EvolDir

November 1, 2003

Month in Review

Forward

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

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

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

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Conferences

Crete EMBO Drosophila Jun20-26

First Annoncement for:

CRETE XIV EMBO Conference The Fourteenth International Workshop on the MOLECULAR AND DEVELOPMENTAL BIOLOGY OF DROSOPHILA Kolymbari, Crete (Greece) June 20-26, 2004

The objective of the workshop, which is supported by EMBO, is to discuss recent findings on gene organization and expression, early development, pattern formation, developmental neurobiology and the evolution of Drosophila. Approximately 80 participants will be selected from the applications, by a majority vote of the organizing committee. The participants are all expected to contribute to the subject coverage. Applications should include a short summary of research interests and a list of five recent, relevant publications to facilitate the selection process. The deadline for receipt of applications is January 9, 2004. For logistical purposes the organizing committee will adhere strictly to this deadline. Please note that acceptance to the meeting is strictly limited to the individual accepted. A registration fee of 500.00 Euro (or US $ equivalent) must be remitted upon acceptance. Local expenses in Crete will be covered. Participants are expected to finance their travel to Crete. However, a small number of grants-in-aid for partial travel support may become available. Applications from junior investigators will be considered favorably, and at least 15% of the available positions will be allocated to investigators who have recently established their labs or who have not previously attended the meeting. The meeting lasts one week with morning (9:00-13:00am) and evening sessions (17:00-21:00pm). All accepted participants are expected to remain for the entire meeting.

The Organizing Committee

U. Banerjee, A. Bejsovec, S. Bray, C. Delidakis, A. Ephrussi, A.Giangrande, D. Ish-Horowicz, T. Kaufman, R. Lehmann, M. Leptin, S.Parkhurst, N. Perrimon, R. Saint, B. Shilo, S. Vincent. Ex-Officio: S. Artavanis-Tsakonas

For more information and access to an application form please go to:

http://flybase.bio.indiana.edu/docs/news/announcements/meetings/crete/start.fr.html

Glasgow ISMB Jul31-Aug4

Call for ISMB/ECCB 2004 Tutorial Proposals

Due date: December 15, 2003 Details available from: http://www.iscb.org/ismbeccb2004/tutorial_call.html The International Society for Computational Biology (ISCB) presents The 12th International Conference on Intelligent Systems for Molecular Biology (ISMB) and the Third European Conference on Computational Biology (ECCB) a joint conference ISMB/ECCB 2004 (www.iscb.org/ismbeccb2004) to be held in Glasgow, Scotland, UK July 31-August 4, 2004.

Tutorials ======== We are now accepting proposals for ISMB/ECCB 2004 Tutorials. ISMB/ECCB 2004 will feature half-day introductory and advanced tutorials. The tutorials will be given on Saturday July 31. The purpose of the tutorial program is to provide participants with lectures and demos on either well-established, or new "cutting-edge" topics, relevant to the bioinformatics field. It offers participants to learn about new areas of bioinformatics research, to get an introduction to important established topics, or to develop higher skill levels in areas where they are already knowledgeable.

Please complete the form located here: http://www.iscb.org/ismbeccb2004/tutorial_call.html Please note: based on feedback received from earlier years, graduate students are not permitted to participate as instructors or demonstrators.

Due Dates: December 15, 2003 Tutorial Workshop (Instructor) Submission Deadline Feb 1, 2004 Notification of Pre-selected Tutorials March 15, 2004 Draft handouts due April 1, 2004 Notification of Final Tutorial Acceptance May 15, 2004 Final Handouts for Reproduction must be Received

Proposals should contain the following information: -Tutorial submissions MUST include a detailed 3-page (max) description of what will be taught or demonstrated. -Brief description of the instructor(s) indicating the relevant qualifications and teaching experience. -Title and expected goals, objectives and motivation of the tutorial. -Tutorial level: Introductory, Intermediate or Advanced. -Intended audience: it should be clearly and precisely indicated to whom the tutorial is aimed and at which level it would be taught with respect to the different underlying scientific fields. In particular if any background (biology, algorithmics, statistics, etc) is expected, this should be very precisely described. -Length: half (4 hours) or full day (8 hours) -Detailed outline of the presentation.

All submissions will be evaluated by a committee and successful Tutorial proposals will be notified of their provisional acceptance by February 1, 2004. A maximum of 12 proposals will be accepted for presentation at ISMB/ECCB 2004.

Each tutorial team will be provided -An honorarium of US$500 -One free registration for the tutorial presented -Free attendance of any other tutorial -One free conference dinner

Tutorial Handouts: The tutors agree to provide participants with teaching materials that should include: -A detailed outline of the presentation -Copies of the slides -A text corresponding to the contents of the tutorial -Copies of relevant articles/book chapters published by the tutors may be provided as Supplementary Information but cannot replace the text material of the handout -A draft version of the handouts will be requested prior to the final acceptance of a tutorial -Draft handouts must be sent by March 15, 2004 -The final acceptance decisions will be made by April 1, 2004 -Final handouts for reproduction must be received by May 15, 2004

In addition, the authors agree that their materials are made available for sale to ISMB participants not attending the tutorial for a period of six months.

The joint conference is hosted by the International Society for Computational Biology (ISCB), the European Bioinformatics Institute (EBI), the Collaborative Computational Project 11 (CCP11), the Scottish Bioinformatics Forum and the Bioinformatics Research Centre at the University of Glasgow.

Chaired by Professor Janet Thornton, CBE, FRS, and Professor David Gilbert

Correspondence for prospective tutorial instructors should be sent to: tutorials04@ismbconf.org

Thank you for your submission.

Bj Morrison <bj@sdsc.edu>

Gordon EvolGenesBehavior Feb8-13

GORDON RESEARCH CONFERENCE IN GENES AND BEHAVIOR

Announcing the first Gordon Research Conference in "Genes and Behavior." The goal of this meeting is to foster a broad approach to this topic by bringing together scientists that use model genetic systems to study behavior with scientists that use model behavioral systems to study behavior. The conference series seeks to help foster a synthesis that involves molecular biology, neuroscience, behavior, ecology and evolutionary biology; lab and field studies; and both mechanistic and evolutionary perspectives. Sessions for the first conference will be devoted to the following topics: social structure; foraging and ingestive behavior; sensory systems and communication; behavior analysis in model genetic systems; nature/nurture; theoretical approaches to genes & behavior; and reproductive behavior.

The GRC will be from February 8 - 13, 2004 in Ventura, California. The Chairperson is Gene Robinson, the Vice Chairperson is Robert Hitzeman, and the members of the Program Committee are Christine Boake, Felix Breden, and Allen Moore.

WHY SHOULD I ATTEND?

The GRCs are wonderful and stimulating because they are organized to be free-wheeling and spirited events with built-in time for lots of audience participation. Everyone is encouraged to participate and to speak with abandon about his or her wildest ideas.

The meetings are structured with sessions in the morning and evenings; afternoons are left open so people can chat, relax, or see the sights.

WHAT IS THE PROGRAM?

The complete program is listed on the Gordon Conferences web site, http://www.grc.org/ .

WHAT IS THE COST OF THE MEETING?

The meeting registration is $800 (actually $750 if you register up until 3 weeks before the meeting) (plus your airfare). This includes all expenses at the meeting such as lodging and food. For details, see Gordon Conferences web site.

We hope to be able to defray some travel or meeting costs for participants from targeted groups (graduate students, postdocs, minorities, attendees from third world countries) although we cannot make any commitments at this time. Please contact Gene Robinson (generobi@life.uiuc.edu).

HOW DO I APPLY?

We will have a maximum capacity of 135 participants of which 55 are speakers or discussants for the sessions. That means that about 80 slots are open for other attendees. We will select attendees to promote diversity in participants (gender, ethnicity, geographical region, level of degree, research interests). But within these categories we will also accept participants on a first come first serve basis. So if you are interested, APPLY AS SOON AS POSSIBLE.

To apply: Go to the GRC website: http://www.grc.uri.edu/grc_home.htm and follow the instructions to apply electronically.

IS THERE A WAY THAT I CAN PRESENT MY RESEARCH IF I AM NOT A SPEAKER?

There will be a poster session, organized by Felix Breden. Please contact Felix for information breden@sfu.ca.

Gene Robinson <generobi@life.uiuc.edu>

Marseille Evol Sep22-24

The 8th “evolutionary meeting at Marseille” will take place September 22 to September 24 2004 As former years Sessions will discuss topics such as : systematics, biodiversity, comparative genomics and post-genomics (at all the taxonomic levels), gene duplication and evolution, functional phylogenesis, concept of evolution.

You will found all the information concerning hotels, registrations fees....... at the following web site

http://evolution.luminy.univ-mrs.fr

The dead line for abstract submission and registration is the First of Mai 2004

Best regards Pierre

– Pierre Pontarotti

Phylogenomics Laboratory

Université d’Aix Marseille I Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 http://evolution.luminy.univ-mrs.fr/phylogenomics-lab/index.html We organize the 8th Evolutionary Biology Meeting at Marseille http://evolution.luminy.univ-mrs.fr

Paris PopGenet Dec5-6

We are pleased to announce the venue of an international symposium

“2nd DNA POLYMORPHISMS IN HUMAN POPULATIONS”

Friday Dec 5th and Saturday Dec 6th

Musée de l’Homme (Museum of Mankind), Paris France

There will be five plenary talks, which will be given by David Balding, Peter Donnelly, David Golstein (confirmation pending), Laurant Excoffier and Stephanie Manel (confirmation pending). Other talks are scheduled in the program.

Population Genetics and related disciplines. This meeting is focused on selection processes and on the geographic analysis of genetic variation.

In the last years, substantial theoretical and experimental progress has been done regarding the different forces shaping the patterns of variability in the human genome. In particular, distinguishing the effects of demography and natural selection remains one the hottest issues among human populations geneticists, demographers and statistical geneticists. There is an urgent need of a public debate on such areas of investigation; their methodological aspects should be discussed in a wide frame that only a symposium can offer. Even though the scientific interests of many speakers are directed towards the understanding of human diversity and the different forces shaping it, this symposium is also addressed to all scholars interested in the methodological aspects concerning genetic diversity and consequently, it may be of great interest for Animal and Plant Population Geneticists, Ecologists, Demographers, GIS, etc. To address an international audience, the official language of this event will be English

A CALL FOR ABSTRACTS IS OPEN, and we will be happy to accept up to 7 oral presentations and about 20 posters.We remind that the symposium is focused onSELECTION PROCESSES and on the GEOGRAPHIC ANALYSIS OF GENETIC VARIATION. All abstracts not concerning these areas of investigation are discouraged.

DEADLINES: Abstract submission: Nov., 3 (notification of acceptance or rejection before Nov., 14) Registration : Nov, 15 (after this date fees will be increased of 50%).

Please visit our web-site http://www.mnhn.fr/mnhn/ecoanthropologie/accueil.html for further information, to submit talk/poster titles and to register.

Evelyne Heyer & Franz Manni Musée de lHomme (Museum of Mankind), Dept. of Men, Natures and Societies Population genetics group 17, Place du Trocadéro 75016 Paris, France Email: manni@mnhn.fr

Franz Manni <manni@mnhn.fr>

Paris PopGenet Dec5-6 2

2nd DNA POLYMORPHISMS IN HUMAN POPULATIONS Friday Dec 5th and Saturday Dec 6th Musée de l'Homme (Museum of Mankind), Paris France

We have now UPDATED the website of the symposium with the abstracts of the invited speakers. http://www.mnhn.fr/mnhn/ecoanthropologie/accueil.html We remind that a call for abstracts is still open until the 3rd of November (LAST DAYS!!!) The FINAL programme with talks and posters selected from the call will be available the 10th of November Registration deadline for discount fees: the 15th of November

Invited speakers: Frederic AUSTERLITZ (University of Orsay - "Paris Sud"); David BALDING (Imperial College, London - United Kingdom); Graham COOP (Oxford University, UK); Laurent EXCOFFIER (University of Bern - Switzerland; David GOLDSTEIN (University College, London - United Kigdom); Raphaël LEBLOIS (University of Montpellier II, France); Stephanie MANEL (University Joseph Fourier, Grenoble - France); Susan PTAK (Interdisciplinary Center for Bioinformatics, Leipzig - Germany); Chris SPENCER (University of Oxford - UK)

Evelyne Heyer & Franz Manni Musée de l'Homme (Museum of Mankind), Dept. of Men, Natures and Societies Population genetics group 17, Place du Trocadéro 75016 Paris, France Email: manni@mnhn.fr

Franz Manni <manni@mnhn.fr>

PennStateU GenomesEvol Jun17-20

Announcing: INTERNATIONAL MEETING Genomes and Evolution 2004 http://www.outreach.psu.edu/C&I/genomes/ Highlighting research at the interface of molecular biology and evolution

Location: The Pennsylvania State University University Park, Pennsylvania, USA

Dates: June 17-20, 2004

Annual Meeting of the Society for Molecular Biology and Evolution Annual Meeting of the American Genetic Association

Plenary talks by: -Sydney Brenner -Leroy Hood -John Avise -Walter Gehring

And international leaders in genomics and evolution speaking in nine diverse symposia: Early Evolution of Life Genome Evolution Molecular Phylogeny and Molecular Clocks Development and Evolution Genome Evolution in Primates Origins and Evolution of Genetic Systems Molecular Polymorphisms and Evolution Molecules and Biodiversity Adaptive Evolution

Plan ahead to attend this key event, and register early to assure a place. A special (low) rate for graduate students has been arranged. See the website (URL above) now for details; online registration begins in December.

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StorrsUConn NEEC Mar26-28

Northeast Ecology and Evolution Conference (NEEC): University of Connecticut, Storrs, March 26-28, 2004.

The Ecology and Evolutionary Biology department at the University of Connecticut will host the second Northeast Ecology and Evolution Conference (NEEC) this Spring. Entirely organized by graduate students, NEEC 2004 will feature talks and posters by grads, post-docs, and advanced undergraduates. The inaugural NEEC, hosted by Rutgers University in 2003, attracted participants from more than 40 institutions.

The Saturday science program will be followed by a banquet featuring a Keynote Address by Dr. Michael Soule, Professor Emeritus in Environmental Studies, University of California, Santa Cruz. Dr. Soule is a founder of the Society of Conservation Biology and the Wildlands Project.

Access will be provided during the conference to the Universitys recently-opened Systematic Research Collections facility, the new home of our vertebrate, invertebrate, and botany collections.

NEEC 2004 represents a fantastic networking opportunity for the regions grads, as well as a chance to introduce the next generation of biologists to the research of their peers.

Conference information, including registration materials and the call for papers, can be found at www.eeb.uconn.edu/NEEC/ . Contact: Chris Martine, Krissa Skogen, or Robynn Shannon, Co-chairs, NEEC 2004 Ecology and Evolutionary Biology Graduate Program University of Connecticut Email: christopher.martine@uconn.edu Phone: 860-486-4156 Fax: 860-486-6364

Dan Vanderpool Graduate Student Department of Ecology and Evolutionary Biology University of Connecticut 75 N. Eagleville Rd. Unit-3043 Storrs, CT 06269 USA Office: (860) 486-4608 Lab (best): (860) 486-3947 Fax: (860) 486-6364

TucsonAZ EvolGenomics Jan16-17

EVOLUTIONARY GENOMICS MEETING

January 16-17, 2004, Marriott Hotel, Tucson, Arizona

The University of Arizona IGERT Program in Genomics is sponsoring an international meeting on evolutionary genomics. It will bring together leading researchers on genome evolution of both prokaryotes and eukaryotes, including empirical, theoretical, and computational approaches. The meeting will take place at the Marriott Hotel adjacent to the University of Arizona campus in Tucson January 16-17, 2004. The format of the meeting will allow considerable time for informal discussion and interaction among participants. Participation by graduate students and postdoctoral fellows is strongly encouraged, and discounted rates for registration are available. For registration and more information, please visit www.genomics.arizona.edu/meeting.html . Invited Speakers: Joy Bergelson (University of Chicago) Andy Clark (Cornell University) Laurent Duret (Université Claude Bernard) Terry Gaasterland (Rockefeller University) Philip Green (University of Washington) Evan Eichler (Case Western Reserve) Michael Eisen (U.C. Berkeley) Jessica Kissinger (University of Georgia) Wen-Hsiung Li (University of Chicago) Michael Lynch (Indiana University) Edward Marcotte (University of Texas) Julian Parkhill (The Sanger Institute) Loren Rieseberg (Indiana University) Christian Schlotterer (University of Vienna) Susan Wessler (University of Georgia)

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

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

UCaliforniaIrvine CalPEG Dec13-14

Announcing

California Population and Evolutionary Genetics Meeting

December 13 & 14, 2003 University of California-Irvine

Join us to revive this annual forum for researchers from throughout the state to share new and interesting results

Graduate students, post-docs and faculty are invited to give 15min. presentations in an informal atmosphere

On-line registration and submission of presentation titles will open on November 10, at <http://bio.uci.edu/-CalPEG03>http://bio.uci.edu/CalPEG03 Registration costs to be $35 for students and post-docs, and will be through credit card, on-line only. Fees cover continental breakfast and lunch for the two days.

Irvine graduate students will offer limited "bunk over" accommodations to their fellow students.

For further information, contact Art Weis

<mailto:aeweis@uci.edu>

Art Weis <aeweis@uci.edu>

Valencia MEEGID Jul19-23 2

08/10/03

The 7th International Meeting "Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases" (MEEGID VII) will be held in Valencia (http:/-/www.valencia-on-line.com/), Spain, 19th-23rd July 2004. As for the 6 first MEEGID meetings, it will be co-organized by the Centers for Disease Control and Prevention (CDC; http://www.cdc.gov/) in Atlanta, the Centre National de la Recherche Scientifique (CNRS; http://www.cnrs.fr/) and the Institut de Recherche pour le Développement (IRD; http://www.ird.fr/) in France.

MEEGID VII will be hosted by the 9th European Multicolloquium of Parasitology (EMOP IX; http://-www.uv.es/emop9/). Many sessions will be organized in common by the 2 meetings. EMOP IX is expected to attract 2000-4000 participants. Communications done in the framework of MEEGID VII will therefore have much impact. EMOP IX is organized by Professor Santiago Mas Coma, professor of parasitology at the university of Valencia, receiving editor of Infection, Genetics and Evolution (Elsevier) for Spain, and co-organizer of MEEGID VII (S.Mas.Coma@uv.es)

Proposals are accepted for: (1) Posters; (2) Oral communications; (3) Organizations of roundtables/symposia (2 hours, 4-6 speakers); (4) Express debates (1 hour, only one speaker with a communication of 15-20 mn followed by free discussion); (4) Plenary lectures (45 mn). Proposals dealing with roundtables/symposia, express debates and plenary lectures should be submitted as soon as possible.

MEEGID is not restricted to evolution only. The scopes proposed can deal with genetics, genomics, proteomics, population biology, mathematical modelling, bioinformatics, molecular epidemiology, molecular diagnosis and morphometrical identification. They can consider the host, the pathogen or the vector. Papers considering host + pathogen or pathogen + vector (coevolution) are particularly encouraged. All pathogens are within the scope of MEEGID: viruses, parasitic protozoa, helminths, fungal organisms, prion. All infectious models can be considered, including those of veterinary or agronomical relevance. As for the former MEEGID congresses, special consideration will be given to communications of high relevance for developing countries.

The papers communicated for MEEGID VII will be published in a special issue of Infection, Genetics and Evolution, as already done for MEEGID VI (Paris, July 2002). Infection, Genetics and Evolution is now covered by Medline and Index Medicus, since the 1st issue of the journal.

Awards will be attributed to the best communication, the best communication by a student and the best communication by a scientist from the Southern World on a problem specifically relevant to these areas.

Limited funds will be made available to travel students and scientists from developing countries.

Hope to see you in Valencia,

Have a very pleasant day.

Michel Tibayrenc, MD, PhD Editor -in-chief Infection, Genetics and Evolution (Elsevier) http:/-/www.elsevier.nl/locate/meegid President Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID) Society Director Unit of Research "Genetics and Evolution of Infectious Diseases" UMR CNRS/IRD 9926 IRD, BP 64501 34394 Montpellier cedex 5, France Tel. 33 4 67 41 61 97 (secretary) 33 4 67 41 62 07 (direct) Fax 33 4 67 41 62 99 Email Michel.Tibayrenc@mpl.ird.fr Website http://-cepm.mpl.ird.fr

GradStudentPositions

ColoradoStateU QuantEvolEcol

The PRogram for Interdisciplinary Mathematics, Ecology, and Statistics (PRIMES) is a new graduate initiative in quantitative ecology at Colorado State University funded by an IGERT grant from the National Science Foundation. PRIMES involves leading faculty and researchers from across the Colorado State University campus, as well as scientists from a variety of government agencies and laboratories. The goal of PRIMES is to equip graduate students interested in ecology, mathematics, and statistics with the skills to tackle modern ecological research problems using an interdisciplinary team-based approach. PRIMES students enroll in a home graduate program at Colorado State University. But, they participate in interdisciplinary research right from the start of their studies while obtaining the necessary research tools through an exciting program of innovative course work, seminars, conferences and workshops, internships, and social events. PRIMES awards both full year and partial year support to participating students. The full year Fellowship stipend for 2003/2004 is $27,500 plus tuition. Applications are invited by new and continuing students; see the website http://www.primes.colostate.edu for further details.

– Michael F. Antolin

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

e-mail: antolin@lamar.colostate.edu Voice: (1)-970-491-1911 FAX: (1)-970-491-0649

CornellU EvolEcol

Graduate Research Associate at Cornell University with Stephen Ellner and Nelson G. Hairston, Jr.

We invite applications from prospective doctoral students to join our research project "The evolutionary ecology of population dynamics: experimental and modeling approaches". Some recent papers from this project are listed below. Interested students should contact us directly and apply for Fall 2004 admission to Cornell through the graduate fields of Ecology and Evolutionary Biology, or Applied Mathematics.

Our broad goal is to understand the proximate and ultimate factors responsible for general patterns of population variability, such as the ubiquity of stability and cycles and the rarity of more complex dynamical patterns. Work to date has centered on predator-prey (rotifer-algal) microcosms having the potential to exhibit a wide range of qualitative dynamics. Linked experimental and theoretical studies have allowed us to show that feedbacks between ecological and evolutionary processes play an essential role in the system's dynamic properties. Future directions for experimental and theoretical work will include: relationships between genetic variability and ecological dynamics; more complex experimental communities; management implications of rapid evolution; and extending the work to natural aquatic communities. We believe in giving students the widest possible scope to independently develop research projects reflecting their interests within the general area of the projec! t.

Funding is available for 3 years of RA support (tuition + stipend); at least 1 year of TA'ing or teaching will be expected. Students in either graduate field are admitted with a guarantee of continued support so long as they make steady progress towards their degree. For additional information please contact us (Stephen Ellner, spe2@cornell.edu; Nelson Hairston, ngh1@cornell.edu).

T. Yoshida, L.E. Jones, S.P. Ellner, G.F. Fussmann, and N. G. Hairston, Jr. 2003. Rapid evolution drives ecological dynamics in a predator-prey system. Nature 424: 303-306.

G. F. Fussmann, S.P. Ellner, and N.G. Hairston, Jr. 2003. Evolution as a critical component of plankton dynamics. Proceedings of the Royal Society of London Series B 270: 1015-1022.

S.P. Ellner and G.F. Fussmann. 2003. Effects of successional dynamics on metapopulation persistence. Ecology, 84: 882-889.

Shertzer, K.W., S.P. Ellner, G.F. Fussmann, and N.G. Hairston, Jr. 2002. Predator-prey cycles in an aquatic microcosm: testing hypotheses of mechanism. Journal of Animal Ecology 71: 802-815.

Shertzer, K.W. and S.P. Ellner. 2002. Energy storage and the evolution of population dynamics. Journal of Theoretical Biology, 215, 183-200.

G. Fussmann, S.P. Ellner, K.W. Shertzer, and N.G. Hairston, Jr. 2000. Crossing the Hopf bifurcation in a live predator-prey system. Science 290: 1358-1360.

Stephen P. Ellner (spe2@cornell.edu) Department of Ecology and Evolutionary Biology Corson Hall, Cornell University, Ithaca NY 14853-2701 Phone (607) 254-4221 FAX (607) 255-8088

IndianaStateU LizardEvolution

The following ad will appear in Science next week:

Victoria University of Wellington is a dynamic, rapidly growing university in the capital city of New Zealand. The School of Biological Sciences (www.sbs.science.vuw.ac.nz) seeks to make four new appointments, including at least one at the Professorial level.

We seek to appoint in areas of existing or developing research and teaching strengths within the School, including: Genetics; Cell & Molecular Biology; Molecular Evolution & Ecology; Marine Biology; Microbiology; Proteomics; Biotechnology; Molecular Pathology and other Biomedical Sciences. Successful applicants will be active and productive researchers in one of these disciplines.

In three of these positions, we are seeking researchers who use contemporary molecular methodologies to advance their biological disciplines. Two of these positions are at the Lecturer/Senior Lecturer/Associate Professor level. The third position is a professorial appointment, where applicants will be required to demonstrate an ability to attract significant external research funding and guide development of molecular technologies and capacities across the School (refs SA0375B Professor of Biological Sciences; SA0376B Lecturer / Senior Lecturer / Associate Professor in Biological Sciences).

The fourth position is dedicated to a person in a research and teaching discipline of particular relevance to Maori and/or Pacific peoples and who can assist us to develop links to Maori and/or Pacific communities. Appointment to this position may be at any level, including Professor (ref SA0377B Lecturer / Senior Lecturer / Associate Professor / Professor - Biology of the Pacific).

The School of Biological Sciences provides a friendly and collegial working environment. We offer innovative teaching and research programmes supported by about 50 academic, research, and general staff, with about 100 research students. The present appointments arise from on-going expansion of the School in response to successes in both teaching and research.

Relocation and establishment costs are available subject to negotiation with successful applicants. In accordance with British and New Zealand conventions, a

New Zealand Senior Lecturer and Lecturer are generally considered to be equivalent to, respectively, a North American Associate Professor and Assistant Professor.

Applications close 24 October 2003. Please quote the relevant reference number on all correspondence.

For further information about these positions, see the website: www.nzjobs.co.nz/vuw An application pack is available from the HR Officer, Faculties of Science, Architecture and Design, tel: +64-4-463 5100, fax: +64-4-463 5122 or email: science-appoint@vuw.ac.nz Victoria University of Wellington is an EEO employer.

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Dr.Linley Jesson School of Biological Sciences Victoria University of Wellington PO Box 600 Wellington NZ

phone +644 463 5573 fax + 644 463 5331

Linley Jesson <linley.jesson@vuw.ac.nz>

5-Year RA position in Behavioral Ecology of Lizards

One fully funded doctoral RA position to study behavioral ecology of lizards starting Fall 2004. Of particular interest are applicants interested in the behavioral aspects of predator avoidance in lizards. The successful candidate would work in collaboration with Diana Hews and Steve Lima. Prospective students working more generally in the areas of lizard territoriality, color or pheromonal signals, and hormonal mechanisms are also encouraged to apply. Interested applicants should submit a CV and a preliminary statement of research interests to Hews. Applications for graduate admission should be submitted by Feb. 1 for full consideration.

For more information please see: http://mama.indstate.edu/users/hews/ for information about the Hews Lab. http://mama.indstate.edu/users/lima/ for information about the Lima Lab. http://oeb.indstate.edu/ for information about the Organismal & Environmental Biology Group. http://biology.indstate.edu/dls/ for information about the Department and graduate applications.

Dr. Diana K. Hews Department of Life Sciences Indiana State University Terre Haute IN 47809 Voice (812) 237-8352 dhews@indstate.edu

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LaTrobeU EnvironmentalStress

PhD programmes: Centre for Environmental Stress and Adaptation Research (CESAR)

RESEARCH AREAS

1. Sustainability of insect-resistant stacked-gene transgenic brassicas for the tropics.

This study will form part in the international public/private partnership lab and field effort to provide stacked-gene Bt transgenic cabbage and cauliflower varieties for the control of insecticide resistant Diamondback moth (Plutella xylostella) in Asia and Africa.

It will involve:

Understanding the genetic and biochemical nature of likely evolved Bt resistance.

Selecting for such resistance in laboratory colonies, for each of the introduced genes singly and in conjunction. Developing diagnostic tools to enable field surveys of field resistance gene frequencies (if any) in Asia and Africa.

Being part of the decision in late 2006 as to whether to commit major donor and private funds to the commercialization of such products by 2011.

2. Determination of host-races in Asias number one insect pest of crops, Helicoverpa armigera (Lepidoptera: Noctuidae).

This study will involve:

Confirming the existence of restricted gene-flow groups within the species, using RAPD, AFLP and mitochondrial DNA methods in additional to classical morphological techniques.

Developing experimental evidence for the restricted gene flow in the field in India. Developing diagnostic tests for particular identified “host races” and field test these against material from across Asia and Australia with a view to commencing the quantification of gene flow between “races”.

ELIGIBILITY Candidates should be Australian or New Zealand citizens qualified to at least Honours level in Genetics, Biochemistry, Entomology or an allied discipline.

FINANCIAL SUPPORT These studies are in association with internationally funded projects. Stipends are available through the LaTrobe University Scholarships Scheme. Closing date for applications is October 31st 2003. Scholarship information and application forms are available from http://www.latrobe.edu.au/rgso/sc/ or Yvonne Parsons (y.parsons@latrobe.edu.au)

CONTACT Further information can be found at http://www.latrobe.edu.au/cesar/ Derek Russell (derek.Russell@latrobe.edu.au) or Ary Hoffmann (a.Hoffmann@latrobe.edu.au)

(a.Hoffmann@latrobe.edu.au)

LincolnUniv NZMites

PhD Scholarship on New Zealand mites PhD Scholarship on New Zealand mites

Measuring the biodiversity of New Zealand's mesostigmatid mites: molecular and morphological approaches

Mites represent a large and important component of worldwide biodiversity and appear to be over represented in the New Zealand fauna. As part of an ongoing study investigating the evolution of parasitism we have discovered several undescribed species of mesostigmatid mites. We will use molecular and morphological approaches to examine the species status and evolutionary relationships of these and other mesostigmatid mites in New Zealand. Important questions about the endemicity of New Zealand's mite fauna and its Gondwanan biogeographical links will be examined. The precise details of the project will be determined according to the background and interests of the student.

The student will obtain a thorough knowledge of the latest techniques in molecular and morphological systematics and phylogenetic and taxonomic methodology. The student will be based at Lincoln University in the heart of New Zealand's South Island, close to Christchurch, with access to a fully equipped molecular lab and entomology research museum and opportunities for field work elsewhere in New Zealand.

The scholarship is for NZ$16,000 per year for up to three years plus tuition fees up to the amount incurred by New Zealand students. Applicants who are not New Zealand residents or Australian, French or German nationals will have to find additional funds to pay international students fees.

Informal enquiries to Dr Adrian Paterson (patersoa@lincoln.ac.nz) or Dr Robert Cruickshank (cruicksr@lincoln.ac.nz), Ecology and Entomology Group, Lincoln University (http://www.lincoln.ac.nz/-), New Zealand.

LundU PlantPopGenet

Lund University announces the following vacancy:

POSTGRADUATE SCHOLARSHIP in Biology, within the discipline of Genetics with placement at the Department of Cell and Organism Biology, Faculty of Science, Lund University, Sweden.

Ref nr: 571 Starting Date: As soon as possible Information: Alf Ceplitis, tel + 46 46 222 78 57 E-mail: Alf.Ceplitis@cob.lu.se

Project Description: The research project deals with the genetic basis of variation in traits of potential ecological importance in natural plant populations. Genomic information from the model plant Arabidopsis thaliana will be used to locate and identify genes controlling phenotypic trait variation in two related plant species, Capsella bursa-pastoris and Brassica cretica. The population genetic structure of the two species will also be studied, with particular focus on population differentiation and linkage disequilibrium. More information on the project is found at: http://www.biol.lu.se/-cellorgbiol/crucifers/index.html Qualifications: The applicant should have received a thorough basic training in population genetics. Some knowledge about the principles of genetic mapping is an advantage. Practical experience of DNA sequencing and genetic marker techniques, such as AFLP and microsatellites, is highly desirable.

Application: Applications are made on a specific application form found on the Faculty's home page: http://www.naturvetenskap.lu.se/-fou/antagn_blankett_eng.pdf The application must reach the Registrar, Kansli N, Lund University, P.O. Box 118, S-22100 Lund, Sweden, not later than Monday, November 3, 2003. All submitted documents must be attested as to their authenticity.

For further information, see: http://www.biol.lu.se/-cellorgbiol/postgrad/vacant.html, or contact Alf Ceplitis (Alf.Ceplitis@cob.lu.se)

Alf Ceplitis, PhD Department of Cell and Organism Biology (Genetics) Lund University Sweden

Postal address: Solvegatan 29, SE-22362 Lund Phone: +46 46 2227857 Fax: +46 46 147874

OhioStateU GeeseMicros

Graduate Research Assistantship (M.S.) in Conservation Genetics in the lab of Dr. H. Lisle Gibbs, Department of Evolution, Ecology and Organismal Biology, Ohio State University. I am seeking a highly motivated student with a demonstrated ability to work independently for a lab-based project that will use microsatellite DNA markers to determine the stock identity of harvested samples of Canada Geese from Ohio. This position, funded by the Ohio Department of Natural Resources, includes a stipend ($16,500/yr) for up to 3 years, full tuition waiver, and partial coverage for health insurance and will begin in September 2004. Candidates should have prior experience with DNA-based genetic analysis and must be willing to work closely with ODNR personnel to coordinate sample collection and analyses and direct lab technicians in the collection of data. Student will join an active lab group pursuing a variety of research projects in the area of molecular ecology (see http://www.biosci.ohio-state.edu/~eeob/faculty/gibbs.html). Please send a letter of interest, photocopy of transcripts and GRE scores and contact information for 3 references to H. LISLE GIBBS, Department of Evolution, Ecology and Organismal Biology, 318 W. 12th Ave. Ohio State University, Columbus OH 43210-1293 (EM: gibbs.128@osu.edu; PH: 614 688 3861). Review of applicants will begin 1 December 2003 and will continue until a suitable candidate is identified. – H. Lisle Gibbs Associate Professor Department of Evolution, Ecology and Organismal Biology Ohio State University 300 Aronoff Laboratory 318 W. 12th Ave. Columbus, OH 43210-1293

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

PortlandStateU MolEvolRNA

GRADUATE FELLOWSHIPS IN MOLECULAR EVOLUTION OF RNA

NSF-funded graduate fellowships in molecular evolution in the Lehman lab at Portland State University are available to study mutational meltdown and recombination in populations of catalytic RNA. Prospective Ph.D. students (or, in exceptional circumstances, M.S. students) with a solid background in biochemistry or molecular biology, and a strong interest in fundamental evolutionary problems such as the origins of life are encouraged to make inquiries at the address below. A current c.v. and names of 2-3 references are desired. Degree options in Chemistry, Biology, and Environmental Science are possible.

Niles Lehman, Ph.D.

Associate Professor Department of Chemistry Portland State University P.O. Box 751 Portland OR 97207 USA

niles@pdx.edu http://www.chem.pdx.edu/%7Eniles/

RoyalBotanicGardens Melbourne

PhD Scholarship opportunity at the Royal Botanic Gardens Melbourne

An exciting opportunity exists for a student to undertake a PhD study:

Conservation and biology of Victorian holly-leafed Grevillea species (Proteaceae)

We are seeking a highly motivated student to undertake a PhD study of Victorian “holly-leafed” Grevillea species. A number of these Grevillea species are nationally endangered and a major aim of the project will be to obtain information of direct benefit to their conservation management. We are interested in the broad relationships between the Victorian “holly-leafed” Grevillea species, and in the population genetic structure, breeding systems and reproductive biology of selected threatened species. The prospective student should have, or expect to obtain, a first-class honours or Masters degree or equivalent plus a strong background in botany and molecular ecology or conservation genetics.

This scholarship is funded by the Cybec Trust and is a joint collaboration between the National Herbarium, Royal Botanic Gardens Melbourne, South Yarra and the Centre for Environmental Stress Adaptation Research based at La Trobe University, Bundoora

Stipend: $19, 000 per annum tax free Applications close, October 31, 2002.

Please send applications, including the names and contact details of two referees and evidence of academic results to

Elizabeth James Royal Botanic Gardens Melbourne Private Bag 2000 South Yarra, VIC. 3141

For further information, contact:

Elizabeth James email: Elizabeth.James@rbg.vic.gov.au phone: (03) 9252-2300 fax: (03) 9252-2350 or Yvonne Parsons email: y.parsons@latrobe.edu.au phone: (03) 9479 2256 fax: (03) 9479 2361 y.parsons@latrobe.edu.au

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TexasTechU TropicalTreeEvol

A position for a graduate research assistantship is available in the Department of Biological Sciences, Texas Tech University, under the supervision of Dr. Chuck Cannon. My research is focused on the tropical trees of Southeast Asia and my students will be strongly encouraged to participate in these studies. Currently, we are pursuing two main projects in my lab: 1) DNA fingerprinting techniques for tropical timbers and 2) phylogeography of three major tree groups.

We are now completing a pilot study in the first project using a single timber species. Our results indicate that sensitive tests for the geographic origin can be performed using standard molecular markers. The ability to determine geographic origin of timber will then allow purchasers to objectively choose legally harvested product. The challenge now is to develop the necessary databases along with high-throughput techniques and to apply the tests for understudied groups of timber species (little things like that...

The second project is an extension of previous work I have done on the phylogeography of Southeast Asian stone oaks. We have examined sequence data from both the chloroplast and nuclear genomes for over 400 individuals in eleven different locations across the region. The results indicate that these populations have experienced little migration and have been persistent for long periods of time (>>1 million years). The stone oaks are upland dominants. To complete the picture, we are now beginning to examine the phylogeographic patterns of genetic variation in two other major groups: one dominant in the lowlands and one dominant in peat swamp forest. Combining and comparing the patterns among these three major groups should provide a very enlightening and comprehensive understanding of the history of tropical rainforest in the region.

Candidates should have a strong background in plant evolution and systematics and be willing to cope with the benefits and frustrations of conducting research based on the other side of the world. Currently, I have funds for two years of support as a graduate research assistant and the Graduate School at Texas Tech University offers competitive packages for graduate teaching assistants (you need to gain some experience teaching anyway!). Interested candidates should send a curriculum vitae, a brief summary of research experience and interests, and two letters of reference to:

Chuck Cannon Texas Tech University Dept of Biological Sciences Box 43131 Lubbock, TX 79409-3131 USA

email submission is fine: chuck.cannon@ttu.edu <mailto:chuck.cannon@ttu.edu>

check out my webpage at: <http://www.biol.ttu.edu/biol2003/faculty_details.asp?fac_id&>

TexasTechU TropicalTreeEvol 2

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email submission is fine: chuck.cannon@ttu.edu <mailto:chuck.cannon@ttu.edu>

check out my webpage at: <http://www.biol.ttu.edu/-biol2003/faculty_details.asp?fac_id&>

UAmsterdam EvolBiol

Faculty of Economics and Econometrics

The Faculty of Economics and Econometrics (FEE) has over 3,000 students in Economics, Econometrics, Fiscal Economics, Operations Research and Management, Actuarial Sciences and in graduate and masters programmes. Research is conducted in a wide range of areas. A large part of the research takes place within the Tinbergen Institute-UvA. The Faculty employs approximately 350 people.

Faculty of Science

The Universiteit van Amsterdam (UvA) is one of the leading institutions for higher education in Europe. It participates in the international science network, collaborating with major universities throughout the world. The faculty has four departments, with about 1,500 employees including researchers and lecturers, 150 full-time and part-time professors operating in eleven research institutes. Each institute has its own research programme that is financed by the faculty, the national research council NWO, the government, EU departments and private enterprises.

Center for Research in Experimental Economics and political Decision making (CREED) and Institute for Biodiversity and Ecosystem Dynamics (IBED)

The Center for Research in Experimental Economics and political Decision making (CREED) and the Institute for Biodiversity and Ecosystem Dynamics (IBED) of the Universiteit van Amsterdam are collaborating in an interdisciplinary project, studying the simultaneous evolution of social behavior and social institutions with techniques from both Evolutionary Biology and Experimental Economics. This project is funded by the Netherlands Organization for Scientific Research (NWO).

The project aims at studying other-regarding behavior (such as altruism) on the one hand and both formal (such as social networks) and informal institutions (such as social norms) on the other hand. The focus will be on how these behaviors and institutions interact at the evolutionary time scale. The project is split in two subprojects: one developing theory from a biological background, the other applying laboratory experiments in the tradition of experimental economics. From the start the interaction between these two subprojects will be intensive. More information about this project is available on http://www.fee.uva.nl/creed/evolution . We invite applications for two positions in this project.

1. PhD student in Evolutionary Biology in a full-time position for four years, based at IBED. The successful candidate will participate in the subproject developing theory from a biological background. job reference number 20176

The tasks include: developing and analyzing evolutionary game theory models, collaborating to design experiments with human subjects, reporting research results in academic publications, and participating in the research activities of the group.

2. Post-doc in Experimental Economics in a full time position for three years, based at CREED. The successful candidate will be involved in the subproject applying laboratory experiments. job reference number 20177

The tasks include: designing, organizing and running laboratory experiments with human subjects. developing and testing theoretical models analyzing experimental data reporting research results in academic publications participating in the research activities of the group

Job requirements 1. PhD student in Evolutionary Biology The candidate is expected to have the following qualifications: an MSc degree in Ecology, Evolutionary Biology or Theoretical Biology (preferably Evolutionary Ecology). Candidates close to finishing their degree are also welcome to apply extensive experience with designing and analyzing theoretical models affinity with experimental model testing an additional background in social sciences will be considered an advantage

The PhD student is expected to follow an educational program in the Research School Functional Ecology and to assist in teaching of undergraduate students. As the position is part of an interdisciplinary project, the work will involve close collaboration with the experimental economics group at CREED. The work should result in a number of publications and a dissertation (thesis), which must be defended in public.

2. Post-doc in Experimental Economics The candidate is expected to have the following qualifications: a completed PhD in a relevant field (Economics or Theoretical & Evolutionary Ecology) or to be expected to have such a PhD completed at the time of the start of the project experience in designing and organizing laboratory experiments theoretical vigor a background in both Economics and Theoretical & Evolutionary Ecology (adaptive dynamics, game theory) will be considered an advantage

Additional information 1. PhD student in Evolutionary Biology

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UEdinburgh QuantGenet

OPPORTUNITIES FOR EUROPEAN PhD STUDENTS

Marie Curie Training Site in Quantitative Genomics

The Institute of Cell, Animal and Population Biology (ICAPB) of the University of Edinburgh has been awarded the status of a Marie Curie Training Site in Quantitative Genomics by the European Commission, for the period 1/10/2000 - 30/9/2004. This is an opportunity for high quality PhD students ('Fellows') registered in other EU countries to come and work at our Institute for a period of up to 12 months. The scheme is well-funded, with travel and subsistence funds for the Fellow and limited funds to cover research costs.

We are now in the final year of the scheme and there are a limited number of fellowship vacancies still available. Current information on the ICAPB Training Site can be found at:

http://improving.cordis.lu/mc/ {e.g. search for "pedigree" using Free Text Search}

If you are a PhD student registered in another EU country and wish to spend some time in an exciting research environment to work on population genetics, quantitative genetics, evolutionary genetics, or aspects of animal and human genetics, please email the contacts shown for specific Vacancies on the Marie Curie Fellowship website. There are currently two Projects listed. For information on the Institute and its research activities, check:

http://www.icapb.ed.ac.uk/

Loeske Kruuk Institute of Cell, Animal and Population Biology University of Edinburgh Edinburgh EH9 3JT, UK Tel: 0131 650 5515 Fax: 0131 650 6564 lkruuk@srv0.bio.ed.ac.uk

UMaryland PlantConserv

GRADUATE ASSISTANTSHIP

A graduate assistantship in Plant Conservation Biology in the Department of Natural Resource Sciences and Landscape Architecture (<http://www.nrsl.umd.edu/->http://www.nrsl.umd.edu/) at the University of Maryland College Park is available starting August, 2004. Possible research projects include 1) Comparative assessment of the effects of fragmentation and landscape context on pollination biology, reproductive success, and gene flow of native plant species. 2) Examination of the evolutionary distinctiveness and systematic relationships of putatively rare species using morphological and genetic approaches. 3) Comparative population biology of endangered plant species endemic to limestone and dolomite substrates in southern California. Students in my laboratory have opportunities to pursue research using a variety of tools and techniques to conservation research, including DNA sequencing and microsatellites, field work, and geographic information system technology. The department has outstanding research and teaching facilities including new classroom, lab, and office space; a new greenhouse complex; and an extensive array of state of the art environmental chambers.

The University of Maryland is an outstanding place to pursue conservation research with potential for training, interaction, and collaboration with faculty and students in different colleges and departments as well as a number of interdisciplinary centers. Included are the Department of Biology, Department of Entomology, Department of Geography, Center for Biodiversity, Center for Bioinformatics and Computational Biology, and Center for Smart Growth Research and Teaching. Proximity to the Smithsonian Institution, other large government research facilities, and headquarters for federal agencies and many conservation groups results in a vibrant community of conservation scientists beyond the University itself.

Support will include tuition remission and a stipend for a combination of teaching and research assistantships, contingent annually upon progress towards a degree. Candidates at both masters and Ph.D. levels will be considered. Outstanding Ph.D.-level candidates who apply prior to February 1, 2004 will also be considered for nomination for a fellowship from the Graduate School. The University of Maryland is committed to increasing the diversity of our graduate students. We offer support to a diverse range of students consistent with the campus principles of equal opportunity (<http://www.vprgs.umd.edu/fellowship/equalopporunities.htm>http://www.vprgs.umd.edu/fellowship/equalopporunities.htm).

For more information please see http://alyxia.umiacs.umd.edu or contact me directly. For information on the Universitys graduate program including application instructions see <http://www.gradschool.umd.edu/catalog/admission.html>http://www.gradschool.umd.edu/catalog/admission.html.

Maile Neel Department of Natural Resource Sciences and Landscape Architecture & Department of Entomology 2116 Plant Sciences Building University of Maryland College Park, MD 20742 USA

Office Phone (301) 405-9780 Cellular Phone (508) 274-6591 Fax: (301) 314-9308 email: mneel@umd.edu

Lab Website: http://alyxia.umiacs.umd.edu

UNevadaReno EcolEvol

PhD studentship at the University of Nevada Reno with Guy A. Hoelzer

I invite applications to the graduate program in Ecology, Evolution, and Conservation Biology to work with me on spatially explicit, computational modeling of evolutionary systems. Ultimate goals of this work are potentially quite variable, and the student will be expected to play a central role in choosing directions taken in the dissertation, although the research should include a systematic exploration of the generic effects of key parameters relating to isolation-by-distance and the spatial configurations and of evolving systems. The dissertation could also include, for example, development of a dynamical network model of representing a specific species or ecosystem in nature, which could have application to management of a system for the conservation of biodiversity and/or ecosystem function. The research program with which this individual would become involved should be of particular interest to someone interested in developing a complex dynamical system perspective, or a thermodynamic perspective, on the process of biological evolution. A successful applicant for this position will come with skills in the use of object oriented programming languages, such as C++ or JAVA, and experience with programming platforms like MatLab is preferred. The stipend supporting this student will initially come in the form of a teaching assistantship, but several colleagues and I are actively pursuing grants that, if successful, would provide a graduate research assistant stipend. Prospective applicants should contact Dr. Guy Hoelzer at <hoelzer@unr.edu>.

– Guy Hoelzer Phone: 775-784-4860 Department of Biology Fax: 775-784-1302 University of Nevada Reno Reno, NV 89557

UNewOrleans ConservBiol

Regents Fellowship in Conservation Biology

The Department of Biological Sciences at the University of New Orleans has two Doctoral Fellowships available commencing Fall 2004. The Fellowship term is a four-year period and includes a full tuition waiver, an annual stipend of $20,000, and a research/travel allowance. The Department offers opportunities to conduct research related to conservation biology in areas including biochemical/physiological adaptations, reproductive biology, genetics, systematics, evolution, and ecology. Applicants must be US citizens. For more information, email inquiries to: biograds@uno.edu or see our website: <http://www.uno.edu/˜bios>. To apply, contact: Director of Graduate Studies, Department of Biological Sciences, University of New Orleans, Lakefront Campus, New Orleans, LA 70148. EEO/AA Employer.

Steve Johnson Associate Professor Department of Biological Sciences University of New Orleans New

Orleans, LA 504-280-7040 (Office) 504-280-6121 (Fax) Web Page: http://www.uno.edu/%7Esgjohnso/-sgjwebpa.html Conservation Biology Ph.D. website: http://www.uno.edu/%7Ebios/phdhome.html

Steven G Johnson <SGJohnso@uno.edu>

Jobs

BrighamYoungU EvolBiol

Postdoctoral Positions in Evolutionary Biology At Brigham Young University

Computational Evolutionary Biology (2 positions) Two postdoctoral positions in computational evolutionary biology are available at the Department of Integrative Biology at Brigham Young University (Provo, Utah, USA). The first position is funded by a National Institute of Health (NIH) grant to evaluate current methods to estimate and characterize recombination, and to assess the role of recombination in HIV, other viruses and bacteria. This work will be collaborative with Keith Crandall (BYU) and David Posada (U Vigo, Spain). The second position is for a computational biologist to collaborate in an NSF supported project to develop parallel computational approaches to phylogenetic analyses under the direction of Michael Whiting (BYU) and Keith Crandall (BYU). Both positions are immediately available and have the potential to continue until the end of 2005. Salary will range between 30,000-40,000 US dollars (including benefits), commensurate with qualifications. The appointed individual will be based at Brigham Young University (Provo, Utah), but for the NIH position, will work a portion of the year at the University of Vigo (Spain). Candidates should have a PhD in genetics, statistics, mathematics or computer science. Experience with biological sequence analysis, parallel computational approaches, and programming (C, Java, Perl) is desirable. Background on population genetics and/or molecular evolution is highly desirable. Applications will be accepted until the position is filled, and they should include a CV, a statement of research interests, and contact information for two references. Please specify in your application if you are applying to the NIH, NSF or either position. Applications should be send these materials to Keith Crandall (keith_crandall@byu.edu) and David Posada (dposada@uvigo.es).

Herpetology/Molecular Phylogenetics/Genomics An NSF-funded postdoctoral position is available in the Jack Sites lab to work on phylogenetic reconstruction of the lizard family Xantusiidae, as a prelude to placing it within the basal Squamata. Support is available for up to two years (starting salary $30k; start date of 1 June or until the best candidate is found), and the primary focus will be to generate a large molecular data set from multiple nuclear and mitochondrial loci. The project includes collaborators at the Univ. of Arizona (B. Bezy), U.S. National Museum (K. de Queiroz), Univ. of Texas Austin (J. Maisano), and Yale Univ. (J. Gauthier), and will involve integration of molecular with fossil and morphological data from the same taxa.

Applicants should have basic molecular skills in modern DNA PCR and sequencing technology, competence in development/optimization of primers for new genes for large-scale sequencing, and be thoroughly familiar with conceptual issues and methods of phylogenetic inference. I anticipate that the ideal candidate would be an investigator interested in using this experience to further develop her/his own research program independent of this project there should be sufficient time for the investigator to complete dissertation manuscripts, pursue side projects, and submit research proposals. There are no nationality restrictions, but individuals from, or with research interests and experience in Latin American herpetology and/or evolutionary biology, are especially invited to apply. Applications should include a CV, a statement of research interests, and contact information for two references. Interested researchers should contact: Jack_Sites@byu.edu for more information.

Bacterial Genetics/Statistical Genetics A NIH funded postdoctoral position is available for a bacterial population geneticist or statistical geneticist. In collaboration with researchers at Johns Hopkins University, we will collect large population genetic data sets from multiple loci across the genome of Neisseria gonorrheae to infer the population history and evolutionary dynamics of this etiological agent of gonorrhea in Baltimore. Candidates for this position should have analytical expertise in population genetics and an interest for developing new analytical approaches for large genomic data sets. Programming experience in C and/or Java is desirable but not necessary. Candidates should have a PhD in genetics, statistics, mathematics or computer science. This position is funded at $32,000 per year plus benefits. Applications will be accepted until the position is filled, and they should include a CV, a statement of research interests, and contact information for two references. Applications should be sent to Keith Crandall (keith_crandall@byu.edu).

Insect Phylogenomics A NSF funded position is available in the Whiting lab to assemble the tree of life for insects. Support is available for up to two years (starting salary $30,000 including full benefits; start date of 1 January or until the

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CaliforniaStateU EvolEcol

Tenure-track position available in Terrestrial Vertebrate Ecology. The Department of Biological Sciences at California State University, Chico invites applications for an Assistant Professor position beginning Fall 2004. Candidates must have: a Ph.D., a specialization in terrestrial vertebrate ecology, a demonstrated ability or potential to establish externally funded research, teaching experience at the undergraduate level, and a strong interest in teaching excellence. Preference will be given to candidates with postdoctoral experience, and additional expertise in such areas as field/population ecology, population genetics, or conservation ecology. Responsibilities will include teaching comparative anatomy, as well as participation in lower-division majors/non-majors biology courses, upper-division majors courses in area of specialty and a graduate course in population ecology. Applicants should submit a letter of application, curriculum vita, a statement of teaching philosophy, representative reprints, complete academic transcripts (student copy acceptable), and three letters of reference to: Dr. Patricia Edelmann, Chair; Dept. of Biological Sciences; CSU, Chico; Chico, CA 95929-0515; Attn: Terrestrial Vertebrate Ecology; Phone: (530) 898-5356. Website: http://www.csuchico.edu/biol/<http://www.csuchico.edu/biol/> . Review will begin 12/01/03. Complete applications received after this date may be considered. As a University that educates students of various ethnic and cultural backgrounds, we seek to create as diverse a pool of candidates as possible. CSU, Chico is an EOE/AA/ADA employer. California State University, Chico employs only individuals lawfully authorized to work in the United States.

Kristina A. Schierenbeck, PhD Associate Professor, Herbarium Director California State University, Chico Department of Biology Chico, CA 95929-0515

email: kschierenbeck@csuchico.edu phone: 530-898-6410 web: www.csuchico.edu/~kschiere

CornellU InsectImmunity ResTech

The following advertisement is for a full time research technician, but I also have positions available for exceptional graduate students and postdocs. Individuals interested in graduate or postdoctoral research should contact me directly at bl89@cornell.edu. Applicants to the technician position are required to apply through the “official” ad, which is linked below, but may contact me directly with informal questions.

A full time technician is sought in the laboratory of Dr. Brian Lazzaro in the Entomology Department at Cornell University. Research in the lab is focused on the population genetics and molecular evolution of insect immune responses. The successful applicant will be expected to spend a small amount of time ordering standard lab supplies, maintaining lab purchasing and safety records, and supervising undergraduate researchers, but will be primarily expected to conduct independent research under Dr. Lazzaro’s direction. The exact nature of the research will depend on the background and abilities of the applicant, but will generally involve basic molecular biology and genetic techniques. These may include, but are not restricted to, DNA and RNA extraction, DNA sequencing, PCR, SNP genotyping, analysis of DNA sequence data, genetic manipulation of and measurement of antibacterial resistance phenotypes in insect cell culture, and infection of live insects with bacteria to measure resistance phenotypes. The opportunity exists for authorship on primary research articles.

Applicants should have at minimum a Bachelor’s degree in a life science and at least one year of practical experience in population genetics or molecular biology. The ideal applicant will also have basic computing proficiency, strong organizational abilities, and good communication skills. The initial appointment for this position is one year, with the possibility of extension. Salary is commensurate with experience.

Ithaca is in the Finger Lakes region of central New York, and is an absolutely beautiful place to live. Photos of the Cornell campus and surrounding area are posted at http://www.explore.cornell.edu/tour_home.cfm . Applicants to this position must apply through the formal job advertisement. This is directly linked at https://cornellu.recruitsoft.com/servlets/CareerSection?art_ip_action=

or can be found by searching for Position Number 01390 under the “Staff Positions” link at http://www.ohr.cornell.edu/jobs/index.html .

Cornell University is committed to creating a more diverse and inclusive campus in which to work, study, teach and serve.

Brian P. Lazzaro, Ph.D. Assistant Professor, Insect Genomics Department of Entomology 4138 Comstock Hall Cornell University Ithaca, NY 14853 USA

tel: 607-255-3254 fax: 607-255-0939 http://www.entomology.cornell.edu/Faculty_Staff/Lazzaro/

Dartmouth EvolGenomics

Faculty Position in Evolutionary Biology Department of Biological Sciences

The Department of Biological Sciences at Dartmouth seeks applicants for a tenure track Assistant Professorship in the areas of evolutionary genomics or the evolution of molecular pathways. We seek candidates who are taking empirical, theoretical or statistical approaches to these problems. The successful candidate will join vibrant and growing groups of researchers in evolutionary biology and bioinformatics on campus. They will be expected to supervise an independent research program that will attract extramural funding, to provide research training for graduate and undergraduate students, and to teach at the undergraduate and graduate levels. Send a curriculum vitae, representative publications, statements of research and teaching interests, and have at least three letters of reference sent to:

Evolutionary Genomics Search Committee Department of Biological Sciences Dartmouth College Hanover, NH 03755-3576

Although materials can be initially submitted by FAX (603-646-1347), original documents are required. Application review will begin on 1 November 2003 and continue until the position is filled. For further information about the department and graduate programs, see http://www.dartmouth.edu/ ˜ biology/ . Women and members of minority groups are strongly encouraged to apply. Dartmouth College is an Equal Opportunity/Affirmative Action Employer.

Dijon EvolEcol

A lecturer position (Maître de Conférences) is available in Dijon (France) on the following general topic : Evolutionary ecology in host-parasite interactions

Location: Group Evolutionary Ecology, UMR CNRS 5561 Biogéosciences (http://www.u-bourgogne.fr/-BIOGEOSCIENCE/)

Teaching activities : Populations biology ; Community ecology ; Landscape ecology and animal ecophysiology. Courses and practical in Licence and Master of Sciences (200-250 hours/years).

Research activities : Host-parasite interactions and evolutionary ecology. Host parasite interactions as a selective force in birds, relationship between immune abilities and life history traits, parasites and sexual selection, avian demography and pathogens.

Application information : Suitable qualification for application : At least, PhD + Qualification aux fonctions de Maître de conférences + french speaking. First administrative step for Qualification aux fonctions de Maître de conférences Section 67: Population Biology & Ecosystems : on line registration following information (in french) on the web site of the Ministère de lEducation National http://www.education.gouv.fr/-personnel/enssup/antares/default.htm See Campagne 2004 Deadline : Octobre 20th, 17:00 Paris Time

Further information and specific enquiries : - Frank Cézilly: frank.cézilly@u-bourgogne.fr (Tel + 33 (0)3 80 39 62 46) : President of the Section 67 jury recruitment at Dijon. - Thierry Rigaud: thierry.rigaud@u-bourgogne.fr (Tel : + 33 (0)3 80 39 39 45) : Head of the team “Ecologie Evolutive” - Bruno Faivre: bruno.faivre@u-bourgogne.fr (Tel: + 33 (0)3 80 39 62 06) : Coordinator of research programs on Population Biology and Evolutionary Ecology in birds

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

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Dorchester EvolGenetics

Molecular Ecologist/Evolutionary Geneticist £24,450 - £30,000

The Centre for Ecology and Hydrology (CEH) is the leading body in the U.K. for research, survey, monitoring and training in the terrestrial and freshwater sciences. CEH Dorset, at the Winfrith Technology Centre near Dorchester, carries out research in terrestrial and river habitats, including population and conservation ecology.

Leading the Molecular Ecology Group, a team of scientists and postgraduate students, you will be responsible for advancing population and evolutionary biology within CEH by developing population genetics theory and applying molecular techniques to ecological questions. Current projects include gene flow in GM plants, conservation genetics of endangered species, and microevolutionary processes. You will develop new research initiatives in these or related areas, often in close collaboration with other groups in CEH and university departments. This is a great opportunity for a young scientist to develop exciting initiatives. With a track record in winning research funding, you will have published high impact papers and led small research teams.

Starting salary will depend on experience and high calibre scientists will have the opportunity for rapid promotion. {pay award pending}

This is a re-advertisement. Previous applicants should not apply.

Further details and application forms available from Diana Morton, CEH Dorset, Winfrith Technology Centre, Nr Dorchester, Dorset DT2 8ZD, UK (e-mail dmo@ceh.ac.uk, telephone 01305 213500). Closing date for receipt of completed applications is 14th November 2003 quoting reference CEHDOR22.

James Bullock <jmbul@ceh.ac.uk>

DukeU CEO OrgTropicalStudies

Please circulate:

Chief Executive Officer Organization for Tropical Studies

OTS is a consortium of more than 60 universities and research institutions that was founded 40 years ago to provide leadership in education, research, and the responsible use of natural resources in the tropics. The Organization operates major research and teaching facilities in Costa Rica and offers educational programs in Latin America and South Africa. This top position oversees all OTS operations and programs, and is responsible for ensuring the financial health and stability of the Organization, as well as providing a vision for the future. OTS seeks a proven leader with excellent management skills, a distinguished record of professional achievement, and a demonstrated record in the promotion of external relations and fund-raising. Requirements include an advanced degree, a substantial period of relevant professional experience, preferably international; fluency in Spanish is an advantage. The position is based in North Carolina at Duke University. See http://www.ots.duke.edu for further information about OTS and the position. A letter of application with details of professional experience, a résumé, and the names and contact information for three references should be sent to:

OTS Search Committee c/o D. E. Stone Box 90630 Durham, NC 27708-0630 Tel. 919-684-5774. Closing date: December 15, 2003. OTS/Duke University is an Affirmative Action/Equal Opportunity Employer.

Amy Barbee Office Mgr./Admin. Assist. Organization for Tropical Studies, Duke University Box 90630, Durham, NC 27708, USA Tel (919) 684-5774; Fax (919) 684-5661 E-mail: <abarbee@duke.edu> or <nao@duke.edu>

Information on OTS and our programs can be found on our website: http://www.ots.duke.edu

ETHZurich StatisticalGeneticist

Job Announcement: Statistical Geneticist

Background The group of Statistical Animal Genetics at the Institute of Animal Sciences, ETH Zürich focuses mainly on fundamental and strategic research covering statistical-molecular genetics and livestock breeding. Internationally competitive and excellent resources exist within the ETH including an Experimental Research station, and functional genomics and molecular genetic laboratories and bio-informatics/computing facilities. We are looking to fill a statistical animal geneticist position at a post-doctoral fellow or senior research associate level. Recent PhDs or post-docs are encouraged to apply.

General Outline of Position The successful candidate will join a team of quantitative and molecular geneticists and work in novel statistical / computational methods in one or more of the following research topics in Livestock: QTL mapping, Marker-Assisted Selection and Introgression, genetic evaluation methods using DNA marker information. Focus will be on categorical data (e.g. health traits). Mostly computer simulations will be used to test different methods or strategies. Candidate may also closely work with geneticists working on QTL mapping and candidate gene experiments starting in 2004 in our Experimental Research station. Appointment will be approximately 80% research and the rest 20% time may be spent on writing manuscripts, help MSc/PhD students in their research and contribute to under-graduate/ masters education in quantitative genetics and animal breeding.

Candidates for this position must have a doctorate/PhD degree in quantitative genetics and (or) animal breeding with a good understanding and background in molecular genetics and mathematics or statistics. Candidates must have experience in Fortran or C/C++ programming under UNIX environment. Some knowledge in standard packages for statistical analysis and database management is desirable. Good interpersonal and communication skills in a university environment would be advantageous.

General Information Written and spoken knowledge of English is essential. Position is available (from March 1, 2004) for 3 years and may be extended for another 3 years. Further extension to another 6 years (total 12 years) may be possible depending on qualifications and experience at the time of appointment, offering excellent long-term job security in good environment. Salary and benefits are internationally competitive.

Your application Please send your curriculum vitae, (scanned), list of courses/training completed, copies of MSc/PhD degree certificates (if available), copy of abstract of the MSc/PhD theses, list of publications, one to two page statement of research experience and future research ideas and career goals, contact details of three professional referees (name with address, phone, fax and e-mail) along with a covering letter. Applications (by post or email) are accepted until suitable candidate is found but selection of candidates for interview will begin on November 1, 2003. Address for applications and informal enquiries:

Dr. Haja Kadarmideen, Head, Statistical Animal Genetics Group, Institute of Animal Science, Swiss Federal Institute of Technology (ETH), Universitätstr. 65 (UNS D7), CH-8092 Zürich, Tel +41 (0)1 632 23 66, Fax: +41 (0)1 632 1260, E-Mail: haja.kadarmideen@inw.agrl.ethz.ch ETH home page: http://www.ethz.ch ; Group home page: http://www.tg.inw.agrl.ethz.ch/

Haja Kadarmideen <haja.kadarmideen@inw.agrl.ethz.ch>

EmoryU EvolGenetics

Evolutionary Geneticist

The Department of Biology at Emory University is seeking a geneticist who uses molecular genetic approaches to study fundamental questions about the processes and mechanisms of evolution. The Department will consider applicants from a wide range of specializations including, but not limited to, evolutionary genetics, molecular ecology, population genetics, experimental evolution and comparative genomics/ bioinformatics. The position is for a tenure-track assistant professor, although an appointment at a higher rank will be considered in exceptional circumstances. Applicants must provide evidence that they will develop a strong, independently funded research program. A commitment to undergraduate teaching is expected and the appointee will also participate in appropriate Ph.D.-granting programs of the interdepartmental Graduate Division of Biological and Biomedical Sciences. Applicants should submit a curriculum vitae and a statement detailing their current and future research plans, and arrange for submission of three letters of recommendation. Please address applications to Dr. Leslie A. Real, Evolutionary Genetics Search, Department of Biology, Emory University, 1510 Clifton Road, Atlanta, GA 30322; Tel.: (404) 727-4234; Fax: (404) 727-2880; E-mail: evol_srch@biology.emory.edu. Review of completed applications will begin January 1, 2004. Information on the Biology Department and Emory's graduate programs can be obtained from the following web sites: http://www.emory.edu/BIOLOGY/ and www.biomed.emory.edu/

Emory is an Equal Opportunity/Affirmative Action Employer.

Nancy Caro Emory University Department of Biology Voice: 404/727-4234 Fax: 404/727-2880

Nancy Caro <ncaro@Biology.Emory.Edu>

InstZoology ButterflyAdaptation

Zoological Society of London INSTITUTE OF ZOOLOGY

Research Technician: Adaptation at the species' edge in the Brown Argus butterfly

Starting Salary £17,461 15 months contract

The Institute of Zoology invites applications for a Research Technician position to work with Dr Jon Bridle on a NERC-funded project Genetic tests adaptation at the species' edge of the UK brown argus butterfly Aricia agestis. The project will investigate the responses of UK populations to ongoing climate change, and will involve a combination of fieldwork, molecular genetics, morphometrics and butterfly rearing. The work will be in collaboration with Prof Chris Thomas (University of Leeds), Prof Jim Mallet (UCL), and Prof Roger Butlin (University of Leeds) and will mainly involve developing and using AFLP markers to look for evidence of selective sweeps. For this reason, some molecular experience, preferably with AFLPs, is essential. Candidates should have a degree in a relevant discipline and be self-motivated and enthusiastic, with a strong interest in ecology/evolution or population genetics. Previous experience of rearing and handling invertebrates, and a clean driving licence is also desirable.

Applicants should send a CV, covering letter and names and full contact details of three referees to the HR Dept., ZSL, Regent's Park, London NW1 4RY or e-mail HR@zsl.org. Informal enquiries to Jon Bridle (tel. +44 020 7449 6627 or e-mail jon.bridle@ioz.ac.uk). Further details and a job description are available from HR or from the website: www.zsl.org The closing date for applications is 1 November 2003.

Registered Charity Number 208728

Jon Bridle Research Fellow Institute of Zoology Zoological Society of London Regent's Park London NW1 4RY

Tel. 020 7 449 6627 Fax. 020 7 586 2870 jon.bridle@ioz.ac.uk

IowaStateU Phylogenetics 2

There was an error in the web link in this evoldir posting of last week.Please see http://www.eeob.iastate.edu for the new departmental web page. The newly formed Department of Ecology, Evolution, and Organismal Biology (EEOB) at Iowa State University seeks one or more tenure-track assistant professors in evolutionary biology whose research focuses on phylogenetics or the evolution of development.EEOB (http://www.ag.iastate.edu/departments/eeob/home.html) comprises 32 faculty members who use integrative approaches that bridge traditional disciplines and span multiple levels of biological organization.Successful candidates are expected to develop a competitively funded research program and contribute to undergraduate and graduate teaching.Applicants must have Ph.D. in Evolution or related field and demonstrate excellent research and teaching potential.Applicants should submit a curriculum vitae, statements of research/teaching interests and selected reprints, and have three letters of recommendation sent to Dr. Lynn Clark, Search Committee Chair, EEOB Department, Iowa State University, Ames, IA 50011-1020 by November 1, 2003 for full consideration.ISU is an EO/AA employer.Women and members of minority groups are encouraged to apply.Contact: Dr. Lynn Clark, Voice: (515) 294-8218; FAX: (515) 294-1337; E-mail: lgclark@iastate.edu lgclark@iastate.edu

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KewLondon Mycology biodiversity

Fungal Diversity Specialist - Ref 750

HOURS OF WORK Full-time

JOB STATUS: Permanent

SALARY PER ANNUM: £24,720 to £32,960 depending on skills and experience

DEPARTMENT: Jodrell Laboratory

JOB DETAILS:

You will be responsible for developing new research initiatives documenting fungal diversity and using modern comparative approaches. You will undertake high level fungal diversity research, using molecular and morphological approaches, on Agaricales and/or Ascomycetes, with emphasis on tropical as well as British species.

ESSENTIALS:

Specialist taxonomic knowledge of Agaricales or Ascomycetes is essential, plus a good working knowledge of larger fungi.

Closing Date: 30 November 2003 with interviews in Jan/Feb 2004.

see http://www.kew.org/aboutus/jobs/ –

Dr Vincent Savolainen Jodrell Laboratory, Molecular Systematics Section Royal Botanic Gardens, Kew Richmond Surrey TW9 3DS London UK phone +44-(0)20-8332-5366 fax +44-(0)20-8332-5310 email v.savolainen@kew.org

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KewLondon Phylogenomics

JOB TITLE: Plant Cytogeneticist - Ref 683

HOURS OF WORK Full-time

JOB STATUS: Permanent

SALARY PER ANNUM: £24,720 to £32,960 depending on skills and experience

DEPARTMENT: Jodrell Laboratory

JOB DETAILS:

You will be responsible for developing new research initiatives in comparative plant cytology. You will use modern cytogenetics tools to investigate questions relating to plant genome evolution in the broadest sense, building on existing skills in the cytogenetics group.

ESSENTIALS:

Experience in plant cytogenetics (including in situ hybridisation) is required. An understanding of the application of genetic data to population genetics and phylogenetics is desirable.

Closing Date: 30 November 2003 with interviews in Jan/Feb 2004.

How To Apply

see http://www.kew.org/aboutus/jobs/ Return your application ideally by post to: Recruitment, 47 Kew Green, Kew, Surrey. TW9 3AB or by email to jobs@kew.org

If you have any queries or would prefer to be sent an application pack please do not hesitate to call the recruitment team on 0208 332 5184 (Office hours) or 0208 332 5150 (24hr).

Home | About Us | –

Dr Vincent Savolainen Jodrell Laboratory, Molecular Systematics Section Royal Botanic Gardens, Kew Richmond Surrey TW9 3DS London UK phone +44-(0)20-8332-5366 fax +44-(0)20-8332-5310 email v.savolainen@kew.org

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LavalU Bioinformatics Conservation

The Faculty of Sciences and Engineering of Laval University is currently seeking candidates for holding Canadian Research Chair (either Tier I and Tier II level). The Faculty offers a unique research environment by grouping together numerous disciplines in sciences and engineering. With more than 5000 students, 250 faculty members from 13 departments, 12 research centres, the Faculty contributes to make of Laval University one of the most important research institution in Canada. Laval University, first French speaking university in North America, is located in Québec City, which is on the UNESCO's World Heritage List and offers an exceptional quality of life.

The fields of research for which candidates are currently needed are:

1. Bioinformatics, or Statistical genetics, or population genetics (theory).

2. Conservation and management of biological resources, including management of natural habitats, management of terrestrial or aquatic resources, conservation biology.

Interested applicants should provide: A letter that specifies which CRC profile thy are applying for, including the level (Tier I or Tier II). An updated C.V. using the CRC form available online at: http://www.chaires.gc.ca/english/Form/index.html A text (maximum 1200 words) describing the proposed research and explaining

its link with the CRC theme chosen by the candidate.

Please send your application before 15th November either by e-mail (as pdf

file) to: vice-doyen.recherche@fsg.ulaval.ca

or by mail to:

Paul Fortier Vice-doyen au développement et à la recherche Faculté des sciences et de génie Pavillon Alexandre-Vachon, bureau 1036-F Université Laval Québec (Québec) G1K 7P4 Canada

For more information please contact Julian J. Dodson, Chair, Biology Department (Julian.Dodson@bio.ulaval.ca) and visit the following site: http://www.fsg.ulaval.ca/crc

Louis Bernatchez, Titulaire de la Chaire de recherche du Canada en conservation génétique des ressources aquatiques

Département de biologie, Pavillon Vachon Université Laval Ste-Foy, QC G1K 7P4 Canada

Tél: 418 656-3402 Télécopie: 418 656-2043 Couriel: Louis.Bernatchez@bio.ulaval.ca Toile: http://www.bio.ulaval.ca/index-alt.html

Chaires de recherche du Canada: www.chaires.gc.ca

LehighU EvolBiol

EVOLUTIONARY BIOLOGY ASSISTANT PROFESSOR LEHIGH UNIVERSITY

The Department of Biological Sciences at Lehigh University is seeking researchers that employ modern analytical methods in the study of fundamental aspects of the evolutionary process. This is a tenure-track position that is part of an ongoing institutional initiative in Bioscience and Biotechnology (www.lehigh.edu/~inbios). Areas of specialization are broadly conceived and may include, for example, field and/or laboratory studies on the molecular aspects of population genetics, molecular mechanisms of phenotypic expression, cell division, human evolution, asexual or sexual development, neural/endocrine processes, genome conservation, or phylogeny. The successful candidate will have the potential to generate extramural funding and have a commitment to instructional excellence at the undergraduate and graduate levels. Applications should be directed to: Prof. M. Itzkowitz, Chair, Evolutionary Biology Search Committee. E-mail: mi00@lehigh.edu. Send curriculum vitae, representative publications, a description of research and teaching interests, and four letters of reference to the search committee chair electronically or to: Department of Biological Sciences, 111 Research Drive, Lehigh University, Bethlehem, PA 18015. Deadline for submission is December 1, 2003. Lehigh University is an AA/EO employer and is committed to recruiting and retaining women and minorities.

Jill Schneider <js0v@lehigh.edu>

LilleFrance

Poste de Maitre de Conferences: 67 MCF 1566

Un poste de maitre de conferences est ouvert en 67eme section à l'Universite des Sciences et Technologies de Lille (Lille I) dans l'unite de recherche UMR 8016 "Genetique et Evolution des Populations Vegetales" (Dir. J. Cuguen).

L'activite de recherche du candidat recrute devra s'integrer dans le projet scientifique du laboratoire dont l'objectif est l'etude de la genetique et de l'evolution des systemes de reproduction, des traits d'histoire de vie et de l'adaptation aux environnements pollues par les metaux lourds.

Lequipe Adaptation et environnements anthropises et son volet ≪Origineet evolution de la tolerance au zinc chez Arabidopsis≫ a besoin de renforcer ses competences en genetique evolutive et biologie de l'adaptation. Lequipe est engagee dans deux programmes nationaux (IFB et PEVS) et dans le reseau europeen "Metalhome". Le projet sinscrit dans le cadre general du Programme de Recherches Concertees Sites et Sols pollues ≪Environnement et Activites Humaines≫ du CPER Nord Pas-de-Calais et dans le volet ≪cycle des contaminants metalliques et organiques≫ de la FR-CNRS 1818. Le theme de recherche propose se situe à l'interface entre ecologie evolutive et genetique des populations. Il est focalise sur la dynamique de l'adaptation et la tolerance aux metaux lourds. Le MCF recrute devra s'investir sur l'evaluation experimentale de la tolerance aux metaux lourds, ainsi que sur la biologie evolutive de la tolerance et de l'accumulation des metaux. En fonction de ses competences il pourra explorer les aspects theoriques de la dynamique de l'adaptation aux environnements extremes.

Le candidat retenu devra posseder une solide formation de base en biologie et genetique des populations et en ecologie evolutive, completee par une experience de recherche dans l'etude experimentale et/ou theorique de l'adaptation.

Il participera aux enseignements de genetique, genetique des populations, biologie vegetale et ecologie en premier et second cycles universitaires.

La date limite de depot des candidatures à l'USTL est fixee au 30 octobre 2003, delai de rigueur (renseignements detailles sur le site web de l'Universite)

http://www.univ-lille1.fr/personnels/recrutement/informations.htm Pour tout renseignement sur le plan scientifique, contacter :

Pierre Saumitou-Laprade Tel : +33 3 20 43 47 42 pierre.saumitou@univ-lille1.fr

ou

Joel Cuguen Tel : +33 3 20 43 40 24 joel.cuguen@univ-lille1.fr

http://www.univ-lille1.fr/gepv/

MichiganStateU Tech

Research Technician Position A research technical position is available immediately in the laboratory of Dr. Kim Scribner in the Departments of Fisheries and Wildlife and Zoology at Michigan State University. The position involves both laboratory and computational data collection and analysis for a large collaborative study of the genealogical basis of disease transmission in free-ranging white-tailed deer. Laboratory work will involve microsatellite genotyping and mtDNA sequence analyses. Knowledge in analytical approaches for estimation of individual relatedness, parentage, and spatial structure would be desirable. The MSU application website address is www.hr.msu.edu/HRsite/forms/-Staffforms.htm. Applicants should send a cover letter and resume including contact information for three references to either Kim Scribner or Gene Rummel. Please send either electronically (scribne3@msu.edu or rummel@hr.msu.edu), fax (517-432-1699) or mail at Dept. Fisheries & Wildlife, Michigan State University, East Lansing Michigan 48824-1222 (KS) or Gene Rummel, Human Resources, 110 Nisbet Bldg. Please refer to position number P30387. Applications should be received by 17 October. Michigan State University is an Equal Opportunity, Affirmative Action Employer

Kim Scribner <scribne3@msu.edu>

NewportOR MolGenetTech 2

Dear Evoldir Colleagues-

Please pass on this message to anyone who might be interested in the position.

I am seeking to hire a full-time permanent laboratory technician to conduct research in the areas of quantitative and molecular genetics of shellfish, especially oysters. The position is with the USDA Agricultural Research Service as part of a program for the selective breeding of cultured shellfish (http://www.ars.usda.gov/research/projects/-projects.htm?ACCN_NO@5577&fy 02) . The position is located in Newport, OR at Oregon State University's Hatfield Marine Science Center (http://-hmsc.oregonstate.edu/). This new laboratory is being set up for high-throughput genotyping of microsatellites, AFLPs, and single-nucleotide polymorphisms, including automated DNA sequencing and liquid handling. Research will focus on using traditional and molecular genetic methods for elucididating the genetic covariance structure, QTL mapping and gene expression analyses of loci contributing to life history traits, stress and disease resistance, economically important characters such as shelf-life and meat quality, and morphological characters such as shell shape and coloration patterns.

The ideal candidate would have a Master's degree, but practical experience in molecular genetics would be considered equivalent if it provided familiarity with the necessary molecular techniques (DNA/RNA isolation, PCR, electrophoresis, molecular cloning, DNA sequencing etc.). Familiarity with the bioinformatic and statistical approaches used to analyze molecular genetic data for population-level patterning and QTL mapping are also highly desirable, but training can be provided. There will be some field work required for animal rearing and data collection.

I am looking for more of a high-level laboratory manager who will contribute to the intellectual aspects of the work rather than simply a pair of hands at the bench. There will be ample scope for independent projects, presentation of results at meetings and in publications, and participation in formulating research agendas. The advertised salary range is large, so there is ample scope for advancement for more junior applicants, and more senior applicants will be given full consideration.

Newport is a small, oceanfront city with unspoiled beaches, an active fishing fleet, and numerous tourist attractions located at the mouth of the Yaquina Bay on the central Oregon coast. The cost of living is very reasonable, especially compared to other west coast areas. Portland is about 2.5 hours north, and Corvallis is about 1 hour east.

Please email or call me with any questions, but be sure to apply according to the instructions in the official announcement below, including a cover letter that specifically addresses the required skills. The federal government can be very exacting when it comes to these details, and applications are filtered by human resources staff before being forwarded to scientists.

<<<<APPLICATION DEADLINE IS 30 SEPTEMBER>>>

Sincerely,

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

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

* OFFICIAL ANNOUNCEMENT: *

USDA - Agricultural Research Service POSITION ANNOUNCEMENT

Announcement Type: ALL SOURCES/ALTERNATIVE MERIT PROMOTION Position Title: Biological Science Technician (Animal)

Series/Grade: GS-0404-06/07/08

Promotion Potential: GS-09

Salary: GS-06: $28,644 - $37,237 per annum

GS-07: $31,830 - $41,380 per annum

GS-08: $35,252 - $45,828 per annum

Type of Appointment: Permanent

Location of Position: Newport, Oregon

Announcement Number: ARS-X3W-3424

Opening Date: August 11, 2003

Closing Date: September 29, 2003

Area of Consideration: All U.S. Citizens

APPLICATIONS WILL ALSO BE ACCEPTED FROM USDA SURPLUS AND FEDERAL DISPLACED EMPLOYEES IN THE COMMUTING AREA.

DUTIES: The incumbent will be engaged in all aspects of a new research program in shellfish genetics and selective breeding using both quantitative and molecular genetics, including assisting with the spawning, rearing and evaluation of animals in the hatchery and field, but emphasizing molecular aspects, including but not limited to: marker development and high-throughput genotyping and gene expression analyses in the laboratory. Duties, therefore, include collecting and archiving tissue samples, DNA/RNA extraction, PCR and reverse PCR, agarose gel electrophoresis, DNA sequencing, molecular cloning, and other related techniques as well as data acquisition, entry, storage, and retrieval in electronic formats. The incumbent will also maintain inventories and stocks of the required consumable laboratory supplies and reagents. Depending on experience, the

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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

NorthCarolina ForestEvolEnto

The North Carolina Division of Forest Resources currently has a job opening for a forest entomologist. The position was posted on 1/3/03 and closes on 1/15/03. To view the vacancy announcement and directions on how to apply, click on the website address below, then scroll down until you see “Forest Pest Specialist” under Job Title (Vacancy # 4304-0000-0004-682). Click on the gray button with the Vacancy Number in it to see details about the job. Don Rogers, NC Division of Forest Resources, requested that I post this message on Forent. Please forward this to any interested individuals you know. If you have questions regarding this position, please contact Don Rogers by phone at (919) 733-2162 ext 256 or by e-mail at: don.rogers@ncmail.net. Thank you – Don Duerr

http://osp.its.state.nc.us/deptsearchresults3a.asp?departmentname=DEPARTMENT%20OF%20ENVIRONMENT%20%26%20NATURAI

Don Duerr Entomology Group Leader USDA Forest Service Forest Health Protection 1720 Peachtree Road, NW Room 862 S Atlanta, GA 30309-2719 Phone: (404) 347-3541 Fax: (404) 347-1880 Cell: (828) 273-4325 E-mail: dduerr@fs.fed.us

OregonStateU MicroTech

Hi, We need a technician to run a large microsatellite genotyping project on steelhead salmon. Official title is faculty research assistant. Cheers, Mike

Responsibilities: Appointee will conduct population genetics research in Michael Blouin’s lab in the department of Zoology at Oregon State University. The primary focus will be high-throughput microsatellite genotyping of salmon populations for conservation applications. Duties will include DNA extractions, PCR, managing the inventory of samples, database management, supervising students, and some ordering and minor paperwork. We need someone who is methodical, pays attention to details, and can handle large, complicated sets of samples without making mistakes. For review of the full position announcement refer to http://oregonstate.edu.jobs.

Feel free to call or e-mail Mike for further information. Info about the project available on my website: http://oregonstate.edu/~blouinm/index.htm To apply: send a letter of application, curriculum vitae or resume, and names, addresses, phone numbers and e-mail addresses of three or more references to: Dr. Michael Blouin, Dept. Zoology, Oregon State University, 3029 Cordley Hall, Corvallis, OR 97331-2914; Tel: 541-737-2362; Fax: 541-737-0501. blouinm@science.oregonstate.edu. For full consideration, apply by 11/14/03, but we may consider later applications. Position can begin as early as 1/1/04. OSU is an AA/EOE. –

Michael Blouin Dept. Zoology, 3029 Cordley Hall Oregon State University Corvallis, OR 97331-

2914 Tel. 541-737-2362 Fax. M. Blouin: 503-714-9907 Fax. Dept. Zoology: 541-737-0501 blouinm@science.oregonstate.edu

PennStateU EvolBiol

Assistant Professor in Astrobiology/Evolutionary Biology

The Eberly College of Science at Penn State invites applications for a tenure track faculty position in Astrobiology with the appointment to be made in one of the departments of the college including Biology, Biochemistry and Molecular Biology, and Chemistry (http://www.science.psu.edu). We seek a candidate interested in pursuing evolutionary research, with either prokaryotes or eukaryotes, on the early evolution of the Earths environment and biota. Potential fields of study include, but are not limited to, molecular, cellular and developmental evolution, and paleontology. The appointee will have the opportunity to join our Astrobiology Research Center (http://psarc.geosc.psu.edu) and is expected to develop a strong, externally funded research program and participate in undergraduate and graduate teaching. Applicants should send a PDF file containing their curriculum vitae, statement of research and teaching interests, and contact information for three references to astrobio@email.bio.psu.edu, or mail to: Chair, Astrobiology Search, Department of Biology, 208 Mueller Laboratory, The Pennsylvania State University, University Park, PA 16802-5301. Review of applications begins December 10, 2003 and will continue until a suitable candidate is identified. Penn State is committed to affirmative action, equal opportunity, and the diversity of its workforce.

NOTE: A separate search is already underway for a second position (Assistant Professor) in Astrobiology, by the Department of Geosciences at Penn State. For information on that position, please see the job announcement (http://psarc.geosc.psu.edu).

S. Blair Hedges, Ph.D. Department of Biology Pennsylvania State University 208 Mueller Lab University Park, PA 16802-5301 tel. 814-865-9991, fax. 814-865-3125 http://evo.bio.psu.edu/hedgeslab/

PortlandStateU PlantEvol

The following ad will appear in Science in a week or two:

Plant Ecology and Evolutionary Biology

The Department of Biology at Portland State University invites applications for a plant biologist at the assistant professor level. We seek an individual with broad research interests in ecological or evolutionary aspects of plant biology, includingbut not limited tophysiology, morphology, reproduction, development, plantanimal, or plantpathogen interactions. Minimum qualification is a Ph.D. in biology, with priority given to candidates with postdoctoral experience and who have demonstrated success in developing a research program through publications or external funding. We encourage applications from individuals whose interests complement existing departmental strengths in ecology, physiology, evolution, and genetics (see the departmental web site: http://www.bio.pdx.edu/). The successful candidate will be expected to develop an externally funded research program, be effective in teaching at the undergraduate level, and participate in the training of graduate students in our masters and PhD programs. This is a tenuretrack, 9month appointment to begin the in the fall of 2004. Review of applications will begin 1 December, 2003, and will continue until the position is filled. A curriculum vitae, statement of current and future research, and three letters of reference should be sent to: Dr. Mitch Cruzan, Chair, Plant Ecology Search Committee, Department of Biology, P.O. Box 751, Portland State University, Portland, Oregon 97207. Portland State University is an Affirmative Action, Equal Opportunity institution and, in keeping with the President's diversity initiative, welcomes applications from diverse candidates and candidates who support diversity.

For additional information please feel free to contact me at the email address below.

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Mitch Cruzan, Associate Professor Department of Biology Portland State University, Box 751 Portland, OR 97207 Phone: 503-725-8391 Fax: 503-725-3888 Webpage: <http://web.pdx.edu/˜cruzan/>

Mitch Cruzan <cruzan@pdx.edu>

RiceU EvolBiol

EVOLUTIONARY BIOLOGY. The Department of Ecology and Evolutionary Biology at Rice University (http://eeb.rice.edu/) is seeking to fill an anticipated tenure-track position at the ASSISTANT PROFESSOR level in any area of evolutionary biology. Rice is a private research university with a strong commitment to the highest standards of research and education at the graduate and undergraduate levels. Applicants should submit a c.v., statements of research and teaching interests, and request four letters of recommendation. All materials should be sent to Evolution Search Committee, Department of Ecology and Evolutionary Biology MS-170, Rice University, P.O. Box 1892, Houston TX 77251-1892. Review of applications will begin November 6. Rice University is an Equal Opportunity/Affirmative Action Employer.

David Queller queller@rice.edu David Queller queller@rice.edu

RoyalBotanicGardensKew MolSyst

Laboratory Manager - Ref LM - Molecular Systematics Section Royal Botanic Gardens, Kew see http://www.kew.org/aboutus/jobs/REFLM.html

HOURS OF WORK: Full Time

JOB STATUS: 1 Year Fixed Term Appointment

SALARY PER ANNUM: £24,720 per annum

DEPARTMENT: Molecular Systematics, Jodrell Laboratory

JOB DETAILS:

We are looking for someone to actively manage the day-to-day running of the Molecular Systematics Laboratory. This role will largely involve ensuring that the laboratory equipment is running smoothly and that staff in this section are operating efficiently including supervising the research of students and visitors as well as delivering training on phylogenetic techniques. You will also conduct your own research programme focussing on the agreed target areas for the Laboratory.

ESSENTIALS:

You will be educated to PhD level with technical expertise in molecular biology, particularly DNA sequencing. Previous experience with DNA fingerprinting would be an advantage. You will have proven managerial experience and be able to effectively to communicate ideas with others. You will also have experience teaching others new techniques and protocols and have a flexible approach to your work.

CLOSING DATE: 9 a.m. Monday 27 October 2003

INTERVIEW DATE: Thursday 6 November 2003

How To Apply

1. Download and read the information below.

Job Description, Person Specification and Additional Information (Word Version - 143KB)

2. Complete an application form:

Application Form (Word Version 166KB)

Application Form (Adobe Version 222KB

3. Return your application ideally by post to: Recruitment, 47 Kew Green, Kew, Surrey. TW9 3AB or by email to jobs@kew.org

If you have any queries or would prefer to be sent an application pack please do not hesitate to call the recruitment team on 0208 332 5184 (Office hours) or 0208 332 5150 (24hr).

Dr Vincent Savolainen Jodrell Laboratory, Molecular Systematics Section Royal Botanic Gardens, Kew Richmond Surrey TW9 3DS London UK phone +44-(0)20-8332-5366 fax +44-(0)20-8332-5310 email v.savolainen@kew.org email v.savolainen@kew.org

RoyalBotanicGardensKew PlantEvol

Senior research scientist post at the Jodrell Laboratory, Royal Botanic Gardens, Kew

Plant Anatomist/Morphologist (ref. 603)

The postholder will be responsible for developing new research initiatives to build an independent high-impact research programme as part of a broader schedule within the Comparative Plant Biology programme. This will include addressing key questions about the evolution of plant form, either reproductive or vegetative.

He/she will have a PhD in a relevant subject and a strong research publication record. Experience in plant anatomy and/or morphology and phylogenetic methodology are required. An understanding of the importance of model organisms as genetic systems and the use of marker-based systems in association with innovative imaging approaches to study plant development are desirable. Experience in successful research applications in desirable.

Starting salary will be from £24 000 to £30 000 and will depend on your experience and range of skills. Benefits include a choice of final salary or stake-holder pension and a generous annual leave allowance.

Application form and further information available from the Personnel Department, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB. Tel: 020 8332 5184/5150. Email jobs@kew.org. Please quote appropriate reference.

Paula Rudall <p.rudall@rbgkew.org.uk>

SpelmanCollege Bioinformatics

The Biology Department at Spelman College is accepting applications for a senior faculty position. We seek a candidate in one of the following broadly defined areas, including Genomics/Bioinformatics, Physiology, Evolutionary, Cellular, or Molecular Biology. The applicant must have a Ph.D. in the biological sciences, qualify for the rank of Associate Professor or Professor, a strong record of publication and extramural funding, and a strong interest in undergraduate teaching, mentoring and research. The Department occupies teaching and research space in the new Albro-Falconer-Manley Science Center. The successful candidate may assist in teaching introductory courses, will develop advanced electives in their area of specialization and will establish a productive research program. Applicants committed to undergraduate teaching with a strong research emphasis should send a letter of interest, detailed curriculum vita, statements of teaching and research interest, official transcripts, recent publications and three letters of recommendation. All application materials must be addressed to: Office of the Provost, Spelman College, Attn: Biology Department Search Committee Chair, 350 Spelman Lane, SW, Box 1209, Atlanta, GA 30314. Review of applications will begin November 1, 2003 and will continue until the position is filled.

Joanne Chu, Ph.D. Assistant Professor Dept. of Biology Spelman College Box #222 350 Spelman Lane, SW Atlanta GA 30314-3399

Tele: 404-270-5712 FAX: 404-270-5725 email: jochu@spelman.edu

JoChu@spelman.edu

UAkron EvolBehavior

The University of Akron Department of Biology invites applications for the Leuchtag Chair, a tenure track position in BEHAVIOR at the rank of Assistant Professor, to begin August 23, 2004. Applicants with research and teaching experience in any area of behavior (broadly defined) are encouraged to apply, and we are especially interested in applicants who will contribute to our growing emphasis on Integrative Biology. Significant set-up funds are available. Candidates must hold a Ph.D. degree, and post-doctoral experience is preferred. Successful candidates will be expected to develop an externally funded research program in their area of expertise, advise graduate students, and contribute to the undergraduate and graduate curricula. The University of Akron is one of the largest state universities in Ohio with over 24,000 students. For further information visit the department's website at http://www.uakron.edu/biology/. Review of applications will begin November 17, 2003. Applicants should submit a curriculum vitae, a summary of teaching interests, a research statement, copies of recent publications, and three letters of recommendation to: Chair, Behavior Search Committee, Department of Biology, The University of Akron, Akron, OH 44325-3908. The University of Akron is an Equal Opportunity/Affirmative Action Employer. Qualified women, minorities, Vietnam-era veterans, disabled veterans, and the disabled are encouraged to apply.

Dr. Randall J. Mitchell Department of Biology University of Akron Akron, OH 44325-3908 330-972-5122 Fax 330-972-8445 rjm2@uakron.edu http://www.uakron.edu/biology/mitchell/

"Mitchell,Randall J" <rjm2@uakron.edu>

UCaliforniaIrvine ComparativeEvolPhysio

COMPARATIVE/EVOLUTIONARY PHYSIOLOGY UNIVERSITY OF California, Irvine Assistant Professor

The Department of Ecology and Evolutionary Biology seeks to fill a tenure-track Assistant Professor position in the area of Evolutionary or Comparative Physiology of animals. Area of research specialization is open, but relevance of research interests to broad evolutionary or ecological issues is important. The successful candidate will be expected to teach in undergraduate courses in animal and human physiology as well as ongoing graduate courses in evolutionary and comparative physiology. By 15 December 2003, please submit a curriculum vitae, description of research and teaching interests, three relevant publications and arrange to have three letters of recommendation sent to Physiology Search Committee, Department of Ecology and Evolutionary Biology, 321 Steinhaus Hall, University of California, Irvine CA 92697-2525. Information about the Department can be obtained at <http://ecoevo.bio.uci.edu/->http://ecoevo.bio.uci.edu . The University of California, Irvine has an active career partner program, is an equal opportunity employer committed to excellence through diversity, and has a National Science Foundation Advance Gender Equity Program.

Jeanne Ingels <jingels@uci.edu>

UCincinnati EvolBehavior

FACULTY POSITION

The Department of Biological Sciences, University of Cincinnati (website: http://www.biology.uc.edu/), announces a tenure-track position for individuals studying MOLECULAR & CELLULAR MECHANISMS of ANIMAL BEHAVIOR to be filled at the ASSISTANT PROFESSOR rank by September 2004. We seek an individual using cellular or molecular approaches to address comparative, integrative, ecological, and/or evolutionary questions involving animal behavior. Specific areas of interest may include behavioral endocrinology, behavioral neuroscience, behavioral neuroendocrinology, behavior genetics, molecular neuroscience, or computational neurobiology. We seek a researcher to complement an emergent faculty group focused on integrative biology of animal behavior. The successful candidate will be expected to develop a rigorous, externally funded research program, and to participate in training of graduate students (M.S. and Ph.D.). Teaching responsibilities may include participation in an introductory course in cellular or molecular biology, an upper-level course in animal physiology, and specialized areas at the graduate level. Applicants must have a Ph.D. or equivalent degree; postdoctoral experience will be advantageous. Applicants should submit a curriculum vitae, statement of research and teaching interests, and three letters of recommendation by November 21, 2003 to Faculty Search Committee, Department of Biological Sciences, University of Cincinnati, Cincinnati, OH 45221-0006. The University of Cincinnati is an equal opportunity/affirmative action employer. Women, minorities, veterans and persons with disabilities are encouraged to apply.

Dr. Michal Polak Assistant Professor Department of Biological Sciences University of Cincinnati Cincinnati, OH 45221-0006 USA

Phone: (513) 556-9736 FAX: (513) 556-5299 http://-www.biology.uc.edu/faculty/polak/index.html

Michal Polak <polakm@email.uc.edu>

UFlorida EvolBiol

ASSISTANT OR ASSOCIATE PROFESSOR IN EVOLUTIONARY BIOLOGY

The Department of Zoology at the University of Florida invites applications for a tenure-track ASSISTANT OR ASSOCIATE PROFESSOR in EVOLUTION. We seek a colleague who is strongly quantitative and is committed to linking data with theory. The successful candidate will integrate with existing strengths in evolutionary biology and complement research in ecology, behavior, genetics, and physiology. Preferred areas of study include, but are not limited to, evolutionary theory, empirical studies of rapid, experimental or applied evolution, and phenotypic plasticity. This colleague will be expected to establish an internationally recognized, externally funded research program; supervise graduate students; contribute to our teaching in general biology, and teach other courses in his or her area of expertise at the undergraduate and graduate levels. Please submit a curriculum vitae, reprints of three representative papers, statements of research interests and teaching philosophy, and have three letters of reference sent to Evolutionary Biology Search Committee, Department of Zoology, PO Box 118525, University of Florida, Gainesville, FL 32611-8525. Applications must be received by December 1, 2003. For more information, see http://www.zoo.ufl/jobs/evosearch.html or contact evosearch@zoo.ufl.edu. The University of Florida is an Equal-Opportunity Employer, and we encourage applications from minorities and women.

Margaret Fields <mfields@zoo.ufl.edu>

UIllinoisUC EvolInsectGenomics

Assistant Professor of Insect Genomics School of Integrative Biology University of Illinois at Urbana-Champaign

We invite applications for a nine-month, tenure-track position as Assistant Professor of Insect Genomics. The position starts as early as August 2004. We seek a broadly trained biologist working on insects who will develop an internationally recognized, externally funded, research program that integrates genomics with other approaches in physiology, neuroscience, behavior, and evolutionary biology. Applicants should be interested in the mechanisms and evolution of socially mediated behavior or physiology. The successful candidate will have the opportunity to be part of dynamic and well-established communities in insect biology and neuroscience, as well as a genomics community that is forming around the Institute for Genomic Biology (IGB), which will make up to 15 hires over the next several years and will be housed in a state-of-the art facility. The IGB will contain laboratory space for research groups organized around scientific themes, teaching laboratories, and facilities for the development and applications of technology for interdisciplinary research in genomic sciences. Participation in both undergraduate and graduate education is required. A Ph.D. in Biology or another relevant biology discipline is required, and postdoctoral experience is desirable. Salary is commensurate with experience. Minorities, women, and other designated groups are encouraged to apply.

To ensure full consideration, applicants should submit a CV, a statement of research and teaching interests, and the names and addresses of three references no later than December 5, 2003. Applicants may be interviewed before the closing date; however, no hiring decision will be made until after that date. Please send materials to Dr. Gene E. Robinson, Insect Genomics Search Committee, School of Integrative Biology, University of Illinois, 286 Morrill Hall, 505 South Goodwin Ave., Urbana, IL 61801 (phone: 217/ 333-3044; fax: 217/ 244-1224; email: sib@life.uiuc.edu).

Gene E. Robinson G. William Arends Professor of Integrative Biology Director, Neuroscience Program Department of Entomology University of Illinois 505 S. Goodwin Ave. Urbana, IL 61801 Tel. 217-265-0309 Fax 217-244-3499 Website: http://www.life.uiuc.edu/-robinson/

Gene Robinson <generobi@life.uiuc.edu>

ULaval CRC

La Faculte des sciences et de genie de l Universite Laval est a la recherche de candidates et de candidats pour occuper des Chaires de recherche du Canada (niveau 1 et niveau 2). La Faculte des sciences et de genie de l Universite Laval se distingue par une structure unique qui reunit sous un meme toit un grand nombre de disciplines des sciences et de l ingenierie. Avec plus de 5 000 etudiants, 250 professeurs-chercheurs repartis dans 13 departements, 12 centres de recherche facultaires ou multifacultaires et avec son personnel professionnel, technique et administratif comptant pres de 200 personnes, la Faculte contribue indeniablement a faire de l Universite Laval l une des plus importantes universites de recherche au Canada.

L Universite Laval, premiere universite francophone d'Amerique, est situee dans la ville de Quebec, ville declaree joyau du patrimoine mondial par l'UNESCO et jouissant d d une qualite de vie exceptionnelle.

Les domaines pour lesquels nous recherchons des candidats sont:

1. Bioinformatique, ou statistiques genetiques, ou genetique des populations (theorie).

2. Conservation et amenagement des ressources biologiques, incluant la gestion des milieux naturels, la gestion des ressources aquatiques ou terrestres, la biologie de la conservation.

Le dossier de candidature doit comprendre : Une lettre de couverture dans laquelle la candidate ou le candidat specifie le domaine de recherche de la Chaire, de meme que le type (niveau 1 ou niveau 2). Un curriculum vitae selon le formulaire des Chaires de recherche du Canada. Ce formulaire en ligne est disponible a l adresse :

www.chaires.gc.ca/francais/Formulaire/index.html .

Un texte d au plus 1200 mots resumant le programme de recherche propose et expliquant comment celui-ci s insere dans la thematique de l un des domaines de recherche vise par l appel de candidatures.

Veuillez acheminer votre dossier de candidature avant le 15 novembre 2003 par courrier electronique (fichiers pdf) a: vice-doyen.recherche@fsg.ulaval.ca ou par la poste a :

Paul Fortier Vice-doyen au developpement et a la recherche Faculte des sciences et de genie Pavillon Alexandre-Vachon, bureau 1036-F Universite Laval Quebec (Quebec) G1K 7P4 Canada

Pour toute autre information, priere de contacter Julian J. Dodson, directeur du departement de biologie (Julian.Dodson@bio.ulaval.ca) ou encore le site suivant: http://www.fsg.ulaval.ca/crc/

Louis Bernatchez,Titulaire de la Chaire de recherche du Canada en conservation genetique des ressources aquatiques Departement de biologie, Pavillon Vachon, Universite Laval, Sainte-Foy, QC G1K 7P4 Canada

Tel: 1 418 656-3402 Fax: 1 418 656-2043 E-mail:Louis.Bernatchez@bio.ulaval.ca

ULeeds ChairEvolGenomics

The University of Leeds has just advertised a series of prestigious Professorial appointments to mark the Centenary of its charter. These include a Chair in Evolutionary/Comparative Genomics in the Faculty of Biological Sciences. We seek a scientist with an international standing capable of establishing a new and vibrant research group within the Faculty. Any approach (empirical, theoretical, statistical) to evolutionary genomic issues is welcome. The Faculty already has an outstanding Ecology and Evolution Group, Bioinformatics Group and various groups using genomics and proteomics in functional studies. For details please go to www.leeds.ac.uk/jobs or email a.e.milner@leeds.ac.uk. I am happy to field informal enquiries.

Professor Roger Butlin Professor of Evolutionary Biology

School of Biology and Centre for Biodiversity and Conservation The University of Leeds Leeds LS2 9JT U.K.

r.k.butlin@leeds.ac.uk www.biology.leeds.ac.uk Tel. +44/0 113 343 3090 FAX +44/0 113 343 2835

UMBCMaryland TeachingEvolBiol

Faculty Position in UMBC (Maryland) Biology Dept.:

The following broad search explicitly seeks to encourage response from evolutionary biologists (especially those whose research bridges with another 'traditional' area of life-science, such as development, biochemistry or neuroscience).

FACULTY POSITION, Tenure-track, Assistant Professor of Biological Sciences. The Department of Biological Sciences, University of Maryland Baltimore County (UMBC) is seeking a colleague who values being in an environment that includes scientists studying basic biological problems using a variety of molecular, cellular, biochemical, physiological, and evolutionary approaches. (www.umbc.edu/biosci). We will consider outstanding candidates in all areas of biology and are particularly interested in individuals whose research programs bridge existing strengths of the Department. The appointee will have a Ph.D. degree with postdoctoral experience, and will be expected to develop a creative, externally-funded, independent research program, and teach at the graduate and/or undergraduate levels. Salaries, start-up funds, and facilities are competitive. Applicants should submit a curriculum vitae, summary of current and future research interests, and have three letters of reference sent to: Faculty Search Committee, Department of Biological Sciences, UMBC, 1000 Hilltop Circle, Baltimore, MD 21250. Review of applications will begin November 3, 2003 and will continue until an appointment is made. UMBC is a Doctoral/Research University-Extensive (the top Carnegie Foundation classification) and an Affirmative Action/Equal Opportunity Employer.

freeland@umbc.edu

UManchester Bioinformatics

BIOINFORMATICS LECTURESHIP

The following position appears in todays issue of Nature advertising a bioinformatics lectureship (in the preferred area of Network Modelling/Systems Biology).

Individuals working in other areas of Bioinformatics are encouraged to apply. The person(s) hired will be based in the new Integrative Centre for Molecular Cell Biology (ICMCB) (http://www.msa.mmu.ac.uk/webcam/) which is near completion. We'd like to encourage both post-docs looking to establish their own groups or well-established researchers to apply. Note, this is one of five identified areas targeted for expansion. Further details and an application form can be obtained from the Universities website http://www.man.ac.uk/news/-vacancies/academic.html#816. For details of bioinformatics research in Manchester visit our website (http:/-/bioinf.man.ac.uk/research) and the website of our colleagues at UMIST (http://www.bi.umist.ac.uk/) with whom we will join with in 2004 in the Faculty of Life Sciences in the new University of Manchester.

######## University of Manchester Lectureship

School of Biological Sciences

Lectureships in Biological Sciences

To sustain and enhance our reputation as a centre of international research excellence, delivering first class undergraduate and postgraduate teaching, we invite high-quality applications for Lectureships within the thematic areas described below.

We seek individuals who have clearly-defined research goals, with the potential to develop a well funded internationally competitive research group.

We aim to make at least one appointment in each area. However, applications from outstanding candidates working in other areas of Biological Sciences will also be considered. For each area initial informal enquiries may be made to the named contact, or to the Dean of the School, Professor Maynard Case: rmcase@man.ac.uk

Network Modelling/Systems Biology Ref: 820/03

Major themes: Exploiting postgenomics research by taking global approaches to address biological problems. In particular, network modelling and systems biological approaches that map onto areas of current research strength.

Professor Andy Sharrocks: a.d.sharrocks@man.ac.uk

This is a particularly exciting period in the School's development. In October 2004, it will join with colleagues in the Departments of Biomolecular Sciences and Optics and Neurosciences at UMIST and others to form the Faculty of Life Sciences in the new University of Manchester.

The School offers a superb research environment with state-of-the-art facilities and unrivalled opportunities for collaboration that will be further enhanced following the merger with UMIST departments. We have an excellent reputation for teaching at all levels, both to bioscience students and to those studying medicine, dentistry, nursing and pharmacy. The salary for these posts will be in the range of Â£21,125 - Â£33,679 p.a. (under review) according to qualifications and experience. Exceptionally, appointment at Senior Lecturer level (Â£35,251 - Â£39,958 p.a. under review) may be considered.

Further particulars and an application form for all the above posts can be obtained from http://-www.man.ac.uk/news/vacancies or from the

Office of the Director of Personnel, The University of Manchester, Oxford Road, Manchester M13 9PL, Tel: +44 (0)161 275 2028, Fax: +44 (0)161 275 2471, Minicom (for the hearing impaired): +44 (0)161 275 7889, E-mail: personnel@man.ac.uk

Formal applications must be received by Personnel no later than 6th November 2003. Please quote relevant reference number.

http://www.biomed.man.ac.uk ######

– David Robertson, (E-MAIL: david.robertson@man.ac.uk) School of Biological Sciences, University of Manchester, 2.205 Stopford Building, Oxford Road, Manchester, M13 9PT, UK. TEL/FAX: +44 (0)161 275 5089/5082, http://-bioinf.man.ac.uk/˜robertson .

UManchester EvoDevo

Dear all,

Below is the text of an ad for a position in Development and Evolution at the University of Manchester, as it will appear in this week's issue of Nature. Please note the tight deadline for the application.

If you require any further information, I will be happy to help, or you may contact the persons mentioned in the ad.

Best wishes, Chris Klingenberg

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Lectureships in Biological Sciences School of Biological Sciences, University of Manchester

Development and Evolution: Ref (818/03)

Major themes: Mechanisms of pattern formation and morphogenesis; or developmental processes in an evolutionary context (invertebrate or vertebrate systems).

To sustain and enhance our reputation as a centre of international research excellence, delivering first class undergraduate and post-graduate teaching, we invite high-quality applications for Lectureships within any area of Evolution and Development.

We seek individuals who have clearly-defined research goals, with the potential to develop a well-funded internationally competitive research group.

The School will make at least one appointment in each of five identified areas targeted for expansion (see ad in 16 October Nature). However, applications from outstanding candidates working in other areas of Biological Sciences will also be considered. Initial informal enquiries may be made to Allen Moore (mailto:allen.j.moore@man.ac.uk), who will chair the search committee, or to the Dean of the School, Professor Maynard Case (mailto:rmcase@man.ac.uk).

This is a particularly exciting period in the Schools development. In October 2004 it will join with colleagues from several departments at UMIST to form the Faculty of Life Sciences in the new University of Manchester. The School offers unrivalled opportunities for collaboration that will be further enhanced following the merger with UMIST departments. We have an excellent reputation for teaching at all levels, both to bioscience students and to those studying medicine, dentistry, nursing and pharmacy. The salary for these posts will be in the range of £21,125 - £33,679 p.a. according to qualifications and experience. Exceptionally, appointment at Senior Lecturer level (£35,251-£39,958 p.a.) may be considered.

Further particulars and an application form can be obtained from http://www.man.ac.uk/news/vacancies or from the Office of the Director of Personnel, The University of Manchester, Oxford Road, Manchester M13 9PL. Tel: 0161 275 2028; Fax: 0161 275 2471; Minicom (for the hearing impaired): 0161 275 7889; mailto:personnel@man.ac.uk

Formal applications must be received by Personnel no later than 6th November 2003. Please quote relevant reference number.

Christian Peter Klingenberg School of Biological Sciences University of Manchester 3.614 Stopford Building Oxford Road Manchester M13 9PT United Kingdom

Telephone: +44 161 2753899 Fax: +44 161 2753938 E-mail: cpk@man.ac.uk Web: http://www.sbs.man.ac.uk/chrisk

Chris Klingenberg <cpk@man.ac.uk>

UMichigan EvolGeneticsGenomics 2

Evolutionary Genetics and Genomics University of Michigan

The Department of Ecology and Evolutionary Biology solicits applications for a tenure-track position as Assistant Professor in any area of evolutionary genetics or genomics. Teaching responsibilities will include courses in evolution, genetics, and/or the individual's area of special expertise. Along with several other new faculty members, the person hired will join a vigorous and growing program in evolutionary biology in a new, dynamic department (see http://www.eeb.lsa.umich.edu). Women and minorities are encouraged to apply. The University is responsive to the needs of dual career couples.

For further information, contact eebevolgen@umich.edu. To apply, please send your curriculum vitae, brief summaries of research plans and teaching interests, evidence of teaching excellence, and copies of representative publications, and arrange to have three letters of reference sent, to:

Chair, Evolutionary Genetics Search Committee Department of Ecology and Evolutionary Biology Kraus Natural Science Bldg, Room 2019E University of Michigan Ann Arbor, MI 48109-1048

Review of applications will begin 24 November 2003, pending budgetary approval. The University of Michigan is a nondiscriminatory, affirmative action employer.

UMichigan FungalEvolSyst

EVOLUTION AND SYSTEMATICS OF FUNGI UNIVERSITY OF MICHIGAN Professor/ Curator

The Department of Ecology and Evolutionary Biology and the University Herbarium solicit applications for a tenured faculty position in evolution and systematics of fungi to fill the Wehmeyer Chair. We seek accomplished individuals whose primary research interests are in aspects of fungal evolutionary biology such as molecular evolution and systematics, evolution of adaptations, or evolution of development. We are also interested in individuals who place fungal evolutionary processes in ecological contexts by collaborating with plant and microbial ecologists in the department. Teaching may include a course in fungal evolution or diversity, and contributions to courses in evolution, systematics, and the individual's research specialization. The candidate will also work with a Collections Coordinator and provide scholarly leadership in the use of the Herbarium's outstanding research collection of fungi and lichens. See http://www.eeb.lsa.umich.edu and http://www.eeb.lsa.umich.edu for more information. Women and minorities are encouraged to apply. The University is responsive to the needs of dual-career couples.

To apply, send a curriculum vitae, statements of research and teaching interests and experience, evidence of teaching excellence, copies of publications, and names and addresses of three references to:

Chair, Fungal Evolution and Systematics Search Committee Department of Ecology and Evolutionary Biology The University of Michigan Ann Arbor, MI 48109-1048

Review of applications will begin 24 November 2003. The University of Michigan is a nondiscriminatory, affirmative action employer.

Diarmaid Ó Foighil Associate Curator of Molluscs, Museum of Zoology Associate Professor, Department of Ecology and Evolutionary Biology The University of Michigan Ann Arbor, MI 48109-1079 USA E-Mail: diarmaid@umich.edu Phone: 734 647 2193 Fax: 734 763 4080 URL: http://www.ummz.lsa.umich.edu/-mollusks/people/diarmaid.html

UNebraska EvolBiol

MOLECULAR ECOLOGIST OR EVOLUTIONARY BIOLOGIST University of Nebraska.

The School of Biological Sciences invites applications for a tenure-track faculty position at the Assistant Professor level with expertise in using molecular techniques to investigate evolutionary and/or ecological questions with an emphasis in organismal biology.Candidates will be expected to develop a rigorous research program and assume teaching responsibilities in undergraduate courses in the areas of biological diversity and/or ecology and evolution, and at the graduate level in their area of expertise.A Ph.D. in the life sciences is required and post-doctoral experience is preferred.

To apply send a curriculum vita and copies of representative publications along with statement of research interests and teaching interests and philosophy.Also arrange for three letters of reference to be sent by January 1 to Jack Morris, School of Biological Sciences, University of Nebraska-Lincoln, 348 Manter Hall, Lincoln, NE 68588-0118.The position will remain open until a suitable candidate is selected.

UNL is committed to a pluralistic campus community through Affirmative Action and Equal Opportunity, and is responsive to the needs of dual career couples.We assure responsible accommodation under the Americans with Disabilities Act.For further information contact Jack Morris at 402-472-6676 for assistance.

tkortum@unlnotes.unl.edu tkortum@unlnotes.unl.edu

UNevadaReno AquaticEvolBiol

AQUATIC BIOLOGIST

The Department of Biology at the University of Nevada, Reno (UNR) invites applications for a tenure-track position (Assistant Professor) to begin July 2004. We seek an AQUATIC BIOLOGIST with interests in CONSERVATION BIOLOGY issues, preferably applicable to the Great Basin. A Ph.D. and postdoctoral experience are required, and applicants should have a strong record of research achievement. The successful candidate will be provided with a competitive start-up package and will be expected to establish a nationally recognized, extramurally funded research program. UNR has a strong, interactive group of faculty working in conservation biology, and Nevada offers excellent opportunities for research on ecologically sensitive species in aquatic environments. The University has outstanding core facilities for genomics, proteomics, and bioinformatics in addition to state-of-the-art facilities and expertise in GIS, stable isotope analysis, remote sensing, ecological modeling, and water resources sciences. Teaching responsibilities will include one undergraduate course per semester and teaching and mentoring graduate students. For more information: http://-www.unr.edu/biology/ and http://jobs.unr.edu. Applicants should send a CV with a complete list of publications, statements of research plans and teaching philosophy, and have three letters of recommendation sent to: Dr. David Zeh, Aquatic Biologist Search, Department of Biology/314, University of Nevada, Reno, NV 89557. Applications received by November 24, 2003 will receive full consideration. AA/EOE – David W. Zeh Associate Professor Department of Biology & Program in Ecology, Evolution & Conservation Biology University of Nevada Reno, NV 89557

Tel: (775) 784-1648 Fax: (775) 784-1302 email: zehd@unr.edu

USDA EvolPlantMolGenetics

RESEARCH, EDUCATION, AND ECONOMICS USDA - Agricultural Research Service

VACANCY ANNOUNCEMENT

NOTE: All application materials MUST be submitted to:

USDA, Agricultural Research Service Human Resources Division ATTN: Lisa J. Porter (ARS-D4W-0007) 5601 Sunnyside Avenue Beltsville, MD 20705-5106

FAX applications to: 301-504-1535 E-MAIL applications to: scirecruit@ars.usda.gov (If submitting applications via E-mail, be sure to mail or fax other required documentation such as college transcripts, SF-50, most recent performance appraisal, and/or DD-214/SF-15 separately and include the vacancy announcement number of the position.)

For informal inquiries, contact:

Nahla V. Bassil USDA/ARS, NCGR 33447 Peoria Road Corvallis, OR 97333

bassiln@science.oregonstate.edu Tel: (541) 738-4214 Fax: (541) 738-4205

Announcement Type: All Sources Position Title: Biological Science Technician (Plants) Series/Grade: GS-0404-5/6/7 Promotion Potential: GS-7 Salary: GS-5 $25.697.00-$33,402.00 GS-6 $28,644.00-$37,237.00 GS-7 $31,830.00-$41,380.00 Type of Appointment: TERM, NTE 2 Years (May be extended up to 4 years total) Location of Position: National Clonal Germplasm Repository, Corvallis, OR Announcement Number: ARS-D4W-0007 Opening Date: October 20, 2003 Closing Date: November 3, 2003 Area of Consideration: ALL US CITIZENS

APPLICATIONS WILL ALSO BE ACCEPTED FROM USDA SURPLUS AND FEDERAL DISPLACED EMPLOYEES IN THE COMMUTING AREA.

DUTIES: Incumbent will assist in one or more phases of the research process by performing a variety of technical duties mostly in a laboratory environment. From the greenhouse and field, collects and verifies plant samples and supporting records. Extracts DNA from a number of plant genera. Carries out a variety of techniques needed for marker development and DNA sequencing. Maintains, calibrates and modifies equipment and automated systems used for test and evaluation procedures. Maintains records and locates and compiles data and other information from various sources. Keeps detailed records of experimental data. Tabulates, statistically analyzes and summarizes data using personal computers and software packages. Maintains inventory of chemicals, prepares solutions and reagents for use in the laboratory, and safely disposes of waste material (both chemical and biological).

QUALIFICATIONS: Applicants must meet the following specialized experience or educational requirements: GS-5: 1 year of specialized experience equivalent to the GS-4 level in the Federal service OR successful completion of a full 4 year course of study leading to a bachelor's degree with a major or at least 24 semester hours in any combination of course such as biology, chemistry, statistics, entomology, animal husbandry, botany, physics, agriculture or mathematics. At least 6 of the 24 semester hours must be in genetics. GS-6: 1 year of specialized experience equivalent to the GS-5 level in the Federal service OR 6 months of graduate education directly related to the duties of the position. GS-7: 1 year of specialized experience equivalent to the GS-6 level in the Federal service OR 1 year of directly related graduate education.

Specialized experience is experience that has equipped the applicant with the following: 1. Knowledge of basic biology techniques including DNA extraction, nucleic acid electrophoresis, PCR. 2. Knowledge of molecular marker analysis techniques and statistical analysis of resulting data. 3. Skill in keeping exact and detailed records of data obtained from experiments in a laboratory environment. 4. Ability to operate personal computer, using word processing and spreadsheet programs, software packages in the data collection, analysis and presentation process.

YOUR EDUCATION AND EXPERIENCE WILL BE EVALUATED AGAINST THE KNOWLEDGE, SKILLS AND ABILITIES (KSAs) AS OUTLINED UNDER SPECIALIZED EXPERIENCE. A SPECIFIC RESPONSE TO THE REQUIREMENTS OUTLINED UNDER SPECIALIZED EXPERIENCE IS HIGHLY

RECOMMENDED TO ENSURE ADEQUATE CONSIDERATION IN THE EVALUATION PROCESS.

APPLICATION INFORMATION

HOW TO APPLY: Send a resume, Curriculum vitae, Optional Application for Federal Employment (OF-612), or SF-171, to the Contact address listed below. The following information is required to evaluate applicant qualifications and to determine if applicants meet legal requirements for Federal employment:

- Announcement number, title, and grade(s)

- Full name, mailing address (including zip code) and day and evening phone numbers (with area code)

- Social security number

- Identify country of citizenship (U.S. citizenship is required)

- Veterans' Preference (If applicable–see "Veterans' Preference" below for required forms and documentation)

- Highest Federal civilian grade held (if applicable)

- Current Federal employees must submit their most recent performance appraisal.

- Current Federal employees and reinstatement eligibles should submit an

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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

USDeptAgr EvolBiol

U.S. Department of Agriculture, Agricultural Research Service, Ames, Iowa, has an opening at the North Central Regional Plant Introduction Station for a two-year term (which may be extended an additional 2 years), full-time Biologist to provide professional support by curating germplasm collections of Echinacea, Hypericum and other medicinal and nutraceutical plants. Must have knowledge of the practices and procedures of plant genetic resource conservation and management, skill in organizing and recording experimental data in a computerized database, the ability to cultivate medicinal and nutraceutical plants and the ability to statistically analyze and interpret quantitative evaluation data. The applicant must also be able to apply horticultural and/or agronomic management practices to the maintenance of living plant collections for research or conservation. Salary is commensurate with experience (GS-9, $38,936 - $50,617 per annum). Must be U.S. Citizen. For information on application procedures, contact Janae Lentz, 515-663-7277, or Gloria Snipes, 301-504-1582, or obtain a copy of the vacancy announcement at www.ars.usda.gov <www.ars.usda.gov . Applications must be marked ARS-D3W-3479 and postmarked by October 20, 2003. The USDA is equal opportunity provider and employer.

Thanks for all your help, Mark

Mark P. Widrlechner, Ph.D. USDA-ARS Horticulturist North Central Regional Plant Introduction Station Iowa State University Ames, Iowa 50011-1170 USA phone: 515-294-3511 fax: 515-294-1903

visit our Station's homepage at: http://www.ars-grin.gov/ars/MidWest/Ames <http://www.ars-grin.gov/ars/MidWest/Ames>

"Widrlechner, Mark" <isumw@iastate.edu>

USFW DexterNM FishEvol

Job is posted at http://jobsearch.usajobs.opm.gov with application information.

Please contact Manuel Ulibarri at 505-734-5910 for additional information or questions.

VACANCY IDENTIFICATION NUMBER: DS181565 OPENING DATE: Oct 29, 2003 CLOSING DATE: Nov 11, 2003 POSITION: INERDISCIPLINARY, GS-0482/0440 -11 / 12 PROMOTION POTENTIAL: GS - 12 SALARY: $47,110.00 - $56,463.00 Annually THIS IS A Career/Career Conditional APPOINTMENT LOCATION(S): DEXTER, NM - 1 vacancy EMPLOYING AGENCY: U.S. FISH AND WILDLIFE SERVICE APPLICATIONS WILL BE ACCEPTED FROM: ALL U.S. CITIZENS

MAJOR DUTIES

Employee serves as the laboratory manager for a modern, independent, fully functional molecular and ecological genetics laboratory. Employee provides administrative oversight and technical direction for all studies carried out in the laboratory. Dexter is assigned the responsibility for holding, studying, and culturing numerous rare, threatened or endangered fish species of the American Southwest. Provides genetics information useful to professionals charged with establishing and maintaining artificial genetic refuge populations, production broodstocks, and progeny used in imperiled fish reintroduction, restoration, and recovery efforts. Employee supplies, equips, and maintains laboratory facilities and ensures proper instrument operation. The employee participates in the planning, design, and execution of applied research studies by selecting appropriate laboratory methodology to achieve experimental objectives. Employee selects, purchases, maintains and operates a variety of laboratory instruments used to perform tests, analyses, and other laboratory procedures. Employee implements and enforces a strong laboratory safety and hazardous waste disposal program. Research focus is on genetic identification and characterization of target and related species including development of population genetic profiles useful in determining population genetic status and trends necessary to establish recovery goals.

Connie Keeler-Foster Fishery Biologist (Genetics) Molecular Ecology Program Dexter National Fish Hatchery and Technology Center P.O.B. 219, 7116 Hatchery Rd. Dexter, N. M. 88230 505-734-5910 fax 505-734-6130 "I've lost all patience with the search for peace of mind" Alice in Chains

USheffield Evol

LECTURER/SENIOR LECTURER/ READER (3 POSTS)

The following advert appeared in Nature several weeks ago, so apologies for the short notice on this list. The Department will consider candidates in a wide range of areas, including both those that would complement current strengths and those that are not currently represented within the Department. A non-exclusive list of examples of areas of potential interest, unconstrained with respect to study taxa, would include: evolutionary genetics and molecular ecology, quantitative genetics, evodevo, molecular evolution, behavioural genetics, conservation biology, ecophysiology, and theoretical and mathematical biology. The department has just been extensively refurbished and re-equipped with excellent molecular laboratories and controlled environment facilities.

UNIVERSITY OF SHEFFIELD DEPARTMENT OF ANIMAL & PLANT SCIENCES LECTURER/SENIOR LECTURER/ READER (3 POSTS) UKP 22,191 - 39,958 pa

The Department has an outstanding international reputation for research (5* RAE 2001) and teaching (QAA 24/24) and seeks to build further on this base through further appointments of high calibre staff. The appointees will join one of three research groups: Molecular and Ecological Physiology; Environment and Biodiversity; and Evolution and Behaviour. Strategic development areas are highlighted in the further particulars (see also: www.sheffield.ac.uk/aps) but candidates with other specialisations are strongly encouraged to apply. Closing date: 3 November 2003 (Ref. No: ADCR3031) Committed to equality through diversity For full post details/application pack visit: www.shef.ac.uk/jobs/ or email: jobs@sheffield.ac.uk/tel: 0114 222 1631 (24hr). Please quote Ref. No. in all enquiries

Informal enquiries can be addressed to the Head of Department, Professor Malcolm Press (M.C.Press@sheffield.ac.uk).

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USouthernCalifornia MarineEvolEcol

MARINE PHYSIOLOGICAL ECOLOGIST University of Southern California

The Marine Environmental Biology section of the Department of Biological Sciences seeks a tenure-track Assistant or Associate Professor working in the area of marine physiological ecology. This position will complement and tie together current departmental interests in organismal biology, physiology and marine microbial ecology with growing strength in population genetics, genomics, and bioinformatics. More information about the department is available at: http://www.usc.edu/schools/college/academics/-biological_sciences.html The successful candidate will have opportunities for research and teaching at the Wrigley Marine Science Center on Catalina Island. Please send a curriculum vitae, statements on research and teaching interests, and names of at least three references to: Marine Physiological Ecologist Search Committee, Department of Biological Sciences, University of Southern California, 3616 Trousdale Pkwy, AHF 107, Los Angeles CA 90089-0371. Review of applications will begin by 1 Dec 2004. USC is an EO/AA employer

Dennis Hedgecock Department of Biological Sciences University of Southern California 3616 Trousdale Pkwy, AHF 107 Los Angeles, CA 90089-0371

Phone: (213) 821-2091 FAX: (213) 740-8123

UTexasArlington Genetics

The Department of Biology at the University of Texas at Arlington seeks two geneticists/genomicists to contribute to an active research group in these areas. We are very interested in candidates whose research is at the interface of genetics or genomics, and evolution or ecology. Salaries and start-ups will be highly competitive. The Department offers both Master's and Ph.D. degrees, and the majority of our graduate students (about 70 in total) conduct research in evolution and ecology. The Department is very research-oriented, is well equipped for molecular work with an ongoing, major expansion in this area, has an extensive, newly constructed animal care facility, and offers ample laboratory space. UTA is the second-largest and fastest-growing component of the University of Texas system, with approximately 25,000 students, about 1400 of whom are undergraduate Biology majors.

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

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

TWO POSITIONS IN GENETICS/GENOMICS: The University of Texas at Arlington

The Department of Biology at The University of Texas at Arlington invites applications for two tenure-track positions at the rank of ASSISTANT PROFESSOR. We seek geneticists/genomicists who will contribute to our focus in these areas. Potential areas of interest include (but are not limited to) population, evolutionary, or ecological genetics/genomics; microbial genomics; quantitative or developmental genetics; and molecular evolution. Applicants must have an earned Ph.D. and a demonstrated record of research productivity commensurate with their experience. The successful candidates will be expected to establish vigorous, extramurally funded research programs and participate in both graduate and undergraduate education. The Department offers several degrees including a Ph.D. in quantitative biology. Located in the Dallas/Fort Worth metropolitan area, UTA is a fast-growing, comprehensive university that is the second largest in the University of Texas system. Hiring will be contingent on final budgetary approval and completion of a satisfactory criminal background investigation for security-sensitive positions. Additional information may be found at website: http//www.uta.edu/biology/. Applicants should submit a curriculum vitae; copies of up to five significant publications; statements of research and teaching interests and philosophy; and the names, e-mail addresses, and telephone numbers of four persons who can provide letters of reference. Review of completed applications will begin November 1, 2003, and will continue until the positions are filled. Send applications to: Dr. James V. Robinson, Chair, Genetics Search Committee, Department of Biology, University of Texas at Arlington, 501 South Nedderman Drive, Arlington, TX 76019-0498. UTA is an Equal Opportunity/Affirmative Action Employer.

Paul T. Chippindale Associate Professor Dept. Biology, University of Texas at Arlington Phone: (817) 272-2703, Email: paulc@uta.edu

UTexasAustin MolEvol

Molecular Evolution Assistant Professor Position at UT-Austin The Section of Integrative Biology of the University of Texas at Austin seeks applications for an Assistant Professor in the area of Molecular Evolution. The successful applicant will join a strong program in evolutionary biology, with particular strengths in population genetics, theoretical evolutionary biology, experimental evolution, behavioral evolution, systematics, and evolutionary developmental biology. Applicants may work on any organisms or model systems, and in any area of molecular evolution. Teaching duties will include a graduate course in Molecular Evolution. The successful candidate will also be eligible for affiliation with the Institute for Cellular and Molecular Biology, which provides state-of-the-art facilities and graduate program support (see http://www.icmb.utexas.edu). Applicants should send a curriculum vitae, a brief statement of research and teaching interests, and up to 5 reprints or preprints, and have at least 3 letters of recommendation sent to: Molecular Evolution Search, Section of Integrative Biology C0930, University of Texas, Austin, TX 78712-1023 USA. Electronic applications can be submitted in PDF format to: molevo@uts.cc.utexas.edu. Review of applications will begin 15 November 2003. For more detailed information see http://www.biosci.utexas.edu/jobs/ .UT-Austin is an EEO/AA employer.

Alisha Holloway <aholloway@mail.utexas.edu>

UWisconsinMadison EvolPopGenet 2

Assistant Professor in Evolution/Population Genetics

The Department of Zoology, University of Wisconsin-Madison, is pleased to announce a search for an assistant professor in Evolution/Population Genetics; below is the formal job announcement. We are particularly interested in attracting candidates with strong backgrounds in theoretical population and/or quantitative genetics, yet who also have broad perspectives in evolution. Although the position is in the Department of Zoology, the position is not taxonomically restricted, and current faculty within the Department study animals, plants, and microbes. We will begin reviewing applications on October 13, 2003 (absolute deadline Nov. 5).

** Job Announcement *************

Faculty Position, Evolution/Population Genetics

The Department of Zoology at the University of Wisconsin-Madison, seeks a tenure-track assistant professor who is committed to excellence in undergraduate and graduate teaching, scholarly research and service. Appointment begins August 2004. Ph.D. required by start of appointment. Area of specialization: evolution/population genetics (regardless of taxa). Teaching expectations include theoretical population genetics at the graduate level.

Candidates should send CV, research statement, 3 publications, and ask for 3 letters of reference sent to:

Evolution Search University of Wisconsin, Madison Department of Zoology 430 Lincoln Dr. 433 Birge Hall Madison, WI 53706-1794

An Equal Opportunity/Affirmative Action Employer. Women and minorities are encouraged to apply. Unless confidentiality is requested in writing, information regarding applicants must be released upon request. Finalists cannot be guaranteed confidentiality. –

Carol Eunmi Lee, Ph.D. Department of Zoology 430 Lincoln Drive, Birge Hall 420 University of Wisconsin Madison, WI 53706

Office: 608-262-2675 Lab: 608-262-9225 Fax: 608-265-6320 Email: carollee@wisc.edu http://www.wisc.edu/zoology/faculty/fac/Lee/Lee2.html http://www.wisc.edu/zoology/faculty/fac/Lee/Lee2.html

UWisconsinMadison Lecturer

Evolution Lecturer, Spring Semester 2004

The Department of Zoology, University of Wisconsin-Madison, invites candidates to apply for a temporary lecturer position to teach Evolutionary Biology for majors (Zoology 410) for the Spring Semester 2004 (Jan 20 - May 15). This is a 50% lecturer position.

Link to the formal posting: http://www.ohr.wisc.edu/pvl/pv_046074.html . Application Deadline: November 15

Please send a CV and cover letter referring to Position Vacancy Listing #46074 to:

Sharon Stern Instructional Program Manager Department of Zoology University of Wisconsin - Madison 145 Noland Hall, 250 N. Mills St. Madison, WI 53706

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phone: 608-262-2741 fax: 608-262-9083 email: sstern@mhub.zoology.wisc.edu –

Carol Eunmi Lee, Ph.D. Department of Zoology 430 Lincoln Drive, Birge Hall 420 University of Wisconsin Madison, WI 53706

Office: 608-262-2675 Lab: 608-262-9225 Fax: 608-265-6320 Email: carollee@wisc.edu http://www.wisc.edu/zoology/faculty/fac/Lee/Lee2.html

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UWisconsinMadison PopQuantGenet

Reminder: Although the absolute deadline for the tenure-track Population and/or Quantitative Genetics position at UW-Madison is November 5th, we have begun reviewing applicants.

Please submit all materials ASAP, if possible (such as references).

Candidates should send CV, research statement, 3 publications, and ask for 3 letters of reference sent to:

Evolution Search University of Wisconsin, Madison Department of Zoology 430 Lincoln Dr. 433 Birge Hall Madison, WI 53706-1794 – carollee@wisc.edu

WashingtonStateU MolPhylogenetics

Dear Colleague,

The School of Biological Sciences at Washington State University invites applications for a tenure-track position at the Assistant/Associate Professor level in animal molecular phylogenetics (see job ad below, which appeared in the 26 September issue of Science). As stated in the ad, we are particularly interested in individuals using modern molecular and computationally intensive approaches for both developing and applying molecular phylogenies to research problems in various areas of evolutionary biology.

Washington State University has numerous strengths in evolutionary biology and genetics, and is only eight miles from the University of Idaho, which also has strengths in these areas. Several active research and educational groups offer splendid opportunities for collaborative interactions, including the Initiative for Organismal Interactions (see http://www.wsu.edu/~mmorgan/ioi/initiativeinorganismalinteractions/index.html) , the Initiative for Bioinformatics and Evolutionary Studies (http://www.ibest.uidaho.edu/), and the Center for Reproductive Biology (http://www.crb.wsu.edu/). In addition, numerous research resources are also available, including core research facilities (e.g., a molecular genetics core facility including DNA sequencing, proteomics and microarray capabilities) and the Conner Museum of Natural History. Taken together, this position offers excellent research opportunities in a dynamic and energetic academic environment. We are also located near numerous natural and wilderness areas and there are abundant opportunities for outdoor recreation.

I am sending this emailto you because I thought that you would know of suitable candidates who might be interested in such a position. Please do pass this information on to such individuals, and do not hesitate to contact me if you would like additional information.

Sincerely,

Mike Webster

Advertisement:

The School of Biological Sciences at Washington State University invites applications for a tenure-track position at the Assistant/Associate Professor level in animal molecular phylogenetics. We are particularly interested in individuals applying modern molecular and computational phylogenetic approaches to problems in evolution, ecology, systematics, functional genomics, development, reproduction, mammalogy, or host/parasite interactions, though other areas of research are also of interest. This individual will also participate in undergraduate instruction and be responsible for a graduate course in molecular phylogenetic methods. The university?s Conner Museum of Natural History, Center for Reproductive Biology and Center for Integrated Biotechnology provide opportunities for involvement and interaction. The position requires a Ph.D. in the life sciences, and applicants with postdoctoral experience, a high potential for grant support, and teaching experience will be given preference. Submit curriculum vitae, three selected reprints, statements of research and teaching interests, and three letters of reference to: Michael Webster, Chair, Molecular Phylogenetics Search Committee, School of Biological Sciences, Washington State University, Pullman, WA 99164-4236. Inquiries can be sent to mwebster@wsu.edu. Review of applications will begin on December 1, 2003. WSU is an equal opportunity educator and employer. Members of protected groups are encouraged to apply.

Mike Webster School of Biological Sciences Washington State University PO Box 644236 Pullman, WA 99164-4236 Phone: 509-335-7180 FAX: 509-335-3184 Email: mwebster@wsu.edu

Other

ACLewis

Hi fellow evoldir members, I wonder if anyone out there knows and has contact info for Alcinda C. Lewis. She was at UC Boulder in 1989, but they don't know where she is now and I can't seem to find her via web searches. I have some questions for her about her past research and would really like to find her. I would greatly appreciate any help that anyone out there can give me.

Thanks a lot, Shanna

If you're not part of the solution, you're part of the precipitate. – Steven Wright

Donuts. Is there anything they can't do?! – Homer Simpson

Back off man. I'm a scientist. – Peter Venkman, Ghostbusters.

It's a mighty poor mind that can only think of one way to spell a word. – Andrew Jackson

Shanna Carney Department of Biology Colorado State

University Fort Collins, CO 80523-1878 970-491-1092 Fax: 970-491-0649 secarney@lamar.colostate.edu http://lamar.colostate.edu/˜secarney/

AFLP problem

Hi everyone,

I am doing some AFLP work on Aspelinium sp (Fern) using the ABI kit for AFLP. I am having problems of getting product in the selective amplification stage (that's what I think). In the beginning we thought there was a restriction problem with Acer but a southern test revealed otherwise. I did PCR and got excellent result which excluded the possibility of PCR inhibitor in my DNA samples. When I ran my restriction/ligation and preamplification product on agarose gel they looked fine but didn't get much product in the selective amplification round. I worked with apple DNA last year using the same kit and had excellent result. I included my apple sample as a control and they were fine as well this time again. I will really appreciate if someone can suggest any solution to come around this problem.

thanks sunita

Mrs Sunita Khatkar Mount albert Research Centre 120 Mt Albert Rd Private Bag 92169 Mt Albert Auckland NZ Ph 64 9 815 4200 ext 7136 Fax 64 9 815 4201 email skhatkar@hortresearch.co.nz

Sunita Khatkar <SKhatkar@hortresearch.co.nz>

Alytes

Does anybody have information about whether or not the French journal Alytes (herpetology)is still in business? Thanks, Moises Kaplan

moiseska@umich.edu

BalzanPrize to WHLi

I am usually the last person to know these things, but perhaps there is someone else out there in my same ill-informed position.

Congratulations are due to W.H.Li for his winning of the Balzan Prize. To quote Nature, the Balzan Prize is "behind only the Nobels in prestige".

It is wonderful that an evolutionary scientist wins such justified praise.

Brian Golding

CWoese wins Crafoord

Following up on Brian's well deserved congratulations for Wen-Hsiung Li, if you haven't heard, last Wednesday Carl Woese was presented with the Crafoord Prize (another one of the "almost Nobels") by the King of Sweden himself.

A symposium in Woese's honor was also presented, with lectures by Norm Pace, Gary Olsen, Karl Stetter, Claire Fraser, and Patrick Forterre. Abstracts are available at: http://www.kva.se/KVA_Root/eng/_news/detail.asp?NewsId=403

With Li and Woese being honored, 2003 really is a "annus mirabilis" for the recognition of molecular evolution.

Jonathan Badger

Centrifuge query

Dear all,

We are experiencing problem with Beckman-Coulter Allegra 21R which we bought about one year back. Has anybody faced any problem with this centrifuge model? Thanks in advance for your feedback with regard to it.

Cheers Alok

Alok Kumar Gupta Forest Genetics & Biotechnology Group Department of Biology, Life Sciences Centre Dalhousie University Halifax, NovaScotia, B3H4J1,Canada. Tel:(off) 1-902-494-2431 Fax:1-902-494-3736

Alok Gupta <akgupta@dal.ca>

Clonal reproduction software

I would like to find a software that can detect clonally related individuals in a population sample (of otherwise sexuals) and estimate their frequencies. Preferably usable for AFLP dominant markers, and with possibilities for adjusting for scoring errors. Can you help me?

I need the software for a study of populations Poa pratensis with both sexual and apomictic reproduction.

Thanks in advance

Thure

Thure P. Hauser, Ph.D., Senior Scientist Plant Research Department, PRD-309 RisøNational Laboratory DK-4000 Roskilde, Denmark Phone: +45 4677 4238 Fax: +45 46774160 http://www.risoe.dk/pbk/staff_uk/thha.htm

Developping primers

Dear all,

I'm actually developping specific microsatellites for the sucker redhorse (Moxostoma hubbsi). I just sequenced some microsatellites from the plamid clones and I'm searching for a good software to develop primers. Any suggestions?

Catherine Lippé (master student) Université Laval, Québec Catherine.Lippe@giroq.ulaval.ca

Developping primers answers

Thanks to all the members. I'm sending a resume of all the answers I received.

QUESTION:

Dear all,

I'm actually developping specific microsatellites for the sucker redhorse (Moxostoma hubbsi). I just sequenced some microsatellites from the plamid clones and I'm searching for a good software to develop primers. Any suggestions?

Catherine Lippé (master student) Université Laval, Québec Catherine.Lippe@giroq.ulaval.ca

ANSWERS :

I also worked on microsatellite development and designed primers for several species yet...I've been using software package LASERGENE - program called "DNA star". It's a program easy to work with and has many useful features (editing sequences, setting preferences for your primers, etc.). Well, I would recommend it, although I have never worked with any other programs, so I can't compare.

We use the online program Primer3 at http://www-genome.wi.mit.edu/cgi- bin/primer/primer3_www.cgi Im in the midst of doing the same thing for Rana boylii, and Ive found that the company Invitrogen has a good primer design site that is free: Oligoperfect Designer, which you can find at this web address - http://www.invitrogen.com/content.cfm?pageid=9716

I also use Integrated DNA Technologies which has a primer analyzer website that is free: OligoAnalyzer at http://biotools.idtdna.com/analyzer/ - If you have funds available though, I would recommend purchasing the software package Oligo which you can find info for at this address: http://www.oligo.net/. It is a bit pricey, and that is why Ive had to use the free web based packages.

I have used the web-based Primer3 to suggest primer sequences from clone sequences and Amplify to check these primers for primer-dimer problems etc. Primer3: http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi Amplify (mac only): http://engels.genetics.wisc.edu/amplify/ Two good programs to use in conjuntion with each other are Primer 3 and amplify. both are available on the web. Primer 3, helps select primers and is a web-based program. amplify run off a Mac and does virtual PCR to test for dimer formation.

I use Primer Designer v. 2.0 with great success for designing primers for my microsatellites. I was not happy with Primer 3 which is available online. When I analyzed primers I designed in Primer 3 primers using Primer 2 most of them had hairpins.

Primer 3 has done a great job picking my primers. I got a good product in 90% of the cases. http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi I know there exist some on-line primer-search programs, such as Primer3. You will find some more links if you go to http://www.hgmp.mrc.ac.uk/GenomeWeb/nuc-primer.html. Otherwise, I used a relatively old version of a DOS-based program called Oligo, which is good but not very user-friendly. Perhaps there are newer versions at http://www.oligo.net/ ... but I just found out it is not for free.

I have cut & pasted the following paragraphs from my PhD thesis. Hopefully they will offer you a possible avenue for exploration! The microsatellite repeat and the flanking region sequence was inputted into the GeneRunner program (available from http://www.generunner.com/). The microsatellite repeat was highlighted, and the PCR Primer Selection function was performed. The default values were initially kept, but changed in the following approach to reduce the suggested primers to below 150 pairs: * Increase minimum primer length to 20. * Increase lower primer melting temperature. * Reduce primer melting temperature difference. * Narrow the %GC range from 35-65 to 40-60, then 43-57. All or some of these steps were needed, depending on the amount of flanking sequence available in each individual microsatellite. The recommended primer pairs, were then assessed for intermolecular and intramolecular secondary structures such as hairpin loops, dimers and internal loops. Primers that displayed a high negative dG (>-9) value were discarded, the greater the negative value, the more stable the duplex formed by the primer.

I have used the following internet based program. I worked fine, I mostly used default options and got some decent primers, though always visually check the primers the program suggests and their suitability for your

— / —

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

Diversity simulation software

Dear all,

I am searching for a software program that can simulate the changes in the level of population genetic diversity (allelic diversity, heterozygostiy). This program should take into account the following variables: number of generations, population size and migration rate.

Any suggestions will be greatly appreciated.

Thank you very much!

Guy Knaepkens University of Antwerp (U.I.A.) Department of Biology Universiteitsplein 1 B-2610 Wilrijk Belgium email: guy.knaepkens@ua.ac.be

Diversity simulation software answers

Thank you to everyone who gave me information concerning software programs that can simulate the changes in the level of population genetic diversity (allelic diversity, heterozygostiy). As requested, I've compiled the advice I received:

1) See http://www.bio.sdsu.edu/pub/andy/ESP.html and for an example: Bohonak, A. J., N. Davies, F. X. Villablanca, and G. K. Roderick. 2001. Invasion genetics of New World medflies: testing alternative colonization scenarios. Biological Invasions 3: 103-111.

2) You could use the METAPOP program. It simulates the evolution of the genetic diversity in a metapopulation. You can specify the number of populations, population size, migration rate, mating system, number of loci etc. See e.g. Le Corre, Machon, Petit & Kremer. 1997. Colonization with long distance seed dispersal and genetic structure of maternally inherited genes in forest trees: a simulation study. Genet. Res. 69:117-125

3) Try VORTEX by Bob Lacy (http://pw1.netcom.com/ ˜ rlacy/vortex.html). It is a bit complex, but very powerful.

4) I've written a population genetics program which can do that, it is available at: http://www2.unil.ch/izea/softwares/easypop.html Depending on your exact needs, you might wish to use a slightly modified version. One option might be a version where you enter the seeds for the random number generator manually, so that you can replicate simulations with the same seeds but different number of generations. Alternatively you might wish to use a version which provides genotypes at different generations. Note that depending on the complexity of your problem it might also be solved analytically.

5) Here's something that might fit your need

(DGS-9D.EXE): http://www.ntnu.no/~jmork/jmork/software/softE.html 6) Try Populus (D. Alstad) and Popgen (J. Aspi & J. Lumme).

7) Try Geneloss (England, P.R. & Osler, G.H.R. (2001). GENELOSS: a computer program for simulating the effects of population bottlenecks on genetic diversity. Molecular Ecology Notes 1, 111-113.)

Kind regards,

Guy

Guy Knaepkens University of Antwerp (U.I.A.) Department of Biology Universiteitsplein 1 B-2610 Wilrijk Belgium email: guy.knaepkens@ua.ac.be

Drosophila StockCenter strains

The Tucson Drosophila Species Stock center is seeking inbred or isofemale strains of the following Drosophila species: D. ananassae, D. willistoni, D. erecta, D. sechellia, D. persimilis, D. mojavensis, D. virilis, D.grimshawi. A proposal to sequence the genomes of these species has been reviewed by the GRASPP panel. A decision by the council anticipated in the near future. In order to be well-positioned to move forward in the event of a favorable decision, and to involve the research community in the selection of strains for possible sequencing, the Stock Center is beginning to catalogue and maintain the candidate strains of these eight species.

Strains to be deposited with the TSC should include collection information (date, location, name of collector) and maintenance history (number of generations of sib-mating, pauses in inbreeding, etc), any available genetic data, and any references reporting the use of the strains.

Flies should be mailed to:

Species Sequencing Collection Tucson Stock Center Biological Sciences West (BSW) Room-606 University of Arizona 1041 E. Lowell St. Tucson, AZ 85721-0088 USA

Therese Markow Regents' Professor of Ecology and Evolutionary Biology Director, Tucson Stock Center

tmarkow@arl.arizona.edu

Lisa Andrus <lgandrus@email.arizona.edu>

Drosophila hematocytes

Dear All, I am interested in measuring immune response in Drosophila to exposure to E. coli (exposure to E. coli growing on medium in a vial NOT injection of E. coli into the fly). I would greatly appreciate any pointers to literature/protocols etc. dealing with how to quantify the number of hematocytes in Drosophila hemolymph, including (a) how to get a known quantity of hemolymph from larvae and adults, (b) how to identify hematocytes, or even types of hematocytes, (c) how to distinguish hematocytes from other cells that may come out, (d) buffers to be used.

Thanks a lot Amitabh reply to: ajoshi@jncasr.ac.in

Amitabh Joshi, Ph. D., F. A. Sc., F. N. A. Sc. Associate Professor Evolutionary Biology Laboratory Evolutionary & Organismal Biology Unit Jawaharlal Nehru Centre for Advanced Scientific Research Jakkur P.O. Bangalore 560 064, INDIA

Phone: (w) 91 80 8462750..57 (8 lines), ext. 2237(off), 2271(lab) (h) 91 80 3418066 Fax: 91 80 8566581, 91 80 8462766 URL: http://www.jncasr.ac.in/eobu/ajoshi-homepage.htm

Drosophila lines

New Drosophila isofemale lines from Baja, Mexico and Sonora, Mexico:

The Tucson Drosophila Species Stock Center has recently received new D. simulans isofemale lines from Mexico. There are fifty seven lines of D. simulans from CAMA, north of El Rosario, Baja, Mexico. These collections were made in August of 2003 by Luis Hurtado and Jessamie Rango. There are four lines of D. simulans from Bacabachi, 20 miles south of Navojoa, Sonora, Mexico. These collections were made in August of 2003 by Sergio Castrezana Isolines are $20/line for orders less than 20 lines. 20 to 50 lines is $10/line or $500 for +entire collection (anything over 50 lines) and will be available until the end of December. They can be ordered by contacting Lisa Andrus, manager, at lgandrus@u.arizona.edu

Lisa Andrus <lgandrus@email.arizona.edu>

EvolSocialBehaviour Journal

Dear Colleagues,

We are pleased to announce a new journal relevant to the evolution of social behaviour, interaction and communication. Details are available by following the web link at the end of the announcement below.

Best Regards,

C. L. Nehaniv Interaction Studies, Associate Editor

Interaction Studies: Social Behaviour and Communication in Biological and Artificial Systems

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The journal aims to advance knowledge in the growing and strongly interdisciplinary area of interaction studies in biological and artificial systems. It intends to act as a medium for dialogues across the boundaries of academic disciplines for research into social behaviour and communication that has traditionally been presented in separate specialist journals.

Understanding social behaviour and communication in biological and artificial systems involves important issues such as evolutionary, developmental and neurobiological aspects of social behaviour and communication; the embodied nature of interactions; origins and characteristics of social and narrative intelligence; perception, action and communication in the context of dynamic and social environments; social learning, adaptation and imitation; investigating social behaviour in human-machine interactions; the nature of empathic understanding, behaviour and intention reading; minimal requirements and systems exhibiting social behaviour; the role of cultural factors in shaping social behaviour and communication in biological or artificial societies. The journal welcomes papers that analyze social behaviour in humans and other animals as well as research into the design and synthesis of robotic, software, virtual and other artificial systems, including applications such as exploiting human-machine interactions for educational or therapeutic purposes. Papers can be experimental, computational, or theoretical studies and should highlight the contribution to knowledge of social behaviour and communication in biological and artificial systems.

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Genetic diversity answers

Dear all, Thanks to all the people who kindly answered and sent information about my question of how to compare genetic diversity values. It seems that a lot of people have the same question and they are interesting to know different opinions. So, I made a compilation of the answers I received. My specially acknowledgement to Dr. Mike Weale (University College London) who has just developed a program to the testing of h "test_h_diff" (http://www.ucl.ac.uk/tcga/software/index.html)

Marina

Question: I estimated the genetic diversity in four populations, and I want to know if the diversity values are significantly different. So, I need to use some statistical test. Does somebody have any idea about which test (and program) should I use? Thanks a lot, Marina

Answers: 1) I did a t-test using microsoft Excel to test statistical significance of difference at genetic diversity parameters between populations. The SAS program can also do a significance test for you.

2) To compare means, Nei (1987) suggests simply the-paired t-test. For microsats you could perhaps do it straight on but e.g. for allozymes it is good to consider arcsine transformation. (You might check our paper, where we experimentally looked at the sensitivity of the test.) Practically all basic statistical programs perform it. Reference: Tapio et al. (2003) Comparison of microsatellite and blood protein diversity in sheep: inconsistencies in fragmented breeds. Molecular Ecology 12, 2045-2056.

3) The basic technique consists in a Wilcoxon paired (by locus) test, but if you have four populations this will make 6 comparisons with a corrected level of significance of 0.008 (very conservative but necessary). Depending on the question you might pool some samples to compare two groups of interest. If not then you can do a Friedman analysis of variance (for three entries), I do not know of any software doing it but it is well described in 'Siegel & Castellan 1988, Non parametric statistics for the behavioural sciences, McGraw-Hill'.

4) This is a problem I have grappled with for some time. It is remarkably difficult to find a robust test for the difference in two h values for the following reasons. a) Permutation tests are not valid. These operate under the null hypothesis of no difference in haplotype frequencies, which is not the same as no difference in h values. b) Bootstrapping methods are biased. Under this method, you resample assuming that observed haplotype frequencies exactly equate to real population haplotype frequencies. This leads to a bias of n/(n-1) between the mean h of the bootstrap samples and the expected h of the real population. If h is close to 1, this bias difference, even for moderately large n (20<n<100), can be so large that the expected real h of the population falls outside of the 95% confidence interval on the bootstrapped h. c) The sampling distribution of h is skewed, especially for values close to 1. Thus, although unbiased formulae exist for the mean and variance of this distributution, Z-tests based on these formulae may fall foul of the departure from assumed Normality.

Currently, the approach I adopt employs both Method (2) and Method (3) above in a conservative double-testing procedure. In Method (2), samples from both populations are bootstrapped, a sampling distribution for the difference in h is obtained, and a 2-tailed P-value is calculated based on twice the smaller frequency of values lying to one side of zero. In Method (3), unbiased h's and their sampling variances are calculated from standard formulae (e.g. see Nei's book on Molecular Evolutionary Genetics), and a P-values for the difference in h is obtained via the standard Z-test. As a conservative measure, the larger of these two P-values is then used. The above approach is heuristic and does not guarantee a conservative Type I error rate, but at least it does something to address the issue.

Reference: Thomas MG et al (2002) Founding mothers of Jewish communities: Geographically separated Jewish groups were independently founded by very few female ancestors. Am. J. Hum. Gen. 70:1411-1420.

One day later: I've created a package for the testing of h differences based on the methods I discussed in the previous email. They should appear as a package called "test_h_diff" within the next 24 hours at the following web site: http://www.ucl.ac.uk/tcga/software/index.html 5) In regard to allelic richness, I refer you to the following paper: Leberg, PL (2002) Estimating allelic richness: effects of sample size and bottlenecks. Molecular Ecology 11:2445-2449. He has apparently written a SAS routine that you can use to perform statistical tests (provided that you have access to SAS).

6) If it's DNA sequences diversity that you want to test for significant

— / —

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

Genetic diversity answers 2

Hi everybody, It seems that it is an interesting point of analysis since I am still receiving answers. I really appreciate all your collaboration. Here I posted the last answers. Thanks a lot. Marina

1) I would recommend you the Arlequin software. You can downoad it from the http://lgb.unige.ch/arlequin/ Take a look at the Users manual, there is the basic theory for a lot of statistical methods for population differentiation and so.

2) I somehow missed your question. Just a quick comment: microsatellite mutation rates differ dramatically among loci-thus you may be better advised to make a paired test (e.g.: sign test). I attach you a manuscript in which we used this approach. Reference: Caracristi and Schoeltterer (2003) Genetic differentation between American and European Drosophila melanoganster Population could be attributed to admixture of African alleles. Mol. Biol. Evol. 20(5):792-799.

3) This is a late answer to your question on comparing genetic diversity values. But I did not see anything closely resembling this in your compilation of answers. Assume that each of P sampled population has its own theta_p through the exchange of m migrants in a population of Ne in an infinite island model. With Markov chain Monte Carlo methods it is possible to get an approximation to the posterior distribution of genetic diversity values (theta_p) for each one of P populations. You can declare two populations different if the posterior values overlap little (e.g. the 95% intervals do not overlap). I attach a preprint, where the method is applied to a sample of Drosophila ananassae populations. Reference: Vogl et al. (2003). Population subdivision and molecular sequence variation: Theory and analysis of Drosophila ananassae data. In press.

4) Arlequin is a good computer programme that enables you to carry out this sort of test. You can do an 'exact test of population differentiation' and there is good documentation with the programme. I am working on a Macintosh computer and I found that the 2001 patch for the programme doesn't seem to work, but the original version (2000) seems to work fine.

Marina S. Ascunce, Ph. D.

Department of Anthropology 1112 Turlington Hall P.O. Box 117305 University of Florida Gainesville, FL 32611-7305 Tel: 352 392 2253 extension: 247 FAX: 352 392 6929 e-mail: ascunce@anthro.ufl.edu

Marina Ascunce <ascunce@anthro.ufl.edu>

Mantel test answers

Hi everyone, Thank you very much to all the people that replied my question. I've received lots of mails, half of them with interesting ideas and literature and half of them asking me to send them the feedback. So here are the most interesting answers I got.

THE QUESTION—-> Fst/(1-Fst) or Fst for mantel test, and why??

THE MAIN ANSWERS:

The answer to your question on the Evoldir network regarding isolation by distance is in Rousset (1997, Genetics; see also his 2001 review in Handbook of statistical genetics, ed by Balding et al.). Using Fst / (1 Fst) is based on a formal population genetics model, under which you actually expect a relationship with distance. The relationship is expected to hold under conditions larger than those modelled by Rousset (1997). See a recent paper by Leblois et al. in MBE.

Fst is distributed between 0 and 1, whereas Fst/(1-Fst) potentially varies between 0 and infinity. When you are doing correlations, upper or lower bounds are a nuisance, and in this way you at least get rid of the former.

As for isolation by distance (ibd), my feeling is that the term is used in two ways, both loosely and strictly. In many recent papers, I see people loosely call ibd any correlation between genetic and geographic distance. In these cases, a Mantel test is Ok. Strictly speaking, though, (which means in the sense of Malècot-Morton and Kimura-Weiss), ibd is the product of genetic drift leading populations to diverge, and short-range gene flow leading them to converge genetically. Both in models where populations are continuously (Malècot-Morton) or discontinuously (Kimura-Weiss) distributed, that combination of drift and gene flow causes an asymptotic decline of genetic resemblance with distance. In other words, kinship between populations decreases up to a certain distance, and then it goes to zero.

In practice, the two different definitions do make a difference, because (1) under the former, but not under the latter any genetic gradient or cline (including those determined by long-range gene flow, range expansion and the like) are taken as evidence of ibd, and (2) over an area much greater than the dispersal distance of the species you are studying, drift and gene flow may generate local clines but not a general correlation between genetic and geographic distances.

I hope these comments did not increase the confusion. The relevant literature is wide, but among the oldies I would still recomment Cavalli-Sforza and Wijsman (1984) Annu. Rev. Ecol. Syst. 15:279-301, Kimura & Weiss (1964) Genetics 49:561-576 and Slatkin (1989) Genome 31:196-202.

I use Fst/(1-Fst) as recommended by Rousset's 1997 Genetics article. Whereas Fst goes to 1 as populations become more differentiated, Fst/(1-Fst) goes to infinity. So if you're regressing against geographic distance, which goes to infinity, it's appropriate to use Fst/(1-Fst). Also, something a lot of authors overlook is that you should specify whether you are considering your populations to be in 1-dimensional arrays or 2-d arrays. If they are essentially 1-dimensional (like along a river) you should regress against geographic distance, but if you consider your populations to be in 2-d arrays, you should use its log transform. Rousset covers this as well- that and Slatkin's 1993 (Evolution) and 1985 (Ann Rev Ecol Syst) articles have been the most helpful to me.

A variety of measures have been used on the "Y" and "X" axis of IBD plots. For examples, see:

Slatkin, M. 1993. Isolation by distance in equilibrium and non-equilibrium populations. Evolution 47: 264-79.

Rousset, F. 1997. Genetic differentiation and estimation of gene flow from F-statistics under isolation by distance. Genetics 145: 1219-28.

Hutchinson, D.W. and A.R. Templeton. 1999. Correlation of pairwise genetic and geographic distance measures: inferring the relative influences of gene flow and drift on the distribution of genetic variability. Evolution 53: 1898-914.

Even the geographic distance axis is log-transformed in some cases and not others.

I suggest that you examine scatterplots and try a variety of metrics, log-transformed or not. If you are interested in the IBD slope, then the most important consideration is that the plot meets the standard assumptions of regression (the relationship is linear, residuals are not skewed, etc.)

See http://www.bio.sdsu.edu/pub/andy/IBD.html for some software to help with this.

Thanks again folks!

Sandra Duran

PhD student Facultat de Biologia. Dept. Biologia Animal, Invertebrats. Av. Diagonal, 645. 08028 Barcelona CATALUNYA

Phone: +0034 934021441 Fax: +0034 934035740 e-mail: sandra@porthos.bio.ub.es

—–Original Message—–

Hi there,

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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

Mantel test question

Hello to everyone on the Evoldir list,

I have a question for anyone who has used a Mantel test in the past. I am comparing genetic and physical distance, and had previously analysed the relationship with a simple correlation. It has been suggested that I use a Mantel test as a control for the pseudoreplication issues that come from using multiple pairwise comparisons. The problem I've run into is that of missing data. My data forms a 8x8 semimatrix - but because of a variety of reasons, approximately 40% of the matrix is just empty cells. All of the programs I have found that calculate Mantel tests don't talk about how to deal with missing data.

Have any of you encountered this problem before? I suppose I could just fill in the cells with the average for the dataset, but I'm hesitant to do that with such a large proportion of missing data.

Thanking you all in advance, Kelly

Kelly Stiver Graduate Student Department of Psychology McMaster University stiverka@mcmaster.ca

Mantel test question answers

Thank you to everyone who provided help with my problem of how to calculate a Mantel test when you have empty cells in the matrices. As requested, I've compiled the advice I received:

Recommendations:

“I used Mantel test and bootstrap analysis (matrix reshuffling), but I did not have to deal with missing cells.”

PASSAGE: “The program PASSAGE is available for free download at http://lsweb.la.asu.edu/rosenberg/Passage/ , where you can find contact information for the author, Dr. Michael S. Rosenberg. He may be able to address the issue of missing data if the user's manual does not.”

EXCEL add-in: “The PopTools add-in for Excel will also do Mantel's test, is available for free download at www.cse.csiro.au/poptools, and is written by Greg Hood. If the help menu isn't helpful regarding missing data, you might give the author an email at poptools.cse.csiro.au or at g.hood@cgiar.org”

GenAlEx: “The program i find easiest to use for PCA, AMOVAs, genetic distances and other simple population genetic work is GenAlEx (Genetic Analysis in Excel). It free to download: www.anu.edu.au/BoZo/GenAlEx and has a mantel test function.”

ECOSIM: “Maybe an interesting way to go is to download a program called ECOSIM (http://homepages.together.net/ ˜ gentsmin/ecosim.htm), transform your matrices in vectors (as if they were regular variables), run a regression analysis and look at the correlation coefficients tab. This program will perform a random permutation of your data (like a Mantel program would), but it will not care whether there are empty cells in the matrices (provided that both matrices have the same number of non-missing cells).”

NTSYS: “try the Programm NTSYS. NTSYS can handle missing data during matrix comparison. Maybe this can help. You can put a certain value (e.g. 9999) as a code for missing data. Also with NTSYS it is possible to do normalization as well as permutations”

“The Mantel test in NTSYSpc (available from Exeter Software) allows missing values.”

“I had some missing data, but nowhere near 40% as you say you have. I used a software package called NTSYS that was designed by one of my professors, Dr. F. James Rohlf at SUNY Stony Brook. I seem to recall that the software allowed one to enter a value of ”??¿‘ to indicate an unknown quantity. One's also had the opportunity to modify the term that could be used to enter an unknown value.”

Cheers, Kelly

Kelly Stiver Graduate Student Department of Psychology McMaster University stiverka@mcmaster.ca

Micro isolation

Two common methods for microsatellite isolation from genomes low in microsatellite frequency (e.g. aves) are 1) selective hybridization using streptavidin-coated magnetic beads, and 2) Lambda Zap (Stratagene). Could I please get input from any researchers who have used either of these methods as to their effectiveness in isolating microsatellites, and any problems or delays encountered and how they were overcome? Please send correspondence to gregos@mcmaster.ca. A summary of all replies will follow.

Thanks,

-Sean Gregory

“S. Gregory” <gregos@mcmaster.ca>

MicroMutRateArabidopsis answers

Dear Evoldir members,

Thanks to all who responded to my inquiry about published microsat mutation rates for Arabidopsis. I did not find any published microsat mut rates for Arabidopsis but I did receive many references. Thanks again!

Sincerely, Tara Marriage

Arabidopsis microsatellite refs

Provan and Campanella 2003. Systematic Botany 28:578 Clauss et al 2002. Molecular Ecology 11:591

Vander Zwan et al 2000. Systematic Botany 25:47 Loridon et al 1998. Theoretical and Applied Genetics 97:591 Innan et al 1997. Genetics 146:1441 Kuittinen et al 1997. Heredity 79:144

Microsatellite evolution refs

Ellegren 2000. Trends in Genetics 16:551-558 Schlotterer 2000. Chromosoma 109:365-371

Miscellaneous microsat refs

Brohede et al 2002. Nucleic Acids Research 30:1997-2003 Steinberg et al 2002. Molecular Biology and Evolution 19:1198-1202

Tara N. Marriage Ph.D. Student Department of Ecology and Evolutionary Biology University of Kansas 1200 Sunnyside Ave. Lawrence, KS 66045

Lab phone: 785-864-3763 E-mail: tmarria@ku.edu

Micros MegaBACE

Dear all,

This mail for asking Evoldir members advice for genotyping on MegaBACE 1000 DNA Analysis System (Amersham Biosciences). We acquired several months ago this 48 capillaries DNA analysis system in our lab. We intend to do sequencing and genotyping (at the moment, microsatellites). For the latter, we would like to share protocols and experience with labs working on this equipment and alike markers. It would concern oligo synthetis, PCR mix, precipitation, run parameters, etc... It would greatly help us to benefit from your experience to reduce the long-time and energy-consuming optimisation step. If several labs are interested, we could create an e-mailing list of the megabace/microsatellites users.

Thanks a lot,

Sincerely

Réjane Streiff

–

Réjane Streiff

Centre de Biologie et Gestion des Populations (CBGP) INRA Campus International de Baillarguet CS 30 016 34 988 Montferrier sur Lez Cedex

http://www.ensam.inra.fr/CBGP

tél: 00 33 (0)4 99 62 33 39 fax : 00 33 (0)4 99 62 33 45 mail: streiff@ensam.inra.fr

Molecular Variance Parsimony

Hi,

I was wondering if anyone knows of a software that can create spanning networks based on molecular variance parsimony (Excoffier and Smouse 1994). I have used MINSPNET, but this creates a network using just one replicate of each haplotype and does not calculate any population statistic based on haplotype frequencies. Any help would be appreciated.

Thank you.

Vidya

– Vidya T.N.C. Research Student Centre for Ecological Sciences Indian Institute of Science Bangalore 560 012 INDIA

email: tncvidya@ces.iisc.ernet.in phone: 91-80-3600985, 2932506 (Extn.321) fax : 91-80-3601428

“Vidya T.N.C.” <tncvidya@ces.iisc.ernet.in>

Molecular markers

Dear all,

Please forgive me if these questions seem a bit basic. Our lab is interested in molecular markers for studying inter and intra specific relationships and gene mapping for wild and cultivated species of tomato. We are currently trying to use as many molecular marker systems as possible.

1) How important is it for any molecular marker, to be selectively neutral ? This is because a fairly recent marker technique known as IMP (Inter MITE Polymorphism) was described by Bureau et al (2001) using MITEs which have a preference for insertion near or within genes - which suggests (to me) that these markers will probably not be selectively neutral.

Will this affect the calculations for linkage and its application in gene mapping? This is because the calculations or linkage...etc seem to be based on allele frequencies obtained from the marker, and if most of the marker loci are not neutral, then how do we distinguish between "real" linkage and selective pressures influencing allele frequencies ?

I would really aprreciate any comments, suggestions, ideas. Thank you all so much,

SM Tam INRA Versailles-Grignon, FRANCE

tam@versailles.inra.fr

Need Newick files

Dear Everyone,

As part of my honours study which aims to improve "Visualisation Techniques for Phylogenies", I am currently testing out my prototype of new visualisation techniques and I would like to test it out on a range of phylogenetic trees. I have some Newick format files that I have dowloaded from the web etc, but it would be very useful if I had more, so as to test the techniques on a range of tree configurations and sizes.

If anyone would be willing to send me some Newick files (10 - 1000 leaf nodes) or direct me to where I can download more, it would be very much appreciated.

Thank you and best regards, Savrina

Honours Information Visualisation Group University of Sydney scarrizo@it.usyd.edu.au

Newick files available

If people want lots of phylogenies (and DNA and protein sequence alignments) that are REAL, as opposed to the easy route of simulating them, take a look at

www.ebi.ac.uk/goldman-srv/pandit You can browse around to pick things you want, or download the whole database (from http://www.ebi.ac.uk/goldman-srv/pandit/dload/Pandit7.6.gz) and parse out the lines you need (for phylogenies with branch lengths, this would be the APH and DPH fields).

Nick Goldman

On Sat, 11 Oct 2003 evoldir@evol.biology.mcmaster.ca wrote:

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Honours Information Visualisation Group University of Sydney scarrizo@it.usyd.edu.au

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

Outcrossing from AFLPs

Dear All, A student of mine is designing her thesis research to estimate outcrossing rate on an endangered plant species. Does she has to use codominant data? Is there any software available that can do a good job for estimating this parameter using dominant data, such as AFLP?

She plans to collect plant materials from the field and the seeds of each plant she collects. The seedlings from the seeds will be included in the analysis. So the "genotype" of the mother and offsprings will be known. In such analysis, how many mother plants and how many offspring from each mother are minimum? Any information and advise will be helpful! Sincerely, Jenny Xiang

jenny_xiang@ncsu.edu

Outcrossing from AFLPs answers

The standard program for estimating outrcrossing rates is Kermit Ritland's MLTR (which I have used quite extensively), however this only accomodates codominant data. Kermit has another program, MLDT, which is intended for dominant data (which I have not used). Both programs are apparently pretty identical, except for the data type. They can be downloaded from: http://genetics.forestry.ubc.ca/ritland/programs.html In terms of number of maternal plants, and number of seeds per plant: I have generally found that 20-30 maternal families, with 5-10 seeds per family will give resonable estimates. Usually, increasing the number of maternal families improves the outrcrossing rate estimate more than adding more seeds per maternal family. However, these numbers are for codominant (allozyme) data. dominant data may give less information per locus, so you may need to use more maternal plants and/or seeds.

Feel free to write back if you have any questions about using MLTR/MLDT

Hope this helps, Chris

Chris Herlihy Department of Biology Queen's University Kingston, ON, Canada K7L3N6 (613) 533-6000 x75125 herlihyc@biology.queensu.ca http://biology.queensu.ca/~herlihyc ————————

The software I made, called FaMoz, is able to make a paternity analysis with dominant markers, like AFLP, I send you in another mail the two corresponding papers. The software is freely available on internet at the following address: http://www.pierroton.inra.fr/genetics/labo/Software/Famoz/index.html I would advise that for a proper evaluation of individual outcrossing, at least 30 offspring per mother should be used.

I hope this helps ! Best regards

Sophie

Sophie Gerber gerber@pierroton.inra.fr INRA - UMR BIOGECO 69 route d'Arcachon tel 33 5 57 12 28 30 (FRANCE) 33612 Cestas cedex fax 33 5 57 12 23 81 http://www.pierroton.inra.fr/genetics/Perso/ Sophie/page_sophie_english.html ——————

We have used microsatellites, which are generally considered codominant, for estimating outcrossing rates and found that null alleles (just like a recessive allele in the analysis) really mess up the estimates of outcrossing rates (manuscript attached to this message). The Holsinger program does estimate outcrossing rates with dominant data, but the error margins are HUGE with dominant data! I strongly discourage you from dominant markers for estimating outcrossing rates. Isozymes give you much better estimates (as long as you can take enough tissue from your plants without causing damage).

Bye

Claus ——————

This paper is not exactly what you want, but should give you some good ideas.

Cheers, a.

@Article{milligan:1993b, author = "Milligan, Brook G. and McMurry, C. Kay", title = "Dominant vs.~codominant genetic markers in the estimation of male mating success", OPTcrossref = "", OPTkey = "", journal = mol_ecol, year = "1993", volume = "2", OPTnumber = "", pages = "275-283", OPTmonth = "", OPTnote = "", OPTannote = "", keywords = "paternity analysis, maximum likelihood, EM algorithm" }

– Allan Strand, Biology http://linum.cofc.edu College of Charleston Ph. (843) 953-9189 Charleston, SC 29424 Fax (843) 953-9199

—————————

I'm not sure whether Kermit Ritland's programs allow for dominant markers, but for an unsuccessful grant proposal a few years ago, I did a few simulations suggesting that with a relatively small number of polymorphic loci (say 30) you can distinguish selfed progeny from outcross progeny by scoring as outcrossed any offspring that do *not* match the maternal genotype at recessive loci.

I'm attaching the Word document that describes the simulations. You can ignore the likelihood/Bayesian stuff that follows, unless you're interested.

Kent

– Kent E. Holsinger kent@darwin.eeb.uconn.edu http://darwin.eeb.uconn.edu – Department of Ecology & Evolutionary Biology – University of Connecticut, U-3043 – Storrs, CT 06269-3043 —————————

It is not really software but a simplified version of how to calculate selfing rates (=1- outcrossing rates) with dominant data.

Have a look and maybe its usefull for your problem. Vrieling, K., P. Saumitou-Laprade, E. Meelis and J. T. Epplen. 1997. Multilocus DNA

fingerprints in the plant Cynoglossum officinale L. and their use in the estimation of

— / —

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

Phylogenetic analysis

Hello, I am trying to do a comparative analysis with one binary and one continuous variable. I have a complete phylogeny and would be really grateful if anyone could suggest a method and program that could do such an analysis or perhaps a reference of some one who has done something similar. I am having real difficulty finding anything.

My email address is j.c.pomfret@qmul.ac.uk Thanks

Joanne Pomfret <j.c.pomfret@qmul.ac.uk>

Phylogenetic analysis answers

I asked a question about how to deal with binary characteristics in comparative studies. Here are the responses I received which a lot of people have asked to be posted on the Evoldir website. Thanks to all those who wrote to me and were extremely helpful

FIRST I believe it must be difficult, but it really should depend on what do you want to correlate with what. What is your question will tell what you need to do.

I have done a very similar thing, even perhaps a little bit more complicated, but the truth is, the method for very complicated things I don't thing is there yet!!! In other words, people may be pseudoreplicating some still....

If you know CRUSH and BRUNCH in CAIC... then you know everything, if you don't know them, or don't know how to use them, then I can help you...

the manual for CAIC explains everything that you need to know, of course, if you have a background (not match) in basic statistics (regression analysis, use of residuals, and so forth).

The problem is to code the phylogeny... even if it is complete... you will need to let CAIC know what the phylogeny is, and that may be tedious...

NEXT

I just had the same problem that I wanted to compare genome size (continuous variable) with life history and breeding system (both coded as binary variables). I used the computer programs Continuous by Mark Pagel: http://sapc34.rdg.ac.uk/meade/Mark/- which is based on the generalised least squares method and CAIC by Andy Purvis: http://www.bio.ic.ac.uk/-evolve/software/caic/ which is a program using the independent contrast method. I strongly recommend comparing different approaches because both methods have their assumptions that cannot be easily met. Both authors were very helpful answering questions about the program.

NEXT

CAIC can do this (if I remember right you need the "BRUNCH" option (don't ask me why it is called this - it is in the manual). You can find CAIC at:

http://www.bio.ic.ac.uk/evolve/software/caic/-index.html NEXT I share your frustration. I too do phylogenetics (molecular cyt-b), and I have been looking into comparative analysis. I have not come across any papers that do comparative analysis at the species-level, most studies use larger datasets drawn from higher taxonomic levels. I assume you know of the program CAIC (Comparative Analysis using Independent Contrasts) (which has two components CardInput, and Phylogeny)? You can download those programs from the web (written by Andrew Rambaut, Oxford University).

NEXT

You should download CAIC (http://www.bio.ic.ac.uk/-evolve/software/caic/). Once you have coded your phylogeny and set up your data files in the appropriate way, you then perform the analysis using the BRUNCH procedure for dichotomous variables. Let me know if you need any more help.

NEXT

Just wanted to point out that you could do this in COMPARE (compare.bio.indiana.edu) using several different methods.

NEXT

You should download CAIC (http://www.bio.ic.ac.uk/-evolve/software/caic/). Once you have coded your phylogeny and set up your data files in the appropriate way, you then perform the analysis using the BRUNCH procedure for dichotomous variables. Let me know if you need any more help.

NEXT

You may have already heard of these programs and found them unsuitable but have you looked into CAIC (available at http://www.bio.ic.ac.uk/evolve/-

software/caic/) or Continuous (available at http://www.bio.ic.ac.uk/evolve/software/caic/). I believe Continuous accepts binary data but I've never used it. Both are available free on the web.

NEXT

You can find PASSAGE, an excellent Windows-based program to do the Mantel tests you described at the following link.

NEXT It depends on whether your dependent variable is continuous or binary. If your dependent variable is continuous (and I assume normally distributed), you can use generalized least squares (e.g. Martins and Hansen 1997) (or equivalently, independent contrasts [Felsenstein 1985]). If your dependent variable is binary (ie binomially distributed), you could use the Generalized Estimating Equation approach (Paradis and Claude 2002). If you have a big phylogeny (> 40 species), you could also look at using the phylogenetic mixed model approach of Lynch (1991). These methods generally assume a brownian motion model of evolution. It is relatively easy to do all these things in R (http://www.r-project.org). email me if you need any more help.

NEXT

— / —

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

Protein alignment

I am trying to find an easy to use protein alignment program that will output the alignment with a seq. I chose as the "consensus" and show similar proteins as a "-" (as in most publications) If anyone has found a program that does this could you please send me the name or website?

Thanks! Kelly East Carolina University kej1216@mail.ecu.edu

"Jones, Kelly Elizabeth" <KEJ1216@MAIL.ECU.EDU>

RAPD software

Dear All.

We are working on population genetics of different endemic plants in Canary Islands. (Diploid species).

We have applied allozymes, and we are now interested in applying RAPD techniques to analyse spatial autocorrelation, genetic differentiation interpopulations (measuring Fst or Genetic distances) and any other index to analyse the genetic relationships between populations such as Dendrograms (UPGMA, NJ), Principal Component Analysis and any other.

Could someone help us about which software we can use? One point: we have missing data.

Thank you very much

Sincerely

Dr. Pedro Sosa Henríquez Catedrático de Botánica Departamento de Biología Universidad de Las Palmas de Gran Canaria Campus Universitario de Tafira 35017 Las Palmas Canary Islands Spain TF: +34 928.45.44.67; Fax: +34 928.45.29.22 Movil 669.82.82.04

RAPD software 2

SORRY, I FORGOT TO INCLUDE MY E-MAIL

psosa@dbio.ulpgc.es

Dear All.

We are working on population genetics of different endemic plants in Canary Islands. (Diploid species).

We have applied allozymes, and we are now interested in applying RAPD techniques to analyse spatial autocorrelation, genetic differentiation interpopulations (measuring Fst or Genetic distances) and any other index to analyse the genetic relationships between populations such as Dendrograms (UPGMA, NJ), Principal Component Analysis and any other.

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Dr. Pedro Sosa Henríquez Catedrático de Botánica Departamento de Biología Universidad de Las Palmas de Gran Canaria Campus Universitario de Tafira 35017 Las Palmas TF: +34.928.45.44.67; Fax: +34.928.45.29.22 psosa@dbio.ulpgc.es

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Relatedness software answers

Dear all,

You can find below the (large) compilation of the answers we receive about

our question concerning familial structure investigation. We hope they will interest other Evoldir members. Thanks for all who responded. Best regards.

Etienne & Claire

Question: Are you aware of any software running on PCR platform that would establish

parentage relationship between individuals and their putative breeder populations. More in details, we have different breeder populations, and we

would like to test whether there exist family structures in some progenies.

Answers:

* Review: There is a review of the subject by M. Blouin (in press in TREE) that you might find useful that you can download from his website at <http://oregonstate.edu/%7Eblouinm/index.htm>http://oregonstate.edu/ ~ blouinm /index.htm. Scroll down to "Representative Publications" at the bottom.

There is also an interesting paper called : A comparison of microsatellite-based pairwise relatedness estimators (Van De Casteele et al. 2001, Mol Ecol, 10 : 1539-1549)

* Useful websites: You can find lot of packages by going to the Rockefeller university linkage

analysis web site: <http://linkage.rockefeller.edu/soft/list.html>http://linkage.rockefeller.ed u/soft/list.html

Another webpage compile lot of interesting software references: <http://www.public.iastate.edu/%7Echkuo/software/useful.html>http://www.publ ic.iastate.edu/~chkuo/software/useful.html

1/ Relatedness Relatedness & Kinship (for Mac only) Relatedness is very interesting software because 1) it allows to explore subgroups and 2) you can use for relatedness calculation either own alleles

frequencies of the studied (sub-)population or other imposed alleles frequencies of for example complete population... <http://www.gsoftnet.us/GSoft.html>http://www.gsoftnet.us/GSoft.html Identix 1.1 (for PC) You can try ≪ Identix ≫, developped for PC (Win98, 2K, XP) by K. Belkhir, V. Castric and F. Bonhomme: <http://www.univ-montp2.fr/%7Egenetix/#programmes>http://www.univ-montp2.fr/ ~genetix/#programmes

The ≪ paper ≫ is there: <http://www.univ-montp2.fr/%7Egenetix/identix_ms.pdf>http://www.univ-montp2 .fr/~genetix/identix_ms.pdf

You can download the software here: <ftp://162.38.181.25/pub/identix.zip>ftp://162.38.181.25/pub/ident This software permit to estimate relatedness with three methods : Queller & Goodnights (1989), Lynch & Ritlands (1999) and Identity. This program implements a resampling procedure (allelic or genotypic) in order to test the mean relatedness coefficient of population and its variance against the null hypothesis of panmixy. But this software can only take account of the own alleles frequencies of the studied sample (without possibility to put reference alleles frequencies to weight the calculation).

2/ Assignment to population

GeneClass This program permit the assigning individuals of unknown origin of population, based on the genetic distance between individuals and populations. You can download GeneClass from <http://www.ensam.inra.fr/URLB>http://www.ensam.inra.fr/URLB Arlequin

though I never tried it I know that Arlequin is capable of a population assignment test, which allows the assignment of an individual genotype to one of several possible population. <http://lgb.unige.ch/arlequin/>http://lgb.unige.ch/arlequin/

Struture 2.1

The program structure uses multi-locus genotype data to investigate population structure. Its uses include inferring the presence of distinct populations, assigning individuals to populations, studying hybrid zones, identifying migrants and admixed individuals, and estimating population allele frequencies in situations where many individuals are migrants or admixed. <http://pritch.bsd.uchicago.edu/>http://pritch.bsd.uchicago.edu/

3/ Parentage assignment

Cervus

Cervus (Tristan Marshall, Univ. of Edinburgh) is an interesting pedigree program which can provides an estimate of the relative likelihood of

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

Relatedness software answers 2

Dear EvolDir members,

Thanks very much to all of you that replied my request about PC-compatible softwares to analyse relatedness/kinship. As I was also asked by several of you, I summarize here the answers I received: Available PC-softwares for relatedness calculations: - FSTAT (http://www2.unil.ch/izea/softwares/fstat.html) - MaRQ (http://www.genetics.forestry.ubc.ca/ritland/programs.html) - IDENTIX (http://www.Univ-montp2.fr/ ˜ genetix/identix01.zip) - SPAGEDI (http://www.ulb.ac.be/sciences/lagev/spagedi.html) - DELRIOUS (http://www.zoo.utoronto.ca/stone/DELRIOUS/delrious.htm) - MER (http://www.zoo.cam.ac.uk/ioz/software.htm) Some of those softwares are available for UNIX/Linux, but the code is available so could be compiled under a PC platform. Here is also a recent and useful review on the subject : Blouin, M.S. DNA-based methods for pedigree reconstruction and kinship analysis in natural populations. TREE 18(10):503-511.

The softwares Cervus, Newpat, Famoz, Gimlet, Parente, Probmax, Papa and the following review (Jones, A.G. and Ardren, W.R. Methods of parentage analysis in natural populations Mol. Ecol. 12:2511-2523) are more directed to kinship and parentage analysis.

Thanks again, Regards

Eva

eva.bellemain@ujf-grenoble.fr Laboratoire d'Ecologie Alpine CMR UMR 5553 Université joseph Fourier BP53 38041 GRENOBLE Cedex 9

Bellemain Eva <Eva.Bellemain@ujf-grenoble.fr>

Relatedness software 2

Dear all,

Does anyone knows a PC software available for analysing kinship and relatedness from genetic data ? I only know the one from Queller & Goodnight (1989) that is available on Macintosh only.

Many thanks in advance for your help.

Eva Bellemain

– Laboratoire d'Ecologie Alpine CMR UMR 5553 Université joseph Fourier BP53 38041 GRENOBLE Cedex 9

Bellemain Eva <Eva.Bellemain@ujf-grenoble.fr>

Requesting used lab equip

Dear Colleagues,

I am in the process of setting up a lab at a small college in NW Florida. At this time my budget is very limited. My goal is to equip this lab to carry out research focused on phylogenetics and population genetics of various organisms. I am looking for sources to obtain some slightly outdated equipment such as a PCR machine, water bath, incubator, centrifuges and other equipment used for DNA isolation and analysis. I am also looking for some decent binocular microscopes, dissecting scopes, and other lab equipment. If anyone has such equipment, or knows of someone who does, this information would be greatly appreciated.

Thanks in advance and best regards, David X Williams, Ph.D.

"Williams, David" <williamsd@owcc.net>

Restriction problems

Dear all,

We use the Eco R I and Pst I enzymes and corresponding adaptors for restriction and ligation as a part of the AFLP procedure. But the problem is that PCR amplification with the corresponding Eco-A and Pst-A primers doesn't yield any product.

We tried many things, among which re-ordering all ingredients (adaptors, enzymes, buffers, primers et cetera) even from different companies (Roche and MBI Fermentas) which did not help at all.

Typically, the same procedure does work for other enzyme/adaptor combinations (e.g. Taq I, Mse I), which seems to exclude our DNA or the PCR being the problem. Moreover, we used DNA from several species (butterflies, plants), which made no difference.

Our most likely conclusion is that the problem must be incomplete restriction for unknown reasons, though we can not 100% exclude problems in the ligation.

Basically, we don't understand what's going on and are desperate to find a solution. Especially since we used Eco and Pst without problems in the past and have to repeat past AFLP runs. A search on the internet hinted into the direction of DNA methylation, but no more than that.

Has anyone experienced similar problems, and more importantly solved?

Any advice is greatly appreciated,

Peter Kuperus (Lab technician) Marc Stift (Ph. D. Student)

Institute for Biodiversity en Ecosystem Dynamics Experimental Plant Systematics Universiteit van Amsterdam P.O. Box 94062 1090 GB Amsterdam The Netherlands Visiting address: Kruislaan 318, Geb I, B003 Tel: +31 20 525 7856 Fax: +31 20 525 7832

stift@science.uva.nl

Science history

dear and reputable members of the evoldir,

you may not yet known about the great-content article freeman j dyson just

published in the latest issue of the new york review of books (he writes mostly in crippled two-word sentences so his prose is not necessarily enjoyable). i think we all should reflect about this tale.

http://www.nybooks.com/articles/16739 best to you all

marcos

ps. the first two paragraphs are below as enticement. ;)

Volume 50, Number 17 November 6, 2003 Review

Clockwork Science By Freeman J. Dyson

Today the name of Einstein is known to almost everybody, the name of Poincaré to almost nobody. A hundred years ago the opposite was true. Then, Albert Einstein was a newly appointed technical expert, third class, examining patent applications in the Swiss patent office in Bern, having failed in his efforts to find an academic job, while Henri Poincaré was one of the leading figures of the French scientific establishment, famous not only as a great scientist but as the author of popular books that were translated into many languages and kept the public informed about the dramatic progress of science during the early years of the twentieth century. A hundred years ago, Einstein and Poincaré were both working hard at one of the central problems of science, trying to find a correct theory to describe how fast particles behave in electric and magnetic fields. Poincaré had published several papers on the subject which Einstein may or may not have read. Einstein had published nothing.

Two years later, in 1905, Poincaré and Einstein simultaneously arrived at a solution to the problem. Poincaré presented a summary of his results to the French Academy of Sciences in Paris, and in the same month Einstein mailed his classic paper, "Electrodynamics of Moving Bodies," to the German journal Annalen der Physik. The two versions of the solution were in substance almost identical. Both were based on the principle of relativity, which says that the laws of nature are the same for a moving observer as they are for an observer standing still. Both agreed with the experimentally observed behavior of fast particles, and made the same predictions for the results of future experiments. How then did it happen that Einstein became world-famous as the discoverer of relativity, while Poincaré did not? Poincaré's lasting fame, such as it is, derives from his discoveries in other areas of science and not from his work on relativity.

Is the verdict of posterity, giving all the credit for relativity to Einstein and none to Poincaré, fair or unfair? I will return to these questions later. [...] questions later. [...]

Sequence saturation software

Dear all,

Does anyone knows a Macintosh software for (easily) computing saturation among DNA sequences, as Ti vs Tv distances plots?

Many thanks in advance.

Yves

Yves Desdevises, PhD Laboratoire Arago, Université Pierre et Marie Curie UMR CNRS 7628, BP 44 66651 Banyuls-sur-Mer Cedex, France http://www.obs-banyuls.fr Email: desdevises@obs-banyuls.fr

Sequence saturation software answers

Dear all,

Here are the answers to my query:

"Does anyone knows a Macintosh software for (easily) computing saturation among DNA sequences, as Ti vs Tv distances plots?"

I should have mention that the "manual" plotting of distances extracted from PAUP was the only method I knew, because it appears to be the typical method used. However, many people asked for a solution, then such a software is really needed !

Many thanks to all responders.

Answers:

- I suggest you to use TREE-PUZZLE that allows to test for the presence/absence of phylogenetic signal in your data set through a graphical approach. You can download it at the following web site http://www.tree-puzzle.de/ To my point of view it is much more efficient than scatter plot analysis to detect the saturation and consequence lost of phylogenetic signal

- I am wondering about the same thing. I was trying to find one software and asked a lot of people about it. But no one was aware of it. Finally I did my scatter plot using EXCEL, which was really painful as the data set was not very small.

- There is a way to get the numbers out of PAUP, but it is'nt straightforward to get the graph (you have to import a table into excel). It works, but is not the easy way.

- It's rather easily done in PAUP, actually. Just export distance matrices to a spreadsheet, first selecting only transitions and then selecting only transversions. You can then quite easily plot them.

- Does Li93 work in an OsX terminal window? It might, and if so, that would be great.

Yves Desdevises, PhD Laboratoire Arago, Université Pierre et Marie Curie UMR CNRS 7628, BP 44 66651 Banyuls-sur-Mer Cedex, France http://www.obs-banyuls.fr Email: desdevises@obs-banyuls.fr

Shrew samples

Dear Evoldir members,

I am looking for tissue samples (for DNA analysis) from the greater white-toothed shrew, Crocidura russula from the following countries: Morocco, Tunisia, Italy (Sardinia), Portugal, Spain, France, Germany and Poland. If you can help me by providing samples, contacts, or information on potential sampling localities, I would be very grateful to hear from you.

Many thanks in advance, best wishes,

Lori

Dr. Lori-Jayne Lawson Handley Département d'Ecologie et d'Evolution Bâtiment de Biologie Université de Lausanne 1015 Lausanne Switzerland

emails: Lori.Handley@ie-zea.unil.ch http://www.unil.ch/izea/people/lhandley.html Tel +41 (0)21 692 4186

Software BAPS

The new version BAPS 2.0 features a GUI and built-in graphics for Bayesian clustering on the basis of molecular marker data. The algorithm from earlier versions has been rewritten to speed up the computations, enhance the convergence, and reduce memory usage, which enables even the analysis of large-scale data sets. It is now possible to use simultaneously multiple MCMC chains which facilitate the investigation of convergence and better ensure that representative samples are generated from the posterior distribution. Data from DNA-pooling techniques can now also be used for clustering. For a typical data set, BAPS 2.0 runs at least 10 faster than the earlier versions. Output from the simulations is now made into a user friendly format and can be easily transferred to any Windows-based text editor. It is also possible to obtain model averaged FST and pairwise genetic distance estimates. BAPS 2.0 is available at: http://www.rni.helsinki.fi/-˜jic/bapspage.html

Jukka Corander Patrik Waldmann Mikko Sillanpää

Rolf Nevanlinna Institute P.O. Box 4 Fin-00014 University of Helsinki Finland

Patrik Waldmann <Patrik.Waldmann@rni.helsinki.fi>

Software GIMLET

Dear Evoldir members,

A new version of GIMLET (version 1.3.2.) is now available. This version is available free at http://pbil.univ-lyon1.fr/software/Gimlet/gimlet.htm The new version features several improvements on the previous version of GIMLET, including:

-.- New features for the estimation of population size with the rarefaction curve method (see pp 15-18 of the Guide):

* the equation used in Eggert et al. (2003 ; Mol Ecol 12:1389-1402) was added, * user can choose to print the results for the parameter b of the equations, *user can choose several distribution parameters (mean, standard deviation, median, minimim, maximum) to describe the distribution of the estimates of a and b parameters of the equations over all iterations, * user can choose the number of iterations when calling the script file in R, * R will try at least 5 times to estimate the asymptote for each iteration of difficult to fit* data sets before skipping the iteration and begin the following iteration calculation (*Hard to fit data sets are for example data where the samples are sampled only once. The data sets where samples are sampled several times each are analysed once and the result is printed, * user can print the observed and predicted rarefaction curves or the histogram of the number of capture per sample.

-.- Program can print more output files in the “Estimate Error Rates” module: file to test the bias in ADO in favor of short or long alleles, file with all detailed errors

All bugs reported by users are wellcome to enhance this new version (register and report to valiere@biomserv.univ-lyon1.fr).

* GIMLET: is a windows based program to analyse data from individual identification using microsatellite data. Different tasks are available: identification and pooling of genotypes, construction of consensus genotypes and estimation of error rates, estimation of allele frequencies and heterozygozities, calculation of probabilities of identity, estimation of population size from genotypes.

Valière N. GIMLET, a computer program for analysing genetic individual identification data. Molecular Ecology Notes (2002) 2:377-379.

GEMINI (windows based program that simulates population study using microsatellites genotyping and allows the determination of the best strategy to adopt, especially in the case where genotyping errors are introduced.) is always avalaible free at http://pbil.univ-lyon1.fr/software/Gemini/gemini.htm Valière, N., P. Berthier, D. Mouchiroud, and D. Pontier. GEMINI: software for testing the effects of genotyping errors and multitubes approach for individual identification. Molecular Ecology Notes (2002) 2:83-86.

Best Nathaniel Valière

——– Nathaniel Valière Laboratoire de Biométrie et Biologie Evolutive UMR 5558 43, boulevard du 11 novembre 1918 F69622 Villeurbane Cedex FRANCE valiere@biomserv.univ-lyon1.fr

Software Treefinder

Hi Folks!

A new TREEFINDER version is online at http://-www.treefinder.de . This time, the focus was on bootstrap analysis, graphic display and the extension of the programming interface.

Bootstrap analysis has now a convenient window dialog and an option to count and output the distinct topologies that are seen in the samples. They are assigned averaged edge lengths and come sorted by frequency.

The tree viewer can now display files containing thousands of trees. The rerooting utility is able to place a root node anywhere in a given tree and rearrangements are exportable into popular formats. A collapse function has been added.

There is an utility to check a sequence alignment for compositional equilibrium and another one to visualize the distribution of differences along the alignment.

Parts of the software have been rewritten in TL language and are included as source code that can be modified by the users. There are dozens of new TL functions covering tree manipulation, graphic display and numerical computations. In particular, there is now a large collection of statistical distributions together with their pdf's, cdf's, quantiles and random numbers.

Again, TREEFINDER is available on Windows, Linux and MacOS X.

Cheers to all, Gangolf Jobb

Statistical Power

Good afternoon,

My name is Claudia, I am phD student in Genetics from Brazil. We are trying to submit a work using Exact test differetiation. The referees are asking the power test to it, but we do not find anything about it.

Do you know a software or someone that can help us?

Thank you very much, Cláudia

Claudia Carvalho <claudiabenedettobr@yahoo.com.br>

Statistical Power answers

Hello,

I have sent a question to evoldir and some researches have answered me, thank you very much. Below are the question and some answers:

Good afternoon,

My name is Claudia, I am phD student in Genetics from Brazil. We are trying to submit a work using Exact test differetiation. The referees are asking the power test to it, but we do not find anything about it.

Do you know a software or someone that can help us?

Thank you very much, Cláudia

Jerome Goudet <Jerome.Goudet@ie-zea.unil.ch> wrote:

Hi Claudia,

I don't know of a software to do this. One way to go would be to simulate data under your hypothesis (i.e., population spacing, migration and mutation rate etc...) using e.g. easypop (http://www2.unil.ch/izea/-softwares/easypop.html) and to estimate the power given your sample size by running many replicates.

As for a reference for which test of differentiation is more powerful, see our paper in genetics (1996) that you can download from

http://www.unil.ch/popgen/research/reprints

Best wishes. Jerome Bob O'Hara

For k=2 and r=2 we can use the odds ratio as a statistic and give it confidence limits. For either one higher it's more difficult, but I think the way to get a statistic is to look at it as a contingency table. If there is no association, then a chi-squared test would not be significant (this is an approximation to the Raymond and Rousset test), and you can use the chi-squared value as a statistic.

I would suggest something slightly different. The chi-squared is an approximation to a log-linear model. So, what you could do is fit a log-linear model with Haplotypes and Populations as factors, and then you will get a residual term (actually the Haplotypes x Population interaction), which under the null hypothesis will have a chi-squared distribution. Even if the null hypothesis is false, it will have an approximately non-central chi-squared distribution, so you can get confidence limits for that.

In practice, what you do is fit a log-linear model with Haplotypes and Populations as factors, and get the residual deviance (call it D), and it's degrees of freedom (which should be (k-1)(r-1), call it df). Then, your point estimate is D, and the 95% confidence limits are C_l*D/df and C_u*D/df, where C_l and C_u are the 2.5% and 97.5% points of a chi-squared distribution with df degrees of freedom. You'll have to find both, because the distribution is not symmetrical.

To interpret these, note that under the null hypothesis the expected value of D/df is 1, so the further you are away from 1, the stronger the association. I don't have any great feel for how far away is from 1 you have to be to have an important effect, but you could do simulations and look at this statistic.

Things are getting complicated, aren't they? It's what happens when biologists try to do statistics. :-(

Bob

Olá Claudia, > >há um programa que se chama "Power and Precision" em que podes fazer a >Power analysis para a maioria dos testes, já confirmei e permite fazer >para o teste exacto. Este programa podes consegui-lo sem pagar para uma >utilizaao durante 30 dias. tentei enviar-te o programa em attachment, mas >é demasiado grande. podes fazer download da internet, se no google >procurares "Power and Precision". > >espero que ajude, >cristina santos >

Claudia,I dont know the exact test to which you refer, but a full proof, if time consuming way to generate the power for any test is to generate random data with the effect size and variation that you wish to determine the tests power to detect, and see if the test detects it. If you repeat this say 1000 times, then the percentage of times that you detect a difference is the power of the test.as a simple example, imagine you wanted to determine the power of a t test to detect a difference of 5 mm, between two groups of 10 fish. Imagine also that you have an estimate of the standard deviation of fish size. You can then get a computer program to generate two groups of random fish by drawing numbers at random from normal distributions, with the appropriate sd, but means that differ by 5 mm. You then do a t test to see if you can detect the difference. Repeat lots of times for an estimate of power. Obviously it would be better to get a computer program to automate the whole process. Excel is pretty good for simpler kinds of things. You will obviously need to come up with a simulation that models the assumptions of the test that y ou are interested in.However, depending on what the editor has asked you to do, you might find the attached paper useful in avoiding it. It basically points out that post hoc power analysis is a waste of time.Nick

Hello Claudia!

— / —

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

Textbook chapters

Dear All,

Thanks to all who responded to my last publication query. My paper is currently in press thanks to the list - cheers!

As you were so helpful last time, I have another publication question: I have written a review of the properties, extraction and storage of mtDNA. A reviewer has suggested it be used as a chapter in a textbook.

How does one go about doing this? I don't know any textbook writers!

I would greatly appreciate any advice,

Regards Tom

Dr Tom Pickerell Fisheries Division II Branch A (Aquaculture & Fish Health)

tel: 020 7270 8227 fax: 020 7270 8827

"Department for Environment, Food and Rural Affairs (Defra)

Tissues in acetone

Dear all, I have received some samples (insects) stored in acetone (for only a few weeks). Does anybody know whether DNA extraction for PCR reaction will be OK for such samples ? Do we need to make something special to make the DNA extraction+PCR successful ? Best wishes A.

Arnaud Estoup Centre de Biologie et de Gestion des Populations (CBGP) Campus International de Baillarguet CS 30 016 34988 Montferrier / Lez cedex

France email: estoup@ensam.inra.fr Fax: 33 (0) 4 99 62 33 45 Phone: 33 (0) 4 99 62 33 38 http://www.montpellier.inra.fr/CBGP

Tree program

Dear All,

I am looking for a program to produce rooted and unrooted trees. The program should (preferentially) be able to read a file containing X sequence names, and then be able to produce at least 10000 X-tipped binary trees (printed to a file).

It seems likely that someone must have written such a program – why reinvent the wheel....

All the best,

Lars – Dr Lars S Jermiin, Lecturer Acting Director, SUBIT Chair, Bioinformatics Degree Program Committee School of Biological Sciences Heydon-Laurence Building A08 University of Sydney New South Wales 2006, Australia

Phone +61 (02) 9351 3717 Fax +61 (02) 9351 4119 E-mail jermiin@bio.usyd.edu.au WWW page http://www.bio.usyd.edu.au/~jermiin

Vole tissue samples

Hi everyone,

I am working on the phylogeny of some European voles, mainly those of the Microtus (Terricola) species. I am currently seeking tissue samples such as pieces of liver, kidney, skin, ear and so on. Samples have to be stored in ethanol (95%). I am mostly interested by the species from Eastern Europe (Terricola daghestanicus, T. tatricus, T. nasarovi, T. schelkovnikovi, T. felteni, T. thomasi). I am also seeking tissue samples of the snow voles (Chionomys nivalis, C. roberti and C. gud) from various localities. Please contact me if you have this kind of samples.

Best regards, Christelle. –

Christelle TOUGARD Biogéosciences-Dijon, UMR CNRS 5561 Université de Bourgogne Centre des Sciences de la Terre 6 boulevard Gabriel 21000 Dijon FRANCE

Tél.: +33 (0)3 80 39 63 79 Fax.: +33 (0)3 80 39 63 87

E-mail : Christelle.Tougard@u-bourgogne.fr http://www.u-bourgogne.fr/BIOGEOSCIENCE/TougardCVT.html

ZebraFinch micros

Dear EvolDir members:

I am looking for microsatellite markers for analysis of parentage in zebra finches (Taeniopygia guttata). If you are currently developing these markers or can help me by providing contacts, I would be grateful to hear from you.

Many thanks in advance, Jennifer Gee

jgee@ucdavis.edu Dept. of Animal Science One Shields Avenue Davis, CA 95616 USA

PostDocs

BrownU PopGenet

POSTDOC IN POPULATION GENETICS, BROWN UNIVERSITY

A postdoctoral position in population genetics is available in Molly Przeworski's group at Brown University.

The successful candidate will develop statistical tools to infer the genomic location of a favorable substitution from patterns of polymorphism and divergence. The project will be pursued in close collaboration with members of Svante Pääbo's lab at the Max Planck Institute for Evolutionary Anthropology (Leipzig, Germany). It is anticipated that there will be the opportunity to apply the new methodology to a number of interesting candidate regions in the human genome.

A main focus of the group is the development of statistical tools to identify targets of natural selection. Other areas of interest include inferences about recombination rates from patterns of linkage disequilibrium and comparisons of humans and close relatives. For more information about the group and the Department at Brown University, see <http://email.eva.mpg.de/~przewors/-> and <http://www.brown.edu/Departments/EEB/-> . Applicants must have either a background in population genetics or come from a quantitative field such as statistics and have a strong interest in genetics. Knowledge of programming in C is essential. Informal inquiries as well as applications (including a CV, statement of research interests, copies of relevant publications and two letters of recommendation) should be emailed to Molly Przeworski at <przewors@eva.mpg.de>. The position is for two years, with the possibility of a one year extension; the intended start date is March 1 but is flexible.

Molly Przeworski

MPI for Evolutionary Anthropology Deutscher Platz 6 04103 Leipzig, Germany

as of 1/04: Dept. of Ecology and Evolutionary Biology Brown University Providence, RI 02912, USA

przewors@eva.mpg.de

INRATours ChemicalResistanceEvolution

We propose a post doctorate position at INRA in France. We are located in Tours (1 hour high speed train from Paris).The salary is 2000euros/months. Duration 18 months. Start on January 2004. English can be the working language on the lab. We (J. Cabaret and A. Silvestre) work on the resistance of nematodes to anthelmintics. The post doc should have experience in molecular biology and the aim is to find in one nematode Haemonchus contortus mutations associated with resistance to non-benzimidazoles anthelmintics, in comparison to what was detected in Caenorhabditis elegans. The deatails are given in the attached file: postdochaem.doc Best regards

cabaret <cabaret@tours.inra.fr>

IndianaU EvolRecomb

TWO POSTDOCTORAL POSITIONS STUDYING THE EVOLUTIONARY CAUSES AND CONSEQUENCES OF RECOMBINATION IN Daphnia Indiana University, Bloomington

Two postdoctoral positions are available to study one of the biggest sets of unsolved issues in biology: The Evolutionary Causes and Consequences of Recombination. Funded by an NSF FIBR grant, a multidisciplinary team of life scientists will exploit the powerful features of the model organism Daphnia, including the soon-to-be-completed complete genomic sequence. This system is ideally suited to our purpose, with populations exhibiting divergent levels of recombination, some populations having dispensed with sexual reproduction entirely, a well-understood ecology, accessible genetics, ease of manipulation in the field and laboratory, and a historical dimension for analysis in the form of ˜200-years of revivable genotypes from lake sediments. The team of 11 PIs at 6 institutions span the fields of cell biology, ecology, evolutionary genetics, genomics, parasitology, and mathematics. Both postdoctoral positions will be carried out at Indiana University, Bloomington.

Postdoctoral position 1: Evolutionary genetics/genomics The successful applicant will be involved in molecular evolutionary studies of the influence of recombination on the rate of mutation accumulation, the spread of mobile elements, and on adaptive potential. Skills in at least one, and ideally more, of the following areas are necessary: population genetics, genomics, and molecular biology. To apply, submit a CV, a description of your background and interests, and email contacts for three potential letters of recommendation to: Michael Lynch at mlynch@bio.indiana.edu or Department of Biology, Indiana University, 1001 E. 3rd St., Bloomington, IN 47405-3700.

Postdoctoral position 2: Functional genomics/genetics The successful applicant will study the genetic pathways controlling sexual and asexual reproduction. This will include functional genomic analyses using full transcriptome microarrays of meiotic egg production, meiotic sperm production, parthenogenetic egg production, and the pathway controlling meiotic versus ameiotic egg production. Skills in at least one, and ideally more, of the following areas are necessary: developmental genetics, molecular biology, and functional genomics. To apply, submit a CV, a description of your background and interests, and email contacts for three potential letters of recommendation to: Justen Andrews at jandrew@bio.indiana.edu or Center for Genomics and Bioinformatics, Indiana University, 1001 E. 3rd St., Bloomington, IN 47405-3700.

Both positions are open now and applications will be accepted until the positions are filled. Those received by November 22 will be assured full consideration. Indiana University is an affirmative action equal opportunity employer.

jandrew@bio.indiana.edu jandrew@bio.indiana.edu

Jena EvolGenomics

Postdoctoral Position in Evolutionary Genomics

A postdoctoral position is available immediately in the Department of Genetics and Evolution at the Max-Planck-Institute of Chemical Ecology in Jena, Germany.

This position is associated with a collaborative project to examine the role of positive selection in the evolution of recently duplicated and rapidly diverging genes in the model plant Arabidopsis thaliana and close relatives. We are currently focussing on genes potentially involved in reproductive isolation, reponse to biotic stress and genes of unknown function (orphan genes) that show signatures of selection.

The work will involve the identification of candidate genes by computational mining of genome databases; the isolation, sequencing and annotation BAC clones; the expression analysis of genes and tests of evolutionary hypotheses using phylogenetic reconstruction and tests of positive selection. A background is molecular biology and molecular evolution is expected. An interest in quantitative aspects of sequence analysis and proficiency in a programming language (our favorite is Python) is highly desired.

The Department of Genetics and Evolution of the Max-Planck-Institute of Chemical Ecology (http://www.ice.mpg.de/tmo/home/home_en.htm) provides an excellent work environment with a modern genomics and bioinformatics infrastructure and a critical mass of scientists working on the interface of evolutionary and functional genomics. The institute is international in character with English as the daily language.

The contact address for applications and further information is:

Dr. Karl Schmid

Department of Genetics and Evolution Max-Planck-Institute of Chemical Ecology Hans-Knöll-Str. 8 07745 Jena, Germany Tel: +49 3641 571465 Email: schmid@ice.mpg.de Internet: vanilla.ice.mpg.de/˜schmid

Karl Schmid <schmid@ice.mpg.de> Karl Schmid <schmid@ice.mpg.de>

MaxPlanck Ploen PopGenet

Max-Planck-Institute for Limnology Tropical Ecology Working Group

Population Genetics: Postdoctoral Research Position

A postdoctoral position in population genetics is available at the Tropical Ecology Working Group, Max-Planck-Institute for Limnology in Ploen, Germany.

The successful candidate will study the evolutionary history and biogeographical distribution of South-American insects (in particular Acrididae, Orthoptera) that are host-specific on aquatic macrophytes. The population structure of the host-plants will be studied in parallel by members of our group. The applicant should have a strong background in population genetics and good expertise in the development and use of microsatellite markers and data analysis of such markers. General interest in Neotropical insects and wetlands will be appreciated. Experience with Orthoptera and/or aquatic macrophytes are a plus.

The position is available for 2 years, the intended start is January 2004. For further information please contact Prof. Joachim Adis, E-mail: adis@mpil-ploen.mpg.de

Applications will be considered until fulfilled. Please submit applications with your CV, publication list, and names and addresses of two scientists who may be contacted to: Prof. Joachim Adis, Max-Planck-Institute for Limnologie, Working Group Tropical Ecology, August-Thienemann-Str. 2, 24306 Ploen, Germany.

Joachim Adis <adis@mpil-ploen.mpg.de>

Montpellier Butterflys

Post-Doctoral Position: Modelling reintroductions of Maculinea butterflies

The position is available beginning 1 September 2004, and is funded by the EEC as part of the research network “MacMan”. My team is developing population biological theory for the reintroduction of Maculinea butterflies in Europe.

The candidate will develop analytical and numerical simulation models with the objective of producing quantitative and qualitative guidelines for reintroduction strategies. These guidelines and the models upon which they are based will incorporate the large empirical knowledge we currently have on the ecology and evolutionary biology of these biological systems.

The successful candidate will have already established an excellent publication record in population biology and be able to conduct independent research.

The position will be based at the Universite de Montpellier, France.

Length of contract: 1 year

Contract to begin: 1 September 2004 or shortly thereafter. The candidate must have finished his/her PhD prior to appointment.

For more information see:

http://www.ufz.de/(en)/spb/bioz/macman/index.html

http://www.isem.univ-montp2.fr/GE/Parasites/-ParasiteHome.php

Please send full CV and two letters of recommendation to:

Dr. Michael Hochberg Genetique et Environnement ISEM - University of Montpellier II Place Eugene Bataillon, CC 065 34095 Montpellier Cedex 5 France e-mail: hochberg@isem.univ-montp2.fr

NOAA FishEvolution

Dear Colleague:

Please make this available to interested finishing graduate students and postdocs.

National Oceanic and Atmospheric Administration, Southwest Fisheries Science Center, Fisheries Resources Division is recruiting for a

National Research Council Postdoctoral Fellow in the area of Evolution and Quantitative Population Genetics of Fishes

Projects in the past have centered on the evolutionary biology, population structure, automated molecular id of larvae, and inferred larval dispersal patterns of the rockfishes (genus Sebastes). Presently we are entertaining research projects in rockfish genetics as well as new projects that would examine Clupeid fishes e.g. Pacific sardine and Lamnid sharks e.g. shortfin mako shark. Projects that seek to use genetic data in novel quantitative ways are particularly encouraged. The position is for one year with a strong possibility for extension.

The deadline for electronic submission of the application package is Nov. 1 to the NRC. Prior to application the candidate should make contact with Russ Vetter of the SWFSC to discuss common interests that would lead to the development of a full research proposal of mutual interest.

The SWFSC Genetics Laboratory is located on the campus of the Scripps Institution of Oceanography of the University of California San Diego. The Laboratory is fully equipped with a ABI 3100 capillary sequencer. The successful candidate is encouraged to interact with fellow scientists in the marine mammal and seaturtle genetics programs at the SWFSC, and with colleagues on the Scripps Institute of Oceanography campus and throughout the San Diego molecular genetics community.

publications such as:

Effects of oceanographic circulation on the gene flow, genetic structure, and phylogeography of the rosethorn rockfish (Sebases helvomaculatus) Can. J. Fish. Aquat. Sci. 56: 803-813

and

Population structure of copper rockfish (Sebastes caurinus) reflects postglacial colonization and contemporary patterns of larval dispersal. Can J. Fish. Aquat. Sci. 59: 1374-1384.

and

Effect of life history strategy, environmental variability, and overexploitation on the genetic diversity of pelagic fish populations Can. J. Fish Aquat. Sci. 56:1376-1388.

are typical of the types of studies undertaken by NRC Fellows.

Russ.Vetter@noaa.gov Russ.Vetter@noaa.gov

OregonStateU PopGenet

POSTDOC needed to conduct POPULATION GENETICS research in Michael Blouin's laboratory in the department of Zoology, Oregon State University. The primary focus will be statistical analysis of pedigree data from salmon populations. Possible projects include estimating effective population sizes, estimating quantitative genetic parameters, and studying selection on various traits, including hatchery vs. wild origin. Candidate will also supervise and assist a technician and graduate student conducting large-scale microsatellite genotyping. The primary qualification is a good background in population or quantitative genetics. Basic molecular skills (PCR, etc...) and experience with management of large databases are desirable.

To apply: send a letter of application, curriculum vitae or resume, and names, addresses, phone numbers and e-mail addresses of at least three references to: Michael Blouin, Dept. Zoology, Oregon State University, 3029 Cordley Hall, Corvallis, OR 97331-2914; Tel: 541-737-2362; Fax: 541-737-0501. blouinm@science.oregonstate.edu. http://oregonstate.edu/~blouinm/index.htm If you have questions about the position, feel free to call. Applicant screening to begin November 14. Position can begin as early as December 15. I'd like someone by January, if possible, but the start date is flexible. OSU is an Affirmative Action/Equal Opportunity Employer and has a policy of being responsive to the needs of dual career couples.

Michael Blouin Dept. Zoology, 3029 Cordley Hall Oregon State University Corvallis, OR 97331-2914 Tel. 541-737-2362 Fax. 541-737-0501 blouinm@science.oregonstate.edu

SanDiegoStateU ComparativeGenomics

Postdoctoral Position in Comparative Genomics/Molecular Phylogenetics of Squamate Reptiles at San Diego State University

An NSF-funded postdoctoral position is available in the Reeder lab at San Diego State University to help reconstruct squamate phylogeny using multiple nuclear protein-coding loci and new genomic databases. This position is funded for up to two years (starting salary $33K, plus benefits), and will be available starting in January of 2004. The project is an international, multi-institutional venture that will involve a phylogenetic analysis of 142 squamate taxa using ~50 nuclear protein-coding loci, analysis of morphological data from the same taxa and ~60 additional fossil taxa, and modeling studies addressing the combination of molecular, morphological, and paleontological data.

The postdoctoral position will involve computational screening of vertebrate genomes for potential loci, development and testing of primers and genes, and large-scale sequencing of some of these markers. Experience in molecular phylogenetics is expected and programming experience in at least one language is highly desirable. Experience in developing nuclear markers, working with genome databases, and/or computational biology are also highly desirable. Previous experience in herpetology is desired, but not required.

The Department of Biology at SDSU is a stimulating interactive environment with several labs interested in diverse aspects of phylogenetics and molecular evolution. In addition to the Reeder lab, the postdoctoral associate will work closely with Dr. Scott Kelley (also at SDSU) on the comparative genomic and computational biology aspects of the early phases of this project. The postdoctoral associate will also interact with the labs of Dr. John Wiens (SUNY-Stony Brook), Dr. Jack Sites (Brigham Young University) and Dr. Michael Lee (Univ. Adelaide), who are also involved in the collection of DNA sequence data for this project.

Review of applications will begin 20 November 2003 and continue until a suitable candidate is found. For additional information, contact Dr. Tod Reeder (619-594-7826; treeder@sunstroke.sdsu.edu). Applicants should send a curriculum vitae, a brief letter describing their prior research experience, current interests and goals, and should arrange to have two letters of reference sent to: SDSU Foundation Human Resource Dept 5250 Campanile Dr. San Diego, Ca. 92182 (Fax: 619-594-3763). Please specify Job # F03-233 on all materials (including letters of reference).

Tod W. Reeder Department of Biology and Center for Applied & Experimental Genomics San Diego State University San Diego, CA 92182-4614 Phone: 619-594-7826 Fax: 619-594-5676 Email: treeder@sunstroke.sdsu.edu Web page: http://www.bio.sdsu.edu/pub/tod/homepage.html "Tod W. Reeder" <treeder@sunstroke.sdsu.edu>

StonyBrook ExptPopGenet

POSTDOCTORAL POSITION - EXPERIMENTAL POPULATION GENETICS at STONY BROOK

An NIH-funded postdoctoral position is available to study the functional and population genetics of metabolic genes in Drosophila. melanogaster. The study involves diverse approaches to evaluate the quantitative genetics of metabolic energy pools, SNP studies of geographic variation, pathway flux analysis using NMR, basic DNA sequencing, and the kinetic characterization of enzyme variants. Knowledge of some of these methods is desirable but not required for consideration for the position.

The position is available immediately, but will remain open until the best candidate is found. Contact: Walt Eanes, Dept. of Ecology and Evolution, State University of New York, Stony Brook, NY 11794, E-mail: Walter@life.bio.sunysb.edu

weanes@notes.cc.sunysb.edu

UAlaskaFairbanks FungalEvol

Postdoc in Fungal Molecular Ecology

The Taylor lab in the Institute of Arctic Biology (http://mercury.bio.uaf.edu/iab/index.html) at the University of Alaska Fairbanks is seeking a postdoctoral associate to contribute to the NSF funded project "Coupling Diversity with Function - Metagenomics of Boreal Forest Fungi." This two year project is a collaboration among several faculty at UAF (Gary Laursen, Tom Marr, Roger Ruess, Lee Taylor) and the Whitehead Institute Center for Genomic Research (http://www-genome.wi.mit.edu/), and aims to carry out the most in-depth sequencing of fungal herbarium specimens and soil amplicons yet conducted. The focus of sampling is the Bonanza Creek LTER site (http://www.lter.uaf.edu/). The resulting comprehensive sequence database will be used for ongoing and future ecological studies. A completed Ph.D., a record of active research and publication, and experience in one or more of the following areas are essential: high-throughput molecular methods, RNA methods, fungal phylogenetics or population genetics, mycorrhizal ecology, and bioinformatics. UAF provides an exciting intellectual atmosphere and a rewarding place to live, especially for those who enjoy scenic wilderness, myriad outdoor activities and a friendly community. We have a strong ecosystem ecology group, and a growing group of molecular and evolutionary biology faculty. To submit an application, follow the instructions at: http://www.uaf.edu/uafhr/Employment/Job0903-383.html. For more information about the position, contact Lee Taylor at fft@uaf.edu or 907-474-6982. 907-474-6982.

UArizona BacterialEvol

POSTDOCTORAL RESEARCHER BACTERIAL GENOME EVOLUTION UNIVERSITY OF ARIZONA

A Postdoctoral Research position is available to study the processes of gene transfer and degradation on the evolution and organization of bacterial genomes. Potential projects include both bioinformatic and experimental studies. Applicants could have skills in molecular genetic or microbiological procedures, in bioinformatics or phylogenetic analysis, and/or in evolutionary or population genetics. Candidates trained in the fields of Evolutionary Biology, Microbiology, Computational Biology, Molecular Biology or Genetics are all encouraged to apply. The position is available immediately; however, the starting date is very flexible. Salary (in the range of $37K to $42K, plus benefits) will be commensurate with experience.

If you wish to apply, please send a curriculum vita and the names of at least two referees to:

Howard Ochman Department of Biochemistry and Molecular Biophysics 233 Life Sciences South University of Arizona Tucson, Arizona 85721 USA 520-626-8355 (phone) 520-621-3709 (fax) hochman@email.arizona.edu

UBarcelona Retrotransposons

Postdoc job: Retrotransposon evolutionary dynamics

A postdoctoral position is available to study Osvaldo retrotransposon expression in Drosophila buzzatii, D.koepferae and their hybrids. Work in our lab has shown that Osvaldo transposes at higher rate in hybrids than in parental species (Labrador et al. 1999, Mol.Biol.Evol. 16: 931-937) and that hybrids generate genetic instability (Naveira and Fontdevila 1985, Chromosoma 91: 87-94). The putative evolutionary implications of hybrid genetic instability, mainly in introgression and hybrid speciation, is going to be investigated in relation to hybrid retrotransposition increase. Combining genomic, molecular, cytogenetic, and population techniques we want to detect and interpret different expression levels of Osvaldo in species, populations, and hybrids. Applicants must have either a strong background in Drosophila molecular evolutionary genetics of transposable elements or a strong background in molecular genetics with a high interest in evolution and transposable elements. Applicants must contact immediately Dr. Antonio Fontdevila at antonio.fontdevila@uab.es sending a cover letter, a CV and the names, affiliation, address, e-mail address, and telephone number of two persons of reference. Deadline for submission is October 20, but immediate notice is encouraged. Salary range is 1270-2325 euros (before taxes) and duration is 18 months. The successful applicant is expected to start working on April 1, 2004, but, if justified, his/her incorporation can be delayed until October1, 2004.

Antonio Fontdevila Grup de Biologia Evolutiva Departament de Genetica i Microbiologia Edifici C Universitat Autonoma de Barcelona 08193 Bellaterra, Spain Phone: 34-93-5811083 Fax. 34-93-5812726 e-mail: antonio.fontdevila@uab.es

UCDavis Phylogeography

Postdocs at UC Davis. I seek one or two postdocs to work on an existing, ongoing NSF and CalFed project on comparative phylogeography of amphibians and reptiles in the central/eastern US (NSF) and California (CalFed). For both projects, I seek an individual with strong molecular skills, an interest in phylogenetics, population genetics, and/or phylogeography, and an interest in amphibians and reptiles. I am particular interested in individuals who are interested in helping to develop new tools (including developing multilocus SNP libraries) and new analytical approaches to solving problems in phylogeographic analysis. UC Davis has great depth in most aspects of evolution and ecology, and there are opportunities to collaborate with individuals within and outside of our laboratory on related projects in micro and macroevolution. Both positions are available immediately. For more information, contact Brad Shaffer (hbshaffer@ucdavis.edu). – H. Bradley Shaffer Section of Evolution and Ecology University of California One Shields Ave. Davis, CA 95616

phone 530-752-2939 fax 530-752-1449 fax 530-752-1449

UCaliforniaIrvine TransposableElements

A Postdoctoral position is available to study transposable element (TE) polymorphisms in Arabidopsis thaliana and A. lyrata. The research is designed to identify evolutionary forces governing the population dynamics of TEs in the A. thaliana genome, using a combination of genomic, molecular and population genetic approaches. The successful applicant must either have a strong background in evolutionary biology and population genetics or a strong background in Arabidopsis molecular genetics, with a desire to learn evolutionary biology. Salary will be commensurate with experience. The successful applicant can begin on January 1, 2004 or perhaps earlier. The position will remain open until filled. Applicants should submit a cover letter, a curriculum vitae and the name, address and phone number of two references to the address listed below.

Applications are currently being screend, but are due no later than November 15, 2003

Contact information: Dr. Brandon S. Gaut Department of Ecology and Evolutionary Biology 321 Steinhaus Hall University of California, Irvine Irvine, CA 92697-2525 e-mail: bgaut@uci.edu

Brandon S. Gaut Phone: 949 824-2564 Dept. Ecology and Evolutionary Biology FAX: 949 824-2181 321 Steinhaus Hall e-mail: bgaut@uci.edu U.C. Irvine Irvine, CA 92697-2525

UCanterbury LifeHistory

POSTDOCTORAL RESEARCH IN NEW ZEALAND: Applications are invited for a 12-month Postdoctoral Fellowship in the area of behavioural ecology in the Department of Zoology, University of Canterbury, Christchurch, New Zealand. The successful applicant will undertake field-based research into evolutionary changes of life history traits in New Zealand birds since the introduction of exotic predators by human settlers. Applicants should have experience in both field-based research and a strong background in evolutionary biology, in addition to possessing a high degree of investigative and interpretative skills. Some work will require visits to remote islands and so a high level of independence and self-reliance is necessary. Enquiries and applications (with three letters of reference) should be directed to Dr. James Briskie (Jim.Briskie@canterbury.ac.nz), School of Biological Sciences, University of Canterbury, Private Bag 4800, Christchurch, New Zealand. Email submissions accepted. Closing date is 30 November 2003, with a starting date as soon as possible after that (before 1 February 2004 preferred). More information on the University of Canterbury and the conditions of appointment can be obtained by visiting www.canterbury.ac.nz .

James Briskie <j.briskie@zool.canterbury.ac.nz>

UOtago FreqDepSel

A03/179

UNIVERSITY OF OTAGO Te Whare Wananga o Otago

Dunedin, New Zealand

Postdoctoral Fellow/Research Fellow (Fixed-term)

DEPARTMENT of zoology

Applications are invited from suitably qualified persons for the full-time position of Postdoctoral Fellow or Research Fellow within the Department of Zoology.

This position in the laboratory of Associate Professor Hamish G Spencer is funded by the Marsden Fund of the Royal Society of New Zealand and is available for three years. The Associate Investigator on the project is Professor Marjorie A Asmussen of the University of Georgia.

The research project entitled “Why are there so many kinds of alleles: Frequency-dependent selection and genetic variability” will involve mathematical analysis and computer simulations of models of frequency-dependent selection, in an investigation of how genetic variation may be maintained in natural populations. The successful applicant will have experience in mathematical population genetics or a similar field.

Applicants must have been awarded the degree of Doctor of Philosophy before taking up this position.

We wish to fill this position by December 2003 or as soon as possible thereafter.

Specific enquiries may be made to Associate Professor Hamish G Spencer, Department of Zoology, Tel 03 479 7981, Email h.spencer@otago.ac.nz

Reference Number: A03/179. Closing Date: Friday 14 November 2003.

APPLICATION INFORMATION

For application information and a full job description go to: www.otago.ac.nz/jobs Alternatively, contact the Human Resources Division, Tel 64 3 479 8269, Fax 64 3 474 1607, Email jenni.whibley@stonebow.otago.ac.nz

Equal opportunity in employment is University policy.

E tautoko ana Te Whare Wananga o Otago i te kaupapa whakaorite whiwhinga mahi.

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

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

UOxford HapMap 2

Deadline October 3rd

University of Oxford

Department of Statistics and The Wellcome Trust Centre for Human Genetics

3 Postdoctoral Research Assistants (PDRA). Academic-related Research Staff Grade 1A: Salary £18,265 to £27,339 p.a.

1 Scientific Programmer. Academic-related Research Staff Grade IA: Salary £18,265 to £33,679 p.a.

Methodology, Analysis, and Software for the Human Haplotype Map Project

The human haplotype map (HapMap) is a major ($100M) international collaborative effort to catalogue the patterns of genetic variation, and in particular association and linkage disequilibrium, in the human genome, through the genotyping of around a million SNPs in each of three population samples. The scale and nature of the data being generated raises novel and challenging analytical questions, which will demand the development of new methodology and software.

Several of the leading groups on the analytical side of the project are based in the University of Oxford. The Mathematical Genetics and Bioinformatics Group in the Department of Statistics, and Professor Lon Cardon's group in the Wellcome Trust Centre for Human Genetics, were two of three internationally to be funded by the SNP Consortium to work on HapMap analysis. Three postdoctoral positions are available, each of two years' duration, to work on the development of analytical methods, and their application to the data being generated by the project. Successful candidates may start immediately, or at a mutually agreed date. Two of the advertised positions will be based in the Donnelly and McVean groups, within the Department of Statistics, the third in the Cardon group in the Wellcome Trust Centre for Human Genetics. There are close collaborative links between these groups, in general and over HapMap, and between them the University has one of the largest centres internationally for human population genetics modelling.

Applications for the PDRA posts are invited from researchers interested in working on this high-impact project: one of major importance in modern genetics. Candidates should have relevant background research experience in quantitative and statistical modelling. Experience in modern computationally-intensive statistical methods, and/or in population genetics, would be an advantage, as would background knowledge of genetics, though neither is essential for candidates committed to moving into the field.

We are also seeking a Scientific Programmer who will work in the Donnelly and McVean groups, in close collaboration with the modellers, to develop software for implementing novel analytical tools. Experience in C++ and/or Java is required. We envisage the post holder as having a central role in the scientific development of the project.

Well-qualified successful applicants for the four posts are likely to be appointed at or near the top of the respective salary scales given above.

Applications should comprise a CV and a list of publications together with the names, addresses, telephone, fax and e-mail details of three referees. Applicants should ask their referees to write directly so that references arrive by the closing date. Additional details concerning the posts, and the application procedure, are given in the further particulars, which are available from jobs@stats.ox.ac.uk, http://www.stats.ox.ac.uk or the address below. Informal enquiries should be directed to donnelly@stats.ox.ac.uk mcvean@stats.ox.ac.uk or lon@well.ox.ac.uk.

Applications and references should be submitted to

Mrs Sue Wood

Department of Statistics,

1 South Parks Road,

Oxford OX1 3TG.

Please quote AM-03-11 on all correspondence. The closing date for applications is 3rd October 2003. The University is an Equal Opportunities Employer.

Gilean McVean Department of Statistics 1 South Parks Road Oxford OX1 3TG UK Tel: +44 1865 281881 Fax: +44 1865 272595 web: www.stats.ox.ac.uk/˜mcvean

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UStThomas PopBiolTeaching

<<UST Biology Postdoc.DOC>>

Postdoctoral Associate

The Department of Biology at the University of St. Thomas invites applications for a postdoctoral associate position integrating research and teaching at the undergraduate level. The position is renewable for up to three years (in 12-month contracts, with benefits) and will include approximately 50% time dedicated to teaching in organismal and population biology, and 50% to research conducted in the lab of one or more faculty sponsors within our department. Interested candidates are strongly encouraged to contact potential faculty sponsors to discuss their research interests. (See http://www.stthomas.edu/BIOL/ for a description of our department and research interests of our faculty). Mentoring partnerships will be established with current faculty. The Biology Department is housed in the 200,000 sq. ft. Frey Science and Engineering Center, which opened in 1997 and is equipped with state of the art instructional and research facilities.

Candidates must have a Ph.D. Minority candidates are especially encouraged to apply. Send: cover letter, identifying potential faculty sponsor(s); curriculum vitae; statements of teaching philosophy and of research experience and goals; and three letters of reference by 1 December 2003 to: Dr. Jennifer Cruise at: www.hr.stthomas.edu , or mail to : #AQU217, 2115 Summit Avenue, St. Paul, MN 55105. AA/EOE

. Regards,

Simon

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

skemms@stthomas.edu 651 962-5228

“Emms, Simon K.” <SKEMMS@stthomas.edu>

UdeBourgogne EvolHostManipulation

Université de Bourgogne, Dijon, France Available Postdoc position

Behavioural mechanisms of host manipulation by acanthocephalan parasites

The post-doc will be involved in an ongoing study on the relationship between infection, altered behaviour, and the modulation of some neurotransmitters using acanthocephalan parasites and their crustacean intermediate hosts as a model study. Various species of acanthocephalan parasites exploit species belonging to the genus Gammarus (Crustacea, Amphipoda) as intermediate hosts. Some of these parasites are able to alter host behaviour (photactism, geotactism) in ways that apparently enhance transmission to the parasite's final host. However, the ability to “manipulate” host behaviour varies between host-parasite interactions. The aim of the project is to determine whether the altered behaviour of infected hosts correlates with modifications of specific brain regions together with altered patterns of neurotransmitters including serotonin. Training in Animal Behaviour and/or Neuroethology will be prefered. Applicants should have obtained their PhD after 1998 and NOT be french citizen.

Duration: 12 months (with a possibility of extension) Starting date: before end of 2003 Salary: 1850 euros per month (net) Send CV plus two letters of reference to:

Professor Frank Cézilly Equipe Ecologie Evolutive UMR CNRS 5561 Biogéosciences Université de Bourgogne 6 blvd Gabriel 21000 Dijon France Phone: 33 3 80 39 62 46 Fax: 33 3 80 39 62 31 e-mail: frank.cezilly@u-bourgogne.fr

WayneStateU Coevolution

RESEARCH ASSOCIATE Mitochondrial-Nuclear Co-Evolution and Adaptation Wayne State University

A postdoctoral position is available starting immediately to study molecular evolution of nuclear encoded genes of the electron transport chain. This is part of a collaborative, NIH-funded project between our labs and those of Caro-Beth Steward (SUNY Albany), Todd Disotell (NYU), and David Pollack (LSU). The emphasis of the project is on positive selection and co-evolution of nuclear genes with mtDNA in primates. References to some of our previous work are below.

Successful candidates would be well trained in both molecular biology and molecular evolution. The position, in a stimulating, interactive environment, will continue for at least two years. A competitive salary and a benefits package are available.

To apply, please provide a curriculum vitae and the names of three references to:

Dr. Lawrence I. Grossman , Center for Molecular Medicine & Genetics [l.grossman@wayne.edu] or Dr. Morris Goodman, Department of Anatomy & Cell Biology [mgoodwayne@aol.com]

Wayne State University School of Medicine 540 E. Canfield Ave. Detroit, MI 48201

313- 577-5326 313-577-5218 Fax

References

T.R. Schmidt, M. Goodman and L.I. Grossman (2002). Amino acid replacement is rapid in primates for the mature polypeptides of COX subunits, but not for their targeting presequences. Gene 286, 13-19.

D.E. Wildman, W. Wu, M. Goodman and L.I. Grossman (2002). Episodic positive selection in ape cytochrome c oxidase subunit IV. Mol. Biol. Evol. 19, 1812-1815.

A. Goldberg, T.R. Schmidt, M. Hüttemann, D. Wildman, M. Weiss, M. Goodman and L.I. Grossman (2003). Adaptive evolution of cytochrome c oxidase subunit VIII in anthropoid primates. Proc. Natl. Acad. Sci. USA 100, 5873-5878.

D.E. Wildman, M. Uddin, G. Liu, L.I. Grossman and M. Goodman (2003). The 99.4% nonsynonymous and 98.4% synonymous sequence identity between chimpanzees and humans: implications for Darwinian selection and for enlarging the genus Homo. Proc. Natl. Acad. Sci. USA 100, 7181-7188. Homo. Proc. Natl. Acad. Sci. USA 100, 7181-7188.

WorkshopsCourses

CostaRica Ants Aug5-15

ANT COURSE 2004 ANNOUNCEMENT

La Selva, Costa Rica August 5-15, 2004

http://www.calacademy.org/research/entomology/ant_course/ COURSE OBJECTIVES. ANT COURSE is designed for systematists, ecologists, behaviorists, conservation biologists, and other biologists whose research responsibilities require a greater understanding of ant taxonomy. Emphasis is on the classification and identification of ant genera of Latin America. Lectures will include background information on the ecology, life histories and evolution of ants. Field trips are structured to teach collecting and sampling techniques, and associated lab work provides instruction on specimen preparation, sorting and labeling. Information on equipment/supply vendors, literature, and myrmecological contacts are also presented.

COURSE SIGNIFICANCE. Ant Course is a unique opportunity to acquire training that is unavailable elsewhere. This course will provide students with 1) the confidence and skills to identify the major ant genera of Latin America; 2) an understanding of modern specimen processing and curation techniques; 3) an appreciation for the biological diversity of ants, and 4) experience keying to the species level.

SPONSORS. California Academy of Sciences and Museum of Comparative Zoology, with funding from The E.O. Wilson Foundation.

BACKGROUND INFORMATION. ANT COURSE will be taught from August 5 - 15, 2004 at the La Selva Biological Station in Costa Rica (http://www.ots.duke.edu/en/laselva/). The Station is centered amid the rich lowland Neotropical ant fauna.

PARTICIPANT ACCEPTANCE CRITERIA. ANT COURSE is open to all interested individuals. Priority will be given to those biologists for whom the course will have a significant impact on their research. An entomological background is not required. We aim to include students with a diverse interest in biology, including ant systematics, ecology, behavioral biology and conservation. The high instructor to student ratio will allow students to receive individual attention. ANT COURSE is presented in English but many of the instructors speak Spanish. The course is limited to 25 participants

COSTS. Tuition for the 10-day COURSE is $475 for current students and $675 for non-students. In addition, La Selva station fees for this period, covering dormitory room and board, are $351. Additional costs to be borne by all participants include transportation costs between home and San Jose, Costa Rica, and hotel stay in San Jose on Aug. 5 and 15.

FELLOWSHIPS. Eight fellowships are available for 2004. Four fellowships cover tuition fees and four fellowships cover station fees. Foreign students may apply for additional fellowships to assist in travel.

SCHEDULE Aug 5. Students and instructors arrive in San Jose. Spend night in San Jose at hotel La Amistad Inn. Aug. 6. Breakfast at 6am, depart San Jose at 7am for La Selva Aug. 15. Students and Instructors depart La Selva, visit INBIO and return to hotel in San Jose around 5 pm. Final dinner in San Jose and party. Aug. 16. Airport day: return flights.

POSSIBLE INSTRUCTORS: 2004 Instructors to be announced spring 2004. –Leeanne Alonso, Rapid Assessment Program, Center for Applied Biodiversity Science, Conservation International, 1919 M Street NW, Suite 600, Washington, DC 20036, (202) 912-1282, l.alonso@conservation.org –Roberto Brandão, Museu de Zoologia, Universidade de São Paulo, Av. Nazaré 481, São Paulo, SP, BRASIL, crfbrand@usp.br –Stefan Cover (Coordinator), Museum of Comparative Zoology, Harvard University, Cambridge, MA 02138, Tel: 617 496 5614, cover@oeb.harvard.edu –Mark Deyrup, Archbold Biological Station, P.O. Box 2057, Lake Placid, Florida 33862, mdeyrup@archbold-station.org –Brian Fisher (Coordinator), Dept. of Entomology, California Academy of Sciences, Golden Gate Park, San Francisco, CA 94118-4599, Tel: 415-750-7240, bfisher@calacademy.org –Bert Hölldobler, Zoologisches Institut II, Biozentrum, Am Hubland, D-97074 Würzburg, Germany: bertholl@biozentrum.uni-wuerzburg.de –John Lattke, Museo Inst.Zoologia Agricola, Universidad Central de Venezuela, Apartado 4579, Maracay 2101-A, Venezuela , fax: +58.243.550.7085, piquihuye@fastmail.fm –Jack Longino (Coordinator), Lab I, The Evergreen State College, Olympia WA 98505 USA, longinoj@evergreen.edu –Mike Kaspari, Dept. of Zoology, University of Oklahoma, Norman OK 73019-0235, mkaspari@ou.edu –Bill MacKay, Dept. of Biological Sciences, University of Texas, El Paso, TX 79968, wmackay@utep.edu –Phil Ward, Department of Entomology, University of California, One Shields Avenue, Davis, CA 95616, psward@ucdavis.edu

Corrie Saux Harvard University Department of Organismic and Evolutionary Biology Museum of Comparative Zoology 26 Oxford Street Cambridge, MA 02138 USA phone (617) 496-4076 fax (617) 495-5667

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

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EastAsiaPacific NSFSummerAbroad

PROGRAM: East Asia and Pacific Summer Institutes for U.S. Graduate Students

SPONSORS: National Science Foundation, National Institutes of Health (Japan only)

OVERVIEW: The East Asia and Pacific Summer Institutes provide U.S. graduate students in science and engineering first-hand research experience in Japan, Korea, Taiwan, China, or Australia, an introduction to the science and science policy infrastructure of the respective location, and orientation to the language and culture. The institutes last approximately eight weeks from June to August. Approximately 175 students will be supported for the summer of 2004.

HOST INSTITUTIONS: University, government and corporate research laboratories, depending on the program.

ELIGIBILITY: Applicants must be U.S. citizens or permanent residents; be enrolled at U.S. institutions in graduate programs (M.S. or Ph.D.) in science or engineering or M.D. programs with an interest in biomedical research; and pursuing studies in fields of science or engineering that are supported by the National Science Foundation. For Japan, fields of study may also include those supported by the National Institutes of Health.

SUPPORT: International round-trip air ticket; living expenses (accommodations, food and professional travel) at the foreign location; and a stipend of $3,000.

DEADLINE: December 23, 2003 (Please complete your application early, as you must include letters of reference and transcripts which may be impossible to get after your university closes for the winter holidays.)

FURTHER INFORMATION:

http://www.nsf.gov/cgi-bin/getpub?nsf03608 http://www.nsf.gov/sbe/int Direct questions to eap-info@nsf.gov.

“Courtney, Mark W.” <mcourtne@nsf.gov>

London FunctionalGenomics Nov20

CEE Workshop Thursday, 20 November 2003

FUNCTIONAL GENOMICS; new challenges to chew on Organisers: Dr Mark Beaumont (Reading), Professor Richard Nichols (QMUL)

Places may be limited. Please email C.J.Foreman@qmul.ac.uk to book your place.

The meeting is designed to promote synergy between groups working at different organisational levels ranging from the analysis of DNA sequences to morphological evolution.

HMM/Bayesian approaches to identifying control regions from sequence data analysis of microarray data modelling of regulatory networks evolution of development and consequences for morphological evolution.

The idea is that we tantalisingly close to the point where these fields will join together to make a coherent account of evolution from the genotype to the phenotype. We hope that the meeting will identify possibilities and impediments.

Venue Education Centre, Zoological Society of London, Regents Park, London, NW1 4RY (See electronic map) Costs: £5 per person, £3 students, at the door For further information contact Professor Richard A Nichols (R.A.Nichols@qmul.ac.uk) CALL FOR POSTERS valuable prizes! Please email C.J.Foreman@qmul.ac.uk if you intend to present a poster.

http://www.gene.ucl.ac.uk/cee/

Christine Foreman <C.J.Foreman@qmul.ac.uk>

London FunctionalGenomics Nov20 2

The web site for the following workshop has had to be changed to

http://www.ucl.ac.uk/˜ucbtcee/cee/Functonal_gen_prog.html The new site includes slight changes to the programme and an electronic map showing the venue. CEE Workshop Thursday, 20 November 2003

FUNCTIONAL GENOMICS; new challenges to chew on Organisers: Dr Mark Beaumont (Reading), Professor Richard Nichols (QMUL)

Places may be limited. Please email C.J.Foreman@qmul.ac.uk to book your place.

Mail signature

Richard A. Nichols Tel: +44 (0)20 7882-3058 Professor of Evolutionary Genetics Fax: +44 (0)20 8983-0973 SBS, Queen Mary, University of London London E1 4NS

Richard Nichols <r.a.nichols@qmul.ac.uk>

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 notifcation 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 one of the keywords "Conference, Grad, Job, Other:, Postdoc, Workshop" and then the message stands a better chance of being correctly parsed.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. So please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating 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.