that bind to the ribosomal intergenic spacer, and determine the impact of intra- and interspecific variation on the interaction between this sequence and these proteins
- 4) determine the impact of breeding system and genomic location on the evolution of a *Daphnia* transposon, Pokey, that is found both inside and outside of the rDNA.

– Teresa J. Crease Associate Professor Department of Integrative Biology University of Guelph Guelph, Ontario N1G 2W1 Canada

Email: tcrease@uoguelph.ca Phone: 519-824-4120 x52723 Fax: 519-767-1656

UHawaiiHilo EvolPlantPopBio

Dear EvolDir Members,

I would be grateful if you would distribute the following announcement to promising students looking for an M.S. position in evolutionary ecology/ plant population biology. Please encourage interested students to contact me ASAP. Mahalo! Elizabeth

M.S. Student Research Position at UH-Hilo

A graduate student position is available at UH-Hilo in an NSF-funded study of the relationship between environmental heterogeneity and cross-fertility in 'Ohi'a lehua (*Metrosideros polymorpha*). The graduate student will participate in cross-pollination, morphometric, and pollen viability studies. He/she will also adopt a component of the study, or develop his/her own related project, to satisfy the research requirements of the M.S. degree.

Partial Abstract Species in the early stages of diversification serve as excellent models for studies of the environmental conditions that drive speciation. The highly variable Hawaiian tree, *Metrosideros polymorpha* ('Ohi'a), is such a species, having derived from a progenitor that colonized the Hawaiian Islands from New Zealand as recently as 0.5 to 1.0 million years ago. Several of 'Ohi'a's varieties co-occur across the volcanic islands, which range in age from the environmentally stable, 5-million-year-old Kauai to the still-forming and highly heterogeneous Big Island. As such, 'Ohi'a provides an ideal system in which to examine the relationship between spatial and temporal environmental heterogeneity and the evolution of reproductive isolation, a precursor to speciation. This two-year study will use hand-pollinations, microscopy, and growth chambers to determine the relative cross-fertility within and between varieties and the viability of the resulting seedlings under a range of conditions. The proposed work will help to illuminate the environmental conditions under which speciation in outcrossed tree species will occur.

Start date: Summer or Fall 2006

Desired Qualifications: Knowledge of basic botany, strong interest in evolution, ability to work with and mentor others, and strong analytical skills.

Students from under-represented groups are especially

encouraged to apply.

The individual selected for this study must be accepted into UH-Hilo's M.S. Program in Tropical Conservation Biology and Environmental Science [<http://tcbes.uhh.hawaii.edu/>]. The application deadline is 1 May. However, interested parties should contact Elizabeth Stacy as soon as possible.

Please direct all inquiries to:

Dr. Elizabeth Stacy Department of Biology University of Hawai'i-Hilo 200 West Kawili Street Hilo, HI 96720
Email: estacy@hawaii.edu Phone: 808-933-3153

estacy@hawaii.edu

UHelsinki EvolQuantGenet

A PhD studentship is available at the University of Helsinki, Finland, to work on the statistical analysis of evolutionary divergence. The successful candidate will develop Bayesian methods for the statistical analysis of the evolution and divergence of populations, and apply these in on-going studies of fish, frogs and birds. The research will involve close collaboration with biologists and statisticians.

The successful applicant will be expected to have numerical and statistical skills, and an interest in developing these abilities in the context of a collaborative project. Much of the work will be conducted using the OpenBUGS programme (www.math.helsinki.fi/openbugs/), which is primarily developed in Helsinki, and there will be the possibility to take part in the development of the programme.

The student will be part of the recently funded Finnish Centre of Excellence in Evolutionary Genetics and Physiology, which includes the Ecological Genetics Research Unit (www.helsinki.fi/bioscience/ecology/merila.htm), and the groups of Prof. Craig Primmer (users.utu.fi/primmer) and Prof. Mikko Nikinmaa (www.sci.utu.fi/biologia/fysiologia/nikinmaa_eng.htm). The project will be supervised by Dr. Bob O'Hara (www.rni.helsinki.fi/~boh/) and Prof. Juha Merilä.

Researchers with previous post-doctoral experience in functional genomics and with the imagination and interest necessary to use their experience to address questions in evolutionary biology are especially encouraged to apply. Interest and/or experience on application evolutionary

quantitative genetic methods is beneficial.

Informal inquiries should be addressed to Dr. Bob O'Hara (bob.ohara@helsinki.fi) or Prof. Juha Merilä (juha.merila@helsinki.fi), and applications to Dr. O'Hara. Applications should include a full CV, and names and contact details of at least two referees. Review of applications will commence at the end of March 2006 with the preferred starting date being prior to September 2006. The position is initially available for two years. The salary range is 1750-2100 EUR per month, depending on the previous experience of the candidate.

Bob – Bob O'Hara

Dept. of Mathematics and Statistics P.O. Box 68 (Gustaf HÅllstrÅkatu 2b) FIN-00014 University of Helsinki Finland

Telephone: +358-9-191 51479 Mobile: +358 50 599 0540 Fax: +358-9-191 51400 WWW: <http://www.RNI.Helsinki.FI/~boh/> Journal of Negative Results - EEB: <http://www.jnr-eeb.org>
bob.ohara@helsinki.fi bob.ohara@helsinki.fi

ULiverpool SpermCompetition

PhD studentship available

Sperm competition and adaptive variation in mammalian ejaculates

Supervised by Dr Paula Stockley, University of Liverpool

Starting October 2006. Funded by The Leverhulme Trust (UK/EU students)

Sperm competition occurs when the sperm of two or more males compete to fertilize a female's ova, and is an extremely powerful selective force in the evolution of male reproductive traits. Our understanding of how males attempt to maximise their reproductive success under sperm competition owes much to the theoretical framework developed in the context of 'sperm competition games' - models designed to predict optimal investment in ejaculates. This project will provide critical empirical tests of sperm competition theory, as a basis for understanding adaptive variation in mammalian ejaculates. Using small mammal models (bank voles, house mice), you will investigate the nature of trade-offs between ejaculate expenditure and other male reproductive investment, and determine how the

number of sperm ejaculated varies in relation to local sperm competition risk and intensity, as well as the phenotypic traits of competing males and their mates. The studentship will provide experience in evolutionary and reproductive biology, including techniques of experimental design, statistical analysis and behavioural observation.

You should have (or expect to receive) a First Class Honours or an Upper Second Class Honours degree in a relevant biological discipline, and a strong interest in evolutionary biology. The successful applicant will join the Mammalian Behaviour and Evolution group

based at the University of Liverpool's Veterinary Field Station, on the Wirral Peninsula (see our website at: <http://www.liv.ac.uk/mbe/>).

Apply by April 30th 2006, sending a covering letter and CV with details of two academic referees, to Dr Paula Stockley, Mammalian Behaviour & Evolution Group, Faculty of Veterinary Science, University of Liverpool, Leahurst Veterinary Field Station, Chester High Road, Neston CH64 7TE (email: p.stockley@liv.ac.uk) Informal enquiries welcome.

p.stockley@liverpool.ac.uk p.stockley@liverpool.ac.uk

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AustMuseum InvertSystematist

Dear All,

The Australian Museum in Sydney has just advertised TWO positions vacant for either short term or permanent appointments. Please note that the closing dates are quite soon (7 April). Non-residents are encouraged to apply, irrespective of current visa status.

Don Colgan.

SCIENTIST (Invertebrate [excluding Entomology] Systematist), Scientific Officer, Grade 2-6, Australian Museum. Job ref: RC2/06. Total remuneration package up to the value of \$100,178.00 p.a. including salary (\$59,937-\$90,782), employer's contribution to superannuation and annual leave loading.

Responsible for implementing and managing research programs; attracting funds; developing networks; supervising students; contributing to management. Advise and work with collection managers and public program staff on collections and exhibitions.

Selection criteria: A PhD or equivalent in relevant fields. A proven track record in invertebrate (not in-

sect) systematics, implementing and managing a program of research in line with Australian Museum priorities, and attracting research funding. Specialist knowledge in one or more of the following: phylogeny and phylogeography, evolutionary biology, biogeography. Demonstrated experience in establishing and maintaining an extensive network of professional and community contacts relevant to the field. High level written and oral communication and interpersonal skills. Ability to work in a team environment. Experience in generating interactive keys. Experience in communicating science to the general public, preferably through developing or participating in high quality public program outputs such as exhibitions, publications and on-line products and/or experience in collection development. Common Selection Criteria also apply.

Notes (a): *Permanent or 3-Year Fixed Term Appointment subject to qualifications, skills and experience.

Notes (b): *Permanent appointment to the NSW Public Service is subject to the applicant being an Australian citizen or permanent resident.

Inquires: Brian Lassig (02) 9320 6297 or email bri-anl@austmus.gov.au.

Information Packages: Access information packages at www.amonline.net.au (<http://www.amonline.net.au/-display.cfm?id#40>) or e-mail hr@austmus.gov.au.

Applications Marked 'Confidential' To: Human Resources Officer, Human Resources Unit, Australian Museum, 6 College St, SYDNEY NSW 2010.

Closing Date: Friday 7 April 2006

Dr Don Colgan Research Branch The Australian Museum 6 College St. Sydney 2010 Australia

ph. 612-9320-6030 fax: 612-9320-6020

The Australian Museum. Australia's first - and leading - natural sciences and anthropology museum. Visit www.amonline.net.au Don Colgan <Don.Colgan@austmus.gov.au>

AustMuseum TerrestrialVerts

Dear All,

The Australian Museum in Sydney has just advertised TWO positions vacant for either short term or permanent appointments. Please note that the closing dates are quite soon (7 April). Non-residents are encouraged

to apply, irrespective of current visa status.

Don Colgan.

SCIENTIST (Molecular Biology Terrestrial Verts), Scientific Officer Grade 2-6, Australian Museum. Job ref: RC1/06. Total remuneration package up to the value of \$100,178.00 p.a. including salary (\$59,937-\$90,782), employer's contribution to superannuation and annual leave loading.

Responsible for implementing and managing research programs; attracting funds; developing networks; supervising students; contributing to management. Advise and work with collection managers and public program staff on collections and exhibitions.

Selection criteria: A PhD or equivalent in relevant fields. A proven track record in terrestrial vertebrate molecular biology (preferably in more than one class), implementing and managing a program of research in line with Australian Museum priorities, and attracting research funding. Specialist knowledge in one or more of the following: population and landscape genetics, phylogeny and phylogeography, evolutionary biology, biogeography. High level skills in DNA and RNA techniques and micro-satellite analysis. Demonstrated experience in establishing and maintaining an extensive network of professional and community contacts relevant to the field. Ability to work in a team environment. High level written and oral communication and interpersonal skills. Experience in communicating science to the general public, preferably through developing or participating in high quality public program outputs such as exhibitions, publications and on-line products and/or experience in collection development. Common Selection Criteria also apply.

Notes (a): *Permanent or 3-Year Fixed Term Appointment subject to qualifications, skills and experience.

Notes (b): *Permanent appointment to the NSW Public Service is subject to the applicant being an Australian citizen or permanent resident.

Inquires: Brian Lassig (02) 9320 6297 or email bri-anl@austmus.gov.au.

Information Packages: Access information packages at www.amonline.net.au (<http://www.amonline.net.au/-display.cfm?id#39>) or e-mail hr@austmus.gov.au.

Applications Marked 'Confidential' To: Human Resources Officer, Human Resources Unit, Australian Museum, 6 College St, SYDNEY NSW 2010.

Closing Date: Friday 7 April 2006

Don Colgan <Don.Colgan@austmus.gov.au>

CentralMichiganU EvolBiol

Dear Evolution Directory,

We are interested in attracting candidates for a full-time, tenure track position within the Biology Department at Central Michigan University. This position will be split as 0.5-time curator for our natural history collections and 0.5-time as a biology faculty member. Tenure will occur within the biology department. The area of research specialty is open, but the candidate must be committed to maintaining an active research program in addition to teaching and curating the natural history collection.

We are an evolving department with 11 new Biology faculty hired in the past 5 years. Please forward this e-mail to qualified post-doctoral associates or finishing graduate students who would be interested in joining a young and vibrant department. Please note that we will begin reviewing applications when they are received as we are hoping for a start date of August 2006.

The CMU natural history collections, consisting of a total of 24,540 specimens (mainly representing Great Lakes species and a few type species), are housed in approximately 1,700 sq ft across multiple rooms in Rowe Hall. In addition, smaller collections are maintained in the Biology Department and on Beaver Island. The museum is well equipped with all of the taxidermy equipment and space required for specimen preparation. A large freeze drier for specimen preparation is housed with the collections to facilitate additions to the collections. As a department we actively seek external support for research activities and this position will be required to obtain external funding to help support the collections.

The Department of Biology supports teaching and research activities with excellent multi-user resources including the CMU Biological Station on Beaver Island (<http://www.cst.cmich.edu/centers/cmubs/>), a greenhouse, a herbarium, 3 ABI PRISM 310 Genetic Analyzers, an ABI 7500 real-time PCR instrument, an automated Biolog microbial identification system (Omnilog ID), and a microscopy facility with confocal, transmission electron and scanning electron microscopes (<http://www.cst.cmich.edu/centers/-microscopy/>). Additional information regarding facilities, the department and position can be found on the Department of Biology's web site (<http://->

www.cst.cmich.edu/units/bio/index.htm).

Please feel free to contact either Dr. Claudia Douglas (Department Chair and Chair of this search) or Dr. Brad Swanson (Chair of Personnel Committee) directly for clarification or additional information.

Thank you, Brad Swanson

– Bradley J. Swanson Asst. Professor Department of Biology Director Applied Technologies in Conservation Genetics Central Michigan University Mt. Pleasant, MI 48859 brad.swanson@cmich.edu (989) 774-3377 <http://www.cst.cmich.edu/users/swans1bj/>-<http://atcg.bio.cmich.edu> swans1bj@cmich.edu

ChicagoBotanicGarden PlantConservationInternship

The Chicago Botanic Garden is seeking applicants for a 6 month paid internship in seed bank/plant conservation. Intern will coordinate seed collections at our Kansas sites as a part of the Millennium Seed Bank Project, an international project that aims to collect 10% of the world's seed bearing flora by 2010 for long-term conservation. The Chicago Botanic Garden aims to collect seeds from 1,500 native tallgrass prairie species throughout the Midwest.

Work description: Intern will work 40 hour/week in Kansas for the duration of 6 months. Pay is \$8.32/hour. Duties include locating and monitoring populations of target species, collecting seed and herbarium specimens, and cleaning seed. Starting date is May 21st, 2006 when training will be held in Chicago; travel and accommodations will be provided for training.

Qualifications: Applicants are required to have a Bachelor's degree at beginning of employment in biology, botany, ecology, or a related major and passion towards conservation and restoration of native plants. We are looking for a highly motivated and independent person who is willing to sometimes work alone and occasional weekends. Because the Millennium Seed Bank Project is dependent on volunteer involvement, individuals need to be committed to using and soliciting help from volunteers. Must be in good physical condition and able to stoop and kneel for extended periods of time. Must possess a valid driver's license.

Application instructions: The deadline for application is April 15th, 2006. Please visit

<<http://www.chicagobotanic.org/internship/-ApplicationInfo05>> for full application instructions.

For further information about the project please visit our website or contact the seed bank coordinator: <<http://cbgseedbank.org/>>. Betsy Allen Millennium Seed Bank Coordinator ballen@chicagobotanic.org (847) 835-6957

PVitt@chicagobotanic.org

NewMexico FieldAssist

Field Assistant Wanted for Field Work in New Mexico

We are looking to recruit a field assistant for a research project investigating the genetics of habitat isolation in sunflowers. Fieldwork assistant post is available May-August for periods of 3-5 days every 20 days. Field activities include measurement of several plant morphology traits as well as eventual collection of sunflower material. Ideally, the field assistant will live close to Socorro, New Mexico, or to The Sevilleta Wildlife Refuge at La Joya, where research will be carried out (<http://www.fws.gov/southwest/refuges/-newmex/sevilleta/>). Compensation is negotiable.

If you wish to apply for this job, then please send a CV with a covering letter and details of one referee (academic or field biology related - with e-mail address) to Dr. Daniel Ortiz-Barrientos indicating dates you are available. E-mail applications are accepted and encouraged. Applications to be received by 15th April 2006.

E-mail: dortizba@indiana.edu

Daniel Ortiz-Barrientos Department of Biology 1001 East Third Street Bloomington, IN 47405-3700 Ph:1(812) 855-9018

http://www.bio.indiana.edu/~rieseberglab/daniel_ortiz-barrientos.html Daniel Ortiz-Barrientos <dortizba@indiana.edu>

NiceSophia-AntipolisU EvolGenomics

The Department of Plant Health at Nice Sophia-Antipolis University (UMR INRA/CNRS/Universite

de Nice-Sophia Antipolis) invites application for a tenure position of Maitre de Conference in genomic evolution of plant nematode parasitism. Expertise in evolutionary genomics and bioinformatics are therefore particularly welcome. The sequencing project of the plant parasitic nematode genome *Meloidogyne incognita* will be achieved by the end of this year at the French genomic center GENOSCOPE. The complete genome sequences of other plant parasitic nematodes, animal parasitic nematodes and other free-living nematodes are on-going processes. The availability of more than ten nematode genomes will offer an unparalleled opportunity for comparative genomics. The comparative analysis will be focused on differential situations such as the mode of reproduction, animal versus plant-parasitic nematode species, and parasitic versus free-living nematode species. Such comparative genomics approaches will help elucidate the evolutive mechanisms involved in the successful adaptation of *M. incognita* to plant parasitism. Applicants are expected to demonstrate the potential to establish an independent, externally funded research program in his or her specific field. The Department has excellent research facilities. For more information, consult our website (<http://www.antibes.inra.fr/unites/ipmsv.htm>). The successful applicant will have also to instruct plant biology courses for undergraduate and graduate (MS) levels. A fluent French speaker is therefore required for this position that will be available for September 2006. This position is referenced as n0259 in the section 66 in the website of Nice Sophia Antipolis University (<http://portail.unice.fr/jahia/Jahia/op/edit/pid/3856>). The closing date for applications is March 30 2006. For more information please contact : Dr. Pierre ABAD (33) 492386402 e-mail abad@antibes.inra.fr

Denis Bourguet <bourguet@ensam.inra.fr>

SimonFraserU CRC AquaticConservation

Canada Research Chairs: Aquatic Conservation in the Department of Biological Sciences Simon Fraser University

The Department of Biological Sciences seeks to appoint two tenure-track Tier II Canada Research Chairs in Aquatic Conservation. Candidates should have a strong international track record in research on conservation of marine or freshwater ecosystems. Ar-

eas of research interest could include fisheries, anthropogenic impacts on habitats, ecosystem dynamics, land-water linkages, and the ecology of threatened species. Appointment will be at the Assistant or Associate Professor level. Successful candidates will be nominated by the university through the Canada Research Chair program <http://www.chairs.gc.ca/>. The positions will benefit from a strong research environment with more than 15 faculty members with common interests in aquatic ecology, conservation and management including the newly-established Tom Buell BC Leadership Chair in Salmon Conservation <http://www.sfu.ca/biology/faculty/reynolds/>. Review of applications will begin on March 31 2006, and the search will remain active until the positions are filled. Applicants should send a curriculum vitae, three representative reprints, a two-page summary of their research objectives and teaching philosophy, and three letters of reference to:

Dr. Tony D. Williams, Chair Department of Biological Sciences Simon Fraser University 8888 University Blvd. Burnaby, B.C. V5A 1S6 Canada E-mail: tdwillia@sfu.ca FAX: 604 291-4312

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. The appointment is subject to final budgetary approval by the University.

Simon Fraser University, located in the greater Vancouver area, is committed to employment equity, welcomes diversity in the workplace, and encourages applications from all qualified individuals including women, members of visible minorities, aboriginal persons, and persons with disabilities.

Michael Hart <mike_hart@sfu.ca>

SouthAfrica VolunteerFieldAssist

Please forward the following advertisement to all that might be interested Volunteers as field assistants and one research station manager needed:

Field assistants needed for the project:

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

What kind of people are needed? Biology/zoology/veterinary students with a BSC/Vordiplom or equivalent are preferred as candidates. Applicants must have an interest in working in

the field and with animals. Whereas the research is mainly non-invasive, this is no job for extreme animal right persons (we take tissue and blood samples). Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o' clock), and stops its activity with dusk. Work during nights might also be necessary. Work in the field will be done for 5-6 days a week. Applicants must be able to manage extreme temperatures (below 0 at night, sometimes over 40C during days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small group.

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

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 500 (around 75 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 1300 or 200 Euro/month). Including extras, you should expect to pay about 300-400 Euros per month.

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

Project: We study the reasons of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

When and how long: From July 2006 onwards for a minimum of 2 months.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to info@stripedmouse.com.

Succulent Karoo Research Station in South Africa:

Research Station Manager required

Requirements: A zoology or biology student with a bachelor or masters degree who would like to gain experience in field work and management. Applicants must be willing to work hard under all weather conditions, be able to cope with the very basic conditions at the research station, the loneliness of the field but also be an active member of a small social group. Applicants

must not fear snakes and must be able to handle very cold and very hot weather. An interest in nature and insight into science are a must, while craft skills are an advantage. Of course the position also offers the opportunity to spend an unforgettable year in the field in Africa.

Period: Preferably for twelve months, to commence in July or August 2006.

Costs and compensation: Accommodation and a weekly trip to town for shopping are provided free of charge. Additionally, a monthly compensation of R2000 will be paid which will cover the basic cost of living (ca. R1300/month) and for some pocket money. Applicants will be responsible for their personal medical insurance, visa fees etc. Transport costs to and from the research station including an air-ticket will be covered by the project but will only be refunded at the end of the period (altogether up to a maximum of 800 Euro or R5800).

Job description: 1. Management of research station (maintenance, refilling water tanks, replacement of empty gas bottles etc.). 2. Trapping, marking, radio-tracking and observation of small mammals. 3. Collection of blood samples from wild living mice. 4. Supervision of field assistants. 5. Management of a captive mouse colony. Five working days a week (Mo, Tue, Thu, Fr, Sat), with Wednesday being used for a shopping trip to town (not counted as working day) and Sundays being free. Included is four weeks of holiday for 12 months, which has to be taken during periods when other students are present at the research station. The trial period is two months.

Place and project: Goegap Nature Reserve near Springbok in the Northern Cape of South Africa. The research projects are on the socio-ecology of small mammals, studying ecological and physiological reasons of social behavior.

How to apply? Please send a CV, a letter of motivation and the names and contact information of at least two scientists available for reference. Application deadline: Until a suitable candidate is identified.

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StanfordU Tech EvolGenet

We are looking for a motivated individual interested in working in an evolutionary genetic laboratory at Stanford University. The position is offered for one year but can be extended further. If interested please apply on the Stanford Jobs web site

([http://jobs.stanford.edu/openings/-display.cgi?Job Req\\$009898](http://jobs.stanford.edu/openings/-display.cgi?Job Req$009898)). Below is a short description of the position:

Under the supervision of the principal investigator and a postdoctoral fellow, perform standard laboratory procedure and data management for research in *Drosophila* population and evolutionary genetics. Conduct molecular analyses, including DNA extraction, PCR, preparation of DNA samples for sequencing, some cloning. Maintain a collection of *Drosophila* strains and carry out genetic crosses. **QUALIFICATIONS:** Knowledge of molecular techniques that include PCR, DNA extraction, restriction enzymes. Bachelor's degree in Biology or Molecular Biology preferred. Experience of working with *Drosophila* is preferred.

– Dmitri Petrov Associate Professor Department of Biological Sciences 371 Serra St. Stanford University Stanford, CA 94305

TEL (650) 736 1169 (office) TEL (650) 736 2249 (lab) FAX (650) 723 6132 WEB: <http://petrov.stanford.edu> e-mail: dpetrov@stanford.edu

“Dmitri A. Petrov” <dpetrov@stanford.edu>

TIGR CompBiology

Dear all,

I would like to call your attention to the following faculty position announcement, soon to appear in *Science* and *Nature*.

Cheers, Joana Silva

Faculty Position Biostatistics and Computational Biology

The Institute for Genomic Research is seeking highly qualified candidates for a faculty position in Biostatistics

tics and Computational Biology. Successful candidates will conduct innovative, independent research, obtain extramural funding, take advantage of interactions with a highly collegial group of scientists within TIGR, and complement existing strengths within the organization. Candidates must have a Ph.D. and a record of accomplishment in computer science, statistics, applied mathematics or a related field, and a demonstrated research emphasis on questions at the intersection of the statistical and biological sciences. Disciplines of major interest include, but are not limited to, comparative genomics, statistical genetics and bioinformatics. The level of appointment will be commensurate with rank and experience. Candidates will be provided with a start-up package.

The Institute for Genomic Research (<http://www.tigr.org>) is a world leader in the fields of genomics and bioinformatics. Our research programs are focused on structural, functional and comparative analysis of genomes and gene products from a wide variety of organisms. TIGR operates a modern 125,000 sq. ft laboratory and office building in Rockville, MD. TIGR provides an outstanding research environment and support infrastructure that include state-of-the-art facilities for DNA sequencing and analysis, transcriptomics, proteomics, and algorithm and database development, and a modern computational grid. TIGR undertakes large scale, data intensive projects which provide fertile ground for a biostatistician or computer scientist wishing to develop new algorithms, statistical measures and applications. In addition, opportunities also exist for graduate student teaching and mentoring through ongoing relationships with the Johns Hopkins University, George Washington University School of Medicine, Virginia Polytechnic Institute and State University, the University of Maryland, and the University of Delaware.

TIGR offers an excellent working environment and a comprehensive benefits package. Interested applicants should submit a CV, a description of research interests and contact information for three references to the address below. The closing date for applications is June 16, 2006. Materials postmarked after this date will not be accepted.

Chair, Faculty Search Committee The Institute for Genomic Research 9712 Medical Center Drive Rockville, MD 20850 or to tigrrecruitment@tigr.org

TIGR is an Equal Opportunity Employer Women and Minorities are encouraged to apply

Joana C. Silva, Ph.D. Assistant Investigator

The Institute for Genomic Research 9712 Medical Center Drive Rockville MD 20850

jsilva@tigr.org voice:301.795.7896 fax:301.838.0208
website: http://www.tigr.org/faculty/Silva_Joana/
jsilva@tigr.ORG

UAmsterdam PlantEvolEcol

The Institute for Biodiversity and Ecosystem Dynamics (IBED) of the University of Amsterdam has a vacancy for a

Plant evolutionary ecologist / assistant professor (UD)

The Experimental Plant Systematics group studies the distribution and origin of genetic variation in various plant genera, mostly relatives of the model species *Arabidopsis thaliana*. One of the main research questions is what role reproductive isolation and gene flow play in this process. The research questions are addressed by a variety of experimental methods, for example molecular analysis of genetic variation and gene expression, analysis of breeding systems, studies of species hybrids and introgression (also in a GMO context), and experiments both in the field and in the greenhouse. The research of the appointee will focus on the evolution of breeding systems and reproductive barriers in relation to habitat fragmentation and adaptation. The work will be carried out in close collaboration with the other scientists (permanent staff, postdocs, PhD students) in the group. A thorough background in plant genetics, ecology and floristics is required.

Full text: Also see url: <http://www.uva.nl/-vacatures/object.cfm/objectid=8462475F-11BD-44E3-B775A26228C03249>

Universiteit van Amsterdam

The Universiteit van Amsterdam (UvA) is a university with an internationally acclaimed profile, located at the heart of the Dutch capital. As well as a world centre for business and research, Amsterdam is a hub of cultural and media activities. The Universiteit van Amsterdam is a member of the League of European Research Universities.

Faculty of Science

The Faculty of Science at the Universiteit van Amsterdam is one of Europe's foremost institutions of higher education and research in its chosen fields of specialization. It plays an active role in international science

networks and collaborates with universities and industry. The Faculty has approximately 2,000 students and 1,500 staff members spread over four departments and ten research institutes. Each institute has its own research programme, a substantial part of which is externally funded by the Netherlands Organization for Scientific Research (NWO), the Dutch government, the EU and various private enterprises.

In 2009, the Faculty will relocate to the Science Park Amsterdam. Ambitious building projects are paving the way for this relocation. The move will make the Park one of the largest centres of academic research in the Netherlands.

The Institute of Biodiversity and Ecosystem Dynamics (IBED) is one of the eleven research Institutes of the Faculty of Sciences. IBED research covers a wide range of subjects, both in pure fundamental and in applied research. Research is directed to the development of fundamental knowledge of the dynamics of ecosystems at all relevant levels, from genes to communities, using a truly multidisciplinary approach. IBED is organized into three thematic clusters (evolution & biodiversity, geo-ecology and community dynamics) that mainly study two related research topics, namely the interaction and communication between organisms and their environment, and the emergent dynamics at different spatial and temporal scales. Strategic research concerns such topics as sustainable harvesting, the prevention of toxic algal blooms, the conservation of endangered species and the potential impact of the introduction of transgenic crops.

IBED has a vacancy for a

Plant evolutionary ecologist / assistant professor (UD)

full-time vacancy number 06-1013 For both internal and external candidates

The Experimental Plant Systematics group studies the distribution and origin of genetic variation in various plant genera, mostly relatives of the model species *Arabidopsis thaliana*. One of the main research questions is what role reproductive isolation and gene flow play in this process. The research questions are addressed by a variety of experimental methods, for example molecular analysis of genetic variation and gene expression, analysis of breeding systems, studies of species hybrids and introgression (also in a GMO context), and experiments both in the field and in the greenhouse. The research of the appointee will focus on the evolution of breeding systems and reproductive barriers in relation to habitat fragmentation and adaptation. The work will be carried out in close collaboration with the other scientists (permanent staff, postdocs, PhD students) in

the group. A thorough background in plant genetics, ecology and floristics is required.

Tasks The appointee will use a variety of methods for his/her research predominantly molecular genetic analyses and experimental manipulations, but also field experiments, (meta-)populations modelling, and the use of geographic information systems. He/she will also contribute to the

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UBerne TheoEvolEcol

POST-DOC AND PhD-POSITIONS IN THEORETICAL AND BEHAVIOURAL ECOLOGY

Dept. Behavioural Ecology, Institute of Zoology, University of Berne, Switzerland.

1) POST-DOC: Theoreticians are invited to apply for a postdoctoral research position to study evolutionary mechanisms of conflict and cooperation, with particular emphasis on reciprocity. Applicants must be experienced in modeling and should have a sound background in theoretical issues in evolutionary biology. The position is initially for two years and can be prolonged. Supervisor: Michael Taborsky.

2) PhD THEORETICAL ECOLOGY: We investigate how environmental conditions experienced early in life may cause ontogenetic changes on life histories through phenotypic plasticity. The successful applicant will develop and study general evolutionary models, as well as models parameterized with experimental lab and field data of African mouthbrooding cichlids. Eligible candidates will have a master's degree (or Diplom) in Biology, Mathematics, or Theoretical Physics and dispose of a sound background in theoretical and evolutionary biology. Research experience in evolutionary modeling is highly welcome. The successful candidate will work part-time at the International Institute for Applied Systems Analyses (IIASA) in Laxenburg (Austria), where the thesis project will be co-supervised by PD Dr. Ulf Dieckmann. The collaboration between IIASA and the University of Bern will provide extensive guidance in Mathematical Biology and Behavioural Ecology. Duration three years; supervisor: Barbara

Taborsky.

3) PhD BEHAVIOURAL ECOLOGY: This PhD-study will investigate (i) proximate and ultimate causes of maternal effects on offspring size and (ii) physiological responses to the environment during early ontogeny, in African mouthbrooding cichlids. The study will involve experimental manipulation of ecological conditions and behavioural observations in the lab, ecological surveys and collection of samples in the field for genetic analysis. Eligible candidates will have a masters degree (or Diplom) in Biology and research experience in animal behaviour, a genuine understanding of evolutionary theory and a strong commitment to basic science. Practical skills in the work with fish, both in the lab and field and/or the measurement of physiological parameters will be very helpful. Duration three years; supervisor: Barbara Taborsky.

The successful candidates will join an active research group consisting currently of 5 advanced research staff, 6 PhD-students and a varying number of guest scientists and masters students. Besides the Behavioural Ecology group, the ecologically oriented Zoological Institute of the University of Bern consists of research groups on Aquatic Ecology (Ole Seehausen), Conservation Biology (Raphael Arlettaz), Evolutionary Ecology (Heinz Richner), Population Genetics (Laurent Excoffier) and Synecology (Wolfgang Nentwig). Salaries will follow the schemes of the national funding organizations of Switzerland and Austria. Besides research, Post-docs and PhD students assist in undergraduate teaching and supervision.

Closing date: Open until filled, but all application materials, including CV, a summary of research experience, copies of any published or in-press papers, and two letters of recommendation should be received by April 15, 2006 to ensure full consideration. The positions will start at the earliest possible date. Candidates should indicate in a cover letter for which of the three positions they apply and when they could take up the position. Please send all application material to the secretarys office, c/o Marlis Gerteis, Dept. Behavioural Ecology, University of Bern, Wohlenstrasse 50A, CH-3032 Bern, Switzerland; or as e-mail attachments to marlis.gerteis@esh.unibe.ch. For inquiries please contact barbara.taborsky@esh.unibe.ch.

barbara.taborsky@esh.unibe.ch

UFribourg EvolBiol

The Faculty of Science of the University of Fribourg/Switzerland (Department of Biology) invites applications for a tenure position of Associate Professor in Evolutionary Biology/Ecology. The successful candidate should have an outstanding record of independent research. She/He is expected to establish an independently funded research program and to teach students in Biology. More information about the position, the application procedure (deadline April 21, 2006) as well as the Department, common facilities and study programs are available at www.unifr.ch/science/positions/. Tadeusz Kawecki Unit for Ecology and Evolution, Department of Biology University of Fribourg Chemin du Musee 10, CH-1700 Fribourg, Switzerland www.unifr.ch/biol/ecology/kawecki phone +41 26 300 88 71 fax +41 26 300 96 98 e-mail tadeusz.kawecki@unifr.ch

UGlasgow ConservationEcol

INSTITUTE OF BIOMEDICAL & LIFE SCIENCES,
GLASGOW UNIVERSITY

LECTURER/SENIOR LECTURER in SPATIAL,
COMMUNITY & CONSERVATION ECOLOGY

We wish to recruit to a Lectureship or Senior Lectureship a spatial, community or conservation ecologist, who will complement our existing strengths in theoretical and empirical ecological and behavioural research. We encourage applications from researchers who seek to understand how organisms function in their environment and the implications for spatial distributions, community structure and conservation. Candidates with interests in interdisciplinary research at the interface between different relevant areas of biology (e.g. molecular, physiological and behavioural ecology, population and conservation genetics, species management and epidemiology) are particularly welcome. The post-holder will be appointed on the Lecturer or Senior Lecturer scale (£24,352 - £43,850 p.a.); s/he will develop an independent research programme and research group, will have and maintain a strong track record of

publication, and will contribute to teaching and to divisional administration.

The Institute of Biomedical and Life Sciences (IBLS) comprises ~140 academic staff members, each of whom is assigned to one of five research Divisions: this post would be based in the Division of Environmental & Evolutionary Biology. Research within IBLS was rated 5/5* at the 2001 RAE. Further information about IBLS and the research interests of staff from each of the Divisions may be found at: <http://www.gla.ac.uk/ibls/>. Method of Application: Further details of the post and host Institute, and full details of the method of application are given at: <http://www.gla.ac.uk/Acad/IBLS/DEEB/> <http://www.gla.ac.uk/Acad/IBLS/DEEB/> Informal enquiries are encouraged and should be made to: Professor Felicity Huntingford, Head of Division of Environmental & Evolutionary Biology, IBLS, Graham Kerr Building, University of Glasgow, Glasgow G12 8QQ. Tel (44) 0141-330-5975, FAX (44) 0141-330-5971 or e-mail f.huntingford@bio.gla.ac.uk Barbara Mable (b.mable@bio.gla.ac.uk) or Dan Haydon (d.haydon@bio.gla.ac.uk) can also be contacted for further information. Closing Date: 31 March 2006. Ref no. 12039/HRL/A3

– 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> Barbara Mable <b.mable@bio.gla.ac.uk>

UGlasgow FieldAssist

Research Assistants Wanted for Field Work in Scotland
We are looking to recruit volunteers for a research project investigating nestling nutrition in blue tits. Fieldwork assistant posts are available April-June for varying periods starting on different dates. Field Activities include: Nestbox monitoring; Measuring of eggs and nestlings; Invertebrate sampling; Nestbox camera setup; Behavioural observations; Video analysis. Travel and living costs covered. Accommodation provided in the University's Field Station, Rowardennan within Loch Lomond National

Park (www.gla.ac.uk/ibls/DEEB/ufs.htm <<http://www.gla.ac.uk/ibls/DEEB/ufs.htm>>). A great opportunity to gain valuable experience in an exciting research project. You will be working as part of a team with Dr Kathryn Arnold and Mr Steve Larcombe of University of Glasgow (<<http://www.gla.ac.uk/ibls/DEEB/>>) If you wish to apply for a post, then please send a CV with a covering letter and details of two referees (academic or field biology related - with e-mail address) to Dr Arnold, indicating dates you are available. E-mail applications are accepted and encouraged. Applications to be received by Monday 13th March 2006. E-mail: K.Arnold@bio.gla.ac.uk

Dr. Kathryn Arnold

Royal Society University Research Fellow

Division of Environmental & Evolutionary Biology, Graham Kerr Building, University of Glasgow, Glasgow G12 8QQ

Tel. + 44 141 3302898 Fax. + 44 141 3305971 <http://www.gla.ac.uk:443/ibls/staff/staff.php?who=PGe~Pn>

UGuelph ProgrammerAnalyst

Job Description:

Position: Programmer Analyst (Canadian Barcode of Life Network)

Organizational Background: The Canadian Barcode of Life Network, which involves more than 50 researchers in university and governmental laboratories, has a lead role in a major international research program that is advancing a DNA-based approach to the identification of life. One critical element of this work involves the further development of BOLD, the Barcode of Life Data System (www.barcodinglife.org), that is a core data repository and analytical tool for DNA barcodes. We now seek a Programmer Analyst to advance the further development of BOLD. This position, which will be based in the new facilities of the Biodiversity Institute of Ontario, based on the campus at the University of Guelph, is ideal for someone who enjoys work in an academic setting on a project that matters. Excellent programming capabilities, good communication skills and a strong work ethic are critical.

Requirements: -Experience in developing with C, C++, Java, and PHP is essential -Experience developing in a cluster or grid environment is essential -Experience in

developing with J2EE technologies and environments is an asset -Experience with each of the following technologies is an asset: Object-oriented Design, XML, XSL, SOAP, HTML, Perl, Ruby, SQL, PostgreSQL, DB2, MPI, OpenMP, RMI -Experience with cluster management is an asset

Job Description: The incumbent will develop, test, implement, debug, document and assist in maintaining programs in the core technologies that are supported by BOLD. The incumbent will also aid development of specifications and provide time estimates for individual system components.

The Programmer Analyst investigates and analyzes ongoing requests and/or problems assigned by the Development Manager. On-going communication with the Development Manager and other members of the programming team and with the Network leadership team is required.

Key Skills and Abilities: -Aptitude for logical thinking, problem solving, and attentiveness to detail -Ability to organize time and work productively under pressure -Basic knowledge of systems analysis, design, and systems development disciplines -Ability to develop grid or cluster applications at a small scale.

Position Details Funding is in place to support this position for the next 4 years, but the prospect for longer-term extension is strong. Remuneration for this position should satisfy those with several years of work experience. This position is available immediately.

Application Procedures Interested candidates should send a statement of interest, a copy of their curriculum vitae and the names of three references by March 15, 2006 to Dr. Paul Hebert, Scientific Director, Canadian Barcode of Life Network, Biodiversity Institute of Ontario, Department of Integrative Biology, University of Guelph, Guelph, ON N1G 2W1. Email applications, which should use Programmer Analyst as the subject header, can be directed to (phebert@uoguelph.ca).

phebert@uoguelph.ca

UHouston FieldAssist

Undergraduate Research Assistants

Two research positions are available for the summer of 2006 (~June 1 to August 10) to assist in research on the effect of colony genetic diversity on colony func-

tion in the western harvester ant. The work is part of a long-term study of harvester ant population biology and evolution (<http://www.bchs.uh.edu/~bcole/pogo/>). The study area is located approximately 20 miles northwest of Grand Junction, Colorado on the Colorado plateau. Field assistants will monitor daily activity patterns, conduct food discovery experiments, and help with estimating reproductive output. Successful applicants must be reliable, tolerant of desert conditions, and must have their own car. We are seeking highly motivated people who can work independently and as part of a research group. In addition to a salary, student housing costs will be covered.

Interested applicants should send or email a cover letter, CV, and have three letters of references sent to: Dr. Blaine J. Cole, Department of Biology & Biochemistry, University of Houston, Houston TX 77204-5001. Electronic applications and letters of reference are encouraged. EMAIL ADDRESS: bcole@uh.edu. In your cover letter, please indicate how this position fits into your long-term career goals. Review of applications will begin April 10th and continue until the positions are filled.

Blaine J. Cole Department of Biology and Biochemistry
University of Houston Houston, TX 77204-5001 <http://www.bchs.uh.edu/~bcole/> Phone:713-743-2679 Fax: 713-743-2636

Blaine Cole <bcole@uh.edu>

UManchester EvolBiol

Dear colleagues

I am pleased to announce a number of position openings in the Faculty of Life Sciences at The University of Manchester. In today's issue of Nature, the Faculty has advertised a total of 20 academic positions throughout the life sciences, of which I am only highlighting those that I think are most directly related to the readership of this list. But I particularly encourage couples who are looking for two jobs in the same place to have a look at the whole list of jobs (<http://www.man.ac.uk/news/vacancies/academic.html#LS031>)

We are advertising these positions broadly. Our priority is to employ the best people rather than to target a specific subject area.

Should you be interested in more than one of the po-

sitions, I think the safest thing to do is to submit a separate application for each of them (I guess our office staff will be a bit overwhelmed with applications, and may not be able to copy applications to all relevant search committees). I definitely encourage such multiple applications.

Further, more formal, information on individual positions is available from the university's web site:

Lectureship in Evolutionary Biology <http://www.man.ac.uk/news/vacancies/LS036.pdf>
Lectureship in Evolutionary Developmental Biology <http://www.man.ac.uk/news/vacancies/LS037.pdf>
Lectureship in Anatomy <http://www.man.ac.uk/news/vacancies/LS033.pdf>
Other positions include Gene Expression, Integrative Plant Biology among others (<http://www.man.ac.uk/news/vacancies/academic.html#LS031>).

Additional information:

Because the ad does not contain much specific information about the institution and the positions, I will provide some information from my own perspective (this is my own experience and the best information I have, but it is not legally binding!).

The Faculty of Life Sciences is very large organization (around 200 academic staff) engaged in both research and teaching. The University of Manchester has resulted from the merger of the Victoria University of Manchester and the UMIST, and the new university has ambitious plans for growth and a substantial improvement of its research and teaching profile. As part of these plans, we anticipate that our Faculty should grow by a further 50% over the next decade. This size and the plans for growth make us a very dynamic place – new ideas and research initiatives can be realized quickly.

The Faculty is structured into research groups (<http://www.ls.manchester.ac.uk/research/themes/>), whose aim is to facilitate research and collaboration (without impeding collaboration across groups). Additional information on these groups is in the Further Particulars for each of the positions.

The ad mentions single positions in each area, but it has happened before that more than one than one person was hired, although only one position was advertised (when I applied, four candidates were interviewed for a single position, and three of us were hired!).

A Lectureship is a junior academic position, comparable to the rank of Assistant Professor in North America. A difference is that tenure is much less of a problem here. I have not yet heard of a person who was denied

permanent employment after the probationary period of 3-4 years. Promotion and permanent employment are not linked here (the ranks are Lecturer – Senior Lecturer – Reader – Professor).

Teaching loads here are comparable or lower than in most universities in North America. An average teaching load includes around 25 hours of lecturing per year, some small-group teaching (tutorials for science students or problem-based learning for medical/dental students), supervision of student projects, and some marking of written work. Efforts are made to coordinate the teaching assignments with the research interests of staff members, but this does vary a bit from person to person.

The Faculty puts major emphasis on excellence in research. Research funding in the UK is competitive, but as far as I know, it is about as good as it gets anywhere these days. There is a range of funding agencies including government research councils (NERC, BBSRC, MRC) and charities (Wellcome Trust, Lister Institute among others) including one charity that specializes if funding projects that are hard to fund otherwise (Leverhulme Trust). Equipment grants can be obtained from the Royal Society and other funding bodies (and equipment can be included in normal grants). Research proposals are shorter than in many other countries (up to 8 pages for a full

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UMelbourne EvolBiol

<<http://www.hr.unimelb.edu.au/pds/Y6540150.pdf>>Y6540150 - LECTURER IN ZOOLOGY (Evolutionary Biology) (Listed 10 March 2006) Department of Zoology Salary: \$62,057 - \$73,692 p.a. (Lecturer, Level B) plus employer superannuation contributions of 17 percent. Full-time Applications close: 10/4/2006 URL for information: <http://www.hr.unimelb.edu.au/pds/Y6540150.pdf> Professor David L. Macmillan Head, Department of Zoology University of Melbourne Parkville Vic 3010

David Macmillan <zoomac@ariel.its.unimelb.edu.au>

UNottingham ResAssist Sticklebacks

Research assistant, host-parasite coevolution in sticklebacks.

I am looking for a graduate research assistant to work on host-parasite coevolution in fish, based at the School of Biology, University of Nottingham, U.K. (Fixed-term, part-time, 15 months).

The successful candidate will be required to assist with studies of host-parasite interactions in natural populations of three-spined sticklebacks. Duties will include: (1) Surveying the parasites of sticklebacks in lochs in Scotland, and waterbodies in the Midlands. (2) Assisting with the execution and monitoring of experiments designed to examine the extent of local adaptation between sticklebacks and their parasites. (3) Assaying parasites in samples of collected material. (4) Entering data into computer databases and performing summary analyses. (5) Assisting with care of aquaria when necessary and developing new research areas as time allows.

Candidates must have a degree in ecology, zoology, parasitology or a related subject and an interest in host-parasite interactions. They should be flexible and willing to carry out fieldwork in remote locations and hold a full driving licence.

Salary will be £20,842 to £22,774 pro rata for this part time post working 80% of a full time post, working pattern to be agreed. Offered on a fixed-term contract for a period of 15 months.

The work is likely to involve long periods (6 to 12 weeks) of fieldwork in isolated parts of Scotland in the spring/summer, and extensive microscope work in winter to assay and identify parasites.

Informal enquiries may be addressed to Dr Andrew MacColl, tel: +44 115 9513410, Email: Andrew.Maccoll@Nottingham.ac.uk.

Candidates should send a detailed CV, together with the names and addresses of two referees, to Dr Andrew MacColl, School of Biology, University Park, The University of Nottingham, NG7 2RD. Email: Andrew.MacColl@nottingham.ac.uk. Closing date: as soon as possible, but formally 14 April 2005.

Andrew MacColl

Lecturer and NERC Postdoctoral Fellow School of Bi-

ology University of Nottingham University Park Nottingham NG7 2RD Tel: 0115 951 3410 Fax: 0115 951 3251

andrew.maccoll@nottingham.ac.uk
andrew.maccoll@nottingham.ac.uk

an-

UOttawa TeachingEvol

Dear Evoldir,

Two full-time, 2-year teaching positions (French preferred for one/required for the other) are available at the University of Ottawa in Ottawa, Canada, at least one of which includes those with an evolution and/or ecology background. The job ads are below.

Cheers, Howard Rundle

THE UNIVERSITY OF OTTAWA The Department of Biology invites applications for two full-time temporary positions at the assistant professor level to commence July 01, 2006. I. A two-year, full-time teaching position. The successful candidate will participate in undergraduate teaching in cell and molecular biology, and/or ecology and environmental science, and/or animal physiology. (S)he may also participate in the supervision of honors research projects. Although there are no expectations regarding research for this position, some accommodation can be made if the candidate wishes. Bilingual candidates will be preferred. II. A two-year, full-time teaching position. The successful candidate will participate in French language undergraduate teaching in areas of organismal and animal biology, vertebrate zoology and/or ecology and evolution. (S)he may also participate in the supervision of honors research projects. Although there are no expectations regarding research for this position, some accommodation can be made if the candidate wishes. An ability to teach in French is essential and preference will be given to bilingual candidates.

Applicants should send a description of their teaching interests and curriculum vitae, and arrange for three letters of reference to be sent before April 15, 2006 to: Teaching Search Committee, Department of Biology, University of Ottawa, 30 Marie Curie, Ottawa, ON, K1N 6N5 Canada. Fax: 613 562 5486. Equity is a University policy; the University strongly encourages applications from women, members of visible minorities, native peoples, and persons with disabilities. In accordance with Canadian immigration requirements,

priority will be given to Canadian citizens and permanent residents of Canada.

L'UNIVERSITÉ D'OTTAWA Le département de biologie invite les candidatures pour deux postes temporaires de professeurs adjoints à temps complet débutant le 1er juillet, 2006. I. Un poste d'enseignant à temps complet, contrat de deux ans. La personne sélectionnée participera au programme d'enseignement de premier cycle en biologie cellulaire et moléculaire, et/ou en écologie et sciences environnementales, et/ou en physiologie animale. Elle pourrait aussi superviser des projets de recherche de spécialisation. Même si ce poste n'implique pas nécessairement d'activités de recherche, il serait possible de fournir les espaces nécessaires si le candidat le désire. La préférence sera accordée aux candidats bilingues. II. Un poste d'enseignant à temps complet, contrat de deux ans. La personne sélectionnée participera au programme d'enseignement de premier cycle, en français, en biologie des organismes et en biologie animale, en zoologie des vertébrés et/ou en écologie et évolution. Elle pourrait aussi superviser des projets de recherche de spécialisation. Même si ce poste n'implique pas nécessairement d'activités de recherche, il serait possible de fournir les espaces nécessaires si le candidat le désire. La capacité d'enseigner en français est essentielle et la préférence sera accordée aux candidats bilingues.

Les personnes intéressées à poser leur candidature doivent faire parvenir une description de leurs intérêts en enseignement, leur curriculum vitae et trois lettres de références pour le 15 avril, 2006 à l'adresse suivante: Comité de sélection-enseignant, Département de biologie, Université d'Ottawa, 30 Marie Curie, Ottawa, Ontario, K1N 6N5, Canada. Télécopieur : (613) 562-5486. Conformément aux exigences d'immigration Canada, toutes les personnes qualifiées sont invitées à postuler; la priorité est toutefois accordée aux citoyens canadiens et aux résidents permanents. L'Université d'Ottawa souscrit en outre à l'équité et encourage donc fortement les femmes, les autochtones, les membres des minorités visibles et les personnes handicapées à poser leur candidature.

Howard D. Rundle Assistant Professor - Professeur adjoint Canada Research Chair - Chaire de recherche du Canada Department of Biology - Département de biologie University of Ottawa - Université d'Ottawa 30 Marie-Curie (277 Gendron) Ottawa, Ontario, K1N 6N5, CANADA

T: +1 (613) 562-5800 x2835; F: +1 (613) 562-5486
Email: hrundle@uottawa.ca; Skype: howardrundle
<http://www.science.uottawa.ca/~hrund050/> hrundle@uottawa.ca hrundle@uottawa.ca

USussex EvolBiol

Dear Evolutionists,

The University of Sussex will soon be seeking several new faculty members to join the School of Life Sciences. There is reasonable chance that one of these new posts will be in the area of evolutionary biology. With this in mind, we would like to solicit expressions of interest in joining our faculty from qualified evolutionary scientists. Applications in any area of evolution are welcome, including molecular studies, behavioural evolution, laboratory-based experimental evolution, and studies of cultural evolution in humans and/or other animals.

If you are interested in the possibility of a permanent faculty position at Sussex, then please email a CV and a statement of your current research interests to Joel Peck at j.r.peck@sussex.ac.uk .

Many thanks, Joel

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

UWurzburg EvolBehavior

The Biocenter, University of Würzburg

* invites applications for a*

* *

W3 ? Professorship

* in Zoology II*

(permanent tenured position)

The Chair in Zoology II is part of the Theodor-Boveri-Institute for Biology (Biozentrum), University of Würzburg. The successful candidate will have the responsibility for teaching animal physiology, and the main focus of research should be in a modern area of animal physiology, in particular behavioral physiology. The appointee is expected to participate in the University's interdisciplinary collaborative research centers (Sonderforschungsbereiche) 554 ?Mechanisms and evolution of arthropod behavior?, and 567 ?Mechanisms of interspecific interaction of organisms?. The successful

candidate should be internationally renowned, and is expected to promote interdisciplinary activities, such as the establishment of a new graduate school at the University of Würzburg, and to assume academic administrative responsibilities.

Requirements include University education and a doctoral degree, good teaching skills, and habilitation or equivalent academic qualifications.

At the time of appointment the candidate should be younger than 52 years of age (exceptions may be possible in special cases according to Art. 12 Abs. 3 Satz 2 BayHSchLG).

The University of Würzburg explicitly encourages applications from female candidates in an effort to increase the representation of women in research and teaching.

Handicapped applicants who meet the expected standard of qualification will be given priority.

Applications, including curriculum vitae, certified copies of degrees, proposed research plan, and documentations of teaching experience and external grants together with a list of publications including reprints of the five most important papers should be sent to the address below *by April 7, 2006.*

Dekan der Fakultät für Biologie

Biozentrum, Am Hubland, 97074 Würzburg, Germany.

–

Dr. Heike Feldhaar Department of Behavioural Physiology and Sociobiology (Zoology II) Theodor- Boveri Institute for Biosciences University of Wuerzburg Am Hubland D- 97074 Wuerzburg Germany

phone: 49- (0)931 - 8884305 fax: 49- (0)931 - 8884309

mail: feldhaar@biozentrum.uni-wuerzburg.de

Heike Feldhaar <feldhaar@biozentrum.uni-wuerzburg.de>

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64bit applications

Hello. I am wondering if any phylogeneticists/pop gen types out there have made the switch to 64 bit machines, and more specifically, how have some of the workhorses of the software world responded. If you have experience running PAUP, Mesquite, Migrate, or any other relevant software I would love to hear from you.

Jim

Jim Austin Joint Assistant Professor Wildlife Ecology & Conservation/ Fisheries & Aquatic Sciences
www.wec.ufl.edu/faculty/austinj austinj@ufl.edu

austinj@ufl.edu

ABI3100-Pop4 Problems

Dear All: Here Im , back again with problems with ABI 3100 sequencer. There are three symptoms that lead us to think that there might be a pop4 problem. Those problems are: 1- red peaks (not real peaks, more like noise peak) 2- high molecular weight standard peaks falling down, notoriusly. 3- high molecular weight microsatellites broadening 4- Elevated current (instead of falling current, which is normal) These symptoms seem to indicate that the cappillary array is stucked. It happens after processing only a few samples in different capillary arrays. But the thing is that we have changed several times the array, the pop (same lote number),

buffers, etc. and the only thing that seemed to make it better is changing pop, but it is only for a few samples, then the problem comes back. This problem is new. We have been working with the same protocol, sample types and materials for a long time and we never saw this problem before. Does anyone have an idea? could it be that the pop4 lote is all wrong? Any idea will be of interest. Thanks!!!

Andrea A. Merás ameras@iib.unsam.edu.ar

“Andrea A. Merás” <ameras@iib.unsam.edu.ar>

ABI3100 standard flat

Dear All: I have written you before asking for some help with ABI3100 sequencer. Since a couple of months, we,ve been seeing standard flattening out (higher molecular weight peaks) and red spike peaks in data. Those problems seemed to be solved by changing polymer lot. Even though red peaks dissapeared (untill now at least), standard flatenning out came back after a few injections. Thats why we are very confussed about the origin of this problem. Any suggestion? Thanks again.

Andrea A. Merás ameras@iib.unsam.edu.ar

Andrea A. Merás ameras@iib.unsam.edu.ar

“Andrea A. Merás” <ameras@iib.unsam.edu.ar>

AFLP answers 2

Scoring AFLP

Hi, Are you using the automatic scoring from Genotyper? My advice is don't, you can not really trust the machine to score your peaks only based on the peak size. Are you defining categories? If you define a category by drawing the square on a peak and then `ctl+1` (give it a name and select highest peak, exclusive, with (scaled) height of at least...) for each band individually you are more likely to extract the real data. It is like giving standards for each band-size individually. You'll probably find that each band-size has its own characteristics and then you'll be able to tell between noise and a real peak. You may have to avoid overlapping categories, since they are very noisy. You'll find that some peaks need the (scaled) height of 1000 and others of 90. It is kind of half-ways between hand-scoring and the automatic method. Yes, it is time-consuming, a good two weeks of scoring only, but is worthy. I have also found that Nei's distances are not appropriate for AFLPs, they assume the same mutation rate across loci. For a dendrogram try Reynolds, Weir and Cocke's 1983 as implemented in Phylip. That one does not assume equal mutation rate. Hope this helps,

Alejandro Nettel-Hernanz Ph.D. Candidate Dodd Lab
UC Berkeley ESPM-Ecosystem Sciences 323 Mulford
Hall Tel (510) 643 3137 anettel@nature.berkeley.edu

Hi Marianne,

I have spent a lot of time also thinking about the problem with calling AFLPs. I have been working with Steve Keller at UVA, and I think an email he sent me recently might be helpful.

Second, I've fiddled with this quite a bit, and thought about it even more (sometimes to the point of keeping me up at night!). As you say, it's subjective. I don't see any way around that. However, my best solution has been the following: First, make sure you assign each individual sample a relative signal strength (Genotyper has a way of doing this automatically), so you normalize signal strength among your samples. Next, define your loci across the entire sample using a very stringent (i.e., high RFU threshold, say 200) criteria. The intent here is that only "real" loci are going to get defined. This approach requires a high signal strength in only one individual for a locus to get defined. After I get my loci definitions this way, I then score all the samples with a less stringent RFU requirement (say 50). That way, you're scoring individuals for loci that you have high confidence are real and not artifactual, but you are lenient on whether any given individual is present for that locus.

I have started to use this technique and feel more con-

fidant when I'm seeing a peak vs. noise. I think that 20 is too low.

Hope this helps.

best, Amy

Hi Marianne, I don't know what instrument you are using to run your AFLP samples, but the ABI capillary system we've been using (ABI 3100) only processes peaks above 50. It's suggested you do not score low peaks as it's close to instrument threshold. So if I'm correct people usually score peaks that are mostly above 100. The problem with smaller peaks is not only the risk that another small peak won't be detected, but also some small peaks can be just AFLP artefacts -> hence 2 possibilities of introduction of noise into your dataset. Using AFLP, you should have a plenty of markers, so using less, but more correct ones should only be an advantage. Another thing to look at is the size of your bins (categories) in Genotyper. I think the recommended size is around 1bp. So adopting rather broader concepts of categories - as size of peaks may vary slightly between runs or capillaries - may also reduce some noise in your data. Especially if you have a lot of markers that are quite close to each other and/or many diverse populations or even species. Hope this helps & good luck with your work! Sarka

Sarka Jahodova Department of Ecology Charles University Vinicna 7 128 44 Prague Czech Republic

Hi Marianne,

I have been wrestling with my AFLP's for a couple of years now, so I can tell you what I've learned. I'd be interested to hear what others advise you as well.

Abundant noise is common for AFLP's, as well as problems with changes in signal strength between runs, and differences in peak size due to heterozygosity and superimposition of different fragments of the same length. Because of these things, it is appropriate to limit your 'loci' to those that you can score reliably, even in weak samples. I focus on peaks that appear several times the strength of the background noise in at least some samples, then go through and look carefully for peaks of any size in those positions in the other samples. I do not feel that differentiation of heterozygotes and homozygotes is possible or reliable or distinguishable from superimposed fragments of different origin, so I score any size peak at a locus equally. It is important to run samples in a randomized manner and to run some duplicates in order to verify that

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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

AFLP scoring answers

Hi everybody, Thankyou very much for your answers. I have attached a file containing them all.

To summarize I found that not only I find it difficult and quite subjective to score AFLP peaks. (thanks that was nice to hear). The advise adds up to making the DNA quality as good as possible. Running at least some samples twice to check the error percent. Try to standazise the samples amplification. Choose a minor level eg. 10 percent of largest peak.

And ofcause it is advisable to mix samples on gels and scoring without knowing the origin of the sample. Also I will score some more peaks so I have at least 125 good ones for my analysis.

Thankyou again for your help.

Marianne Lindhardt
mariannel@bi.ku.dk

AFLPs GeneMarker

Dear Colleagues,

We are interested in purchasing GeneMarker to analyze AFLP data, and we are curious about your opinions concerning the software. If anyone has any good or bad comments please let me know. Thank you!

<http://www.softgenetics.com/gm/index.htm> Leslie Rissler Ecology, Evolution, and Systematics Department of Biological Sciences University of Alabama Tuscaloosa, AL 35487

rissler@bama.ua.edu

Algal Micro mutation rate

Dear all, I received this question and I would like to

pass it to Evoldir members.

I hope anyone could help with these two questions: Does anyone know any estimates of microsatellite mutation rate for brown algae and the generation time for Fucus?

Any information is much appreciated and if you can send me some references as well, even better.

Thanks in advance

Milena Polifrone

Dr. Milena Polifrone Department of Biology University of Las Palmas Campus Universitario de Tafira 35017 Las Palmas Canary Islands, Spain

mpolifrone@becarios.ulpgc.es

Cheap BAC libraries

Hello,

we are thinking about having a BAC library built for our favorite ant. Google turns up a few north american companies that can do this sort of thing.

But maybe you have experience with an overseas company that could be less expensive?

Thanks for any tips,

yannick

yannick.wurm@unil.ch - Doctoral student Department of Ecology and Evolution <http://www.unil.ch/-dee/page28685.html> #3106, Biophore, Université de Lausanne 1015 Lausanne, Switzerland land: +41.21.692.4182 fax: +41.21.692.4165 cell: +41.78.87.87.001

Yannick.Wurm@unil.ch

Cheap micros answers

Thanks to all of you who answered my question about cheap ways to score microsatellites, looks like they still have to invent a really cheap and precise device, anyway here they are:

Hi Andrea, The spreadex system from Vhbio resolves

to 2bp and scores 96 samples for c.£20. Unfortunately you'll only be able to score one loci at a time but it provides a relatively cheap solution with a small set up cost. You can stain the gels with Syber gold which is less time consuming than silver staining. The gels are fairly robust but you need a special rig and power pack to run them. The obvious alternative is a sequencer if you run your PCR products in a multiplex PCR etc. Our company charges £2.00 per run. For instance we use an eight primer multiplex PCR to genotype cherries which makes it a more cost effective solution. Best of luck. Jake Hi

We use a Licor sequencer and we are very happy because the reagents and glass for gels are very cheap. We only have one banding colour but it works quit well and you can do a lot of PCR's on multipelx depending on mSats number of bp.

Good luck

Best regards Hello Dr. Verardi, I am responding to the email you sent to the EvolDir concerning scoring of microsatellite data. Our not-for-profit facility (in Canada) does this for academic labs at a very reasonable cost (on our ABI 3730 instruments)- what is your sample size and number of loci (are they multiplexed or pooled). I would happy to give you an estimate for this, if you decide not to purchase an instrument for your facility. However, I would recommend the ABI 3100 instrument as a reasonably-priced instrument to score fluorescently-labelled microsatellite fragments - it can run approx. 3 plates of 96 samples per day. Best Regards, Tara Paton Hi Andrea,

One alternative would be to look for a used sequencing machine. It's likely that this may actually be just as, or more, expensive as sending samples out but you never know. Maybe something on e-bay or other used lab equipment sites. The only caution there is whether you can still obtain the necessary supplies to continue running the machine. Actually, one more caution is whether the machine you decide on has a history of problems. If so, you would want to make sure that the manufactuer still supports the machine.

Another alternative may be to try to collaborate with someone at an institution that already has a sequencer. You could prepare all of you samples locally and then spend a bit of time in the lab of someone who has a bit of space and would be willing to sponsor you. Just another thing to consider.

Good luck!

Hi Andrea, I know of cheaper prices for sequencing work at Cardiff University - they are one of the cheapest services but still relatively expensive. There is also a se-

quencing service in Korea Macrogen but you have to ship it there and you really have to do above a certain number of runs before it becomes worth while but surprisingly if you have enough it can be one of the best options. In the UK there is a NERC facility that you can apply for a sheffield University but I'm not sure what the eligibility foir this facility is exactly. If you need further information on any of these let me know and I'll give you some more details.

If you find out about any other good cheap facilities that are better than the ones I've listed please could you pass on the details. Good luck, Vittoria

I am currently using a Li-cor system (4300) and I have previously used a Corbett Research GelScan2000. Both are very useable. The Gelscan is cheaper and I could push samples through quicker, but is only has one channel and, outside of Australia where Corbett is based, support is poor. The Li-cor is more expensive, may take longer (but could actually be as fast with the short plates. I only have the long plates) but it has two channels (i.e., you can run two different colored dyes at the same time) and probably has better support. The dyes are quite expensive for the Li-cor machine, whereas the Corbett machine uses the same dyes as PE machines.

Hope that helps. Any further questions, drop me a line.

Mike

We use LiCor DNA sequencers to score microsatellites. They're reliable, and the customer support is outstanding (much better than ABI).

www.licor.com Best wishes, Mohamed Noor

— evoldir@evol.biology.mcmaster.ca ha scritto:

Hi everybody, Thankyou very much for your answers. I have attached a file containing them all.

To summarize I found that not only I find it difficult and quite subjective to score AFLP peaks. (thanks that was nice to hear). The advise adds up to making the DNA quality as good as possible. Running at least some samples twice to check the error percent. Try to standazise the samples amplification. Choose a minor level eg. 10 percent of largest peak.

And ofcause it is advisable to mix samples on gels and scoring without

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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>

Contig Assembly Update

Dear Colleagues,

Last summer I posted a plea for DNA sequence editing software that would 1) align contigs (to each other, across individuals), 2) allow access to chromatograms with a simple mouse click (so that data can be compared quickly and easily both between primer reads from one individual and between multiple individuals in a data set), 3) work with Beckman sequencer data, 4) be economical for evolutionary biologists without huge grants, and 5) be relatively easy to use and bug-free.

At that time, I felt positive about the Codon-Code Aligner (<http://www.codoncode.com/aligner/new.htm>) program that did many of these things, but did not do #1, a feature that I had only seen in the cumbersome and expensive ABI SeqScape program. I am happy to report that the new version of Aligner (1.5.1) will make a contig of contigs and thus satisfies criterion #1. It does NOT require a reference sequence. The cost for the first license is unchanged (\$960 US), but the price of the second license has increased a bit (from \$480 US to \$720 US). This is still an excellent bargain compared to Sequencher and Seqscape and many other programs. CodonCode Aligner is easy to use and the developers are responsive to suggestions.

I don't work for these guys, and have no financial interest in the product. I don't even know them. I am just psyched to share a solution that will save me (and many others based on the responses to my first message) many hours of sequence editing.

Thanks,

Steve

Steve Jordan Department of Biology Bucknell University Lewisburg, PA 17837 Office: 310 Bio. Bldg. +1 570-577-1254 Lab: 331 Bio. Bldg. +1 570-524-3816 Fax: +1 570-577-3537 <http://www.facstaff.bucknell.edu/sdjordan/jordan.html>

sdjordan@bucknell.edu sdjordan@bucknell.edu

DNA from etoh

Dear colleagues,

We are conducting a population genetic study in our lab with charr and other salmonid microsatellites. At present we are having real problems with extracting good quality DNA from our older fin clip samples, which have been stored in ethanol for around 10+ years (in +4 C). Can any of you give us some advice on how to get our extraction protocols working on older samples too?

The protocols we've been using are as follows:

Ethanol removal (for 1+ year old samples only): Remove ethanol from eppendorf tubes and add an equal amount of 0,1x TE buffer, incubate overnight.

Proteinase K digestion: Mix 5600ul salt extraction buffer, 560ul 20% SDS and 130ul proteinase K, then add 60µl of this mix to each well of the 96-well plate. Add tissue piece(s) (ca 1 mm³) and seal with strip caps. Incubate @ 60 C for a few hours

DNA extraction: The protocol is basically the glass beads extraction method described in: Elphinstone, MS, Hinten, GN, Anderson, MJ & Nock CJ 2003. An inexpensive and high-throughput procedure to extract and purify total genomic DNA for population studies. Mol. Ecol. Notes 3:317320.

(More detailed workflow can be downloaded from http://users.utu.fi/albval/tutkimus/M13-Tailed_PCR.pdf)

The protocol (without ethanol removal) and used PCR primers work well with new samples. Using the TE-buffer incubation we've been able to get good results also from samples 5+ years old. Only with the 10+ years old samples the amount and quality of extracted DNA is too poor for most PCR reactions, although a few loci in a few individuals manage to amplify.

Thank you in advance for your help and comments,

- J. Albert Vallunen, Graduate student Laboratory of Genetics, Department of Biology 20014 University of Turku Finland tel. +358 2 333 7085

albval@utu.fi

Decapod lowcopymarkers

Dear colleagues,

We are presently trying to amplify low-copy nuclear markers of decapod crustaceans but haven't had much success yet using standard primers for Elongation Fac-

tor 1a, Calmodulin, Amylase and Aldolase. The samples do, however, amplify readily with various primer combinations for COI, 12S, 16S, 18S and ITS. Is anybody out there using primers for low-copy nuclear markers that routinely work on decapods?

Thanks, 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 http://www.ru.ac.za/academic/departments/-botany_research/Peter/

my populations does not come out with the other populations of the same species. Also it is only possible to reallocate (using AFLPOP) 47% back into the population of origin. The results seem much better if I use only peaks of 50 or over in Genotyper, but does that not leave too much information out? It leaves out many smaller peaks. This is my first time using these methods, so I feel quite insecure about what is most correct.

Cheers, Marianne Lindhardt Dpt. of Population Biology University of Copenhagen

mariannel@bi.ku.dk

Decay indices

Dear all,

I am trying to calculate Decay indices in the resulting maximum parsimony trees, obtained from a molecular data set (16S rRNA gene). I did this analysis using MacClade and PAUP, treating gaps as missing data and it worked perfectly. But when I tried doing this analysis treating gaps as a fifth character state, MacClade won't accept this condition and will treat gaps as missing data.

How could I calculate Decay indices in my MP trees, treating gaps as a

fifth character state?

Thanks,

Alexandra

Alexandra Hiller Department of Animal Ecology Justus-Liebig University Heinrich-Buff-Ring 26-32 35392 Giessen Germany Tel: ++49-641-9935624 Fax: ++49-641-9935299

Alexandra.Hiller-Galvis@allzool.bio.uni-giessen.de
Alexandra.Hiller-Galvis@allzool.bio.uni-giessen.de

Difficulties Scoring AFLP

Hi everybody,

I hope that somebody can help me! I have problems with too much noise in my AFLP dataset. First I scored all peaks of 20 or over which gives so much noise that

ErnstMayrAward SSBMeeting StonyBrook

Ernst Mayr Award

General Information. The Ernst Mayr Award is given to the presenter of the outstanding student paper in the field of systematics at the annual meetings of the Society of Systematic Biologists, as judged by the Ernst Mayr Award Committee. The award consists of \$1000.00 and a set of a set of available back issues of Systematic Zoology/Systematic Biology.

Who is Eligible. Members of the Society who are students or have completed their Ph.D. within the last 15 months are eligible. Students should submit their titles for the SSB Meeting in Stony Brook, New York, and indicate at the time of submission that their talk is a potential competitor for the SSB Ernst MAYr Award (this category is now in the drop down menu on the Tilete registration page). Students should ALSO submit a 400-word abstract of their talk to the current awards chair (Kelly Zamudio, krz2@cornell.edu) by March 31, 2006. Please include your abstract in the text of your e-mail, and include your name and complete contact information.

** Please note that the registration deadline for the talks at Stony Brook is mid April, but to be eligible for the Mayr Awards, contenders must submit their abstracts to Kelly Zamudio by the earlier deadline (end of March).

Based on the submitted abstracts, the Mayr Awards committee (appointed by the Awards Chair) will select the best 15 for inclusion in the actual competition at the meetings, which will be held at a single venue in a separate session. Previous winners are not eligible.

Judging. Papers will be judged on creativity, quality, excellence of research, and quality of presentation. Abstracts should clearly indicate methods used, the relevance to systematics and the conclusions. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible.

Co-Authors. The paper may be co-authored. It is understood that the ideas, data and conclusions presented are primarily and substantially the work of the student presenting the paper and the intention is that person will be senior author on the published version of the paper.

Notification of Winner. The winner of the award will be announced at the SSB business meeting at Stony Brook, during the banquet at the annual meetings, and an announcement will be published in Systematic Biology.

Application submission and confirmation

Applications should be sent to Dr. Kelly R. Zamudio, SSB Award Committee Chair, at krz2@cornell.edu E-mail submissions are required.

Application deadline is March 31, 2006.

To ensure that applications are not lost in electronic transfer, the awards chair will send each applicant a confirmation e-mail. If you do not receive this confirmation within 3 days of your submission, please contact the awards chair to arrange for re-submission.

krz2@cornell.edu krz2@cornell.edu

EtOH DNA

Dear evoldir members,

I am having difficulties in extracting DNA from some old (>10 years) ethanol preserved tissue samples. My extracts contain DNA but its quality is very low. I am guessing they contain too many short fragments which inhibit the amplification of the gene i need (mitochondrial Dloop control region). I have tried to amplify both a short part of the gene (around 500 bp) and the complete sequence (around 900 bp) but none worked. I would like to ask if anyone knows of some way to remove the shorter DNA fragments keeping only the bigger ones. I have tried running the extracts on agarose gel and then purifying the DNA from the gel, but it doesnt work (maybe the DNA concentration prior to

PCR is not high enough to allow it?). Any help would be much appreciated, my email is below,

cheers, bruno

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Bruno.Nevado@naturalsciences.be

European samples *Nasonia vitripennis*

Dear All,

I am a PhD student at Groningen University (Netherlands) and I am working on the biogeography of the Jewel Wasp (*Nasonia vitripennis*). *N. vitripennis* is a cosmopolitan parasite of cyclorrhaphous fly pupae. It can usually be found in bird nests and on carcasses. It has been used extensively in the laboratory but field studies are rare.

To complete my sample set, I am in need of additional samples, preferably from Europe. I would greatly appreciate any ethanol preserved samples that anybody could supply. If you can provide some material or you know somebody how might ... please contact me. Thanks a lot !

Regards

Bernd

Bernd Grillenberger

Evolutionary Genetics Center for Ecological and Evolutionary Studies University of Groningen Kerklaan 30 NL-9751 NN Haren P.O. Box 14 NL-9750 Haren The Netherlands Phone: +31 (0)50 363 2128 Email: B.Grillenberger@rug.nl

ExoSAP-IT Answers

EvolDir community,

I have been using ExoSAP-IT for PCR cleaning prior to sequencing and it has worked great. However, has anybody tried to use less than recommended (2ul per 5 ul of PCR product)? Any experimental results with this product would be helpful.

Thanks, Greg Douhan

Greg W. Douhan, Assistant Professor Department of Plant Pathology Fawcett Lab RM 238 University of California Riverside, CA 92521-0122 (951) 827-4130 gdouhan@ucr.edu

Here are the responses about my ExoSAP-IT post. I did not post all of them but this gives the range of answers. The bottom line is you can use 'much less' and buy the reagents separately to 'save money'-that's what I like to hear. The answers should interest many of you out there.

Thanks so much. Greg

***** Greg W. Douhan, Assistant Professor Department of Plant Pathology Fawcett Lab RM 238 University of California Riverside, CA 92521-0122 (951) 827-4130 *****

We make up our own concoction of Exonuclease I and Shrimp Alkaline Phosphatase that works great.

To 5ul PCR product, add 0.5ul of 1U/ul SAP + 0.5ul of 10U/ul ExoI. Incubate in a thermal cycler 30 minutes at 37deg then 15 minutes at 80deg.

Both chemicals are sold separately by GE Healthcare (formerly Amersham Biosciences).

We usually make up a fresh "ExoSAP" mastermix everytime we do a round of PCR and add 1ul of the mastermix to 5ul product. I've never experimented with making up batch volumes for further down the road, but feel free to try and let us know if it works! If you need more product for sequencing, just scale up.

Hope that helps! Elizabeth

Hi Greg, I have successfully used 2 ul of exosapit / 10ul reaction. To test this, I mixed the same amount of product with different amounts of exosapit, then compared the sequence data. If it looks good with less exosapit, then you can probably get away with less. Hope this helps, Jen Knies UNC-Chapel Hill

***** Dear Greg,

We also use ExoSAP-IT in my lab. We routinely use 1 ul of ExoSAP-IT for 5 ul PCR product rather than the

recommended 2 ul. I have not tested it further to see if 0.5 ul or less would also work. However, we are also now saving a lot of money by making our own ExoSAP-IT. Here's the recipe.

89 ul ddH2O 1 ul Exonuclease I (10 u/ul; USB cat# 70073Z) 10 ul Shrimp Alkaline Phosphatase (1 u/ul; USB cat# 70092Y) 100 ul Total It works great! I couldn't believe it when someone first brought it to my attention because you don't use any buffer. I thought for sure the enzymes would denature. But they don't and it works just as well as the premixed ExoSAP-IT we used to buy from USB.

I mix it up in 100 ul batches about 5 at a time and keep them in the -20 and they seem to last pretty much indefinitely.

Good luck!

Randy Small ***** Hello,

I buy my Exonuclease and SAP from Amersham and only use 1ul of each for 12 ul of PCR product. Did someone tell you needed to add this much or is this from the company you are purchasing it from? I have sequenced on ABI (model 3100) at our genomics facility and on our own Beckman CEQ 8000 and it seems to always work great.

BTW I am UCR alumni....miss the campus.

Noelle

Noelle A. Barkley PhD Molecular Geneticist USDA-ARS PGRCU 1109 Experiment St. Griffin, GA. 30223 770-412-4035 *****

Dear Greg, we are used to clean PCR product in our lab with 1ul of exosap mix (0.5 exo+0.5sap if you have separated vials of the two components) and it works really well. Of course if you need particularly clean PCR for very important sequences you may go back to your concentrations. I hope this helps Best regards Chiara

Dr. Chiara Papetti Biology Dept University Of Padova Via G. Colombo I-35100 Padova Italy e-mail cpapetti@bio.unipd.it chiara.papetti@unipd.it Tel 0039 049 8276222

Hi

I have used 2ul in a 10ul reaction and that works perfectly well Cheers

Kerry evoldir@evol.biology.mcmaster.ca wrote: ***** Hi Greg,

I did some testing a few months ago with primersolution, and it seems you can use 4 times less ExoSAP-it. I attached a picture with my test results (sorry, the text

is in Dutch on the picture). This is what I did :

1. I prepared a 25 μ M primer solution 2. I took 5 μ l of that primersolution for each test 3. on the picture starting from left : 2 - 1 - 0.5 μ l ExoSAP-it -> all primer is gone 4. middle part on picture : ExoSAP-it diluted (10 times) in distilled water, and from that dilution I took 5 - 3 - 2 - 1 - 0 (blank) μ l for testing. 5. right part of picture : ExoSAP-it diluted (10 times) in 1x PCR buffer, and from that dilution I took 5 - 3 - 2 - 1 μ l.

Results : - dilution in distilled water gives not so good result - dilution in PCR buffer gives better results, 5 μ l of 1/10 dilution in 5 μ l primer removes all primer, this is the same as 0.5 μ l pure ExoSAP-it.

— / —

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>

ExoSAP-IT PCR

EvolDir community,

I have been using ExoSAP-IT for PCR cleaning prior to sequencing and it has worked great. However, has anybody tried to use less than recommended (2ul per 5 ul of PCR product)? Any experimental results with this product would helpful.

Thanks, Greg Douhan

Greg W. Douhan, Assistant Professor Department of Plant Pathology Fawcett Lab RM 238 University of California Riverside, CA 92521-0122 (951) 827-4130

gdouhan@ucr.edu

G-50 Sephadex Cleanup

My lab has recently started a new bottle of G-50 (DNA Fine grade) used in the Sephadex cleanup of Cycle Sequenced material. We are ending up with a pellet of excess white powder after we dry our samples with a vacuum centrifuge, when before we had none. Should

we ignore this? Will this damage the ABI-3100 in our core facility?

Thanks for any assistance -Anson Koehler

University of New Mexico

GeoDis problems

I am working on my thesis using GeoDis 2.4 looking at phylogeographic gene flow of Horned Lizards. The problem is that the program is having issues with my input files. Here is an example-

Clade 1-1 2 II III 1 0 1 1 1 1

Error message reads : the number of haplotypes for location X can not be one-you need genetic variation for this analysis. I do believe that II and III of line 3 represents 2 haplotypes! I've tried entering 2 i.e. 2 haplotypes at location 1-same thing (2 was entered for line 7) Also just entering 1 under location 1 just to see-same thing Another example

Clade 3-3 2 2-5 2-2 1 0 2 2 5 1 0 0 1

The program error is the same-it flags location 2 as being problematic and not 5. The same thing happens in another file and the clade is flanked before and after with clades that have the exact same scenario (clade 1-1 o.k 1-2 not o.k 1-3 fine). Why it chose the middle one and was happy with the rest-I don't know. If you have any insight into this, I would welcome your help.

Thanks, Austin austin.burt@juno.com

austin.burt@juno.com

Help with Migrate answers 2

Dear Tatjana and other evoldir members.

I want to make a couple of comments to some of the comments you got.

***Consistency of results of ML programs, such as migrate, fluctuate, lamarc, (or Bayesian programs such as IM, etc) MCMC is difficult as Joseph clearly outlined, programs based on MCMC can fail for various reasons, the most common one is that the programs

are not run long enough. This is especially serious with data that is not very informative (for example has only few variable sites) and were researchers have sampled many individuals.

- few variable sites: It is obvious that results will be hard to obtain if there is nothing to show differentiation, with MCMC-ML (likelihood approximated by MCMC) almost every change will be accepted resulting in a Brownian motion walk in the solution space, and of course short runs will deliver different results, MCMC is working only in the limit, so for such data every run might be too short. MCMC-Bayes in contrast to MCMC-ML is changing the driving value (often called `parameter_0`, or `Theta_0`) using a prior distribution for the MCMC chain more often than the MCMC-ML runs where the driving values is typically fixed. If no information is contained in the data the prior is defining the outcome. It is important to recognize that under Bayes failure to achieve good results delivers the prior distribution (several runs actually will deliver the same result when run using the same prior) whereas ML delivers different MLE estimates and we then consider the results inconsistent. With Bayesian programs, like IM, you need to be able to distinguish informative posterior (data is overpowering the prior) versus posterior is similar to the prior (prior is overpowering the data). To my knowledge IM or the other Bayesian programs out there (migrate-bayes included) do not produce good statistics on this, yet. A immediate solution is to use different prior settings and compare the posteriors (if the data is informative the will look the same). Of course one always can run these programs with no data and compare with the data-runs, but this will work only if all parameters fail to be pushed the data [the population sizes are most often much easier to estimate than the migration rates].

- variable data but very complex scenario: I get often email about difficulties to run on machine x that turns out to be often a problem that is unrelated to computers but to researchers (and perhaps the manual). Programs like migrate can estimate a large number of parameters: in fact from 1 to n^2+n+1 , where n is the number of populations. You can imagine that a researcher has investigated 10 populations -> typically a default migrate run will try to estimate 100 parameters. Now, if you sample 20 individuals per population then you will have 200 individuals, for single locus data this is not a lot of data to estimate the 100 parameters and most often such an analysis will fail because many of the individuals are "relatives" and so not perfect replicates. Would you run a regression analysis with 100 parameters and 200 data points? Probably not with lots of confidence. Another problem is that sometimes researchers have sampled 5

populations (25 parameters) and have 300 individuals per populations. In principle this is good, but because of the MCMC runs, we need to calculate likelihoods on large trees (1500 for the example), in phylogenetic research, people believe that this is a "very" difficult problem. As a result the MCMC runs will not explore the solution space exhaustively, in short, the runs will be too short and return inconsistent results. A remedy of this is to subsample each population randomly and run 10 or 20 individuals per population. Pluzhnikov and Donnelly (1996) and Felsenstein (2006) describe that results from coalescent studies show smallest variance when sampling about 6-10 individuals per locus but using many loci: so a study with 1500 individuals and 1 locus will produce worse results than to a study with 150 individuals and 10 loci.

*** Estimates from many populations (e.g. migrate, lamarc, batwing, genetree, ...) versus pairwise estimators (FST based, IM) In the standard statistical literature they tell you that is a very bad thing to test pairs of sets of data when their is interaction among all sets, that's why people use Bonferoni correction and the like. For estimation of molecular clock or time of divergence in earlier times researchers used pairs and calibrated Nei distance and geology events, these procedures are almost completely abandoned because superior methods that can take all lineages jointly into account arrived (for example, mdivtime). The same caveat holds for population genetics studies, I do not see why pairwise-methods (i.e. IM) should work better than others, for what it worth, you can run migrate on pairs, too; but that is not what I would suggest. The comparison

— / —

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>

ID in Nevada

Greetings colleagues,

I'm sure it will not surprise you to hear that the political forces pushing for the teaching of intelligent design in high school biology classes have made their way into another state. This time I am sad to say it is my own - Nevada. Here is a link to a recent news paper article announcing the initiative:

<http://news.rgj.com/apps/-pbcs.dll/article?AID=/20060228/-NEWS18/602280389&SearchIDs237250172019>

It looks like they are continuing to adapt their rhetoric in response to past failures in the courts. The telling phrase this time is that they want high school biology teachers to “teach the evolution controversy” as opposed to evolution per se.

Here we go again.

Guy Hoelzer

“Guy A. Hoelzer” <hoelzer@unr.edu>

Introduced Species

Dear EvolDir Members,

I am conducting a meta-analysis on 'common garden' studies on introduced species and would be grateful to hear if anyone knows of any additional studies that I have missed. In particular, I have focused on plants and I am hoping to add some animal studies for non-drosophilid species. Below is a list studies I have already included. Please note that I am only interested in studies that (a) use populations of the same species from both its native and introduced range, and (b) grow/raise individuals in a common garden/laboratory setting. It isn't necessary that these studies control for maternal effects or include family structure. Thanks in advance.

Rob Colautti Department of Botany University of Toronto Toronto, Ontario, Canada M5S 3B2 Phone: (416)978-5603 Fax: (416)978-5878

Plants: >Bastlov D and Kvt J (2002) Differences in dry weight partitioning and flowering phenology between native and non-native plants of purple loosestrife (*Lythrum salicaria* L.) *Flora* 197: 332-340 >Blossey B and NR (1995) Evolution of increased competitive ability in invasive nonindigenous plants: a hypothesis. *Journal of Ecology* 83: 887-889 >Bossdorf O, Prati D, Auge H and Schmid B (2004a) Reduced competitive ability in an invasive plant. *Ecology Letters* 7: 346-353 >Bossdorf O, ShcrS, Prati D and Auge H (2004b) Palatability and tolerance to simulated herbivory in native and introduced populations of *Alliaria petiolata* (Brassicaceae). *American Journal of Botany* 91: 856-862 >Cipollini D, Mbagwu J, Barto K, Hillstrom C and Enright S (2005) Expression of consti-

tutive and inducible chemical defenses in native and invasive populations of *Alliaria petiolata*. *Journal of Chemical Ecology* 31: 1255-1267 >Clement SL (1994) Resistance among populations of yellow starthistle to thistle-head insects: results from garden plots in Italy. *Biological Control* 4: 149-156 >DeWalt S, Denslow JS and Hamrick JL (2004) Biomass allocation, growth, and photosynthesis of genotypes from native and introduced ranges of the tropical shrub *Clidemia hirta*. *Oecologia* 138: 521-531 >Joshi J and Vrieling K (2005) The enemy release and EICA hypothesis revisited: incorporating the fundamental difference between specialist and generalist herbivores. *Ecology Letters* 8: 704-714 >Kaufman SR and Smouse PE (2001) Comparing indigenous and introduced populations of *Malaleuca quinquenervia* (Cav.) Blake: response of seedlings to water and pH levels. *Oecologia* 127: 487-494 >van Kleunen M and Schmid B (2003) No evidence for an evolutionary increased competitive ability in an invasive plant. *Ecology* 84: 2816-2823 >Leger EA and Forister ML (2005) Increased resistance to generalist herbivores in invasive populations of the California poppy (*Eschscholzia californica*). *Diversity and Distributions* 11: 311-317 >Leger EA and Rice KJ (2003) Invasive California poppies (*Eschscholzia californica* Cham.) grow larger than native individuals under reduced competition. *Ecology Letters* 6: 257-264 >Maron JL, Vil M and Arnason J (2004a) Loss of enemy resistance among introduced populations of *St. Johns wort* (*Hypericum perforatum*). *Ecology* 85: 3243-3253 >Maron JL, Vil M, Bommarco R, Elmendorf S and Beardsley P (2004b) Rapid evolution of an invasive plant. *Ecological Monographs* 74: 261-280 >Meyer G, Clare R and Weber E (2005) An experimental test of the evolution of increased competitive ability hypothesis in goldenrod, *Solidago gigantea*. *Oecologia* 144: 299-307 >Stastny M, Schaffner U and Elle E (2005) Do vigour of introduced populations and escape from specialist herbivores contribute to invasiveness? *Journal of Ecology* 93: 27-37 >Vil M, Gmez A and Maron JL (2003) Are alien plants more competitive than their native conspecifics? A test using *Hypericum perforatum* L. *Oecologia* 137: 211-215 >Vil M, Maron JL and Marco L (2003) Evidence for the enemy release hypothesis in *Hypericum perforatum*. *Oecologia* 142: 474-479 >Willis AJ and Blossey B (1999) Benign environments do not explain the increased vigour of non-indigenous plants: a cross-continental transplant experiment. *Biocontrol Science and Technology* 9: 567-577 >Willis AJ, Tomas MB and Lawton JH (1999) Is the increased vigour of invasive weeds explained by a trade-off between growth and herbivore resistance? *Oecologia* 120: 632-640 >Willis AJ, Memmott J and Forrester RI (2000) Is there evidence for the post-invasion evolution of increased size among

invasive plant species? Ecology Letters 3: 275-283

Jacqui Eales – bsp030@bangor.ac.uk

Italian Systematics texts

I'm teaching an introductory course in Molecular Systematics / Phylogeny to "masters" level students in Italy and am looking for a suitable text to recommend to my students. I was wondering if anyone knows what might be in print in Italian. I am covering alignment, substitution models, distance methods, parsimony and basic Likelihood and Bayesian methods (focusing on phylogenetic methods rather than lab-based techniques). Any suggestions would be most gratefully received.

Thanks in advance

David

Dr David S. Horner

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David Horner <david.horner@unimi.it>

Looking for SNPsoftware

Hi everyone

I'm looking for software you can use to download specific SNPs from GENBANK together with specified flanking sequences and information about other SNPs in that flanking sequence. I know the software SNPhunter (<http://www.hsph.harvard.edu/ppg/software>) does precisely this, but I am looking for a program in which you can do batch queries for specific SNPs using a file that lists SNPs according to their rs numbers. The batch queries of SNPhunter only involve genes, as far as I know, and my SNPs are not associated with genes.

Looking forward to some suggestions

Thanx

Carina Schlebusch

cschlebu@yahoo.com

MegaBACE size standard

Does anyone know of a size standard compatible with Amersham's MegaBACE other than the MegaBACE Et standards that have been backordered for weeks?

Any advice would be greatly appreciated.

Cheers, Gigi

– D. Gigi Ostrow Genetic Analysis Laboratory Interdisciplinary Center for Biotechnology Research University of Florida Gainesville, FL 32611-8525 USA

Phone: 352-392-3948 email: ostrowdg@ufl.edu

ostrowdg@ufl.edu

Large trees

Dear members

I am currently attempting to analyse a data set with around 120 taxa and between 1200-1900 characters, to create a phylogenetic tree. At present I am using PAUP* to do this, and have used MrBayes for bayesian analyses, both of which are taking huge amounts of time to run! Apart from the slowness created by the large number of taxa, many of the taxa are less than 1% different, causing repeated, inefficient terminal node swapping. If anyone has any suggestions (or moral support) that may help I would be infinitely grateful! A colleague has suggested TNT (Tree Analysis using New Technology) which I am at present unfamiliar with, any feedback on this would be great

Thanks

Micro data

I am a 3rd year undergraduate student at Brock University and I am working on a final project for a Molecular Ecology course. I am looking for a set of microsatellite data in order to perform some analyses calculations. Taxa and length or data does not matter.

Thanks a lot! Denise Stein

ds03bk@brocku.ca

Micro screening

Hi everybody, I was wondering if any of you could suggest a cheap (relatively speaking) sequencer or something similar to score microsatellites. Silver staining is very laborious and inaccurate and sequencing companies that I am aware of charge too much if one intends to screen multiple loci for a big sample. Cheers Andrea

PER FAVORE RISPONDETE A QUESTO EMAIL verardino@gmail.com PLEASE REPLY TO THIS EMAIL verardino@gmail.com POR FAVOR CONTESTAR A ESTE EMAIL verardino@gmail.com Dr Andrea Verardi Dipartimento di Genetica e Biologia Molecolare Università La Sapienza Roma mobile (+39) 340 97 17 555 email verardino@yahoo.com

verardino@yahoo.com

Microsat problems answers

Hi everyone, I would just like to apologize for the delay in posting the responses and say thank you to everyone who offered advice, it was very much appreciated.

Deborah

INITIAL EMAIL

Hi, I have been developing microsatellites for 3 species of Galatheididae for the past year and although the developmental process went well and plasmid sequencing gave microsatellites and flanking regions which were sufficient to develop primers I am now having problems with optimisation and amplification. I am somehow amplifying product of incorrect size (as to what the primers were designed for- larger fragments) and am getting multiple bands and lots of background noise when trying to screen samples. Of the two micros that I

have managed to optimise the screening concluded that they were uninformative (everything I screened including 19 adult individuals from a single area as well as a mother and 75 eggs were all found to have identical heterozygote bands!). I am confused by this result and was wondering if anyone has had similar problems with crustaceans or could offer advice as to possible problems that could be causing this or how to proceed. Thanking you in advance for any comments you could offer

Deborah

VERY KIND AND MUCH APPRECIATED RESPONSES:

* I haven't much experience with crustaceans but I would've thought that mining non-unique sequences by chance was very unlucky. I realise that enrichment success is species dependant but I need to know more about your protocols before I can offer advice. Have you tried SSCP with your 'monomorphic' primers to check whether there's any conformational polymorphism? Perhaps you could look on the database for EST sequences to see whether you can design SSR markers from them. Jake Jake Clarke (EMR) [Jake.Clarke@emr.ac.uk]

* Have you tried a HotStart Taq, touchdown, and touchup PCR??? Cheers, Fabio

Fabio M. Diniz [F.M.DINIZ@soton.ac.uk]

* I have experience with plant and insect microsatellites, but not Crustacean, so I can not really comment if your amplification problems are species-specific... Nevertheless, some hints perhaps: Although you have not mentioned the PCR conditions, I suppose you have tried selective conditions (e.g. higher annealing temperature), in order to amplify only specific bands. So, if you do get multiple bands or incorrect size, can be that your primers match with more sequences and so amplify more/different loci, in fact. Perhaps, the best to check on that is to cut out the suspicious bands from the gel and sequence them. Thus, you can precisely check whether you have amplified microsatellites. If so, you may then decide to try and re-design the primers. Also, you have not specified what is difference from expected and your observed length ...my own experience is that some microsatellite loci can amplify alleles within relatively broad range like 90 bp or so.

Zavodna, Monica [M.Zavodna@nioo.knaw.nl]

* you have to separate if the problem is: 1/ technical and general 2/ technical to do with this organism 3/ non-technical to do with this organism, ie a property of this organism

1/ can be ruled out if you can borrow some microsatellite primers and DNA from someone in the lab working on some other organism and get scoreable gels with your reagents and equipment.

2/ you might approach by seeing if you can get sensible results using nuclear primers that are supposed to work on your taxon, or at least related crustacea. If successful this will tell you that there is nothing too wrong with your DNA for example.

Jarman SN, Ward RD, Elliott NG (2002) Oligonucleotide primers for the amplification of coelomate introns. /Marine Biotechnology/ *4*, 347-355. is a good potential source. You might develop some useful primers anyway that could supplement microsatellites

3/ some organisms are just hard. you probably know the crustacean literature. I seem to remember that Shane Lavery found that prawns have very long pure repeats that were stutter, and other decapod studies have had a hard time too.

There are lots of reasons for microsatellites to fail - invertebrates seem to be generally a lot more difficult and unpredictable in yielding good loci. In my group we have encountered some very difficult animals. My advice would be that if you work out that 3/ above applies, you have a few more goes at a few more microsatellites, then try alternative approaches (Garrick RC, Sands CJ, Rowell DM, Tait NN, Greenslade P, Sunnucks P (2004) Phylogeography recapitulates topography: very fine-scale local endemism of a saproxylic 'giant' springtail at Tallaganda in the Great Dividing Range of south-east Australia. /Molecular Ecology/ *13*, 3329-3344. contains some suggestions).

Paul Sunnucks [paul.sunnucks@sci.monash.edu.au]

* I had a wretched time getting micros to work on stone and blue crabs.

— / —

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>

Microsatellite stutter

I am looking for suggestions on how to reduce stutter at dinucleotide microsatellite loci.

Thank you, Katie

katieshul@gmail.com

k s <katieshul@gmail.com>

Migrate answers

Dear Members

Many thanks for all your helpful suggestions with the program Migrate. Some people pointed out the fact that it is not a very reliable program and others gave some suggestions for the program parameters. I've added the answers below just in case someone else might need them.

Many thanks Tatiana

Tatiana Zerjal The Sanger Institute UK
tz1@sanger.ac.uk

Hi Tatiana,

I've played around with Migrate some myself. Before you continue, I would take a serious look at the following article: Evaluating the performance of likelihood methods for detecting population structure and migration ZAID Abdo, Keith A. Crandall, PAUL Joyce Molecular Ecology 2004 13:4 837

They find that the results from Migrate are not very reliable or accurate. I might choose different software (Jody Hey's IM, Prtichard's STRUCTURE, etc.) to get at this question.

-Jeff

Hi Tatiana - I've had major problems with consistency for the Migrate, Fluctuate, Lamarc programs and despite multiple runs of the same dataset, I never got convergence. Depending on which way the wind blows, you will get all kinds of numbers. Like flipping a coin. It doesn't matter what your starting parameters are or number of chains.. the programs are horrible. So, I suggest you steer clear of that batch of programs - there's a paper about Migrate by Paul Joyce, Zaid Abdo, and Keith Crandall that shows how bad the Migrate program is - it's in Mol Ecol. Most of the time, Migrate didn't find the simulated theta within the 95% confidence interval... and worse yet, it was *really* far off most of the time.

There is a program called IM by Jody Hey (he's at Rutgers) which does consistently give you "ballpark" theta and migration estimates. I typically do 10 identical runs to watch if they are converging, and I mark down

the estimates. You have to run 2 populations at a time, so you get a θ_1 , θ_2 , $\theta_{\text{ancestral}}$, m_1 , m_2 , and time since divergence. I haven't used the program yet for usats, but it takes sequence data and usats. I then cancel the runs that are really different from the others... typically, 2 or 3 will converge on some strange number while all the others will hit the same ballpark. Then I take the run that falls in the middle of that convergent set and let it run until the effective sample sizes (ESSs) for time to convergence are well over 1000. This means I let the thing run for a few weeks. You'll get an output file that has probabilities for each of the estimates (θ , m , and t) and 90% posterior density confidence intervals. I used IM for my Mol Ecol paper - it's in the Dec 2005 issue... cave crayfish with Keith Crandall. And Rasmus Nielsen and Jody Hey are great and have published in Genetics using usat data for the IM program - they actually write back and respond to your questions, unlike the Lamarck crew.

I hope that helps, Jen

Other people may have more detailed/technical suggestions...

A simple thing you can do is repeat the analysis. If the results are very different (eg. no or small overlap in confidence intervals for parameters) you definitely need to run it for longer. Also if the confidence intervals are large, you may need to run it for longer, although I would not like to specify how large is too large.

Hope this helps.

Karen Bell [karen.bell@wku.edu]

I would suggest you to start with FST values. Do some runs with say 10 short chains and 1 long chain starting with different random seed numbers. Try to play with parameter that explore the sample space, such as how many trees to discard etc. Compare the results and see if they converged to something common or if the results are completely disparate. You will acquire confidence in your runs as you see the results and experiment with the parameters. Once you are confident with the parameters you prepare the "official" run with the parameter set you have determined in your trials. Follow the manual for that and try to optimize the number of runs in relation to the computer time and power you have available. Do three or four runs, starting the first with FST parameters and the subsequent with what you obtained in the previous. Do a single very long run at last.

Good luck

Julianno

Hello Tatiana. I have run Migrate ad infinitum, and

so hope I can offer some good suggestions. First I'll give you my advice, and then a blurb from something I wrote on MCMC sampling a while ago, if you are interested.

Running the Program 1) Run it multiple times, starting from random positions in parameter space. If you get consistent results, you be confident that you have sampled adequately. 2) Use heated chains, typically one cold and three hot (NOTE: this is not a default for the program, so you will have to specify this in your parm-file). This will greatly improve convergence and mixing of the chains. Please note, however, that adding heated chains will slow down your analysis substantially (you are doing four searches rather than

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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>

Migrate help

I am trying to use the program Migrate to estimate proportions of gene flow among populations using Y-chromosome microsatellite data. I have tried some runs but I don't know if the results I get are reliable or not. The program allows to set many parameters and for many of them I used the default setting. Because I didn't know how long it would have run for, I started using a small number of chains. Could someone be so kind to give me some suggestions? What "start parameters" (θ and migration rates) are better to use? What is the minimum number of chains for a data set of 16 microsatellites typed in 200 samples? Any suggestion will be appreciated.

Many Thanks

Tatiana Zerjal The Sanger Institute UK
tz1@sanger.ac.uk

MolEcolNotes Barcoding

The editors of Molecular Ecology Notes (MEN) and the Consortium for the Barcode Of Life (CBOL) are

pleased to announce an expansion of the journal to include:

Technical reviews Full-length technical papers A new section on barcoding papers The first two initiatives are intended to provide an outlet for comprehensive technical papers and reviews that currently do not have a home in the journal. The third initiative is intended to recognize the tremendous promise bar-coding holds for ecological studies and to provide a suitable venue for these kinds of papers. We envision that barcoding papers would deposit their data to appropriate databases such as BOLD and GenBank and to follow the standards developed by CBOL.

To facilitate this expansion, we are pleased to announce that Brian Golding, McMaster University, has agreed to join our Editorial Board as an Associate Editor for barcoding papers. Jared Strasburg, Indiana University, will assume editorial responsibilities for technical reviews and full-length technical papers.

To read a statement from CBOL endorsing Molecular Ecology Notes (MEN) as a publishing vehicle for DNA barcoding papers visit www.blackwellpublishing.com/pdf/CBOL_Endorse.pdf Kevin Livingstone, Harry Smith, and Loren Rieseberg, Molecular Ecology Notes

David Schindel, Executive Secretary, Consortium for the Barcode Of Life

Loren Rieseberg <lriesebe@bio.indiana.edu>

Molluscan Basommatophorans Samples

Dear all,

I am looking for samples of three species of Basommatophorans (Mollusca) from all over Europe for phylogeographic analysis: *Radix* sp., *Ancylus fluviatilis* and *Hippeutis complanatus*. If you yourself don't have that kind of samples, but know of people who would be susceptible to have them, I would be happy to have their E-mail, to contact them myself. Thanks a lot for your help

Please contact me:

Mathilde Cordellier

Ökologie, Evolution, Diversität J.W. Goethe University Siesmayerstraße 70 60054 Frankfurt am Main GER-MANY

Tel: +49-69-798-24721 Fax: +49-69-798-24910

Mathilde Cordellier <m.cordellier@zoology.uni-frankfurt.de>

Multiple Sequence Alignment answers

Thank you for your many helpful responses to my original post. Many people responded to request that I share the outcome. Hence, copies follow, in no particular order, with email addresses, salutations, signatures, and affiliations scrubbed (as a spam/ phishing prevention measure).

In hindsight, I ought to have clarified that I am working on whole-genome alignments of the hepatitis C virus, which spans both coding and non-coding regions, and encodes one polypeptide without introns or rearrangements. The sequences are ~9.5K nt for ~30 taxa.

Per the moderator's instructions, any discussion should be taken off-list to the USENET/Google groups...

Best regards,

Peter Hraber

<part 1 of original post> Do you know of a multiple sequence alignment algorithm that uses an objective goodness-of-fit criterion? I am presently working with *clustalw(x)* and *t-coffee*. Both use penalty scores for mismatches. However, I see no way to compare the quality of alignments obtained with varied parameters.

I'm surprised that no one has applied an information-based model-selection criterion (AIC, BIC, MDL) to this problem. Am I mistaken? How do you know when an alignment is near optimal? Is this an entirely subjective decision? </part 1of original post>

<response> >From Jeff Blanchard:

We use a partial order graph approach implemented in POA (<http://www.bioinformatics.ucla.edu/poa/>) for some of our work. However, this is mainly because it scoots the unaligned sequences to the end for easy trimming with the initial settings we tried. I have also heard the some of the EST alignment methods do something similar.

There is no optimal alignment. Usually the goal is to try and align sites that share a common ancestry. Thus there is a circular problem of wanting to use a tree to build the alignment. Then using the alignment to build

a tree. The use of Bayesian approaches that allow the incorporation of prior knowledge is rapidly changing this field, but there is no easy answer. </response>

<response> >From Ilya Nemenman:

Another objective, and formally very sound, way to quantify the sequence similarity is to measure the length of the shortest program that can transform one sequence into another. This is obviously related to Kolmogorov complexity, and Li and Vitanyi, some of the biggest names in the theory of algorithmic complexity in the recent years, have worked on this subject. The algorithm, described in <http://www.ams.org/mathscinet-getitem?mr=2005f%3A68028> works quite nicely for phylogeny studies. There might have been later works on this approach, but I am, unfortunately, unfamiliar with them. </response>

<response> >From Joe Felsenstein:

Why do you think that the issue has never been addressed? There is an active literature on statistical approaches to multiple sequence alignment, using models of insertion and deletion (there are major unsolved problems, including treatment of multiple-base insertions and deletions). The literature goes back to Bishop and Thompson 1986 and to Thorne et al. 1991 and 1992. In addition there is a minimum message length approach of Allison and Yee (1990). References are in my phylogenies book (2004), chapter 29. </response>

<response> >From Will Fischer:

This is an excellent question, and there is distressingly little formal work in the area. Most "alignment accuracy" studies simply compare the alignments from algorithm A or algorithm B to a set of hand-curated alignments, e.g. BaliBase.

One objective criterion for alignment quality is the length of the most parsimonious tree derived from the alignment – this is unfortunately too time-consuming to compute for each step of an alignment procedure, but can be used to compare alignments from different methods.

I would encourage you to explore some alternatives to the programs you are using:

muscle (www.drive5.com/muscle) is freely available, is much faster than either clustalw or t-coffee, and produces excellent amino-acid alignments (certainly more accurate than clustalw's, and as good or better than t-coffee's according to published data; I haven't done a side-by-side muscle/t-coffee comparison since t-coffee is so slow). Nucleotide alignments may require more post-alignment tweaking than amino acids. It builds an initial guide tree using common-substring counts.

Muscle references: <http://nar.oxfordjournals.org/cgi/content/full/32/5/1792?ijkey=-48Nmt1tta0fMg&keytype=ref>

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Multiple Sequence Alignment methods

Dear Colleagues,

Do you know of a multiple sequence alignment algorithm that uses an objective goodness-of-fit criterion? I am presently working with clustalw(x) and t-coffee. Both use penalty scores for mismatches. However, I see no way to compare the quality of alignments obtained with varied parameters.

I'm surprised that no one has applied an information-based model-selection criterion (AIC, BIC, MDL) to this problem. Am I mistaken? How do you know when an alignment is near optimal? Is this an entirely subjective decision?

This seems to be an issue of fundamental importance in phylogenetic inference, as the quality of a tree is limited by the quality of the input alignment.

Alternatively, does there exist an algorithm that will utilize amino acid translations to inform alignment of nucleotide sequences?

Thank you, and best regards,

Peter Hrabec, PhD Northern New Mexico

phrabec@gmail.com

Munidopsis mtDNA polymorphism

Hi, I am working with the squat lobster *Munidopsis* polymorpha, and I have several problems with the mitochondrial DNA amplifications and restriction digests. I have tried to clean my samples using various methods, including columns from Qiagen and the ChargeSwitch

system from Invitrogen. I have also tried more standard methods such as diluting the DNA template, changing Taq and using agents such as BSA. For the digests, I have tried diluting the DNA and adding more enzyme. The extracted DNA is of good quality and the solution is clear with no visible pigment. However, I continue to have problems, suggesting that some form of inhibitor is co-amplifying with the DNA. I will be grateful for any ideas on how to resolve this problem or to hear from people who have encountered similar problems. Patricia

Hola, Estoy trabajando con el cangrejo *Munidopsis polymorpha*, y estoy encontrándome con varios problemas para amplificar el ADN mitocondrial y para realizar digestiones con enzimas de restricción. He intentado limpiar las muestras usando varios métodos que incluyen columnas de Qiagen y el kit ChargeSwitch de Invitrogen. También he intentado otros métodos como diluir el ADN, diferentes Taq y otros componentes como BSA. Para las digestiones, he diluido el ADN y he añadido mas enzima. Las extracciones de ADN son de buena calidad y la elución es limpia y no parece que tenga ningún pigmento. Sin embargo continuo teniendo problemas, que creo pueden deberse a que algunos inhibidores están coamplificándose con el ADN. Estaría muy agradecida si alguien tuviese algunas ideas de cómo resolver los problemas o si alguien se hubiese encontrado con problemas similares. Patricia

Patricia Cabezas Padilla Dpto. Biodiversidad y Biología Evolutiva Museo Nacional de Ciencias Naturales C/Jose Gutierrez Abascal, 2 28006 Madrid

Teléfono: +34 91.411.13.28 Ext. 1126 Fax: +34 91.564.50.78

Patricia Cabezas <mcnpc774@mncn.csic.es>

Notropis stramineus samples

Dear All, I am a Ph.D. candidate at the University of Kansas and am studying the phylogeography of the Sand Shiner (*Notropis stramineus*). I am in need of additional samples to supplement my work (particularly from the northern reaches of its distribution). I would greatly appreciate any ethanol preserved samples that others could supply. If you would be willing to collect some specimens, please contact me. Thanks!

N. stramineus is a commonly occurring and widespread

minnow species in eastern North America. For a map of its distribution and other info, please see:

<http://www.natureserve.org/explorer/servlet/-NatureServe?searchName=Notropis%20stramineus>

K.J. Pittman Ph.D. Candidate Department of Ecology and Evolutionary Biology University of Kansas Higuchi Hall (Kansas Biological Survey) 2101 Constant Avenue Lawrence, KS 66045 (785) 218-0804 kjpi@ku.edu

Other venues

Dear members of the evolutionary biology community,

I was wondering if anyone would be able to suggest venues similar to this, or complimentary to this list where either PhD positions are listed, or employment/research opportunities within evolutionary biology.

Thank you in advance, ~Joanna Malukiewicz
arcova@yahoo.com

Phylogenetic trees replies

Dear Members

Many thanks for all your helpful replies in my problem of resolving a phylogenetic tree with <1-2% sequence difference between taxa. In summary, the programs TNT, PAUP ratchet, PhyML, Repeated Heuristic searches using PAUP MP, and collapsing data into groups with <'a threshold' difference, were the main suggestions to get a tree search to at least complete, or take less time than in a conventional PAUP analysis. As a general note, for the suggestions I have tried so far, time taken has been improved (although with the inherent problem of too little information in the data, resolution has not). For anyone who would like more details feel free to email me directly,

Jacqui Eales University of Wales, Bangor

– bsp030@bangor.ac.uk

“Eales,Jacquelyn” <bsp030@bangor.ac.uk>

Protein alignment

Dear colleagues,

I got a relatively large dataset of protein-coding genes, and I'm looking for the best way to align it. I'm aware of approaches that use things like BLOSUM matrices, but I'd like to use a method that does both tree search and alignment simultaneously (e.g. the optimization alignment used in POY, although I'm not aware of a way to set it up so that it won't allow gaps only between codons). Any suggestions?

Best,

Jason

jas2339@yahoo.com

SMBE Absts Titles

Abstract submission deadline for presenting contributed talks in the SMBE 2006 annual meetings is March 15, 2006. Please go to <http://www.smbe.org/geb/abstracts.php> The confirmed list of participants and symposia is at <http://www.smbe.org/geb/events.htm> A list of contributed titles can be seen at http://www.smbe.org/geb/abstract_submissions.php Encourage your graduate and undergraduate students to apply for many travel awards. Details are given at <http://www.smbe.org/geb/awards.htm> Genomes, Evolution & Bioinformatics (GEB) Conference May 24-May 28, 2006 Arizona State University, Tempe, Arizona, USA

To register visit <http://www.smbe.org/geb/registration.php> The SMBE/GEB conference will open on the evening of Wednesday, May 24 with a Welcome Social and Registration from 7:00 p.m. - 11:00 p.m. The opening symposia and contributed sessions will begin at 8:00 a.m. on May 25. The closing symposia and contributed sessions will take place from 8:00 a.m.- 12:00 noon on Sunday, May 28.

SUDHIR.KUMAR@asu.edu
HIR.KUMAR@asu.edu

SMBE TravelAwards

Abstract submission deadline for Travel awards to attend the SMBE 2006 annual meetings is March 15, 2006. There are many graduate, postdoc, and undergraduate travel and poster awards. <http://www.smbe.org/geb/awards.htm> (1) Walter M. Fitch Prize Beginning with the first annual meeting of the SMBE in 1993, the Walter M. Fitch Symposium has provided a forum for young investigators (graduate students and postdocs) to showcase their exemplary research. There are 10 travel awards in this category.

(2) Graduate Student Travel Award SMBE announces competition for another 10 graduate students travel awards.

(3) Travel Award for Undergraduate Students from Under-Represented Groups The SMBE is pleased to make available 10 travel awards for undergraduate students from under-represented and minority groups (including women).

(4) Best Graduate Student Poster Award This award will be given to the graduate student with the most outstanding poster presentation at the conference, as determined by appointed SMBE judges.

(5) Best Postdoctoral Student Poster Award This award will be given to the postdoctoral student with the most outstanding poster presentation at the conference, as determined by appointed SMBE judges.

For more information on award eligibility and details, go to www.smbe.org/geb/awards.htm

The confirmed list of participants and symposia is at <http://www.smbe.org/geb/events.htm> Genomes, Evolution & Bioinformatics (GEB) Conference May 24-May 28, 2006 Arizona State University, Tempe, Arizona, USA To register visit <http://www.smbe.org/geb/registration.php> The SMBE/GEB conference will open on the evening of Wednesday, May 24 with a Welcome Social and Registration from 7:00 p.m. - 11:00 p.m. The opening symposia and contributed sessions will begin at 8:00 a.m. on May 25. The closing symposia and contributed sessions will take place from 8:00 a.m.- 12:00 noon on Sunday, May 28.

SUD- SUDHIR.KUMAR@asu.edu
HIR.KUMAR@asu.edu

SUD-

Sciaenidae samples

Hi, My name is Mona Elsmaili - I am a graduate student at the University of Windsor (in Canada) conducting research on the evolution of hearing in Sciaenidae. I need to generate a phylogenetic tree for that family and I am looking for tissue samples of any species that belong to it. Inserted below is a comprehensive list of all the species of Sciaenidae - I would be interested in getting samples of any species on that list. Would you be able to supply me with any samples or would you be able to suggest a resource that may be able to do so? If you have any information, please contact me at elsmail3@uwindsor.ca. Thanks in advance - your help is greatly appreciated.

Scientific Name	English Name	Aplodinotus grunniens
Freshwater drum	Argyrosomus amoyensis	Amoy croaker
Argyrosomus beccus		

Argyrosomus coronus	Dusky kob	Argyrosomus heinii
Arabian sea meagre	Argyrosomus hololepidotus	Southern meagre
Argyrosomus inodorus	Mild meagre	Argyrosomus japonicus
Japanese meagre	Argyrosomus regius	Meagre
Argyrosomus thorpei	Squaretail kob	Aspericorvina jubata
Prickly croaker	Atractoscion aequidens	Geelbeck croaker
Atractoscion nobilis	White weakfish	Atrobucca adusta
Scorched croaker	Atrobucca alcocki	

Atrobucca antonbruun

Atrobucca bengalensis

Atrobucca brevis

Atrobucca geniae

Atrobucca kyushini	Black-spot croaker	Atrobucca marleyi
African blackmouth croaker	Atrobucca nibe	Longfin kob
Atrobucca trewavasae		

Austronibeia oedogenys	Yellowtail croaker	Bahaba chaptis
Chaptis bahaba	Bahaba polykladiskos	Spine bahaba
Bahaba taipingensis	Chinese bahaba	Bairdiella armata
Armed croaker	Bairdiella batabana	Blue croaker
Bairdiella chrysooura	Silver croaker	Bairdiella ensifera
Swordspine croaker	Bairdiella icistia	Ronco croaker
Bairdiella ronchus	Ground croaker	Bairdiella sanctaeluciae
Striped croaker	Boesemania microlepis	Boeseman croaker
Cheilotrema saturnum	Black croaker	Chrysochir aureus
Reeve's croaker	Cilus gilberti	Corvina Collichthys lucidus

Collichthys niveatus

Corvula macrops	Vacuocua croaker	Ctenosciaena gracilicirrhus
Barbel drum	Ctenosciaena peruviana	Peruvian barbel drum
Cynoscion acoupa	Acoupa weakfish	Cynoscion albus
Whitefin weakfish	Cynoscion analis	Peruvian weakfish
Cynoscion arenarius	Sand weakfish	Cynoscion guatucupa

Cynoscion jamaicensis	Jamaica weakfish	Cynoscion leiarchus
Smooth weakfish	Cynoscion microlepidotus	Smallscale weakfish
Cynoscion nannus	Dwarf weakfish	Cynoscion nebulosus
Spotted weakfish	Cynoscion nortoni	hake weakfish
Cynoscion nothus	Silver seatrout	Cynoscion othonopterus
Gulf weakfish	Cynoscion parvipinnis	Shortfin weakfish
Cynoscion phoxocephalus	Cachema weakfish	Cynoscion praedatorius
Boccone weakfish	Cynoscion regalis	Gray weakfish
Cynoscion reticulatus	Striped weakfish	Cynoscion similis
Tonkin weakfish	Cynoscion squamipinnis	Weakfish
Cynoscion steindachneri	Smalltooth weakfish	Cynoscion stolzmanni
Stolzmann's weakfish	Cynoscion striatus	South American striped weakfish
Cynoscion virescens	Green weakfish	Cynoscion xanthulus
Orangemouth weakfish	Elattarchus archidium	Bluestreak drum
Daysciaena albida	Bengal corvina	Dendrophysa russelii
Goatee croaker	Equetus iwamotoi	Blackbar drum
Equetus lanceolatus	Jack-knifefish	Equetus punctatus
Spotted drum	Genyonemus lineatus	White croaker
Isopisthus parvipinnis	Bigtooth corvina	Isopisthus remifer
Silver weakfish	Johnius amblycephalus	Bearded croaker
Johnius australis	Bottlenose jewfish	Johnius belangerii
Belanger's croaker	Johnius borneensis	(Johnius vogleri)
Sharpnose hammer croaker	(Little Jewfish)	Johnius cantori

Johnius carouna	Caroun croaker	Johnius carutta
Karut croaker	Johnius coitor	Coitor croaker
Johnius distinctus		

Johnius dorsalis	Small kob	Johnius dussumieri
Sin croaker	Johnius elongatus	Spindle croaker
Johnius fasciatus		

Johnius fuscolineatus	Bellfish	Johnius gangeticus
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Johnius glaucus	Pale spotfin croaker	Johnius goldmanni
Johnius grypotus		

Johnius heterolepis	Large-scale croaker	Johnius hypostoma
Small-mouth croaker	Johnius laevis	Smooth croaker
Johnius latifrons	Broad-head croaker	Johnius macropterus
Largefin croaker	Johnius macrorhynchus	Big-snout croaker
Johnius mannarensis	Mannar croaker	Johnius novaeguineae
Paperhead croaker	Johnius novaehollandiae	

Johnius pacificus	Pacific croaker	Johnius philippinus
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Johnius plagiostoma	Large-eye croaker	Johnius tra-
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chycephalus Leaf-tail croaker Johnius trewavasae Trewavas croaker Johnius weberi Weber's croaker Kathala axillaris Kathala croaker Larimichthys crocea Croceine croaker Larimichthys pamoides Southern yellow croaker Larimichthys polyactis Yellow croaker Larimus acclivis Steeplined drum Larimus argenteus Silver drum Larimus breviceps Shorthead drum Larimus effulgens Shining drum Larimus fasciatus Banded drum Larimus pacificus Pacific drum Leostomus xanthurus Spot croaker Lonchurus elegans Blackfin croaker Lonchurus lanceolatus Longtail croaker Macrodon ancylodon King weakfish Macrodon mordax Dogteeth weakfish Macrospinosa cuja
Megalonibea fusca
Menticirrhus americanus

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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>

Scientia Marina journal

Does anyone has this journal that can send me a copy?

Scientia Marina 60 (Supl. 2): 1996 - THE EUROPEAN ANCHOVY AND ITS ENVIRONMENT

Thanks.

Gonalo Silva

BioCon - Biodiversity and Conservation Laboratory (<http://www.biocongroup.com>) CCMAR - Centre of Marine Sciences, and CIMAR ? Associated Laboratory Department of Biological Sciences Faculty of Marine and Environmental Sciences, University of Algarve

Contacts: Mail address: F.C.M.A., Univ. Algarve, Gambelas, 8005-139 Faro, Portugal Fax: +351-289-818353, E-mail: gfsilva@ualg.pt

Gonalo Silva

goncalojfsilva@yahoo.com.br

Seeking info on Darwins Nightmare

"Darwin's Nightmare" is an Oscar-nominated documentary film by the Austrian filmmaker Hubert Sauper. It deals with the introduction of Nile Perch into Lake Victoria (arguably one of the great ecological tragedies of the 20th century) and its ecological, economic and political consequences. It is reviewed, quite favorably, in the 6 March, 2006 issue of The New Yorker.

I am trying to get a video or DVD version of this film for teaching purposes. Does anyone know if these are available, their sources, etc?

Thanks, Bruce Turner, fishgen@vt.edu

"Bruce J. Turner, Dept. Biological Sciences, VPISU, Blacksburg, VA 24061" <fishgen@vt.edu>

Sequencing polymer

Dear All,

Does anyone know of a cheaper alternative to be used instead of the ABI POP polymers?

Best,

Jason jas2339@yahoo.com

Softare FAMOZ

Dear Colleagues

A new version of FaMoz is now available freely on internet at this address: <http://www.pierroton.inra.fr/-genetics/labo/Software/Famoz> In this version, you can now look for most likely fathers or parent/parent pairs of some offspring with codominant, dominant, cytoplasmic markers (or combinations of these), using log likelihood ratio (lod score) AND/OR delta scores of each father/parent/parent pair. Delta was not available before, you can build tests with delta exactly the way it was done with lod-scores, and compare the quality of the different tests thanks to simulations.

Gene flow can be simulated and evaluated, in a different manner than before. The size of the total reproducing population, a value difficult to obtain in an easy way, is not used anymore by the simulation step, with an original idea from Olivier Hardy (thanks Olivier !). You

only need the observed gene flow observed in your experiment after the paternity or parentage test. The different types of gene flow observed after the simulation are given (real, apparent, cryptic gene flow, ...).

Any feedback is very wellcome

With my best regards

Sophie

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

gerber@pierroton.inra.fr

Software BAPS

We would like to inform population geneticists (and other with interest for population genetic structure analysis) about the upgrade of the BAPS software to version 4. BAPS 4 contains all the functionality of BAPS 3.2, and introduces two new models for genetic clustering: a spatial model for genetic discontinuities in populations and a model for linked marker or sequence data. The new version is currently available for Windows XP/2000, however, we aim to release a Mac OS X version shortly. For further details, visit <http://www.rni.helsinki.fi/~jic/bapspage.html> Best, Jukka

– Jukka Corander, PhD, Docent

Department of Mathematics and statistics P.O.Box 68 University of Helsinki FIN-0014 Helsinki, Finland

<http://www.rni.helsinki.fi/~jic/> Fax: +358 9 191 51400 Visiting address: Gustaf Hällströmin katu 2b, 3rd floor, room B330 — Edelleenlähetetty viesti päättyy —

– Jukka Corander, PhD, Docent

Department of Mathematics and statistics P.O.Box 68 University of Helsinki FIN-0014 Helsinki, Finland

<http://www.rni.helsinki.fi/~jic/> Fax: +358 9 191 51400 Visiting address: Gustaf Hällströmin katu 2b, 3rd floor, room B330

corander@mappi.helsinki.fi corander@mappi.helsinki.fi

Software Geneious

SOFTWARE: for organizing sequences, alignments, phylogenetics trees and abstracts

We have recently released a new software system (Geneious version 0.9e) which allows evolutionary biologists to easily manage their data and access web-based databases such as NCBI. It also integrates several core tasks that are essential for evolutionary biologists to perform quickly, often and easily, including

- * phylogenetic reconstruction (NJ with bootstrapping)
- * tree viewing
- * pairwise sequence alignment
- * multiple sequence alignment
- * dot plots
- * sequence viewing, including sequence annotations from NCBI database
- * translating from DNA to amino acids
- * export to Endnote, Nexus, Newick, Fasta
- * import trees, sequences alignments and bibliographies in a variety of formats
- * adding user information and notes to sequences, alignments and trees

The novel thing about this software is that for the first time these tasks can now be done in an integrated way using a tool that also allows local database storage and retrieval of all sequences, proteins, and research publications in formats including PDF. The result is that much of the drudgery of downloading, sorting and analysing sequences is now streamlined, so that you can spend more time on genuine research. The other major innovation is that any existing bioinformatics applications that you are using can be rapidly integrated into the product so that your workflow becomes even faster.

- Significantly increases your chance of finding the research paper you are looking for - in minutes, not hours
- and being automatically told when new ones come in
- Organise, search, and perform non-exact searches through all PDF- format research publications for keywords
- By creating a well-organised searchable, continuously updating local database of sequences, you can perform much more complicated searches and analyses much quicker than if you had to search from scratch on the whole of NCBI and/or EBI each time

You can download Geneious without charge at www.geneious.com. Versions for Mac OS X, Windows and Linux are available.

Geneious will grow as we continue to build new tools through open- source upgrades and new features. We will plan to focus special attention on developing analy-

sis tools for sequence alignment and phylogenetics and welcome any and all feedback on current and future features in the product.

Biomatters plans to release version 1.0 of Geneious in Q2 2006.

Inquiries

Dr Alexei Drummond Chief Scientist Biomatters Ltd (Auckland, New Zealand) 64 9 3737599 ext 88298 or 021 1601959 alexei@biomatters.com

Dr Daniel Batten Chief Executive Officer Biomatters Ltd (Auckland, New Zealand) 64 9 3795064 or 021 747131 daniel@biomatters.com

alexei@cs.auckland.ac.nz

Software IBDWS 2 6

Colleagues,

We have posted an update to Isolation By Distance, Web Service (IBDWS). (current version is 2.6)

IBDWS is a specialized package for isolation by distance analyses of codominant markers (raw data), or user-provided distance matrices for any type of data.

IBDWS is hosted at <http://phage.sdsu.edu/~jensen/> Recent improvements include a cleaner user interface and some minor bug fixes. Most significantly, you now have the ability to return to the IBDWS page and retrieve results for large analyses that take a significant amount of time to run. (Most web browsers time out in 2-5 minutes.)

Andy Bohonak

–

Andrew J. Bohonak

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

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

Software MTgui 1 5

Hello EvolDir

I have finished the development of a new version of the ModelTest interface, MTgui. The new version 1.5 is only available to Windows systems at the moment, and the Linux new version will be out soon.

Version 1.5 is a major improvement on the last available release and includes the possibility of running PAUP from the interface directly. By clicking a button and selecting your NEXUS file, MTgui will start PAUP, run the modelblock and run ModelTest at the end. All you need to do is check the result and edit your NEXUS file (and you can do this by clicking another button).

This feature was only tested with the PAUP4b10 console version (command line, DOS version), as I do not have a full PAUP Windows version to test.

MTgui 1.5 is available at:

<http://www.genedrift.org> (click on software and then on MTgui)

If someone is interested in helping the development of this simple, yet useful interface, or has interest in creating an interface for some other command-line tool just send me an email.

Thanks for the interest.

Paulo Nuin

Software TRANSFORMER-3

Dear colleagues, We are announcing the release of TRANSFORMER-3, a computer program for the analysis of molecular population genetic data which is suitable for codominant (allozyme or microsatellite) and dominant (AFLP, RAPD, RFLP, PCR-RFLP) matrices for at least 60 enzyme/primers with up to 10 loci (each containing a maximum of 20 alleles) per enzyme/primer in 65,000 diploid individuals.

At present, the program transforms raw genotype data or (only for allozymes) drawings of the gel interpretations to the formats of Arlequin, BIOSYS, Bottleneck,

Fstat, GenePop, Genestat, PopGene, NTSYS-pc and SPAGeDI (codominant data), and Arlequin AFLPsurv, GDA, GenAlex, PopGene, NTSYS-pc, PASSAGE and SPAGeDI (dominant data) for any groupings of populations the user may be interested in. Thus, the program allows you to define population subsets, compare independent groups of populations, include the same population(s) in more than one group and make all possible data combinations you can think of just with a few easy mouse clicks and without formatting errors. For co-dominant data only, it also calculates all the parameters related to the probabilities of allelic loss (sensu Bengtsson et al. 1995).

Through saving a lot of research time while increasing accuracy and versatility in data analyses, Transformer-3 permits the effective implementation of urgency in the growing number of practical applications of molecular population genetic information, and allows the researcher to concentrate in what really matters: the critical discussion of results and hypotheses.

This program is the result of a collaborative effort between the Laboratorio de Biodiversidad Molecular at the Jardín Botánico Canario Viera y Clavijo and the Departamento de Software of EXEGEN. It can be downloaded without charge under the link “software” at the web page of EXEGEN

<http://www.exegen.org> Users just have to provide a valid email address to which EXEGEN will send the link where the program, the example files and the users manual can be downloaded. A mailing list will also send them updates and other information concerning future developments of the Transformer project.

Use the program only in a PC and avoid Windows XP. Since Transformer-3 runs macros, check that your macro security is set at least to medium, and also make sure that you do not have Excel add-ins in your computer, as these might interfere with some commands in Transformer-3.

Transformer-3 can be downloaded without charge, and may be distributed freely if and when (i) it does not undergo any modification, (ii) the manual and the three example files are attached without changes, and (iii) it is adequately cited in all papers and communications as follows:

Caujapé-Castells J, Baccarani-Rosas M (2005) Transformer-3: a program for the analysis of molecular population genetic data. EXEGEN software & Jardín Botánico Canario “Viera y Clavijo”.

To those who requested and tested the beta versions of the program, thanks a lot for your feedback and encouragement; we hope all of you will find yourselves in the

acknowledgements of the manual. Users can also send comments, criticisms, suggestions and bug reports on Transformer-3 to

julicaujape@grancanaria.com or to mbaccarani@wanadoo.es

Your citations and comments are important to raise funds to complete the next version of the program. Transformer-4 is already being designed by EXEGEN software and the Laboratorio de Biodiversidad Molecular of the Jardín Botánico Canario Viera y Clavijo to include a much wider range of possibilities, transformations and calculations.

Cheers,

Juli and Mario

Dr. Juli Caujapé Castells Head Molecular Biodiversity labs & DNA bank Jardín Botánico Canario “Viera y Clavijo” Ap. de Correos 14 de Tafira Alta 35017 Las Palmas de Gran Canaria Spain

email: julicaujape@grancanaria.com phone: ##34 928219421 ext. 4770 fax: ##34 219581 <http://www.step.es/jardcan/> julicaujape@grancanaria.com

Software goldMINER

Dear All,

I am releasing a Windows software goldMINER to the scientific community at:

<http://dambe.bio.uottawa.ca/goldminer.asp>

The software was originally written to annotate a large set of ESTs (expressed sequence tags) from goldfish brain in a study to elucidate the response of goldfish to environmental hormone-like chemicals (especially estrogen-like chemicals). Hence the gold part in its name.

goldMINER is the first EST annotation software that automate functional annotation by using the Conserved-Domain Database (CDD, which imported and validated functional classifications from pFAM, SMART, COG, etc., and added many functional annotations of proteins curated by NCBI staff led by A. Marchler-Bauer). CDD is, in my view, the best one-stop database for functional annotation of unknown sequences.

If you happen to have ESTs or whatever unknown sequences and you wish to know its detailed function,

then you will be impressed by goldMINER's functionality.

Online help is provided in the form of a tutorial. Just press F1 after starting goldMINER.

Enjoy!

Best. Xuhua

Dr. Xuhua Xia CAREG and Biology Department University of Ottawa Room 278, Gendron Building 30 Marie Curie, P.O. Box 450, Station A Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 Fax: (613) 562-5486 URL: <http://dambe.bio.uottawa.ca>

xxia <Xuhua.Xia@uottawa.ca>

SquatLobster samples

Hi,

Could anyone help me, I am trying to get my hands on samples of *Munida rugosa* and *M.sarsi* from the English Channel?? Any advice or direction would be much appreciated

Deborah

Deborah Bailie Fisheries Genetics and Evolutionary Ecology Lab School of Biology and Biochemistry Queens University of Belfast 97 Lisburn Road Belfast BT9 7BL Northern Ireland Tel: 028 90972247 Email: d.bailie@qub.ac.uk

d.bailie@qub.ac.uk

TREEs birthday cover

Subject heading: Faces of the future.

We are editing two special issues of Trends in Ecology and Evolution to mark TREE's 20th birthday. These issues take a hard look at the future of our subject, and to celebrate this, we would like to construct one of the covers as a collage of the people who are the future: the graduate students and young post-docs of today. A poster size rendition of the cover is also likely to be produced.

If you would like to appear in this visualisation of the

next twenty years, please send a picture of yourself to tree@elsevier.com by the end of March, along with the statement of permission below. The pictures will be used without attribution. The pictures will be small on the cover, so we need faces only, and filling the image like a passport picture. The pictures must be no bigger than 100kb and saved as a .jpeg or .tif file. We will use them in order of arrival if we get too many, and if we get too few, we will assume the worst for the future of our subject.

Statement of permission: "I (your name) grant permission to reproduce this photograph worldwide as part of the cover image of TREE and in all revisions and translations of the cover image in print and in all the forms of media, now or hereafter known (including books, journals, CD-ROMs, online and internet), derivative works based on this journal, and other publications or advertising material published by Elsevier."

Best wishes, Andrew Read (Edinburgh) & Jim Clark (Duke), Birthday editors, & Katrina Lythgoe, TREE Editor.

Many thanks and best wishes,

Katrina

"TREE, ETJ (ELS)" <tree@elsevier.com>

Taxonomic rss feeds

In case you haven't seen it, this web site allows you to quickly view recent papers published that contain information on particular taxonomic groups. It has a convenient, taxon-level browser and those with an interest in particular taxa can also set up a personalized RSS feed. Way cool.

David Remsen, uBio Project manager comments (in a note to Taxacom):

"uBioRSS is a taxonomic RSS aggregator that provides taxonomic browsing of thousands of articles from hundreds of journals. Viewers can select taxonomic groups or input their own species lists for monitoring. <http://names.ubio.org/rss> "

Rich Palmer –

A. Richard Palmer Systematics and Evolution Group Department of Biological Sciences University of Alberta Edmonton, Alberta T6G 2E9 CANADA phone: (780) 492-3633 message: (780) 492-3308 FAX: (780) 492-9234

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

Tree Rot

I answered a query concerning decay indices for phylogenetic trees directly, but thought the information may be useful for other members of the group.

TreeRot by Sorenson <http://people.bu.edu/msoren/-TreeRot.html> is a very easy program to use for determining Bremer indices (decay indices). It is also capable of providing partitioned DI, and after your analysis is complete, the program can parse your output log and give you the DI at each node (so you don't have to go through the log file yourself and do the arithmetic).

Alan Meerow

Alan W. Meerow, Ph.D Research geneticist and systematist USDA-ARS-SHRS National Germplasm Repository 13601 Old Cutler Rd. Miami, FL 33158 (305) 254-3635, cell: (786) 412-1821, Fax: (305) 969-6410 email: ameerow@saa.ars.usda.gov

ameerow@saa.ars.usda.gov

UGroningen EcolEvol

Dear colleagues: Please distribute this information to potential students.

International Master's Programme in Ecology and Evolution

The Centre for Ecological and Evolutionary Studies at the University of Groningen (Netherlands) organizes a highly successful master's programme on the interface between ecology and evolution. This two-year "top master" programme is designed to provide an optimal preparation for a subsequent PhD programme and eventually for a scientific career in academic research. Through intensive student-teacher interaction during courses, seminars, practicals and individual research

projects, students get an intense training in modern research paradigms and techniques. Much emphasis will be placed on the development of critical thinking and the training in "soft skills" like efficient communication or writing grant proposals. The programme is highly selective and aimed at the brightest and most ambitious students from all over the world. All foreign students admitted are eligible for a two-year scholarship. The deadline for application is 15 April 2006. For more information visit www.rug.nl/biol/evobio or contact

Franz J. Weissing Professor of Theoretical Biology Centre for Ecological and Evolutionary Studies University of Groningen Kerklaan 30 9751 NN Haren The Netherlands tel: +31-50-363-2131 fax: +31-50-363-3400 email: f.j.weissing@rug.nl URL: www.rug.nl/biol/theobio

Weighing Drosophila

Hello all,

I am wondering if anyone could recommend an affordable and accurate micro-balance for weighing individual Drosophila? I am trying to calculate offspring-parent regressions and need precise and accurate estimates (one fly weighs around 0.20 mg).

thanks,

Sam Yeaman (yeaman@zoology.ubc.ca)

Weighted Phylogenetic Trees

Respected Sir

With due respect I would like to ask you a query regarding making of weighted phylogenetic tree based on morphological characters of cyanobacteria. Please tell me how to give weight to particular character as colour, presence/absence of akinete, heterocyst position & its frequency, vegetative cell shape, apical cell shape & vegetative cell width & length. Which one of the software we must install to do this job well.

Thanking You With best regards Swati

swati_mishra23@yahoo.com

walter.durka@ufz.de walter.durka@ufz.de

WintoMac conversion software ABI answers

thanks all for your immediate help!

For all who do not know, you can download the conversion programs (Win->MAC, and MAC -> Win) from the ABI site:

www.appliedbiosystems.com/support/software/3100/-conversion.cfm regards Walter

– **** Register for “Plant Population Biology” <<http://www.ufz.de/PopBio2006>> *** A conference from 24.05.-27.05.2006 in Halle, Germany *

Dr. Walter Durka Dr. Walter Durka UFZ - Centre for Environmental Research Leipzig-Halle UFZ - Umweltforschungszentrum Leipzig-Halle Dept. Community Ecology Department Biozönoseforschung Theodor-Lieser-Strasse 4 Theodor-Lieser-Str. 4 06120 Halle 06120 Halle Germany Deutschland Tel.: (+49)345/558-5314 Tel.: 0345/558-5314 Fax: (+49)345/558-5329 Fax: 0345/558-5329

email: walter.durka@ufz.de
<<mailto:walter.durka@ufz.de>>

INVASIONS: <http://www.ufz.de/index.php?en=2773> <<http://www.ufz.de/index.php?en=73>> Home:
<http://www.ufz.de/index.php?en=798> <<http://www.ufz.de/index.php?eny8>>

fastatoNWconverter answers

Question: Does anybody know of a freely available program that converts fasta / nexus / mega / phylip etc. files to the *.rdf files used by the NETWORK program

Answer: Seems everybody use dnasp. Its free; <http://www.ub.es/dnasp/> I tested it and it works. Import your fasta (or whatever) file to dnasp and the export it to the Roehl format.

But even easier. You can use Network as it is if you do it correctly:

You do not need to convert a file to the *.rdf format. Just go directly to the “Calculate Network: Network Calculations: Median Joining” menu (if that’s the type of analysis you want to perform). That will open a new window. After that, you can go to the “File: Open” menu, which will open a conventional Windows file dialog box. From there, just select the type of file you want to open using the drop-down menu at the bottom of the dialog box. You should see a list of different types of files that can be directly read by the program (including nexus and phylip files).

Thanks for all the Answers All the best Carina
Carina.Schlebusch@nhls.ac.za

PostDocs

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BrnoSheffield OstracodReproduction

Marie Curie Research training network (MRTN) SEXASEX - postdoctoral position available in molecular genetics

Researchers interested in the paradox of sex in evolutionary biology are strongly encouraged to apply for a research position in the European Union Marie Curie Research Training Network SEXASEX, which is coordinated by Prof. Dr. Koen Martens, RBINSc, Brussels. One postdoctoral ('Experienced Researcher') position is vacant, out of a total of 10 positions supported by the network. Criteria of eligibility include: EU citizenship, less than 10 years of research experience (defined as starting when the candidate is awarded a degree that permits entry to a PhD programme, usually a Masters degree), and a willingness to work in a European country other than the country of origin. We seek candidates who are enthusiastic about evolutionary biology, travelling and living abroad, learning in a multidisciplinary research environment and working in teams. This appointment will be for 2 years but we may consider making two one-year appointments for suitable candidates.

The application of female candidates is especially encouraged; detailed information on child care facilities at the different institutions will be provided upon request. Aid can be sought if accompanying spouses also require employment abroad.

Project overview: Sex is the queen of evolutionary problems. It will be tackled by SEXASEX in a multidisciplinary approach, providing training and transfer of knowledge for a total of 360 person-months. 10 network researchers (6 young researchers (YR) and 4 experienced researchers (ER)) will receive training in 9 institutions across as many countries. A wide array of research tools will provide excellent training opportunities, for example through individual career de-

velopment plans, individual tutoring and secondments, which will be supplemented by participation in courses and external workshops. Network-wide training will exploit the extensive experience of the partner institutions through five courses and summer schools for all network researchers. Complementary skills such as management and communication (verbal, written) will be developed, and gender awareness will be raised, in two network-wide meetings. The network's theoretical and empirical research will apply 13 major approaches, including novel genetic and cytogenetic approaches, intraspecific phylogeography, ecology, behavioural studies, GIS analyses and theoretical modelling. With this multidisciplinary toolkit, SEXASEX will investigate why sex exists at all, given its evolutionary costs, using the model organism *Eucypris virens*, a non-marine ostracod species with both sexual and asexual reproduction. What determines its gender, what are the genomic consequences of long-term asexuality, what is the cohesiveness of a species with mixed reproduction, how do asexuals and sexuals compete and what is their historical zoogeography? The pluralistic approach of SEXASEX is unique and timely, using highly novel methodologies and dealing with cutting edge science based on European excellence and tradition. Please refer to <http://www.naturalsciences.be/EVIRENS/> for more information.

POSTDOCTORAL POSITION: MOLECULAR GENETIC AND CYTOGENETIC APPROACHES TO THE CAUSES AND CONSEQUENCES OF ASEXUAL REPRODUCTION. Starting date: 1st July 2006 or as soon as possible thereafter Duration: 24 months (or 2 x 12 months) Salary: country-specific plus tax-free mobility allowance Scientists in charge: Prof. Dr Jan Zima, Czech Republic

Prof. Dr Roger Butlin, UK Locations: Brno, Czech Republic & Sheffield, UK (12 months funded in each location but the final arrangements are open to negotiation with the appointee). Visits to other partner laboratories will be encouraged and may be required, especially for cytogenetic training in Munich. Places of work: 1) Academy of Science, Institute of Vertebrate Biology & Charles University, Department of Zoology;

2) University of Sheffield, Department of Animal and Plant Sciences

Approach and methods to be applied: Sex determination mechanisms in freshwater ostracods in general and in *E. virens* in particular remain elusive: are they chromosome based (XY or XO systems) or environmentally cued, or are other factors at play? What genetic changes underlie the transition to asexual reproduction and what changes accumulate as a result of long term asexuality? We will investigate these questions with a range of modern genetic and cytogenetic approaches. Correlations between chromosomal architecture and/or other cytological factors and reproductive mode will be examined, using fluorescence in situ hybridization techniques. Gene expression will be examined with Suppression Subtractive Hybridisation (SSH). This will be used to search for genes that are expressed differently in sexual females

— / —

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>

BrookfieldIllinois ConservationPopGenet

Conservation Associate-Population Genetics (Postdoctoral Researcher) Chicago Zoological Society (Brookfield Zoo), Brookfield, Illinois

Position description: Work with a team of collaborators to develop and test improved methods for genetic management of breeding programs for wildlife populations. Develop methods for analyzing pedigrees and managing captive populations in which pedigrees are incomplete. Use analytical and simulation methods to test alternative strategies and algorithms.

Requirements: Ph.D. degree in evolutionary biology, population genetics, population biology, or a related field. Familiarity with programming and simulation methods. Knowledge of Visual Basic, C, or C++ highly desirable. Experience with statistical methods for analyzing DNA data and/or pedigrees. Good communication skills.

This is a full-time, two-year, grant-funded position. Approximate salary: \$40,000/year, with excellent benefits.

The position will be filled 1 June 2006, or as soon thereafter as a suitable candidate is chosen.

Inquiries about the position may be made to Robert Lacy by emailing: rlacy@ix.netcom.com.

To apply, send resume, cover letter, and three letters of reference to: Brookfield Zoo; Attn: Human Resources Department; 3300 Golf Road; Brookfield, IL 60513; or if preferred may be sent via e-mail to: greatjobs@brookfieldzoo.org; or fax to: (708) 485-0986.

Robert C. Lacy rlacy@ix.netcom.com www.vortex9.org
<<http://www.vortex9.org/>>

Population Geneticist Department of Conservation Biology Chicago Zoological Society Brookfield, IL 60513 USA www.brookfieldzoo.org

Bob Lacy <rlacy@ix.netcom.com>

BrownU SpliceSiteRecognition

Postdoctoral Associate

My lab employs computational approaches to identify and understand the role of individual sequence elements in complex recognition events. In yeast, splice sites are defined by strong consensus sequences. Yet in vertebrate genes these signals appear much weaker even though the search space is much larger (bigger genomes, bigger pre-mRNAs, more introns). The information necessary for recognition appears to have migrated outside the sites and into the surrounding sequences. We have identified subtle enhancer and silencer sequences that appear to help explain this recognition event.

we want to: 1) identify functional variants using these models and inferences of selection. 2) test the enhancer activity of both version of the alleles in a high-throughput system 3) implement computational methods in multiple genomes to study the evolutionary history of these elements - concomitant loss/gain of cis-element and trans acting factor

I am looking for a postdoc with quality molecular biology experience coming from an evolutionary/computational background. Salary will be commensurate with experience but will definitely start higher than the institutional minimum (28K). There may also be some opportunity to transition into a CCMB teaching fellow next year if that is something that is interesting to you.

Unfortunately I have to require more than PCR/sequencing expertise - please do not respond if you have not made a construct or performed a hybridization of some sort. Thanks. Will

Will Fairbrother, PhD Assistant Professor of Biology BioMed- Molecular, Cellular Biology Biochemistry Box G-E404 Brown University, Providence, RI 02912-G Telephone: (401)863-6215 Fax: (401)863-9653

William.Fairbrother@brown.edu

DalhousieU SalmonidConservationGenetics

A postdoctoral position is available in the laboratory of Daniel Ruzzante at Dalhousie University in Halifax, Canada. The position is available for two years starting in the spring/summer of 2006 and is to conduct research on conservation genetics of salmonids. The research will have a significant field component and fieldwork is to be conducted in northern areas within Gros Morne and Terra Nova National Parks in Newfoundland and the Torngat Mountains National Park Reserve in Labrador. The successful applicant will have a record of relevant publications in conservation genetics. S/he will ideally also have experience working in northern regions or an excellent predisposition for fieldwork in the north. The work is to be conducted in collaboration with Parks Canada scientists (Drs Tom Knight and David Coté). The Department of Biology at Dalhousie has strengths in evolutionary/population and conservation genetics and the successful candidate will conduct the molecular aspects of his/her research in the Gene Probe Laboratory, a centralized molecular facility at Dalhousie University with ample opportunities for interaction with faculty, postdocs and students.

Interested candidates should send a CV, statement of research interests as well as the names and affiliations, e-mail addresses and phone numbers of at least two referees to Daniel Ruzzante (Daniel.ruzzante@dal.ca).

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

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

Gatersleben EvolPlantReprod

Hello,

I have a 2 year post doctoral position beginning in April 2006 to develop high throughput and automated flow cytometric methods to analyze leaf and seed tissue from both experimental and crop plants.

The position will involve a number of different projects, both in my research group and in conjunction with European seed companies, and will include (to name but a few):

1. Seed analyses of sexual and apomictic plants (my group)
2. Somatic tissue analyses of induced polyploids
3. Genome size analyses of wild accessions from various crop plants

The work will involve analyses using automated pipetting and flow cytometric systems which have been recently purchased for my lab, and will entail development of extraction methods, buffer systems, and downstream automated software analyses. I'm thus looking for someone who is very comfortable with computers, and who has experience with flow cytometry and karyological methods. There is also the possibility of joining these analyses with a number of genotyping projects we have running.

My group is at the IPK in Gatersleben, which is about 2 hours southwest of Berlin in the foothills of the beautiful Harz Mountains. The IPK is a very well endowed institute with a wide range of research groups working on both model systems (Arabidopsis) and crop plants.

Knowledge of German would be helpful, but is not required.

Please don't hesitate to contact me if you have any questions, or require more information.

Best wishes, Tim

Dr. Tim Sharbel Apomixis Research Group Dept. of Cytogenetics and Genome Analysis Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstraße 3, D-06466 Gatersleben Germany Apomixis Group Webpage <http://www.ipk-gatersleben.de/en/02/04/05/index.html> IPK Webpage www.ipk-gatersleben.de tel: +049 (0)39482 5608 fax: +049 (0)39482 5137

Tim Sharbel <sharbel@ipk-gatersleben.de>

Helisinki EvolGenet

Post-doctoral position in Evolutionary Genetics, Helsinki, Finland.

A post-doctoral position is available in Ecological Genetics Research Unit (see <http://www.helsinki.fi/bioscience/ecology/merila.htm> for more details) at the University of Helsinki, Finland, as a part of the recently funded Finnish Centre of Excellence in Evolutionary Genetics and Physiology which also includes the research groups of Professor Craig Primmer (see <http://users.utu.fi/primmer>) and Professor Mikko Nikinmaa (http://www.sci.utu.fi/biologia/fysiologia/nikinmaa_eng.htm).

The successful applicant will be expected to have the necessary molecular skills and scientific enthusiasm to contribute significantly to functional and population genomics aspects of on-going projects on (i) three-spine stickleback adaptation and differentiation in northern Europe, and (ii) development of molecular genetic tools for studies of evolutionary and population genetics of wild vertebrate populations (Atlantic salmon, common frog and birds). These projects provide extensive opportunities for collaboration with researchers and students working with quantitative genetic and statistical aspects (see also: <http://www.rni.helsinki.fi/~boh/>) of the same projects.

In addition to playing a major role in these projects, the successful applicant will be encouraged to develop their own research program within the scope of the Centre of Excellence (including supervision of graduate students), and research funding will be provided to support this. A certain amount of supervision of post-graduate students will be involved.

Researchers with previous post-doctoral experience in functional genomics and with the imagination and interest necessary to use their experience to address questions in evolutionary biology are especially encouraged to apply. Interest and/or experience on application evolutionary quantitative genetic methods is beneficial.

Informal inquires and applications should be addressed to Prof. Juha Merila (juha.merila@helsinki.fi). Applications should include a full CV, a statement of previous research and supervision experience as well as an outline current research interests and names and contact details of at least two referees. Review of applica-

tions will commence at the end of March 2006 with the preferred starting date being prior to September 2006. The position is initially available for two years. The salary range is 2200-2600 EUR per month, depending on the previous post-doctoral experience of the candidate.

More information about the Department and its research groups it hosts can be found from: <http://www.helsinki.fi/bioscience/ecology/research.htm> –

Juha Merila Ecological Genetics Research Unit Department of Biological and Environmental Sciences PO Box 65 (Biocenter 3, Viikinkaari 1) FIN-00014 University of Helsinki Finland

Fax: +358-9-191 57 694

juha.merila@helsinki.fi juha.merila@helsinki.fi

IndianaU BehavioralEvolution

We are looking for a postdoc with interests in behavioral mechanisms to work on a large, collaborative zebrafish project in the lab of Emilia Martins (<http://www.indiana.edu/~martinsl>) at Indiana University, Bloomington. The project aims to uncover the genetic, hormonal and biochemical bases of evolutionary shifts in complex behavior seen in comparisons of natural populations of zebrafish and also in comparing the behavior of domesticated and recently-wild-caught strains. Individuals with interest and previous experience working with steroid hormones, pheromone biochemistry, quantitative genetics, fish behavioral ecology and/or fieldwork in India are especially encouraged to apply, but other combinations of skills and knowledge backgrounds may also be welcome. The position (including stipend and benefits package) is available as early as July 1, 2006, and can continue for up to two years.

The successful candidate will join IU's large and active behavior community (<http://www.indiana.edu/~animal>) and a Biology Department (<http://www.bio.indiana.edu>) especially strong in evolutionary research. Bloomington is located in the heavily forested hills of South-Central Indiana and is renowned for its attractive quality of life and modest cost-of-living. The cultural environment provided by the University is exceptionally rich in art, music and theater. For further inquiries, please contact Emilia Martins at emartins@indiana.edu. All applications (letter of inter-

est, CV and contact information for 3 references) should be emailed to malockha@indiana.edu, enter Martins - Postdoc position, in the subject line. Please indicate in your cover letter the date at which you are available to begin the position. Review of applications will begin immediately and continue until the position is filled.

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

emartins@indiana.edu emartins@indiana.edu

Madrid EvolBiol

POSTDOCTORAL POSITIONS IN SPAIN

The funding program "Juan de la Cierva" has just been announced. This will support 350 new 3-yr postdoctoral positions in all areas of knowledge, of course including Evolutionary Biology. Applicants can be of any nationality provided that they will have earned their PhD between 3-April-2003 and 30-June-2006 (some exceptions apply, see link below). However, host institutions must be from Spain. It is necessary that candidates contact their prospective research groups and coordinate with them for the application process. Deadline is April 3rd, 2006.

More (and formal) info at: <http://www.mec.es/ciencia/delacierva> Best of luck,

- - - Alberto G. Saez Depto. de Biodiversidad y Biología Evolutiva Museo Nacional de Ciencias Naturales, CSIC Jose Gutierrez Abascal, 2. 28006 Madrid, Spain <http://www.mncn.csic.es/saez.htm> "Alberto G. Sáez" <asaesz@mncn.csic.es>

MaxPlanck EvolSleep

Max Planck Institute for Evolutionary Anthropology
Postdoctoral Position to Study the Evolution of Sleep in Mammals

1600 to 2200 per month (19200 to 26400 per annum), depending upon qualifications and experience.

We seek to appoint a post-doctoral research associate to investigate the evolution of sleep patterns in mam-

mals using phylogenetic methods applied to comparative data. The research will take place at the Max Planck Institute for Evolutionary Anthropology. The position is available starting in May 2006 (and ideally not later than July 2006), and the initial term of the contract will be 18 months. The postdoctoral research will be supervised by Dr. Charles Nunn (Max Planck Institute and University of California), in conjunction with Dr. Robert Barton (University of Durham) and Dr. Patrick McNamara (Boston University). The postdoctoral research associate will be involved in collating and analyzing comparative data on mammalian sleep patterns in relation to ecological, behavioral, and physiological traits. The ideal candidate should have expertise in phylogenetic comparative methods, along with experience in one or more of the following areas: database development and management (particularly mysql), mammalian behavior and ecology, and programming.

Review of applications will begin right away and will continue until the position is filled. Applications should include a CV, brief description of research interests and names and contact information for two references. Please send applications or questions to Charles Nunn via email (nunn@eva.mpg.de). Further information is available at http://www.eva.mpg.de/primat/-staff/charles_nunn/index.htm . Charles L. Nunn http://www.eva.mpg.de/primat/staff/charles_nunn/-index.htm Max Planck Institute for Evolutionary Anthropology Deutscher Platz 6 04103 Leipzig, Germany email: nunn@eva.mpg.de tel.: ++49 (0) 341 3550 204 fax: ++49 (0) 341 3550 299

and

Department of Integrative Biology University of California Berkeley, CA USA tel.: ++1 510 643 2579

nunn@eva.mpg.de nunn@eva.mpg.de

McMasterU StatGenetics

Location: McMaster University

Application deadline: April 30

Project Title: Statistical molecular evolution

Description: A postdoctoral position is available in the lab of Dr. Brian Golding in the Biology Dept. of McMaster University Hamilton, Ontario.

The project will involve developing new statistical

methods and/or using pre-existing bioinformatics tools for the analysis of gene sequence data. Candidates for the Postdoctoral Fellowship must have completed a Ph.D. in the field of statistical genetics, theoretical population genetics, molecular evolution or a related discipline. Experience in molecular evolution or population genetics, statistical analysis and bioinformatics/computer programming are required.

To apply: Send a complete CV, a description of your research achievements and interests, and the names of at least two referees via email to Golding@McMaster.CA. Include a subject header that clearly states "Application for StatGenetics Postdoc".

Brian Golding E-mail: Golding@McMaster.CA Department of Biology FAX: 905-522-6066 McMaster University Tel: 905-525-9140 ext 24829 1280 Main Street West Hamilton, Ontario, L8S 4K1

Smithsonian MarineEvolBiol

Marine Postdoctoral Fellowship, Smithsonian, Panama
The Smithsonian Tropical Research Institute (STRI), in the Republic of Panama, is accepting applications for one 2-year Marine Postdoctoral Fellowship.

This fellowship will support marine biological research on either or both the Atlantic and Pacific coasts of Panama. Preference will be given to projects that are based at STRI'S Caribbean research station at Bocas del Toro.

The stipend is US\$35,000/year plus allowance for travel to Panama.

Before submitting a formal application, applicants are strongly encouraged to consult with STRI staff scientists who will serve as potential advisors (see: http://www.stri.org/english/scientific_staff/index.php)

A complete application (double spaced, 12pt font, as a PDF file or Word document) includes the following: a. Curriculum vitae. b. Abstract (up to 1 page) c. Proposal (up to 6 pages) d. Bibliography relating to the proposal e. Research budget and justification.

Submit your application by email to MarineFellowship@si.edu.

Letters of recommendation: Have two recommenders send letters by email (with "your name - recommendation" in the subject line, and including details of the recommender's institutional affiliation, and contact

data) to MarineFellowship@si.edu. Receipt of all emails will be acknowledged by return email within 24 hours.

Application deadline: April 15, 2006.

Starting date: As of October 1, 2006

Adriana Bilgray <BilgrayA@si.edu>

StanfordU MammalianSubstPatterns

An NIH-funded one year postdoctoral position, with possible renewal for up to 5 years is available to work with Dmitri Petrov at Stanford University. The project is done in collaboration with Peter Arndt (Max Planck Institute for Molecular Genetics in Berlin) and Terry Hwa (UCSD). The project focuses on understanding the evolution of patterns of substitution (including nucleotide substitution, insertions, and deletions) through evolutionary time and across genomic space. We will use dead copies of transposable elements, pseudogenes, and intergenic sequences to provide crossvalidated estimates of substitutional patterns. The SNP data and newly developed methods of inference will be used to understand evolutionary forces that have acted on patterns of substitution. We are seeking applicants with research interests in evolutionary and molecular biology. Strong quantitative skills and experience in computational biology is required.

Please send a CV, names and contact details of three academic referees, and a statement of research interests to dpetrov@stanford.edu. Review of applications will begin right away and will continue until the position is filled.

Remuneration will be in line (or above) with the guidelines at <http://postdocs.stanford.edu/handbook/-salary.html> For relevant papers please see:

P. F. Arndt, D. A. Petrov, T. Hwa, *Mol Biol Evol* 20, 1887 (2003). P. F. Arndt, T. Hwa, *Bioinformatics* 21, 2322 (2005). P. F. Arndt, T. Hwa, D. A. Petrov, *J Mol Evol* 60, 748 (2005). M. Lipatov, P. F. Arndt, T. Hwa, D. A. Petrov, *J Mol Evol* 62, 168 (2006).

Dmitri Petrov Associate Professor Department of Biological Sciences 371 Serra St. Stanford University Stanford, CA 94305

TEL (650) 736 1169 (office) TEL (650) 736 2249 (lab)
FAX (650) 723 6132 WEB: <http://petrov.stanford.edu>
e-mail: dpetrov@stanford.edu

“Dmitri A. Petrov” <dpetrov@stanford.edu>

UAlbany ExpViralEvol

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

UBerne TheoEvolEcol

POST-DOC POSITION IN THEORETICAL AND BEHAVIOURAL ECOLOGY

Dept. Behavioural Ecology, Institute of Zoology, University of Berne, Switzerland.

1) POST-DOC: Theoreticians are invited to apply for a postdoctoral research position to study evolutionary mechanisms of conflict and cooperation, with particular emphasis on reciprocity. Applicants must be experienced in modeling and should have a sound background in theoretical issues in evolutionary biology. The position is initially for two years and can be prolonged. Supervisor: Michael Taborsky.

The successful candidate will join an active research group consisting currently of 5 advanced research staff,

6 PhD-students and a varying number of guest scientists and masters students. Besides the Behavioural Ecology group, the ecologically oriented Zoological Institute of the University of Bern consists of research groups on Aquatic Ecology (Ole Seehausen), Conservation Biology (Raphael Arlettaz), Evolutionary Ecology (Heinz Richner), Population Genetics (Laurent Excoffier) and Synecology (Wolfgang Nentwig). Salaries will follow the schemes of the national funding organizations of Switzerland. Besides research, Post-docs assist in undergraduate teaching and supervision.

Closing date: Open until filled, but all application materials, including CV, a summary of research experience, copies of any published or in-press papers, and two letters of recommendation should be received by April 15, 2006 to ensure full consideration. The positions will start at the earliest possible date. Candidates should indicate in a cover letter when they could take up the position. Please send all application material to the secretary's office, c/o Marlis Gerteis, Dept. Behavioural Ecology, University of Bern, Wohlenstrasse 50A, CH- 3032 Bern, Switzerland; or as e-mail attachments to marlis.gerteis@esh.unibe.ch. For inquiries please contact barbara.taborsky@esh.unibe.ch.

Please see also <http://www.zoology.unibe.ch/behav/index.e.php> for further information on our department

Dr. Barbara Taborsky Zoological Institute Behavioural Ecology University of Bern Wohlenstrasse 50A CH-3032 Hinterkappelen Switzerland

e-mail: barbara.taborsky@esh.unibe.ch tel: +41/ 31/ 6319 157 fax: +41/ 31/ 6319 141

barbara.taborsky@esh.unibe.ch

UConnecticut Hybridization

Postdoctoral position: Hybridization and evolution in slender salamanders (Batrachoseps) at the University of Connecticut

An NSF-funded postdoctoral position is available in the laboratory of Elizabeth Jockusch, Department of Ecology and Evolutionary Biology, University of Connecticut, to support research on hybridization and evolution in slender salamanders (genus *Batrachoseps*). The research will use multilocus sequence data to investigate the evolutionary history of *Batrachoseps* and to analyze the role that hybridization has played in the diversification of this group. Applicants must have completed

the requirements for a Ph.D. degree in evolutionary biology or a related field before the start date. Individuals who are proficient in molecular biology laboratory skills, have a demonstrated record of achievement, and have a background in molecular phylogenetics, population genetics, or the development of nuclear markers are preferred; experience with amphibians is also a plus.

The preferred start date is September 1, 2006, and the position is renewable annually with support available for a total of up to 28 months. Salary and benefits are competitive.

For additional information on the Jockusch lab, please visit: <http://hydrodictyon.eeb.uconn.edu/people/jockusch/jockuschlab/> The Department of Ecology and Evolutionary Biology (www.eeb.uconn.edu) at the University of Connecticut, Storrs, has a large and active group of systematists and evolutionary biologists.

To apply, please send a C.V., brief description of research interests, and letters from three references (these may be sent separately) to the address below. Electronic submission is encouraged. Informal inquiries about the position are also welcome.

Elizabeth Jockusch elizabeth.jockusch@uconn.edu
Ecology and Evolutionary Biology 75 N. Eagleville Rd., U-3043 University of Connecticut Storrs, CT 06269

phone: (860)-486-4452 FAX: 860-486-6364

Review of applications will begin on April 7, and continue until the position is filled.

elizabeth.jockusch@uconn.edu
beth.jockusch@uconn.edu

eliza-

UEdinburgh MaternalAllocation

Post: Postdoctoral Research Fellow
School/Department: Biological Sciences, University of Edinburgh
Vacancy Ref. No: 3005583
Duration: up to 9 months
Hours: Full-time
Informal enquiries: e.cunningham@ed.ac.uk

Background:

To investigate the effects of maternal allocation on offspring fitness and how this is affected by genetic and age-related effects. The project will involve complementary experiments with both avian and invertebrate systems.

Job Profile:

The avian part of the work will examine how precocial birds allocate resources within the egg to their offspring under experimental conditions and the implications this has for offspring health. The successful candidate will be responsible for continuing the breeding of experimental lines of an established colony of blue-breasted quail to look at sources of variation in allocation levels, and to assay allocation levels within this experimental set up. The invertebrate part of the work will involve using *Callosobruchus* beetles as a model system to examine how age related allocation decisions influence offspring longevity and reproductive fitness. Further details can be found at homepages.ed.ac.uk/ecunning. There is also scope for the candidate to conduct side projects of interest within the general maternal allocation framework.

Person specification:

You should have a PhD in an appropriate discipline. You should be a highly motivated and organised individual with a strong experimental background and an interest in applying principles of evolutionary ecology to improve animal health. Statistical experience in mixed modelling approaches and/or experience of conducting immunological assays would be an advantage.

Applicants who would be interested in using this opportunity to prepare funding applications for continued support to remain working within our group after this period are particularly encouraged to apply.

Salary

The role is grade AR1A and attracts an annual salary of £20,044 - £22,289.

Applicants can apply online at http://www.jobs.ed.ac.uk/vacancies/index.cfm?fuseaction=vacancies.detail&vacancy_ref=3005583.

Informal enquiries can be made to Dr Emma Cunningham by e-mail (e.cunningham@ed.ac.uk).

– Dr Emma J A Cunningham Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh King's Buildings West Mains Road Edinburgh EH9 3JT Tel 0131 651 3602 Fax 0131 650 6564 E-mail e.cunningham@ed.ac.uk

Emma Cunningham <e.cunningham@ed.ac.uk>

UEdinburgh ParasiteResistance

University of Edinburgh Institute of Evolutionary Biology Postdoctoral Research position on the genetics of parasite resistance

Molecular geneticist required to join a NERC-funded consortium investigating the ecology and evolution of nematode-vertebrate systems. The post will focus on the study of host-parasite co-evolution in a nematode-sheep system, including experimental work on Black-face sheep and studies of free ranging Soay sheep on St Kilda. The project will involve expression analysis using microarrays and genetic analysis of identified candidate genes to characterise the molecular basis of resistance of sheep to the common gastrointestinal helminth *Teladorsagia circumcincta*. In addition the study will develop molecular assays for non-invasive monitoring of helminth diversity in sheep.

Funding body: NERC Duration: up to 36 months
Start date: by 1 July 2006 Hours: Full-time PI:
Professor Josephine Pemberton Informal enquiries:
J.Pemberton@ed.ac.uk

Please apply electronically through the University of Edinburgh's website at www.jobs.ed.ac.uk where this position carries the reference number 3005581.

Closing date: 24 March 2006

j.pemberton@ed.ac.uk

UFlorida StatGenetics

There is an opening for two postdoctoral research associates with Dr. Lauren McIntyre at the University of Florida Department of Molecular Genetics and Microbiology, Department of Health Policy research Epidemiology and Biostatistics.

The positions will be affiliated with the UF Genetics Institute. www.ufgi.ufl.edu Dr. McIntyre's research is in the area of statistical genetics/ genomics. For more information on her program visit her website at <http://www.genomics.purdue.edu/people/lmcintyre.shtml> The successful applicants will be able to choose among a variety of collaborative projects focused on the analysis of genomic and proteomic data. Some of the projects include: the quantitative genomics of sex dimorphism in *Drosophila*, identification of virulence factors in *Staphylococcus aureus* associated with clinical outcome, integration of genomic and proteomic data in an analysis of nitrogen deprivation in Maize roots. Work is focused on methodological development

with relevance to the biological problem at hand. Skills expected include: in depth knowledge and interest in Genetics, particularly Evolutionary Genetics, as well as substantial quantitative skill. Candidates with PhD's in either "Genetics" or "Statistics" will be considered for this position. The work will be highly interdisciplinary and require interaction among a diverse group of scientists. The most important qualities are analytic thinking and problem solving, highly developed writing skills, and a genuine interest in working in a successful team. The initial term of the position is one year, with renewal for up to three years, pending successful analytic and writing endeavors.

To apply: Send a complete CV, a description of your research achievements and interests, and the names of at least two referees via email to Dr. Lauren McIntyre mcintyre@ufl.edu

UGroningen EvolBiol

Dear colleagues:

Please distribute this information to talented researchers who are just about to obtain their doctorate of who have completed their doctorate in the past year.

Rubicon programme of the Dutch Science Foundation

The Dutch Science Foundation (NWO) has recently established a new programme (called Rubicon) that intends to further the mobility of talented young researchers who have just completed their doctorate. Rubicon offers Dutch researchers the opportunity to gain experience at a top research institute outside the Netherlands, and it offers talented researchers from abroad the opportunity to obtain a one-year grant for conducting research at a top research institute in the Netherlands. For example, talented young researchers in the fields of ecology and evolution might take this opportunity to spend a year at the Centre for Ecological and Evolutionary Studies (CEES) at the University of Groningen.

The Rubicon programme is highly attractive and, as a consequence, highly competitive. There are three selection rounds a year. The next deadline for submitting an application is 18 April 2006. For more information on the programme visit the Rubicon website

www.nwo.nl/subsidiewijzer.nsf/pages/-NWOP_6H2G7R_Eng .

For more information on the CEES institute visit www.rug.nl/biol/cees or contact

Franz J. Weissing Professor of Theoretical Biology Centre for Ecological and Evolutionary Studies University of Groningen Kercklaan 30 9751 NN Haren The Netherlands tel: +31-50-363-2131 fax: +31-50-363-3400 email: f.j.weissing@rug.nl URL: www.rug.nl/-biol/theobio

UHelsinki 12 EvolBiol

12 postdoctoral positions at University of Helsinki, Finland

The University of Helsinki is currently advertising 12 three-year postdoctoral positions across all scientific disciplines (application deadline: April 20th). This may be of interest to evolutionary biologists, as research in evolutionary biology and ecology was recently evaluated to be at a very high international level at this university. Interested applicants should get familiar with the instructions available at

http://www.helsinki.fi/jobs/postdoctoral_general.html before getting in touch with local researchers (see <http://www.helsinki.fi/bioscience/ecology/-research.htm>).

Hanna Kokko Laboratory of Ecological and Evolutionary Dynamics, Dept of Biological and Environmental Sciences, PO Box 65, 00014 University of Helsinki, Finland tel +358 9 1915 7702, fax - 7694, hanna.kokko@helsinki.fi <http://www.helsinki.fi/~hmkokko> Hanna Kokko <hanna.kokko@helsinki.fi>

UMontpellier BactEvol

“Poste Rouge” Postdoctoral Fellow at the University of Montpellier II

We are looking for an evolutionary biologist with microbiological training to take a leading role in our research program on the experimental evolution of bacteria - phage interactions. Our research team is unique in bringing together theoretical and experimental biologists on projects ranging from coevolutionary interactions between bacteria and phage to ecosystem per-

spectives on adaptation in microbial communities. The successful candidate will actively participate in the design and execution of experiments, will take responsibility in the daily running of our P2 microbiology lab, and will co-supervise students.

The successful candidate will have a PhD degree, an excellent publication record, and will be able to provide contact details for 3 letters of recommendation upon request. The initial contract would begin in the autumn of 2006 for 12 months and can be extendable for an additional year. The “Poste Rouge” Fellowship is limited to non-French nationals. We are particularly interested in candidates who would consider applying in 2007 or 2008 for a permanent research position in France with the Centre National de la Recherche Scientifique.

Candidates fulfilling the above criteria should address a letter of motivation along with CV to:

Dr. Michael Hochberg ISEM, Université de Montpellier II CC065, Place Eugène Bataillon 34095 Montpellier Cedex 5 France email: mhochber@univ-montp2.fr

Michael Hochberg <mhochber@univ-montp2.fr>

UNebraska EvolBiochem

A two-three year postdoctoral position is available to work on the biochemical basis of life history trade-offs in a wing-polymorphic insect at the School of Biological Sciences, University of Nebraska, Lincoln, Nebraska. This project focuses on biochemical and molecular mechanisms underlying differences in lipid metabolism, which, in turn, underlie morph specializations for flight vs. reproduction in a dispersal polymorphic insect. Specifically, research will investigate morph differences in gene regulation, post-translational modification, and/or catalytic activity of lipogenic enzymes that contribute to previously documented differences in flux through lipogenic pathways in the cricket, *Gryllus firmus*. This species is one of the most intensively studied models with respect to variation in biochemical and physiological mechanisms underlying a life-history trade-off (for recent publications on this topic see: Zhao and Zera, Proc. Natl. Acad. Sci. USA 99:16829-16834, 2002; Zera and ZHao, Evolution 57:586-596; Zera, Integr. Comp. Biol. 45:551-524, 2005).

Individuals applying for this position should have experience in some of the following molecular techniques (PCR, cloning, gene sequence analysis, gene expression

analysis), or enzymological techniques (enzyme purification, antibody production and ELISA, enzyme kinetic analysis). Of equal importance, the applicant should have the desire to learn new molecular and biochemical approaches, and the ability and desire to move boldly into uncharted regions of life history biochemistry. Additional information on research in the Zera laboratory can be found in the following web site: www.biosci.unl.edu/faculty/FacPages/zera.asp. Starting salary will be \$30,000 per year. Start date is flexible, optimally June-August 2006. Initial appointment is for 2 years, with appointment to year 2 contingent upon satisfactory completion of research in year 1. Additional funds may be available for a third year of this position. Applicants should send a CV, letter describing research interests, and the names and email addresses of three references. Applicants need to apply electronically at the following: <http://employment.unl.edu/> Click on "SEARCH JOB OPENINGS" and add "060070" in the box entitled "requisition number". UNL is committed to AA/AEO and ADA/504. Please feel free to email me directly (azera1@unlnotes.unl.edu) if you have additional questions on this position. Review of applicants will begin March 22, 2006 and will continue until the position is filled or the search closed. The University of Nebraska is committed to a pluralistic community through affirmative action and equal opportunity. We assure reasonable accommodation under the American Disabilities Act.

Tony Zera Professor School of Biological Sciences University of Nebraska Lincoln, NE 68588-0118

azera1@unlnotes.unl.edu

UReading PlantConservation

This two year and three month postdoc post starts 1st May 2006 and is part of an ongoing project funded by the Darwin Initiative to develop DNA technologies to support the conservation of Mexican desert cacti. The successful candidate will have laboratory experience in microsatellite development and will have used molecular marker data to address questions in evolution/ecology. Their primary responsibility will be to screen microsatellite markers in order to determine whether plants in trade are the ex-situ progeny of parents collected under permit. This work supports a DNA-based certification scheme for traded cacti. The project will also pilot DNA sequencing strategies for species identification. The successful candidate will

play a role in the development of a this scheme through supervision of visiting Mexican scientists; an interest in DNA bar-coding technologies would therefore be desirable. The successful candidate will be an employee of The University of Reading, working with Dr Julie Hawkins in the School of Biological Sciences. Short periods will be spent collecting and contributing to a short training workshop in molecular marker technologies in Mexico.

Informal enquiries and requests for further particulars to Dr Julie Hawkins, School of Biological Sciences, University of Reading, email j.a.hawkins@reading.ac.uk or Tel 0118 378 6546.

Application forms and further particulars are available from the Personnel Office, The University of Reading, Whiteknights, PO Box 217, Reading, RG6 6AH. Telephone (0118) 378 6771 (voicemail). Application forms are also available in Word/RTF format from www.reading.ac.uk/Jobs Closing date for applications 30 March 2006. Please quote reference number R0626.

Dr Julie A. Hawkins, School of Biological Sciences, Plant Sciences Laboratories, University of Reading, Reading, Berkshire, RG6 6AS. UK.

Julie Hawkins <j.a.hawkins@reading.ac.uk>

USaarland Evol Of Transcriptional Regulation

Advertisement of a Vacancy at the University of Saarland

The following position is available at the Medical Faculty, Department of Theoretical Medicine and Biosciences, Institute of Human Genetics

Job Specification: Requisites: We are seeking a highly motivated postdoctoral researcher to investigate transcriptional regulation of human endogenous retrovirus sequences. The successful applicant will have well established expertise in the characterization of eukaryotic promoter sequences and, preferably, repetitive elements. He/she will join an established research group at the Department of Human Genetics at the University of Saarland (Homburg, Germany). Desired: High motivation and interest in scientific work, team spirit. Duties: To conduct research in the field of human endogenous retroviruses, in particular, molecular genetic characterisation of cellular promoters.

Mode of Employment: Scientific Assistant (Postdoc)
 Qualification: University degrees Diploma and Ph.D.
 in biology or biochemistry Post: Department of Human
 Genetics, Medical Faculty, Homburg/Saar Start of
 contract: As soon as possible Volume of employment:
 Full-time (100%) Duration of employment: 2 years (ac-
 cording to §§57aff HRG)

Salary will accord to tariff and other applicable terms
 of the University of Saarland. Full-time positions are,
 in principle, divisible. (§7 Abs. 1 TzBfG). University of
 Saarland pursues a higher proportion of women in this
 field of activity according to the affirmative action plan
 for women. Women are therefore emphatically invited
 to apply. Severely handicapped persons will be favored
 when equally qualified.

Please send complete applications by e-mail or reg-
 ular mail until April 15 2006 to: Dr. Jens
 Mayer FR 2.6, Human Genetics, Medical Faculty
 Building 60 University of Saarland 66421 Homburg
 Germany jens.mayer@uniklinik-saarland.de (reference
 number Z03)

Please send copies only as application documents will
 not be returned. Also, do not send binders or the like.

–

Dr. rer. nat. Jens Mayer Human Genetics, Building
 60 Medical Faculty University of Saar 66421 Homburg
 Germany

phone-office: (49) 06841-1626627 phone-lab: (49)
 06841-1626189 fax: (49) 06841-1626186 e-mail:
 jens.mayer@uniklinik-saarland.de

jens.mayer@uniklinikum-saarland.de
 jens.mayer@uniklinikum-saarland.de

USouthCarolina LifeHistories

Postdoctoral Position: Genetics of Behavior and Life
 Histories

A postdoctoral position is open in the lab of Dr.
 Tim Mousseau at the University of South Carolina,
 Columbia. The ideal candidate will have experience
 in the use of quantitative genetics, molecular markers,
 and SAS, and be willing to participate in lab and field
 studies of behavior and life history variation. The can-
 didate must have demonstrated writing skills and be
 willing to help with the supervision of graduate and
 undergraduate research assistants. Ongoing projects in
 the lab include the immunological consequences of mat-

ing behavior in a cricket, the ecological implications of
 infection by a male-killing bacterium in a beetle system,
 a QTL analysis of maternal effects on development in
 a cricket system, and studies of mutation-accumulation
 in fruit flies and birds from Chernobyl. Salary: \$30 -
 \$35k USD plus benefits. Start date: Open until posi-
 tion is filled.

The average daily high temperature in February is 60F
 (16C), and the average annual snowfall is 1.6 inches (al-
 though it is zero for this year). It's not San Diego, but
 the cost of living index is 30.4% less! (CLI San Diego
 = 141; Columbia, SC = 97).

Interested applicants should send the following infor-
 mation to Mousseau@sc.edu : CV, a brief statement
 of research interests, and names and contact informa-
 tion for three references. Applications will be reviewed
 as they are received and the position will remain open
 until filled.

Dr. Timothy A. Mousseau Professor of Biological Sci-
 ences Dept of Biological Sciences University of South
 Carolina Columbia, SC 29208 USA tel: 803-777-8047
 fax: 803-777-4002 mailto:mousseau@sc.edu
 mousseau@sc.edu

UTexas TheoCompEvolBiol

A postdoctoral position is open at the University of
 Texas, Section of Integrative Biology, in the lab of Claus
 Wilke. One third of the position will be to work on
 an NIH-funded project on the population genetics of
 RNA viruses. The remaining two thirds can be on
 any aspect of theoretical and computational evolution-
 ary biology. Current areas of interest in the Wilke lab
 are RNA virus evolution, protein evolution, determi-
 nants of genome-wide substitution patterns in coding
 sequences, and population genetics theory.

This position requires a Ph.D. and a record of published
 research in areas related to virus evolution, population
 genetics, molecular evolution, or other computational
 or mathematical biology. The successful applicant will
 have strong analytical and computational skills. Pro-
 ficiency in any specific software tool or programming
 language is not required, but past programming expe-
 rience is a must unless the applicant has exceptional
 analytical abilities. Most of the computational work in
 the lab is done in python, R, and C++. The appoint-
 ment will be initially for two years, subject to review

after one year. Renewal beyond the initial two years will depend on the availability of funding.

Qualified candidates, including minorities and women, are strongly encouraged to apply. Please submit applications (cv, statement of research interests, and the names and contact information of at least two references) via email to Claus Wilke, cwilke@mail.utexas.edu, preferably as pdf files. Review of applications will begin immediately, and continue until the position is filled.

Claus Wilke Section of Integrative Biology and Center for Computational Biology and Bioinformatics University of Texas at Austin 1 University Station C0930 Austin, TX 78712 cwilke@mail.utexas.edu

Utah EvolMammalianDetoxGenes

Post Doctoral Research Associate in the area of plant-mammal interactions: evolution of mammalian detoxification genes. Specifically, this project involves investigation into the recent evolution of creosote feeding by the desert woodrat (*Neotoma lepida*). Within the past 10,000 yrs, the desert woodrat has evolved the capability to deal with the large quantities of toxic resin ingested while foraging on creosote leaves. This capacity for resin tolerance differs among desert woodrat populations such that populations with evolutionary experience with creosote voluntarily ingest greater quantities of creosote. Furthermore ³experienced² populations have higher enzyme activities, particularly cytochrome p4502B. The central goal of this project is to understand the evolution of woodrat detoxification enzymes, particularly CYP2B, with respect to creosote feeding.

Qualifications: Candidates should have experience with molecular evolution approaches techniques and analyses. Strong writing skills are essential. Prior experience trapping and handling small mammals preferred but candidates enthusiastic to learn will be considered. To apply, send a cover letter detailing your interest and suitability for the position, CV, 1-2 page research statement, representative reprints, names and email addresses of at least three references to Dr. Denise Dearing dearing@biology.utah.edu. Start date June 1 (nego-

tiabile). Starting salary \$31,500 and healthcare benefits. [kathysmith <kathysmith@bioscience.utah.edu>](mailto:kathysmith@bioscience.utah.edu)

WashingtonU Obesity

POSTDOCTORAL RESEARCH ASSOCIATE GENETICS OF OBESITY, DIABETES, GROWTH AND BONE BIOMECHANICAL PROPERTIES

Positions are available for postdoctoral research associates to work on a variety of projects relating to mapping genes affecting growth, obesity, diabetes, neural morphology, and osteoporosis in mice. Current projects include fine-mapping and identification of previously identified quantitative trait loci (QTLs) in the LG/J by SM/J mouse intercross, mapping and identifying QTLs for dietary obesity and diabetes-related traits and for bone morphology and biomechanical properties in an Advanced Intercross line and a set of Recombinant Inbred lines generated from the LG/J by SM/J intercross. We are especially interested in the context dependence of gene effects and the role of epistasis and genotype by environment interaction in the genetic architecture of complex traits. It is desirable that candidates have a familiarity with the molecular methods used in gene mapping studies, including development of genetic markers, primer design, sequence analysis, and gene expression studies using qPCR and/or the statistical analysis of gene mapping data. Positions are available immediately or over the next year. Interested candidates should submit a letter of application and their vitae to:

James M. Cheverud Department of Anatomy & Neurobiology Washington University School of Medicine 660 S. Euclid Ave. St. Louis, MO, 63110, USA

E-Mail: Cheverud@pcg.wustl.edu Phone: 314-362-4188 FAX: 314-362-3446 AA/EOE M/F/D/V

James M. Cheverud Department of Anatomy & Neurobiology Washington University School of Medicine Box 8108 660 S. Euclid Avenue St. Louis, MO 63110 USA Phone: 314-362-4188 FAX: 314-362-3446 E-mail: cheverud@pcg.wustl.edu

Jim Cheverud <cheverud@pcg.wustl.edu>

WorkshopsCourses

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Copenhagen PlantPopStructure May15-19

Ph.D. course Molecular marker analysis of plant population structure and processes, 15-05-2006 -19-05-2006 at the Royal Veterinary and Agricultural University, Copenhagen. The course provides the participants with advanced knowledge of the analysis of genetic structure, mating patterns and processes in plant populations, using molecular marker data. The course includes theoretical lectures, discussions of scientific articles and student projects, and exercises and practicals with various computer programs. This course is Module 3 of the course package: Molecular plant breeding and genetic resource, <http://www.kursus.kvl.dk/-shares/phdmarker/index.htm>. Course content Estimation of inbreeding level, restricted geneflow, population admixture, hybridisation, selfing rate, paternity assignment, allocation to parental populations, allocation of hybrids to genealogical classes. Assumptions and limitations behind diverse procedures used in relevant computer programmes: GenA1Ex, Spagedi, Structure, MLTR, Two-gener, Population Graph, Split tree, New Hybrids, AFLPOP, Famosz, Cervus, etc.

Discussion of scientific articles using the methods presented. Discussion of student projects (please use this opportunity to discuss your Ph.D. research). Course credit 3 ECTS points. Requirement for obtaining credit: approval of a written synopsis of the course content and compiled results of computer exercises, max. 10 pages. Students who are using, or going to use, some of the techniques for their Ph.D. research are invited to present and discuss their projects during the course.

Course material All course material, such as discussion articles, presentations and software, will be available through a restricted course web site. All software to

be used is freely available. Practicals Maximum number of participants is twenty. PhD students are given preference until 15/4. After 15/4 remaining seats are open to non-PhD student. The course will take place at KVL, 1958 Frederiksberg C (part of Copenhagen). For the exercises, there will be computers available for all; if you prefer to bring your own laptop computer, do that. Coffee and tea will be served, all other meals and lodging is to be organised and paid by the participants on their own.

Course fee To be decided, maximum 500 DKK.

Teachers: Erik D. Kjær, Professor in Forest Genetics, edk@kvl.dk Thure Hauser, Associate Professor in Plant Ecology, tpha@kvl.dk Ole Kim Hansen, Ph.D. in Forest Genetics.

Registration and questions Thure Hauser, tpha@kvl.dk, +45 3528 2818

Edinburgh BBSRC MolEvol Jul17-21

BBSRC Theoretical Genetics And Evolution Summer School on Molecular Evolution and Diversity 2006

Deadline for applications: March 31st 2006.

The BBSRC will be running a summer school (course) for Postgraduate and Postdoctoral researchers working on quantitative aspects of evolutionary biology, dealing with variation both within and between species. The course will take place in Edinburgh, and the dates are:

Monday July 17th 2006 (starting at 2pm) - Friday July 21st (ending at noon)

The course is intended for young scientists with an ongoing and broad interest in molecular evolutionary biology, who wish to gain a greater understanding of

quantitative and theoretical tools and approaches that will aid their interpretation of evolutionary data. The course will include plenary talks from experts in population genetics and molecular evolutionary analyses, including people who are working on developing methods, and people who are applying them to biological data from a range of organisms. There will be a few practical (computer) sessions, intended to help participants learn how to approach analyses of sequence and other types of data, and to think about how they can be used in studying biological questions. Those chosen for the course will be asked to present a short talk or a poster about their research project (or planned project).

Places on the course, and accommodation during the course, are free. Places are not restricted to BBSRC-funded students or post-docs, but are limited to people who have not attended the course in previous years. Travel to Edinburgh will be at your own expense.

Applications are via the web site: <http://www.biology.ed.ac.uk/public/conferences/molevoldiv2006/> You will be asked for a talk or poster title and abstract as well as your name and supervisors name and your institution and department. The deadline is March 31st 2006.

Places are limited to 35 "students". Applicants who have been chosen to attend the course will be notified in April.

The Summer School will cover the following areas of micro- and macroevolution:

Theme A: Genetic diversity within populations The neutral theory and the coalescent Mutation Human minisatellites Genomic context and molecular evolution Theme B: Genetic variability between populations. Theme C: Macroevolution and variation between species Alignment of sequences Reconstruction of Phylogenetic Trees, Detecting natural selection from gene genealogies Gene families, Gene duplications in evolution Genome alignment Theme D: Evolution of development Theme E: Evolution in microorganisms

Lecturers in 2006 will include: Nick Barton, Peter Keightley, Toby Johnson, Brian Charlesworth and Deborah Charlesworth (Edinburgh University) John Armour, John Brookfield, and Paul Sharp (University of Nottingham), Gil McVean (Oxford University) Michael Akam (Cambridge, Zoology) Timothy J.C. Anderson (Department of Genetics, Southwest Foundation for Biomedical Research, San Antonio) Jaap Heringa (Centre for Integrative Bioinformatics, Free University, Amsterdam) Susan Ptak (Max Planck Institute for Evolutionary Anthropology, Leipzig) – 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

EvolBiol in Guarda

Course: Workshop in evolutionary biology for master students and first or second year PhD students.

It is my pleasure to announce this years Guarda workshop in Evolutionary Biology. The main aim of this 1 week course is to develop the skills to produce an independent research project in evolutionary biology. The course is for students with a keen interest in evolutionary biology.

The course takes place in a remote place in the Swiss alps (the village Guarda) during the last week of June 2006. Course faculty this year includes Andrew Read, Louis Du Pasquier, Sebastian Bonhoeffer, Tad Kawecki and Dieter Ebert (organizer).

The course is intended for master (= diploma) students and early PhD students. For the course 4 ECTS credit points are awarded.

The web page with all the details can be found under:

<http://www.evolution.unibas.ch/teaching/guarda/-index.htm> Please communicate this information to interested students.

dieter ebert

<dieter.ebert@unibas.ch>

<http://www.evolution.unibas.ch/>

Universität Basel, Zoologisches Institut, Vesalgasse 1 4051 Basel, Switzerland Tel. +41-(0)61-267 03 60

dieter.ebert@unibas.ch dieter.ebert@unibas.ch

Helsinki GenesUnderNatSel May15-19 Deadline

DEADLINE: 15 MARCH 2006

EMBO practical course: Statistical methods for identification of genes under natural selection

Helsinki 15th-19th May 2006

Organizers: J. Corander & C. Schlötterer

The identification of genes subjected to natural selection has been one of the primary research interests in population genetics over the past decades. With the recent technological advancements and the availability of numerous fully sequenced genomes, the emphasis is shifting from the analysis of single genes towards genome scans for genes subjected to selection.

The course aims to train biologists with the fundamental techniques on how to use statistical methods for the identification of selected genes. Furthermore, we will also show how the statistical tests could be improved by the incorporation of available data from genome scans.

Participants of the course will be provided with the background of the statistical tests, they will be trained in the use of available statistical software packages, and finally they will have the opportunity to apply this knowledge to their own data.

Teachers: Mark Beaumont Jukka Corander Joachim Hermisson Christian Schlötterer Ziheng Yang

More information can be found at:

<http://cwp.embo.org/pc06-02/> Christian Schloetterer <christian.schloetterer@vu-wien.ac.at>

HinxtonUK HapMap July31-Aug2

The Wellcome Trust Course: Working with the HapMap July 31st - August 2nd, 2006 Held at the Wellcome Trust Genome Campus, Hinxton, Cambridge, UK.

The deadline for application is 7th April 2006. Further information can be found at: http://www.wellcome.ac.uk/doc_wtx030611.html and details of how to apply.

Organisers: Barbara Stranger and Manolis Dermitzakis (Sanger Institute)

Course Summary This 3-day residential course will provide a comprehensive overview of the International HapMap Project, and will include practical experience of working with the HapMap data to map phenotypic traits to locations in the human genome. Theoretical lectures will be combined with hands-on practical ses-

sions and introduction to relevant databases and tools.

Programme Introduction to Association Studies The history of genetics association studies in humans, including Mendelian and complex traits will be discussed and will clarify the goals and motivation for the HapMap.

Introduction to the HapMap The project design, including choice of populations, sample size, SNP density, and community engagement plan will be presented. Ethical, legal and social implications of genetic research in human populations will be discussed.

Data collection SNP discovery and the NCBI dbSNP database will be covered. HapMap genotyping and data quality will be discussed alongside commercially available genotyping platforms.

Genetic variation and selection Key findings from the Phase I HapMap will be presented, including patterns of recombination, population structure, and Linkage Disequilibrium in the human genome, and identification of regions of the genome with unusual patterns of variation.

Resource Accessibility Introduction to the HapMap web-site and software tools, including Haploview, Tagger and others. The concept of 'tag SNPs' and their effectiveness will be presented with practical tools for choosing them.

Association mapping Methods for association studies will be reviewed along with issues related to reducing false positives in the face of multiple testing. Practical examples will be provided.

Course instructors Goncalo Abecasis (University of Michigan) Paul de Bakker (MIT) Andy Clark (Cornell University) Panos Deloukas (Sanger Institute) Jonathan Marchini (Oxford University) Albert Vernon Smith (CSHL) Ellen Wright Clayton (Vanderbilt University) Gil McVean (Oxford University) Steve Sherry (NIH/NCBI) Mike Feolo (NIH/NCBI) How to apply Prerequisites Applicants should be postdoctoral scientists or senior PhD students engaged in relevant research.

Cost The course is subsidised by the Wellcome Trust for scientists in academic institutions anywhere in the world. This is a residential course, without exception, and there is a charge of £330 towards board and lodging costs for academic applicants. The fee for commercial (non-academic) applicants is £1,020.

Applications Applicants are required to complete an application form containing their CV together with a one-page outline of their current and ongoing research plans, indicating the relevance of the course to that re-

search. Please note that documentation supporting the application will be required from the applicant's supervisor/head or department.

To submit an application please use the following link: <http://firstcontact.hinxton.wellcome.ac.uk/> We are unable to accept incomplete applications

If you have any questions please contact:

Wellcome Trust Advanced Courses Wellcome Trust Genome Campus Hinxton Cambridgeshire CB10 1SA UK Fax +44 (0)1223 495130 Email advanced-courses@hinxton.wellcome.ac.uk

Barbara E. Stranger, PhD Post-doctoral Researcher Population and Comparative Genomics The Wellcome Trust Sanger Institute Wellcome Trust Genome Campus Hinxton, Cambridge CB10 1SA UK e-mail: bes@sanger.ac.uk Tel: +44 (0)1223 834244 ext.7297 Fax: +44 (0)1223 494919

Barbara Stranger <bes@sanger.ac.uk>

KelloggBiolStation MathFieldEcol

****Scholarship Support Available****

Mathematics and Field Ecology/Evolution Summer Program

12 June - 28 July for Undergraduate and Graduate Students at Kellogg Biological Station, Michigan State University <http://www.kbs.msu.edu/ELME> This summer the Kellogg Biological Station (KBS) will continue a summer program called ELME, Enhancing Linkages between Mathematics and Ecology. ELME is a coursework based research experience designed for students with an interest in applying mathematics to questions in ecology and evolution. Students both with and without formal training in mathematics have benefited from these courses. Students can take 3 one week math courses on topics that are relevant to ecology/evolution and then apply these tools in a field ecology/evolution course.

Mathematics 1-week courses:

Introduction to Theoretical Population Biology - MTH 490.431 Robin E. Snyder, Case Western Reserve University June 12 - June 16

Theory and Modeling in Behavioral Ecology - MTH 490.432 Thomas Getty, Kellogg Biological Station, MSU June 19 - June 23

Maximum Likelihood Analysis in Ecology - MTH 490.433 Chad E. Brassil, Kellogg Biological Station, MSU June 26 - June 30

Ecology 4-week course:

Field Ecology and Evolution - ZOL/PLB 440 Gary Mittelbach and Jeff Conner, Kellogg Biological Station, MSU July 5 - July 28

Undergraduate Fellowships (\$2500, plus housing, travel, and tuition) are available for students enrolling in the full ELME program. Graduate scholarships are available for tuition and housing. Students can enroll in a subset of the ELME courses if that better fits their needs and schedules. More information about KBS and the ELME program is available at <http://www.kbs.msu.edu/ELME>. The application deadline for enrollment and scholarships is 15 March 2006.

brassilc@kbs.msu.edu brassilc@kbs.msu.edu

UFlorida EnrichedMicros Apr3-7

Molecular Markers: Tools for developing enriched microsatellite libraries

Date: 4/3-7/2006

Time: 8:00AM - 5:00PM

Location: Communicore Building, Room CG-29 (MDL6) Fees: \$500.00 for all registered UF Students, Faculty and Staff. \$900.00 all others.

Instructors: Dan Brazeau Ph.D. and Ginger Clark

This intensive laboratory and lecture workshop allows participants to build and screen a microsatellite-enriched, plasmid library using the genomic DNA of their choice. Repetitive probes immobilized on magnetic particles are used to capture microsatellite-containing fragments from genomic DNA digests. A session is dedicated to DNA fragment analysis (GeneScan and Genotyper software). Complementary lecture topics focus on the use of microsatellites in determining genetic relationships, molecular probes for analysis of population structures, and applications of RAPDs in population genetics.

For online registration fill out form here: <http://www.biotech.ufl.edu/WorkshopsCourses/-calendar.html>

or contact Sharon Norton @ 352-846-1337

Sharon E. Norton Education Coordinator University of Florida ICBR Education and Training Core Laboratory PO Box 100156 Gainesville, FL 32610 (352) 846-1337 fax (352) 846-3225 www.biotech.ufl.edu Sharon Norton <norton@biotech.ufl.edu>

Instructions

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

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

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as \LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.