
E v o l D i r

August 1, 2003

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

Forward

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

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

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



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Conferences

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CapeTown Science Jan19-23

Conference: Southern Connections 2004 Date: 19-23 January 2004 Venue: University of Cape Town, Cape Town, South Africa. Web site: www.uct.ac.za/-conferences/sc2004 Email: sc2004@botzoo.uct.ac.za (case sensitive) Brief description: Southern Connections is a large group of scientists from all continents who study aspects of biology and earth history of the Southern Continents. Previous meetings have taken place in Australia, New Zealand and Chile. This will be a chance for scientists to experience the other major Southern Connector, southern Africa, and to continue and build on their interactions, discussions and collaborations concerning this bit of Gondwana. The theme in 2004 will be "Towards a Southern Perspective". The literature in most fields of biology is dominated by a northern perspective. One of the main aims of Southern Connections is to develop and emphasise differences between North and South. Africa, for example, with its long history of hominids and its relatively well preserved megafauna, is a stark contrast to most of the Northern Hemisphere. Besides this theme there will be several other more specific themes relating to, for example, ecology, forest ecology, paleontology, applied ecology, ethno botany, forest management, zoology (fishes, birds, etc), arid land ecology, biodiversity management, community issues, biogeography, phylogeny, phylogeography, history and utilization. A common thread is the Gondwana link.

many thanks

Elizabeth, Secretariat SC2004

Elizabeth Danckwerts <aecon.e@mweb.co.za>

Hawaii Sciences Jan15-18

Call for Papers/Abstracts/Submissions Hawaii International Conference on Sciences January 15 - 18, 2004 Renaissance Ilikai Waikiki Hotel, Honolulu Hawaii, USA

Submission Deadline: August 25, 2003

Web address: <http://www.hicsciences.org/> Email address: sciences@hicsciences.org

The 2004 Hawaii International Conference on Sciences will be held from January 15 (Thursday) to January 18 (Sunday), 2004 at the Renaissance Ilikai Waikiki Hotel in Honolulu, Hawaii. The conference will provide many opportunities for academicians and professionals from sciences and related fields to interact with members inside and outside their own particular disciplines. Cross-disciplinary submissions are welcome.

Topic Areas (All Areas of the Sciences are Invited)

*Agricultural Sciences *Anatomy *Animal Sciences
 *Astronomy *Astrophysics *Biochemistry *Biology
 *Biophysics *Botany *Chemistry *Entomology *Environmental Science *Exercise Health Science *Fisheries and Wildlife *Food Science *Forensic Science *Forestry
 *Geology *Horticulture *Marine Biology *Meteorology
 *Microbiology *Neuroscience *Oceanography *Physical Therapy *Physics *Science Education *Soil Science
 *Toxicology *Zoology *Cross-disciplinary areas of Science with other areas are also encouraged *Other Areas of Science

The Hawaii International Conference on Sciences encourages the following types of papers/abstracts/submissions for any of the listed areas:

Research Papers - Completed papers. Abstracts - Abstracts of completed or proposed research. Student Papers - Research by students. Poster Sessions/Research Tables - informal presentation of papers or abstracts. Work-in-Progress Reports or Proposals for future projects. Reports on issues related to teaching. Panel Discussions, Practitioner Forums and Tutorials are invited. Workshop proposals are invited.

For more information about submissions see: <http://www.hicscienc.es.org/CallForPapers.Sci.htm> Submission Guidelines 1. Submissions may be made electronically via e-mail to sciences@hicscienc.es.org or mailed. Electronic submissions are preferred. Submissions will be acknowledged within 48 hours.

If submissions are mailed, submit two copies of your paper, report, abstract, proposal or study. Submissions imply that at least one author will register for the conference and be present at the time designated in the conference program. Submissions must be received by August 25, 2003. E-Mail, fax or mail submissions to:

Hawaii International Conference on Sciences P.O. Box 75036 Honolulu HI, 96836, USA

Telephone: (808) 949-1542 Fax: (808) 947-2420 E-mail: sciences@hicscienc.es.org

There is a limit of two contributed papers per lead author.

2. Each submission must include a separate title page as outlined below:

a. title of the submission, b. topic area of the submission (available at <http://www.hicscienc.es.org/CallForPapers.Sci.htm>), c. two or three keywords that describe the submission, d. name(s) of the author(s), e. mailing address(es), f. e-mail address(es), g. phone number(s), h. fax number(s), i. corresponding author if different than lead author.

Correspondence regarding receipt of submission will be made by e-mail unless another mode of correspondence is requested. BE SURE AND INCLUDE THE TOPIC AREA AND TWO OR THREE KEY WORDS DESCRIBING THE SUBMISSION.

3. Submissions will only be published in the conference proceedings if at least one of the authors attends the conference. Instructions for submitting a computer readable format for the proceedings will be provided when the submission is accepted.

4. If you wish to be a reviewer, session chair, or discussant, please e-mail your request to sciences@hicscienc.es.org and indicate the topic area in which you are interested. Registration for the conference is required to be a session chair or discussant.

Web address: <http://www.hicscienc.es.org/> Email Address: sciences@hicscienc.es.org

To be removed from this list, please reply to this e-mail with the word remove in the subject heading.

Hawaii International Conference on Sciences P.O. Box 75036 Honolulu, Hawaii 96836, USA Telephone: (808) 949-1542 Fax: (808) 947-2420 E-mail: sciences@hicscienc.es.org Website: <http://www.hicscienc.es.org/>

USussex PopGroup Dec16-19

Population Genetics Group Meeting

University of Sussex

Tuesday Dec 16th to Friday Dec 19th

The annual Pop Group meeting will be at the University of Sussex this year. Pop Group is a small (~150 delegates) informal meeting of scientists interested in all fields of population genetics and evolutionary biology. This year the plenary lectures will be given by John Maynard Smith, Tim Birkhead and Laurent Duret. The cost is expected to be about 170 UKP for registration, accomodation and meals.

This is an advance notice - further details, including details of how to register will follow.

Adam Eyre-Walker Centre for the Study of Evolution & School of Biological Sciences University of Sussex Brighton BN1 9QG

tel : 01273 678480

Virginia SEEPAGE Sept19-21 2

Dear Colleagues:

Time to register for SEEPAGE2003! Particularly if you are planning to present a talk or a poster.

2003 SEEPAGE (South-East Ecology, PopulAtion Genetics and Evolution Meeting) will be held at Camp Sequoya, on South Holston Lake in VA on September 19-21 2003. Titles of talks and posters are now being accepted. Details on location, registra-

tion and (soon) program - at <http://faculty.etsu.edu/yampolsk/SEEPAGE2003> . Those who have already registered, please send registration fee promptly. I need to make a down payment for the camp.

Please note that for several my registration form has not been working properly for some people weeks due to server problems . It now works fine, but please update your bookmarks, since the form's URL has changed. I will be e-mailing registration confirmations shortly. If you don't receive one, it probably means that your registration has not reached me. I will, of course, contact all people from whom I receive checks but not the

registration.

Please contact me <yampolsk@mail.etsu.edu> or <SEEPAGE2003@mail.etsu.edu> if you have any questions about the meeting, its location and program.

Lev Yampolsky <mailto:SEEPAGE2003@mail.etsu.edu>

Department of Biological Sciences <<http://www.etsu.edu/biology>> East Tennessee State University <<http://www.etsu.edu/>> Johnson City TN 37614-1710 Phone 423-439-4359 Fax 423-439-5958

"Yampolsky, Lev" <YAMPOLSK@mail.etsu.edu>

GradStudentPositions

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BielefeldU Bioinformatics

The Graduate Program "Bioinformatics" at Bielefeld University offers 6 PhD scholarships, starting autumn/winter 2003.

Prerequisites are a Diploma or M.S. in Bioinformatics, Computer Science, Biology or Mathematics, as well as willingness to become acquainted with the fascinating interdisciplinary field of bioinformatics. Enrolment for a qualifying year on the basis of an appropriate B.S. is possible as well.

For more information see <http://www.TechFak.Uni-Bielefeld.DE/GK635>, for other ongoing research activities in Bioinformatics see e.g. <http://bibiserv.techfak.uni-bielefeld.de> Submit your application (preferably in PDF format) to the head of the graduate program before 31.08.2003.

Prof. Dr. Robert Giegerich Technische Fakultät Uni-

versität Bielefeld Postfach 10 01 31 33501 Bielefeld Germany

robert@techfak.uni-bielefeld.de

JyvaskylaU SexualSelection

a graduate student position in Jyvaskyla University, Finland:

The thesis work deals with phenotypic (morphological traits, male courtship songs and female song preferences) variation within and between *Drosophila montana* populations and its consequences in the context of sexual selection. This species is of a special interest in evolutionary studies as it has genetically (and morphologically) diverged populations on different continents, and as the females of this species have very high requirements with respect to male courtship

song quality. A phylogeographic analysis of *D. montana* populations presently being made within an EU Research training Network, will provide a theoretical framework for the interpretation of the patterns of chromosomal, morphological and behavioural variation among populations. The graduate student may also take part in studies on the role of chromosomal rearrangements in creating reproductive barriers (especially behavioural changes) via position effect, reduced levels of recombination and selective sweeps in polymorphic populations of the species. The work can be started at the University of Jyväskylä, Finland 1.9.2003 or later. If you are interested in participating into this kind of research, please contact Dr. Dominique Mazzi (Dominique.Mazzi@oulu.fi) in July or Prof. Anneli Hoikkala in August (Anneli.Hoikkala@oulu.fi).

Anneli Hoikkala Department of Biology University of Oulu PL 3000 90014 Oulu Finland

Phone +358 8 5531784 Fax +358 8 5531061 <http://cc.oulu.fi/~genetwww/behgen/behgene.htm>

Anneli Hoikkala <anneli.hoikkala@oulu.fi>

PurdueU VanEckScholars

Van Eck Scholars Graduate Assistantships

Hardwood Tree Improvement and Regeneration Center
At Purdue University

Description: The Hardwood Tree Improvement and Regeneration Center (HTIRC) at Purdue University is seeking outstanding candidates interested in obtaining MS or Ph.D. degrees. Research program areas include: development of plant tissue culture and genetic modification technologies for tree improvement; conservation and population genetics; forest tree breeding; functional genomics of heartwood formation; and nursery, outplanting, and silvicultural stand management.

Qualifications: Candidates should have strong quantitative skills, and knowledge and experience in an area of biological science such as forestry, horticulture, botany, plant biology, genetics, physiology or pathology. Candidates should have a GPA of at least 3.2 and a strong GRE score.

Assistantships will be awarded at \$17,500 (MS) and \$20,000 (Ph.D.) per year. In addition, an annual research budget will be available for research support.

Interested candidates that do not meet requirements for

a Van Eck Scholar Graduate Assistantship are encouraged to apply for additional graduate assistantships that are available through HTIRC.

Applications or Additional Information: Please e-mail or mail a short (1-page) letter of interest, including cumulative GPA, GRE scores, and three references (telephone numbers and e-mail addresses) to: Janis@fnr.purdue.edu. Feel free to visit: www.fnr.purdue.edu/Htirc/-HTIRCindex.htm and contact Drs. Jacobs (djacobs@fnr.purdue.edu), Michler (cmichler@fnr.purdue.edu), Pijut (ppijut@fnr.purdue.edu) or Woeste (kwoeste@fnr.purdue.edu) prior to formal application.

Women and minorities are encouraged to apply. Purdue University is an equal opportunity-affirmative action employer.

“Michler, Charles” <cmichler@fnr.purdue.edu>

SoutheasternLouisianaU EvolEcol

Master's of Science Degree in plant evolutionary ecology and systematics

To work with Rick E. Miller Assistant Professor of Plant Evolutionary Genetics

I recently received funding (Louisiana Board of Regents) for a masters student to work in my lab on a project that combines an investigation of the evolutionary ecology of seed size and seed number with a study of morning glory systematics. This research program integrates studies of selection and constraints on ecologically important traits with research on the molecular phylogenetics of a diverse and species-rich group of plants. There are a wide variety of masters projects that would make suitable contributions to this research program including greenhouse studies, field studies, and molecular work.

The Department of Biological Sciences at Southeastern Louisiana University includes an active group of scientists with strengths in evolutionary biology, systematics, and molecular evolution (B. Crother, M. White, W. Font, K. Piller, C. Fontenot), ecology (P. Keddy, C. Jackson, G. Schaffer), and microbiology (G. Childers, G. Howard).

For a description of our graduate program please refer to the information provided at (www.selu.edu/-

Academics/Depts/Biology/grad/index.htm). A description of how to apply to our program is available at: (www.selu.edu/Academics/Depts/Biology/grad/-prospect.htm). While the application deadline for Fall 2003 was in March, the graduate position in my lab is open. If you are interested in applying please contact me and I will make the appropriate arrangements. In addition to the funding from my research grant, teaching assistantships are available, as well as Louisiana Board of Regents fellowships awarded to outstanding candidates.

For further explanation of my research interests please visit my web site. Also do not hesitate to contact me by email with questions or general inquiries.

Rick E. Miller Department of Biological Sciences Southeastern Louisiana University Hammond, LA 70402 985 549-5556 (phone) 985 549-549-3851 (FAX) E-mail: rickmiller@selu.edu Web: <http://www.selu.edu/Academics/Faculty/rickmiller>

UDublin Supertrees

Title: Large trees, supertrees and the grass phylogeny: a high performance computing approach (funded by Enterprise Ireland)

Department of Botany and Trinity Centre for High Performance Computing, University of Dublin, Trinity College, Ireland Jodrell Laboratory, Royal Botanic Gardens, Kew, UK

A three year PhD studentship is available to work on a collaborative research project between TCD and the Royal Botanic Gardens Kew. The student will work under the supervision of the project principal researcher, Dr Trevor Hodkinson (<http://www.tcd.ie/Botany/Staff/THodkinson>), Dr Nicolas Salamin, Univ. of Washington, (<http://evolution.gs.washington.edu/-salamin>), Dr Vincent Savolainen, Royal Botanic Gardens Kew, and Professor James Sexton, Director of the Trinity Center for High Performance Computing (<http://www.maths.tcd.ie/pub/-official/StaffPages/sexton>).

The project aims, with the aid of high performance computing, to produce comprehensive phylogenetic trees of the whole grass family, by using multi-gene analyses and meta-analysis approaches such as supertrees. The information from these large phylogenetic trees will be used to study macroevolutionary and

phylogenomic processes and for systematic purposes. The grasses are one of the largest families of higher plant and are undoubtedly the most important from an economic perspective, representing four of the world top five crops. These comprehensive phylogenetic trees will be an essential tool in understanding grass evolution.

The student will be expected to a) generate new DNA sequence data to contribute to existing data sets to produce large matrices for phylogenetic analyses based on multiple genes and b) utilise existing data for phylogenetic and phylogenomic purposes, employing state of the art high performance computers. It is anticipated that the student will travel to the Royal Botanic Gardens Kew on numerous occasions to generate fresh data and to other countries to collect plants and attend international conferences. The student will become part of an active and successful research group working on the grass family and the phylogenetics of large and speciose groups. It will link closely with worldwide initiatives to assemble a comprehensive 'Tree of Life' using DNA sequence information.

The student will be based at Trinity College and receive an annual stipend of 15,000-18,000 Euro for maintenance and to cover university fees. Fees are approximately 4,000 Euro for EU students or 8,000 Euro for non-EU students. There will be opportunities to get extra money teaching and demonstrating on undergraduate courses.

To apply or to obtain further information, please send a CV including research interests and contact details of two referees and a letter of motivation to trevor.hodkinson@tcd.ie with copy to v.savolainen@kew.org and salamin@gs.washington.edu by August 1st 2003.

– Nicolas Salamin Felsenstein Lab Department of Genome Sciences Box 357730 University of Washington Seattle WA 98195-7730

tel: (206) 616 9581 e-mail: salamin@gs.washington.edu
web: <http://evolution.gs.washington.edu/salamin>

UFrankfurt EcolGenet

Ph.D. STUDENT POSITION ON ecological genetics of Chironomus

A Ph.D. Student Position is available in a project funded by a Baden-Württemberg Program (BWPLUS; Lebensgrundlage Umwelt und ihre Sicherung).

The project will test whether local adaptation or stochastic processes (e.g. genetic drift) in Chironomus mediate microevolutionary change. Natural populations will be subjected to different levels of toxic substances (TBT and cadmium) for several generations and changes in genetic diversity will be monitored over time. Life-history experiments will be conducted to assess the variation in quantitative traits. Parallel, an extensive genetic analysis will reveal levels of variation in neutral genetic markers among populations. Comparing spatial genetic variation with genetic variation in ecologically relevant (quantitative) traits will allow to test hypotheses on local adaptation and determine long-term population genetic effects of chemical contamination.

The successful candidate should have the equivalent of a master's degree or Diplom in Biology, a firm background in evolutionary ecology, and a strong commitment to basic research. The position is available initially for two years, with likely extension for maximum one further year. Salary and conditions are according to the German BAT-IIa/2 scale for civil servants.

A complete application should include a curriculum vitae, a description of the MSc or Diplom research, and the names (address/phone/fax/e-mail) of two references, and be sent to Dr. Klaus Schwenk, Department of Ecology & Evolution J.W. Goethe-University Frankfurt am Main, Siesmayerstraße 70, 60054 Frankfurt am Main, Germany (k.schwenk@zoology.uni-frankfurt.de). Closing date for applications is 25. Juli 2003.

Klaus Schwenk <k.schwenk@zoology.uni-frankfurt.de>

ULausanne EvoGenomics

PHD POSITION IN EVOLUTIONARY GENOMICS

A PhD position is available beginning September 1 (2003) in the group of Henrik Kaessmann at the Center of Integrative Genomics, University of Lausanne, Switzerland.

I am interested in the origin, evolution, and polymorphism of genes and noncoding DNA sequences in the human genome. We will explore available data from genomic databases and generate complementary data by large-scale experimental analysis. My current research focuses on the origin and evolution of primate genes and gene architectures. For more information see the web site: <http://home.uchicago.edu/~kaessm/> I am seeking

highly qualified and motivated applicants with experimental and/or computational experience and a strong interest in one or several of the following fields: computational biology (bioinformatics/data mining), molecular evolution, population genetics, and/or statistics.

Please note that a master degree or equivalent is required for starting a PhD in Switzerland.

Although living costs in Switzerland are relatively high, the salary still is attractive: ~45.000 CHF (~30.000 Euro) the first year, ~52.000 CHF after 3 years.

The Center of Integrative Genomics (CIG) is a new (starting September, 2003) interdisciplinary research and training institute of the University of Lausanne covering all aspects of genome evolution and functional genomics. It is set up in collaboration with the University of Geneva and the Swiss Federal Institute of Technology in Lausanne. The CIG is also supported by the Swiss Institute for Experimental Cancer Research, the Ludwig Institute for Cancer Research, the Swiss Institute for Bioinformatics and the University Hospitals at both Geneva and Lausanne.

The Lausanne region is known for its excellent public schools, an attractive cultural atmosphere, a growing economy, and its beautiful environment next to Lake Geneva.

Informal inquiries may be addressed to Henrik Kaessmann kaessm@uchicago.edu. Applications including a CV, statement of research interest, copies of relevant publications, and two letters of recommendation should be emailed or mailed to me at the address below. Review of applications will begin immediately. Starting dates after 1 September 2003 are flexible.

until September 1, 2003: Dr. Henrik Kaessmann
Department of Ecology and Evolution University of Chicago Chicago, IL 60637 USA Phone: +1-773-834-3965 Fax: +1-773-702-9740

After August 1, 2003: Dr. Henrik Kaessmann, Assistant Professor Center for Integrative Genomics BEP University of Lausanne Phone: +41-21-692-2054 Note: please use my Chicago email address until further notice on my webpage!

UTilburg AnimalBehaviour Economics

PhD studentship in animal behaviour & economics

For the research project 'Economic behaviour in vervet monkeys' we look for a PhD candidate with an interest in animal behaviour (ethology - behavioural ecology) as well as in economics (microeconomics - game theory). The goal is the development of theoretical models of cooperation and economic behaviour in non-human primates on the basis of experimental research in vervet monkeys. The project is funded for 4 years (starting the fall of 2003) by the Netherlands Organisation for Scientific Research (NWO) in the framework of the programme 'Evolution and Behaviour'. (www.nwo.nl)

The CentER for Economic Research (<http://center.uvt.nl>) of the University Tilburg, The Netherlands (Prof. Eric. van Damme), will be the home base of the candidate. The empirical work will be done in the Centre de Primatologie (www-ulp.u-strasbg.fr) of the Université Louis-Pasteur in Strasbourg, France (Prof. Ronald Noë) and in South-Africa (in cooperation with dr. S. Peter Henzi, Bolton Institute, UK, and dr. Louise Barrett, University of Liverpool, UK.).

Some experience with animal behaviour and field work is required. We further expect good mathematical skills and an affinity with theoretical modelling and with game theory. A good command of English is required; knowledge of French and Dutch will be an advantage.

Please apply by sending an email (attachments in Word or PDF) with CV, relevant publications if any and the names, (email)-addresses and telephone numbers of two referees to:

Petra Ligtenberg, secretary to Prof.dr. E.E.C. van Damme, CentER for Economic Research, Universiteit Tilburg; P.A.M.Ligtenberg@uvt.nl

deadline: Monday 14 july.

For further information please contact:

Prof. dr. E.E.C. van Damme CentER for Economic Research Univ. van Tilburg, Postbus 90153, 5000 LE Tilburg - Tel. +31-13-4662813; Fax +31-13-4663066 <http://center.uvt.nl/staff/vdamme> Prof. dr. R. Noë Ethologie et Ecologie comportementale des Primates (CEPE CNRS UPR 9010) 7, rue de l'Université, 67000 Strasbourg, France. Tel. +33 (0) 388 96 59 61 of +33 (0) 390 24 19 11; Fax. +33 (0) 390 24 19 63/noe@neurochem.u-strasbg.fr. <http://ss20w.mpi-seewiesen.mpg.de/~knauer/noe/markt.html>

Prof. Ronald Noë Ethologie et Ecologie comportementale des Primates CEPE (CNRS UPR 9010) / Université Louis Pasteur 7 rue de l'Université, F - 67000 Strasbourg, France

office: tel (+33/0) 390 24 19 11/secr. 19 20 /fax 19 63 tel. home: (+33/0) 388 96 59 61 ULP: noe@neurochem.u-strasbg.fr home/Tai Monkey Project : Ronald.Noë@wanadoo.fr

webpages:<<http://ss20w.mpi-seewiesen.mpg.de/~knauer/noe/taan.html>> <<http://ss20w.mpi-seewiesen.mpg.de/~knauer/noe/taan.html>>Tai Monkey Project - <<http://ss20w.mpi-seewiesen.mpg.de/~knauer/noe/markt.html>>Biological Markets - <<http://ss20w.mpi-seewiesen.mpg.de/~knauer/noe/markt2.html>> "Economics in Nature" (book)

"Ronald.Noë" <Ronald.Noë@wanadoo.fr>

UWindsor SalmonGenetics

Graduate Studentship in Salmon Gene Expression/Genomics. A funded Ph.D. or M.Sc. position is available immediately to study the impact of triploidization on chinook salmon. The position is a collaborative venture between faculty members at the University of Windsor, UBC, UNBC, and aquaculture companies on Vancouver Island. The student will study the effect of dosage compensation and overall gene expression on salmon performance, possibly focussing on disease resistance. A critical component of the project involves using salmon DNA chips for microarray analysis of gene expression differences between diploid and triploid salmon. Ideally, students should have some molecular biology experience together with an understanding of fundamental genetic mechanisms and preferably some fish biology, although we are prepared to train otherwise qualified candidates.

Please send your C.V. to either Dr. Adnan Ali (aali@uwindsor.ca), Dr. Andrew Hubberstey (ahubber@uwindsor.ca) or Dr. Daniel Heath (dheath@uwindsor.ca) at the University of Windsor. We will consider seriously all applicants; however, only those selected for an interview will be contacted.

Daniel Heath Great Lakes Institute for Environmental Research University of Windsor Windsor, Ont, Canada N9B 3P4

Phone: (519) 253-3000; Ext 3762 Fax: 971-3616
dheath@uwindsor.ca

Jobs

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ANU PlantMicrobial

The Australian National University Faculty of Science School of Botany and Zoology Lecturer in Plant-Microbial Interactions (Level B)

Reference No: BOZO 1582

The School of Botany & Zoology is seeking to appoint a level B Lecturer in the field of plant-microbe interactions. Research in the School primarily concerns whole organism biology and we are seeking a person whose research interests will complement those of the School. Consequently, we require a person interested in exploring the association between fungi, bacteria or viruses and their plant hosts from an ecological or evolutionary perspective. Expertise with plant-pathogen interactions or with the role of microbes in structuring plant communities would be an advantage. We expect the successful candidate to be committed to establishing a strong externally funded research program and to supervise research students. The candidate will be expected to contribute to undergraduate teaching, and in particular, to develop and participate in a course concerned with the biology of plant-microbe interactions.

The position is a continuing appointment and is partially funded, including some research funds, by the Grains Research & Development Corporation of Australia. The position is available from 1 January 2004. Further information concerning the School can be viewed at <http://www.anu.edu.au>. Enquires to Dr. Mike Crisp, Head, phone: (61 2) 6125 2866, email: Head.BoZo@anu.edu.au. Selection documentation should be obtained before applying from: <http://www.anu.edu.au/hr/jobs> . Salary: Lecturer (Level B)

\$53,640 - \$63,287 pa plus generous superannuation provisions

Closing date: 31 July, 2003

Information on how to apply may be obtained from the ANU Web page - <http://www.anu.edu.au/hr/jobs> or by telephoning/emailing the contact.

DalhousieU SequenceTech

MOLECULAR BIOLOGY/GENOMICS TECHNICIAN

One to two MOLECULAR BIOLOGY TECHNICIANS/LAB MANAGERS are required to run and manage an automated sequencing facility for the A.J. Roger, M.W. Gray and W. F. Doolittle laboratories in the Biochemistry and Molecular Biology Department, Dalhousie University. The positions are available starting in August 2003.

The successful candidate(s) should have an M.Sc. in biochemistry, genetics, molecular biology or a related field and must be able to work productively and independently. They should have substantial experience in molecular biological techniques including: DNA purification/preparation, DNA sequencing, PCR amplification and associated techniques. Experience with the 377 automated sequencers is an asset, but not essential. In addition, the candidate(s) must be highly organized and efficient. Familiarity with sequence manipulation software, bioinformatics applications and with the UNIX or LINUX operating system would be an asset. Can-

didates with extensive relevant experience but without an M.Sc. degree may also be considered.

The successful candidate(s) will be responsible for routine preparation of template DNA, performing automated sequencing reactions and associated molecular biological techniques in high-throughput formats and operating an ABI 377XL automated sequencer (or overseeing those activities) as well as retrieving & editing sequence trace data on a computer. One of the technicians will be also be a lab manager for the Roger lab and will be responsible for ordering, preparing solutions and reagents, trouble-shooting technical problems, monitoring costs and communicating effectively with service representatives and his/her supervisor. Depending upon qualifications the technician(s) could participate in ongoing protistan genomics projects in the Roger laboratory.

Salary commensurate with qualifications.

Please forward a curriculum vitae or resume including a list of references to:

Lesley Davis, Rm 8B1 Sir Charles Tupper Medical Building Department of Biochemistry Dalhousie University Halifax, NS, B3H 4H7 telephone: 902-494-2881 FAX: 902-494-1355 email: ldavis@hades.biochem.dal.ca

Dorset PopGenet

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 on terrestrial and river habitats, including population and conservation ecology.

Population Geneticist 24,450 - 30,000 (UK pounds)

Leading the Molecular Ecology Group, a busy laboratory of 6 scientists and several postgraduate students, you will be responsible for advancing molecular ecology within CEH by securing funding to develop population genetics theory and to apply molecular techniques to practical problems. You will develop new research initiatives, and provide statistical advice on current projects (e.g. gene flow in GM plants, conservation genetics, evolutionary genetics). You will have a track record in winning research funding, publishing high impact papers and leading research teams. Starting salary will depend on experience and high calibre

scientists will have the opportunity for rapid promotion.

Further details and application forms available from Diana Morton, CEH Dorset, Winfrith Technology Centre, Nr Dorchester, Dorset DT2 8ZD (e-mail dmo@ceh.ac.uk, telephone 01305 213500). Closing date for receipt of completed applications is 25th July 2003 quoting reference CEHDOR22.

migg@ceh.ac.uk

ImperialCollege PopBiol

Lectureship/Senior Lectureship in Population Biology

Department of Biological Sciences, Imperial College London

Salary: Lecturer: £29,621 - 33,679 / Senior Lecturer: £36,712 - £39,958

The Department of Biological Sciences' (RAE 5*) Ecology & Evolution Section and the NERC Centre for Population Biology are based at Imperial College's Silwood Park campus and conduct research on a wide range of topics in ecology, evolution and associated fields. We seek to appoint a staff member who works in the broad area of population biology (i.e. including theoretical and experimental approaches; work on plant, animal and microbial systems; focus on population, community or ecosystem issues; and pure and applied problems). We are particular interested in candidates who will bring new skills to the community of population biologists at Silwood Park.

The successful applicant will have a PhD in a relevant subject and a strong research publication record. He or she will be expected to develop an independent and externally-funded research programme; to contribute to teaching at undergraduate and postgraduate levels; and to assist in the activities of the Centre for Population Biology. The open-ended appointment will be at lecturer / senior lecturer level depending on experience and we will consider candidates who seek part-time positions.

For further information and application forms contact Mrs Diana Anderson at Department of Biological Sciences, Imperial College London, Silwood Park Campus, Ascot, Berks, SL5 7PY (d.anderson@imperial.ac.uk).

Closing date: Thursday 24 July 2003 –

Ian P. F. Owens Department of Biological Sciences Im-

perial College London Silwood Park Ascot, Berkshire SL5 7PY

email i.owens@imperial.ac.uk fax +(0)20 759 42215

Ian Owens <i.owens@imperial.ac.uk>

IowaStateU parttime

Molecular Evolution Instructor needed this coming fall semester (late August start) for a one-term replacement for Jonathan Wendel's graduate course in Molecular Evolution. Position is half-time, but opportunities exist to supplement with additional teaching and/or post-doctoral research at Iowa State University. Excellent opportunity for a recent Ph.D. to acquire teaching experience in a collegial setting. For additional information, please contact J. Wendel at jfw@iastate.edu.

Jonathan F. Wendel, Professor and Chair Department of Ecology, Evolution, and Organismal Biology, Iowa State University Ames, IA 50011 Voice (515) 294-7172; FAX 515-294-1337; jfw@iastate.edu <http://www.eeob.iastate.edu/jwendel/> Jonathan F Wendel <jfw@iastate.edu>

JointGenomeInstitute ResAssoc

Senior Research Associate in Evolutionary Genomics

The Evolutionary Genomics Department of the Joint Genome Institute (JGI) in Walnut Creek, CA (San Francisco Bay area), has an opening for a Senior Research Associate.

The JGI is a high-throughput genomics center with extensive laboratory and computer facilities, currently producing more than 1,800 million nucleotides of DNA sequence per month (about 50,000 nt per minute). The JGI has produced random shotgun, high depth draft sequences of the puffer fish *Fugu*, the tunicate *Ciona*, the fungi *Phanerochaete* and *Trichoderma*, the green alga *Chlamydomonas*, the diatom *Thalassiosira*, and dozens of prokaryotes. Several other large-scale genome projects are underway, including those of the poplar tree, the frog *Xenopus*, two species of the basidiomycete *Phakopsora*, two species of the oomycete *Phytophthora*,

and scores of other prokaryotes, including community microbial sequencing.

Within the JGI, the Evolutionary Genomics Department is a team of molecular evolutionary biologists focusing on numerous aspects of genome evolution using these and other publicly available genome sequences, as well as sponsoring many projects that compare mitochondrial and chloroplast genomes and selected regions of the nuclear genome (e.g., Hox gene clusters).

This Group currently has an opening for a Senior Research Associate. It is expected that this person will function as a full member of the Department, participating in all aspects of a project, from design to publication, to the limit of his/her ability. There will be substantial opportunities for training and professional development. This person will regularly collaborate with other scientists within and outside of the JGI.

This person may perform work that is primarily in the lab or primarily computational or a combination of both. Examples of the type of work that may be undertaken include (1) performing computerized analyses of DNA and amino acid sequences, genome structure, etc.; (2) writing computer code for comparative genomics projects; (3) performing PCR amplification, cloning in plasmid, cosmid, or BAC vectors, hybridization, and other molecular biology techniques; and (4) improving and developing laboratory protocols.

The person selected will have these qualifications: (1) B.S. in Biology or Computer Science or related field (M.S. desired); (2) Either broad experience in a variety of laboratory techniques or strong programming skills, especially in PERL; (3) Strong computer user skills with PC and/or Macintosh operating systems (strong UNIX skills desired); (4) Some familiarity with the concepts of evolutionary biology and molecular evolution.

Further information on this facility can be seen at <<http://www.jgi.doe.gov/>> and on the Evolutionary Genomics Department by following the link from this page. Those interested should contact Dr. Jeffrey Boore by e-mail at JLBoore@LBL.gov; by mail at 2800 Mitchell Drive, Walnut Creek, CA 94598; or by phone at 925-296-5691 as soon as possible.

–

Jeffrey L. Boore, Ph.D. Evolutionary Genomics Department Head and Associate Adjunct Professor, University of California, Berkeley DOE Joint Genome Institute 2800 Mitchell Drive Walnut Creek, CA 94598

phone: (925) 296-5691 fax: (925) 296-5666

Jeffrey Boore <JLBoore@LBL.gov>

UAntwerp Biostatistics

VACANT POSITION

“BIostatistician-POPULATION BIOLOGIST”

University of Antwerp, Department of Biology, Antwerp, Belgium

Task description:

Teaching: (i) Biostatistics for the Biology and Applied Biological Sciences programmes, and specialized optional courses: - 1ste licentie Biology (3rd year undergraduate): Biostatistics I, 30h Theory - 2de licentie Biology (4th year undergraduate): Biostatistics II, 30h Theory - 1st Engineer Applied Biological Sciences (3th year undergraduate): Data analysis and modelling: 45h Theory, 60h Exercises (ii) Participation in the candidate (lower undergraduate) programme of Applied Biological Sciences - 1ste kandidatuur (1st year undergraduate) Applied Biological Sciences (partim: 60h Theory) (iii) Support for statistical applications to undergraduate (thesis) students and research groups in the departments of Biology and Applied Biological Sciences

Research: - Development of an independent research programme within the broad field of Evolutionary and Population Biology, in collaboration with the research groups Animal Ecology and Evolutionary Biology - Contribution to the research of the new department Applied Biological Sciences

Profile and requirements

The position will fill up a gap in statistical expertise for the programmes Biology and Applied Biological Sciences, both with respect to teaching and giving support to research. We are looking for a candidate with a strong biologically oriented research background who will be capable of teaching applied statistics specifically for these domains and programmes. The research activity of the candidate will be situated in the field of Organismal and Population Biology. An important focus of attention is the study of patterns of genetic variation (quantitative genetics, population genetics).

Requirements: - PhD in Sciences (Biology) or Applied Biological Sciences (Bio-Engineer) - Additional specialisation or strong research experience in Biostatistics - Research experience in population biology

In principle, the job is opened at the level of docent (lowest rank of Professor). However, a higher degree

can be awarded based on the candidate's application. The position is full-time with tenure awarded after three years on condition of a positive evaluation. Relevant professional experience will be taken into account for the salary.

Candidates have to send their application, including a detailed curriculum vitae and the necessary documents attesting their qualifications, to Prof. dr. Alain Verschoren, rector of RUCA, Groenenborgerlaan 171, 2020 Antwerpen no later than 1 september 2003.

Note: due to legal requirements it is necessary to fill in a specific form which can be downloaded at <http://www.aiv.ruca.ua.ac.be/e-Loket/personeel/-personeel/wat%20te%20doen%20bij%20aanwerving/-inlichtingsformulier.pdf>

For more information, contact Erik Matthysen, Herwig Leirs or Ron Verhagen (firstname.lastname@ua.ac.be)

UBritishColumbia EvolBiol

ASSISTANT PROFESSOR IN EVOLUTIONARY BIOLOGY

The Department of Zoology at the University of British Columbia invites applications for a tenure track position at the assistant professor level in evolutionary biology. We seek an outstanding individual working on any taxon who would fit well with the evolutionary biology group at UBC (<http://www.zoology.ubc.ca/~otto/Evolution.html>). The successful applicant will have a meritorious record and will be expected to develop and sustain a strong externally funded research program that involves the training of graduate students and will be expected to contribute to the teaching of core biology courses at the undergraduate and graduate level. Salary will be commensurate with experience. Appointment will be at the assistant professor level and is subject to final budgetary approval.

Applicants should send a curriculum vitae, a summary of research interests and teaching philosophy, reprints of three key publications, and the names and e-mail addresses of three referees to Dr. Bill Milsom, Head, Department of Zoology, University of British Columbia, 6270 University Boulevard, Vancouver, BC, Canada, V6T 1Z4 (e-mail head@zoology.ubc.ca; FAX: (604) 822-5780). Candidates should ask referees to send supporting letters to the same address. Screening of applications will begin October 1, 2003 and continue until a

suitable candidate is found.

The University of British Columbia hires on the basis of merit and is committed to employment equity. We encourage all qualified persons to apply; however, Canadians and permanent residents of Canada will be given priority.

UCSD 3 EcoEvol

Ecology, Evolution & Conservation Biology The University of California, San Diego Section of Ecology, Behavior & Evolution Division of Biological Sciences <http://biology.ucsd.edu/> The Section of Ecology, Behavior and Evolution in the Division of Biological Sciences at UCSD invites applications for two senior and one junior faculty positions. Appointment level will be commensurate with qualifications and experience with salary based on UC pay scales. Applications from women are especially encouraged.

The areas of scholarship are open but we are interested in ecology, evolution, and conservation biology. Applicants should have Ph.D.'s and outstanding records of research achievement for their stage of career. Appointees are expected to develop strong, extramurally supported, independent research programs and participate fully in both undergraduate and graduate teaching.

Applications will be reviewed upon receipt beginning September 2 and accepted until the positions are filled. Send curriculum vitae, publication list, synopsis of professional goals, research and teaching interests, and three letters of reference (mailed directly from referee) to: EBE Search Committee, Attention: Ms. Romel Hokanson - Mail Code 0116-E, Division of Biological Sciences, 9500 Gilman Drive, La Jolla, CA 92093-0116.

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

Posted by: David S. Woodruff, Professor and Chair Section of Ecology, Behavior and Evolution, Division of Biological Sciences University of California, San Diego
dwoodruf@ucsd.edu dwoodruf@ucsd.edu

UHawaii GeneticsLabSupervisor

CORE GENETICS FACILITY LAB SUPERVISOR-ID# 23313. University of Hawaii. Regular, Full-Time, RCUH Non-Civil Service position, located at the University of Hawaii, Hilo. Continuation of employment is dependent upon program/operational needs, satisfactory work performance, and availability of funds. Salary: Commensurate with qualifications Duties: Manages the operations of a small to medium size molecular genetics core laboratory. Supervises, trains, and schedules students, assists faculty and visiting researchers in the completion of projects. Purchases and inventories equipment and supplies. Maintains molecular and computer equipment associated with core sequencing, genotyping and microarray facilities. Establishes a centralized laboratory information management system that includes a server-based interface for data archiving, dissemination, manipulation and analysis for core facilities. Organizes and runs an annual workshop designed to train researchers, students and technicians on basic and emerging molecular research techniques. Minimum Qualifications: Bachelors degree from an accredited college or university in Biology, Molecular Genetics, Conservation Genetics or other appropriate field. One to three (1-3) years of molecular genetics experience in the collection and management of large datasets. Experience with the operation and troubleshooting of core facility equipment including: Beckman CEQ 8000 for sequencing and genotyping needs, gene arrayer and scanner, web/data/storage servers and associated workstations. Experience in basic molecular methodology and troubleshooting including: PCR, AFLP, microsatellites, RFLP, and gel electrophoresis. Knowledge of molecular biology and personnel management skills. Working knowledge of Apple and PC software, including word-processing, and presentations. Should be familiar with Mac, Win, and general knowledge of genetics analyses software including Sequencher, McClade, PAUP, Bionumerics, Areliquin, MEGA, PHYLIP. The work may require periods in a biosafety cabinet or at a laboratory bench. Desirable Qualifications: Master's degree from an accredited college or university in Biology, Molecular Genetics, Conservation Genetics or other appropriate field. Three to five (3-5) years experience in the management of a molecular genetics laboratory. Inquiries: Dr. Sue Jarvi 974-7358 (Hilo) jarvi@hawaii.edu. Ap-

plication Requirements: See www.rcuh.com and click on "Employment" for additional information regarding employment. You must apply through our on-line web application process by navigating to Current Job Vacancies unless you do not have access to the Internet. Other applicants may apply by submitting resumes, cover letter with ID#, referral source and narrative of your qualifications for position; salary history, names, phone numbers and addresses of three supervisory references and copy of degree(s)/transcripts/certificate(s) to qualify for position via: a) fax: (808) 956-5022 or b) mail: Director of Human Resources, Research Corporation of the University of Hawaii, 2530 Dole Street, Sakamaki Hall D-100, Honolulu, HI 96822. Closing Date: July 21, 2003. EEO/AA Employer.

Sue Jarvi Biology, UH Hilo jarvi@hawaii.edu

UKonstanz EvolBiol

Position as Junior Group Leader

IN EVOLUTIONARY BIOLOGY (preferably in molecular evolution, comparative genomics or devo-evo)

A position as "Assistant" (German government SALARY SCALE BAT II a / C1) in the Department of Biology at the University of Konstanz is available immediately.

The person we are looking for should work on current research topics in the fields of either molecular evolution / phylogenetics, comparative genomics, and / or the evolution of developmental mechanisms. The position is for a Ph.D. biologist, ideally with prior postdoc experience in molecular or developmental biology. A total of three research groups, two of which are headed by an Junior Group Leader each representing their particular subdisciplines of evolutionary biology, make up the Evolutionary Biology group (Lehrstuhl Evolutionsbiologie) in the Department of Biology.

However the taxonomic emphasis is also open for: work on fishes, particularly the zebrafish and cichlid fish model systems is favoured. Space in a modern animal care facility is available. Excellent opportunities are available in terms of space, equipment, departmental facilities and annual financial support from the University of Konstanz for research expenses. The lab has state-of-the-art facilities for molecular and developmental biology, including 2 ABI 3100 DNA-Sequenzers, a pipetting robot, a DNA-chip reader, etc. The University of Kon-

stanz and the Department of Biology in particular are among the most highly rated institutions in Germany and provide a lively and academically outstanding research environment. Konstanz is a lovely historic town located at Lake Constance near the border to Switzerland.

Appointments are initially for 2 - 3 years and are renewable for up to 6 years with an annual gross salary (depending on age, marital status, etc.) of up to 43.000 Euro (about 50.000 US\$). Habilitation is possible, and some teaching (English or German) is required.

Additional information can be obtained from axel.meyer@uni-konstanz.de. Phone: + 49 7531 884163, Fax: + 49 7531 883018 or directly from the internet page: <http://www.evolutionsbiologie.uni-konstanz.de> The University of Konstanz is an equal opportunity employer and in particular encourages female applicants. Also, the University encourages applications by disabled persons, who can reach the University office for disabled persons service at + 49 - 7531 / 88 - 3725.

Please send me applications including a statement of research interests, a full CV, names and email addresses of 2-3 referees to axel.meyer@uni-konstanz.de before July 31st, 2003. Axel Meyer, Ph.D. Professor of Zoology and Evolutionary Biology Department of Biology University of Konstanz Universitätsstr. 10 D-78457 Konstanz Germany

email: axel.meyer@uni-konstanz.de

tel. + 49 7531 88 4163 fax. + 49 7531 88 3018 tel. secretary + 49 7531 88 3069 email: (christiane.ehmann@uni-konstanz.de)

<http://www.evolutionsbiologie.uni-konstanz.de> Axel Meyer <axel.meyer@uni-konstanz.de>

UMelbourne Genetics

LECTURER POSITION The Department of Genetics at the University of Melbourne, Australia seeks a Lecturer who will conduct research in the area of Genetics and will be expected to teach in the areas of evolutionary genetics, population and quantitative genetics, genomics and bioinformatics. The position will be expected to conduct research which leads to publication in quality international journals and will contribute to teaching and course design at undergraduate and postgraduate levels including supervision of

B.Sc(Hons) and postgraduate students. For more information contact Assoc. Prof. James Camakaris or Assoc. Prof Meryl Davis, tel: + 61 3 8344 6246, email genetics-info@unimelb.edu.au or for a position description and details on how to apply please go to: <http://www.hr.unimelb.edu.au/jobs>

Position Description

Department of Genetics, The University of Melbourne
LECTURER Position No: Organisation Unit: Department of Genetics Budget Division: Faculty of Science Classification: Lecturer (Level B) Salary: \$56,602 - \$67,214 p.a. (Level B) Superannuation: Employer superannuation contributions of 17 percent Employment Type: This is a full-time (continuing) position. Other Benefits: Salary packaging and staff training and development opportunities are available. Contact: Assoc. Prof. James Camakaris tel: + 61 3 8344 6246 email: genetics-info@unimelb.edu.au Closing Date: 29 August 2003 Applications To: Deputy Principal, Human Resources, The University of Melbourne, Victoria, 3010; fax +61 3 8344 6080 or email hr-applications@unimelb.edu.au by the closing date. Applicants must address the selection criteria and provide a detailed curriculum vitae by the closing date. Please quote the position number and include the names, phone, facsimile numbers and email addresses of three referees in your application.

1. Position Summary The Lecturer will conduct research in the area of Genetics. The applicant will be expected to teach in the areas of evolutionary genetics, population and quantitative genetics, genomics and bioinformatics. The appointee will establish an active externally funded research program leading to publications in peer reviewed international journals of high standing and have the ability to form and lead a strong research team. He/She will contribute to teaching excellence at undergraduate and postgraduate levels including supervision of B.Sc (Hons) and PhD students, and in activities such as course design and development, and administrative responsibilities such as department and University committees as defined by the Head of Department. The position will report to the Head of Department.

2. Selection Criteria 2.1 Essential a PhD in Genetics or related discipline demonstrated teaching ability in Genetics demonstrated track record in research expertise through training or research experience, in evolutionary, population and/or quantitative Genetics, preferably with a genomics orientation demonstrated ability to deal efficiently with administrative tasks demonstrated ability to interact positively with academic and administrative, technical and support staff 2.2 Desir-

able a track record of publication in international peer-reviewed journals success with attracting external research funding from national competitive grant schemes and/or industry

2.3 General Statement on Selection Criteria - Lecturer. A person appointed to Lecturer will have the capacity to: undertake independent teaching and research in his or her discipline or related area. In research and/or scholarship and/or teaching, make an independent contribution through professional practice and expertise and coordinate and/or lead the activities of other staff, as appropriate to the discipline. contribute to teaching at undergraduate, honours and postgraduate level, engage in independent research and activities appropriate to his or her profession or discipline. undertake administration primarily relating to his or her activities at the institution and may be required to administer and coordinate components of the award program of the institution.

3. Key Responsibilities Provide excellence in undergraduate and postgraduate teaching. Provide supervision and support for B.Sc. Honours, post-graduate diploma, and M.Sc. and PhD students and provide assistance with coordination of one of these programs of study in the Department. Contribute to the discipline by participating in professional bodies and in scholarly meetings and conferences, by undertaking professional activity in the field and by acting as reviewer or assessor of major research grants and scientific publications. The Lecturer is required to participate in these activities on behalf of the Department and The University. Make a contribution to Department and Faculty meetings and

— / —

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>

USouthernCal ResTech

Laboratory Research Technician Population and evolutionary genetics of marine organisms University of Southern California, Los Angeles

We seek a research technician to join our lab group as early as September 1. Work in our lab focuses on 1) the genetics of speciation using a marine copepod as a model, and 2) population genetic structure of a num-

ber of different marine species. Duties of the technician will include maintaining copepod cultures, conducting a variety of molecular assays, managing data, ordering supplies and maintaining equipment. The ideal candidate would have a bachelor's or possibly master's degree in biology, a strong interest in population genetics/evolution and experience with molecular techniques such as PCR, DNA sequencing, microsatellites and AFLPs. Specific training will of course be provided. The position is initially for one year but may be extended pending additional funding. Salary is dependent on experience.

To apply send a letter of interest, a resume, and contact information for three references to the address below via either email (preferred) or regular mail. Review of applications will begin August 1 and continue until the position is filled.

Suzanne Edmands Department of Biological Sciences, AHF 107 University of Southern California Los Angeles, CA 90089-0371 sedmands@usc.edu (213)740-5548 <http://www.usc.edu/dept/LAS/-biosci/faculty/edmands.html> Suzanne Edmands <sedmands@usc.edu>

UZurich AnimalEvol

The Faculty of Science of the University of Zürich invites applications= for an

Assistant Professorship in Animal Evolution or Animal Systematics

(non-tenure track)

Applicants should demonstrate outstanding scientific achievements in animal evolutionary biology or animal systematics and expect to develop an internationally competitive research program. There are no restrictions on the animal groups investigated.

The professorship is in the Zoological Museum of the University. The Museum, which has a public display area and is fully integrated in the teaching of the University, has extensive collections, experienced staff and stimulating, close collaboration with colleagues in the Consortium for Evolution and Biodiversity. Experience in museum displays or in furthering the public understanding of science would be advantageous, as would proficiency in German. The successful candidate will participate in teaching evolutionary biology. The position is available for a maximum of six years.

Applications including a curriculum vitae, a publication list, short summaries of current and future research, of teaching activities and copies of three recent key publications should be sent by 15th August to Prof. K. Brasel, Dekan der Mathematisch-naturwissenschaftlichen Fakultät der Universität Zürich, Winterthurerstrasse 190, CH-8057 Zürich, Switzerland. At the same time please submit your CV and publication list as a single PDF or Word file to jobsmnf@zuv.unizh.ch.

For further information please contact Prof. Paul Ward, pward@zoolmus.unizh.ch, Zoologisches Museum, Winterthurerstrasse 190, CH-8057 Zürich, Switzerland. – PLEASE NOTE NEW PHONE AND FAX NUMBERS

Prof Paul I Ward Zoologisches Museum der Universität Zürich Winterthurerstrasse 190 CH 8057 Zürich Switzerland

Phone +41 1 635 4760 Fax +41 1 635 4780
pward@zoolmus.unizh.ch pward@zoolmus.unizh.ch

Other

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Asteraceae NuclearGenes

Other: Nuclear genes in the Asteraceae We are working on the genus *Senecio* (Asteraceae) with the aim of determining origins of a number of polyploids. We are hoping to be able to sequence single-copy (or low copy) nuclear genes such as *Adh*, *PgiC*, *CHS*, *Tpi* and have met with limited success. Our searching so far has found that studies using these genes have been carried out in distantly related species, eg cotton or rice, and suspect the primers will not work. We would therefore like to hear from anyone who has used these genes in a species related to *Senecio* and any information about primers would be greatly appreciated. Many thanks in advance Mark

Mark Chapman (mac7@st-and.ac.uk) Sir Harold Mitchell Building School of Biology University of St Andrews St Andrews FIFE KY16 9TH

Mark Chapman <mac7@st-andrews.ac.uk>

Authorship criteria

Greetings! I have heard for a very long time that a publication exists that lists five criteria for authorship, of which coauthors must meet three.... but I have not found anyone that knows how to find that article. Any suggestions on criteria for authorship, or references to the original article would be greatly appreciated.

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

Connie_KeelerFoster@fws.gov

Authorship criteria answers

Greetings! Responses to my inquiry were substantial. It appears this is an issue of increasing concern, particularly in regards to honorary authorships. The list of references include:

Schmidt, R. H. 1987. A worksheet for authorship of scientific articles. *Bulletin of the Ecological Society of America*. 68:8-10

Dickson, J. G. et al. *Wildlife Society Bulletin* 6:260-261.

Hunt, R. 1991. Trying an authorship index. *Nature* 352: 187. (I have a copy now as a pdf file if anyone wants it and can't access it)

Rennie, D. and D. Kennedy. 2002. A proposal for Transparency. *Science* 298 (5598): 1544c.

Evolutions instruction to authors includes specific authorship criteria: <http://lifesciences.asu./evolution/-instruct.html> Many individuals familiar with medical literature cited: <http://www.icmje.org> which lists criteria for authorship for a group of medical journals. (I

have now as a pdf file if anyone wants it and can't access it)

BMS Views and News, Editorial, by Emma Veitch
Reviewing Peer Review: The Fourth International
Congress on Peer Review in Biomedical Publication.
(I have now as a pdf file if anyone wants it and can't
access it)

Thank you so much for the many responses. Connie

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

Connie_KeelerFoster@fws.gov

Biogeography

Hi everybody, I'm actually working on sexual selection
in birds and the interaction between the presence of
birds in the tropical zone and the occurrence of sexual
dichromatism. I would need some information, that
I really found nowhere: What are the total areas of
emerged land inside the tropical zone and outside the
tropical zone? What area the total areas of earth inside
the tropical zone and outside the tropical zone? I would
be very grateful if someone could help me. Thanks a
lot in advance for any answer! All the best,

Marine

Marine DANEK-GONTARD Laboratoire de Para-
sitologie Evolutive CNRS UMR 7103 Université Pierre
et Marie Curie Bât. A, 7ème étage 7, Quai St
Bernard, Case 237 F-75252 Paris Cedex 05 France
Tel.: +33 1 44 27 31 45 Fax.: +33 1 44 27 35 16
mgontard@snv.jussieu.fr

Bonferroni correction

Dear all, I recently had a problem while applying Bon-
ferroni correction (Rice, 1989) to pairwise F_{st} values on
a "large" set of data: The p value is so small that almost
none of the values remain significant after that correc-

tion (the p value become less than 1/1000). However,
it looks like this is a very conservative way of trying to
avoid type I errors, and it actually may induce a very
high amount of type II errors. It seems to me that it
should be a real source of concern when analysing large
dataset, and then potentially losing a lot of important
information. However, I still see a lot of studies using
it and not interpreting the values that are not signifi-
cant after Bonferroni correction. Moreover, in a lot of
cases, it looks like you would then have more chance to
keep your value significant while reducing your dataset,
which is quite unusual. I did not find, so far, a lot of re-
ferences trying to estimate the problem Bonferroni could
induce in terms of type II errors. I heard only about
one good reference on this: Sachs, L. 1980. Applied
statistics: a handbook of techniques. Springer-Verlag.
New York. but I could not find it. I would like to ask
you if some of you would have this reference, or another
one reporting strong points and weakness of Bonferroni
correction, or a personal advice, I would be interested
in hearing from you. Thanks Sophie

Sophie ARNAUD-HAOND, PhD. Centro de Ciencias
do Mar Faculdade de Ciencias do Mar e Ambiente
(F.C.M.A.) Universidade do Algarve Campus de Gam-
belas P-8005-139 Faro, Portugal Tel: 00 351 289 800
900 ext 7359 Fax: 00 351 289 818 353 Email : sar-
naud@ualg.pt

Sophie ARNAUD-HAOND <sarnaud@ualg.pt>

Bonferroni correction answers

Dear all, I received a lot of interesting comments, sug-
gestions and references following my request on Evoldir
about Bonferroni correction for multiple tests. It seems
to be an important source of debate, thinking and in-
terest for a lot of people. Here below is the compilation
of the personal comments that I have been sent, and,
at the end, a list of useful references I received. Thanks
again to all the people who kindly answered and sent
information Sophie

I have been doing association studies with the most
polymorphic expressed genetic system, the HLA loci.
Multiple comparisons is a painful issue in my research
and I have had several papers rejected early in my car-
eer with a simple statement that "correction for mul-
tiple comparisons was not made and the results are in-
valid." Now in a later phase in my career (and as a
reviewer myself), I see this more as an excuse for a

busy referee to avoid a comprehensive review. I got so fed up that I educated myself and created my own webpage on statistical analysis of HLA association studies with particular emphasis on multiple comparisons issue: <http://home.att.net/~dorak/stat.html> Please have a look at this page and you will see an extensive discussion of this issue with a lot of references. The two that specifically discuss type II errors are those rather accessible ones:

I feel that the best way of dealing with the problem is simply decreasing the number of tests. I find that a matrix of pairwise p-values mostly provides only little insight, and it's more useful to perform a hierarchical Fst-analysis, which is also more powerful (make biologically meaningful groups of populations and test between them). This also gives a better estimate of Fst as it will be averaged over several populations. If you do not have logical groupings, but do have a lot of populations, you might wanna try Jerome Goudet's PCAGEN method. Nevertheless, I also acknowledge the fact that it is sometimes inevitable to look at the pairwise matrix.

I have no answer for the question you posted on EvolDir (except that I think it depends on what you want: if you want to examine candidates for something, you don't need Bonferroni; if you want to be sure that an individual observation is significant, there is no way around it).

However, I'd be very interested in the responses you get. It would be great if you could either post them on EvolDir, or send me a copy of those that you find most useful

am sorry i cannot help, but i have thought about the same problem when correcting our own data sets. I refrained to correcting only within small units of the analysis but not the entire table. In the article towards the end Rice ask to apply the correction within the correct unit and leaves you some space for interpretation (as i interpreted it).

However, if units are larger i really wonder whether the technique is wise anymore. If you get good advise or/and come to an interesting conclusion yourself, please let me know!

What you have seen is correct, as is Bonferroni. There is a penalty that we must pay when we want to ask a lot of questions on the same data, that is just the nature of statistical inference. Perhaps instead of asking the same question in a pair-wise fashion amongst your $K(K-1)/2$ data points, you can ask more direct questions of all data simultaneously and thus only loose a single degree of freedom. I can't provide any more in-

sights since I don't know the domain of your question you are using Fst to answer. If you'd like to discuss it further, drop me a line.

You might want to try the Dunn-Sidak version of the sequential Bonferroni correction, which is slightly less conservative than the usual Bonferroni. A description of it can be found on page 241 of

Sokal, R. R. and F. J. Rohlf. 1995. Biometry. New York: W. H. Freeman.

Regarding your more general question about the loss of information due to correction for multiple comparison, you have to decide in the context of the specific statistical tests you are conducting whether type I or type II errors are more important. If you are screening for carriers of a disease, making a type II error is worse (because you will miss some carriers and allow the disease to spread), but if you are comparing the effects of a new medication to a placebo, a type I error is worse (because you would approve a medication that is no better than placebo). So, the interpretation for your own data set would depend on the context—more controversial results would warrant a more conservative interpretation of the statistics, more mundane results might give you some more wiggle-room.

I had the same sorts of questions while looking at coevolution in proteins (Pollock et al, JMB 1999). I had thousands of comparisons, and the Bonferroni correction requires a 95% probability of for the statistic for

— / —

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>

Cimicidae samples

I would like to ask for help in obtaining samples of Cimicid bugs (Hemiptera: Cimicidae) to be used in constructing a molecular phylogeny of this group. These insects may be found in the roosts or nests of many birds and bats or sometimes on the hosts themselves. I would be grateful for any samples to be placed in 95% ethanol, together with information on the collection location and host species, to be sent to me at Department of Ecology, Evolution & Marine Biology, University of California, Santa Barbara, CA 93106, USA.

Many thanks Ted Morrow morrow@lifesci.ucsb.edu

Cupressus chromosomes

Hello, I am actually working on in situ hybridisation on cupressus sempervirens chromosomes. We have problems in synchronising mitosis in cypress roots. Has anyone worked on cupressus sempervirens chromosomes? I would like to know what is the best treatment in order to observe a maximum of cells at the metaphase stage. Thank you, Benjamin

Benjamin.liens@avignon.inra.fr

DNA in acetic acid

Dear colleagues,

Does anyone have any experience with long-term (~6 months) stability of DNA in glacial acetic acid?

I've been using phenotypic pollen traits to estimate the somatic mutation rate of a tree and have anthers from >800 flowers stored in glacial acetic acid. I will be doing acetolysis/pollen counts starting in about two weeks, and am wondering if extra bits of anther/filament tissue might be useful for parallel DNA work.

Thanks for any help, I will summarize to the list if there's interest.

Douglas Scofield Department of Biology
d.scofield@umiami.edu University of Miami off:
 (305) 284-3778 P.O. Box 249118 fax: (305) 284-3039
 Coral Gables, FL 33124-0421

DNA in etoh-benzene

Does anyone have any experience extracting DNA from specimens stored in ethanol that is 1.5% benzene? The specifications from the manufacturer are:

Ethyl Alcohol 96.4% - 95% volume Benzene - 1,5% volume Butyl alcohol - 3,5% volume

A colleague has been given this ethanol but is not sure if it suitable for tissue preservation. Thank you very much for any information.

-Michael

Michael T. Monaghan Department of Entomology The Natural History Museum London SW7 5BD U.K.

m.monaghan@nhm.ac.uk

Dendrogram scales

Hello, My name is Lianna Sliwczynski, i am a student from RMIT university and working in Melbourne, Victoria Australia.

I was hoping someone knows how to calculate Dice Coefficients, percentage similarity and percentage divergence. Each of these are represented in dendrograms of amplified fragment length polymorphism (AFLP) analysis, after the pseudonucleotides have been put through distance matrix programs and alignments or something. I have looked at TREEVIEW, but the scale is in "PAMS". Can you help? email this address or s2007782@student.rmit.edu.au

References that show dendrograms with scales i am hoping to create (once someone can tell me how).

Thank-you. <<Hookey et al 1999 fAFLP and MRSA.pdf>> <<Grady et al 1999 fAFLP and MRSA.pdf>> <<Grady 2001 FAFLP and PFGE for MRSA.pdf>>

"Sliwczynski, Lianna J"
 <Lianna.Sliwczynski@mh.org.au>

Drawing networks

Hi there,

We are currently using Network 3.0 to construct median joining networks from mitochondrial data. We are trying to work out a way to manipulate the outputted network (i.e. show the various populations represented for a single haplotype by using different colours for that circle in the network). It appears that the network can

only be saved as a bmp file although it looks like emf may be an option in the future.

Does anyone have any bright ideas that would allow further manipulation of these images? What we would like to do is export the image to something like CoralDraw and be able to do further editing there.

Thanks for your help.

Andy Given

– Andy Given

PhD Candidate Dept. of Zoology, University of Toronto and Centre for Biodiversity and Conservation Biology, Royal Ontario Museum

ph. 416 586 5761 fax 416 586 5553

Andrew Given <andrew.given@utoronto.ca>

Drosophila Rsp-i32 strain

Dear colleagues, I am trying to obtain the Rsp-i32 (responder satellite insensitive 32 allele) strain of *D. melanogaster*. If you have this and/ or derived strains that you would be willing to send us, please send me an email at the following address: hsmalik@fhcrc.org. Thanks for your time. Harmit

Dr. Harmit Singh Malik Assistant Member, Basic Sciences, Fred Hutchinson Cancer Research Center 1100 Fairview Avenue N, A1-162, Seattle WA 98109-1024. (206) 667-5204 hsmalik@fhcrc.org

Harmit Malik <hsmalik@fhcrc.org>

FTA cards testimonials answers

Here is a summary of the information I received back from list members after asking for advice on collecting blood using FTA Whatman cards. I was not able to get whatman cards in time for my recent field collecting trip, so I used the Whatman filter paper for some samples and lysis buffer for others, as described below. I'll email the list if it doesn't work, otherwise you can assume it is a fine method.

Heather

Hi, here is the email for the scientist who invented the FTA card: Leigh.Burgoyne@flinders.edu.au I have used them myself for cuttlefish tissue and they work fine. I think with blood its even better. I am sure Leigh would answer all your questions better than I can, so contact him.

Hello Heather. I haven't used the FTA cards, but what I do use is simple Whatman filter paper. I just soak up the blood with strips of filter paper, stick them in a tube of EtOH, and store them at room temperature. I have successfully amped both microsatellites and mtDNA genes using this procedure (all birds). Considering you will be taking fresh blood (i.e. lots of good DNA), you can use a digestion followed by a simple phenol-chloroform extraction. This is the cheapest way I know of (though tedious) and gives good DNA preps. If money is not an issue, you can use kits such as QIAGEN DNEasy - this is the cleaner approach, but costs a lot more. If I had the funding then this is the way that I would go - faster, cleaner, and avoid the nasty phenol-chloroform fumes (phenol is a carcinogen).

OR Just take a scalpel and cut a square ~ 5 mm x 5 mm from the filter paper, digest in lysis buffer with Pro K in a waterbath (55-65 degrees) overnight, and perform a phenol-chloroform extraction the next day. It's that simple. Hope this helps.

----- I'd collect blood in lysis buffer unless there is some serious reason not too. Presumably you need needles to make a prick with the FTA card method and maybe also capillaries to transfer the blood to the card. That's all you need to collect blood in lysis buffer in screw-cap tubes and I would think you could get more blood into the tube.

Second and more importantly, if you're planning mtDNA work, collect a feather or two in addition to the blood sample. Nuclear copies are a potentially pesky problem with blood samples and feathers generally provide clean mtDNA sequences in cases where blood samples produce a co-amplified product,

Sorenson, M.D. & T.W. Quinn. 1998. Numts: A challenge for avian systematics and population biology. *The Auk* 115: 214-221.

Sorenson, M.D. & R.C. Fleischer. 1996. Multiple independent transpositions of mitochondrial DNA control region sequences to the nucleus. *Proceedings of the National Academy of Science USA* 93:15239-15243.

Heather R.L. Lerner, M.S., PhD candidate University of Michigan Museum of Zoology, Department of Ecology and Evolutionary Biology 1109 Geddes Rd.

Ann Arbor, Michigan 48109-1079 734-763-0310 <http://www.umich.edu/~hlerner> hlerner@umich.edu

Formaldehyde fixed samples

Dear all,

I have five very valuable samples of voles (Rodentia) from Romania, that were originally stored in formaldehyde and after a year or two transferred to alcohol. Most methods that deal with DNA extraction from such a material state that the sufficiency is only about 20% of all samples and none of them succeeded in a PCR product from my samples. Does anyone have a protocol that gives any better results? Is a 300bp PCR product too long to believe in? I'll be grateful for all the replies.

Natalia Martinkova Institute of Vertebrate Biology Academy of Science Kvetna 8 603 65 Brno Czech Republic e-mail: stmartinek@volny.cz

GelCompar AFLPs

Hi

we are trying out the GelCompare software to analyse AFLP banding patterns in plants. The software seems to be quite useful, but we are not sure about the best settings for AFLP's. Does anyone has any experience with GelCompar and AFLP's especially on sensible sensitivity settings, i.e. on the best value for "minimum profiling" and the percentage "optimisation"?

Thanks for any feedback

Jasmin –

Dr. Jasmin Joshi Institute of Environmental Sciences University of Zurich Winterthurerstrasse 190 CH-8057 Zuerich Switzerland

NOTE NEW PHONE NUMBER!!

Tel. ++41 (0)1 635 6128 Fax ++41 (0)1 635 5711 e-mail joshi@uwinst.unizh.ch <http://www.unizh.ch/~uwinst/>

Genotyper GelCompare

Dear EvolDir members

I would be most interested in corresponding with anyone who is currently working (or has recently worked) with two software designed for automated scoring of AFLP and SSR - GENOTYPER and GelCompare.

Thanks very much. Svetlana

Dr. Sviatlana Trybush

Plant Population Biology and Genetics Plant and Invertebrate Ecology Division Rothamsted Research Harpenden, Herts AL5 2JQ UK

“sviatlana trybush (RRes-Roth)”
<sviatlana.trybush@bbsrc.ac.uk>

HybridZone micros

Dear all, I am working with microsatellite loci in a tetraploid specie. And I have found some different alleles in a supposes hybrids individuals. On the other hand, some authors not recommend use microsatellite in Hybrid zone, species boundaries and phylogeny. Any body know if there are any problem to use microsatellite loci to study hybrid zone?

Thank in advance

Miguel Angel

Dr. Miguel Angel González Pérez Departamento de Biología Universidad de Las Palmas de Gran Canaria Campus de Tafira 35017 Las Palmas Islas Canarias Spain e-mail: mgonzalez@becarios.ulpgc.es

canariensis750@hotmail.com

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gunter.wagner@yale.edu

MarieCurie TrainingPositions

Short Predoctoral Marie Curie Training Positions

Two Vacancies !!!

<http://www.ub.es/molevol/MarieCurieAnuncio.html>

The Molecular Evolutionary Genetics Group at Universitat de Barcelona <http://www.ub.es/molevol> has been selected as a Marie Curie Training Site in Molecular Population Genetics and Evolution by the EU Commission (Contract No. HPMT-2000-00108). Short training fellowships of 6-12 months are available to non-Spanish EU registered predoctoral students. Fellows will receive an allowance of 1200 euros per month.

Within the area of Molecular Population Genetics and Evolution, the host group studies nucleotide variation at both the intraspecific and interspecific levels in different species of *Drosophila* and of *Cruciferae*. This work aims to establish the role of natural selection in shaping nucleotide variation, and also to infer the evolutionary history of populations and/or species.

Further details of the research programme of the group, and the job description for the present vacancies are available from the group's web site. <http://www.ub.es/molevol/MarieCurieAnuncio.html> <http://www.ub.es/molevol>

Main Marie Curie Requirements:

Nationality

All fellows must be nationals of an EU Member or Associated State, or have resided in the EU for at least

five years immediately prior to their selection.

Mobility

They must not undertake their fellowship in the country of their nationality or recent centre of activity.

Age

At the time of selection the fellow must be 35 years old or less.

Research Experience

The scheme is directed to postgraduate researchers pursuing doctoral studies in a subject area similar to that of the Training Site. Applicants should be affiliated to a University as PhD students both at the time of application and during the Marie Curie training fellowship.

Julio Rozas Carmen Segarra Departament de Genetica, Facultat de Biologia, Universitat de Barcelona Diagonal 645, 08028 Barcelona Spain

jroz@ub.edu

Marker choice

EvoDir,

Can anyone actually justify spending time, effort and money on randomly generated molecular markers (e.g. AFLPs and RAPDs/ISSRs) for ecological studies that assume (hope) markers are selectively neutral? Has anyone attempted to correlate any of these randomly generated markers with ecological variables?

Any thoughts would be of interest.

John McMullan

jjm13@le.ac.uk

Micro checker

Dear Evol. Dir. members,

Regarding Tom's email on the scoring of microsatellites, and in particular possible genotyping errors due to stuttering, large allele drop out and null alleles, we have designed software that can help you identify such scoring errors.

The software is free and can be downloaded from: <http://www.microchecker.hull.ac.uk/> The software, called MICRO-CHECKER, is a Windows-based (Windows 98 SE, 2000 and XP, not yet tested on NT or ME), and can test the genotyping of microsatellite data from diploid populations. The program aids the identification of various genotyping errors, and can also detect typographic errors. MICRO-CHECKER estimates the frequency of null alleles at a locus using a series of algorithms. If null alleles are detected, MICRO-CHECKER can also adjust allele and genotype frequencies of the amplified alleles, which allows the data to be used in further population genetic analysis, for instance with GenePop, Arlequin or Fstat.

Regards, Cock van Oosterhout – Dr. Cock van Oosterhout NERC Research Fellow University of Hull Hull HU6 7RX, UK Tel.: +44(0)1482 465505 Tel.: +44(0)1482 466434 Fax.: +44(0)1482 465456 <http://http://www.microchecker.hull.ac.uk/> <http://www.hull.ac.uk/biosci/staff/vanoosterhout.html>

C.van-Oosterhout@hull.ac.uk

Micro sizes

Hello:

Can anyone give me advice on scoring microsatellite fragment sizes? I'm running m13 tailed di- and trinucleotide repeats on an ABI 3100 capillary sequencer. We are getting nice clean runs but are seeing quite a bit of stutter for large repeat fragments. Between the stutter and poly-a addition, I'm worried about the accuracy of calling the actual fragment size for the large repeats. Are there any tricks to reduce stutter?

Tom tjuenger@mail.utexas.edu

MiltonRoySpectronic software

A serious problem is mostly accompanied by another one! We have a "Milton Roy Spectronic 3000" whose motherboard (PC 286) crashed and beyond that the harddisk became unreadable! However, the harddisk contained the software organizing the photometer and enzyme kinetics, and today there is no chance to get

the ten year old software from a dealer!

Does anybody have copies of the programmes

rapscan version 2.1.1, enzyme kinetics version 2.0.2 and rate analysis version 2.0.2

?

If yes, it would be a great help for us. Thanks Jürgen Tomiuk

Dr. Jürgen Tomiuk phone: +49-(0)7071-29-76883 - Professor - fax: +49-(0)7071-29-5233 University of Tübingen e-mail: juergen.tomiuk@uni-tuebingen.de Institute of Human Genetics Division of General Human Genetics Wilhelmstrasse 27 D-72074 Tübingen Germany

Jürgen Tomiuk <juergen.tomiuk@uni-tuebingen.de>

Nested Clade Analysis 2

New gene functions

A volume edited specifically for discussion about new gene evolution and its related problems, "Origin and evolution of new gene functions", has appeared in two forms: *Genetica* 118 (No.2-3), 2003 and a hardbound book as Volume 10 of "CONTEMPORARY ISSUES IN GENETICS AND EVOLUTION". More information can be found in two websites:

<http://www.wkap.nl/prod/b/1-4020-1396-5> and <http://www.kluweronline.com/issn/0016-6707>

–

Manyuan Long, Ph.D.

304 Zoology Building Department of Ecology and Evolution & The Committee on Genetics The University of Chicago 1101 East 57th Street Chicago, IL 60637 (773) 702 0557 (office) (773) 834 3567 (lab) (773) 702 9740 (fax) <http://pondside.uchicago.edu/~longlab/longlab.html>

Manyuan Long <m-long@midway.uchicago.edu>

blouinm@science.oregonstate.edu

Outsourcing AFLP work

Hello,

Has anyone outsourced their AFLP work? If so, I'd be interested in asking you a few questions.

Ciao,

Rodney Dyer

- Department of Botany Iowa State University
rdyer.botany.iastate.edu

rodney@iastate.edu

Pop Foundings

Hi, I could use suggestions on the best way to answer a particular question using microsats. Say you have two remnant populations of a species. One of them is smaller and is much less diverse than the other. I would like to distinguish between two scenarios for the origin of those two populations. (1) The large population was the only surviving remnant of the original species, and then the less diverse population was recently founded by individuals from the larger population, or (2) each population is an independent remnant from the originally widely distributed species. At two out of 11 loci the small population has private alleles (i.e. not seen in my sample from the large population). This argues for the latter scenario. However, this is just a verbal argument. It is possible that the two populations were part of a common gene pool and the larger population just lost those alleles owing to drift since the two remnant populations were isolated (or the alleles are rare and weren't seen owing to inadequate sampling of the large population). I would like to estimate a relative likelihood for the two scenarios. If the two populations were historically differentiated to a large extent then R_{st} should be greater than F_{st} (I haven't checked yet). Any other suggestions on ways to distinguish between the two scenarios? Thanks, Mike

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

Relatedness software

Dear all,

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. Any information is very wellcome !! We will post in return all the informations we get. Thank you for your help,

Claire

- Claire BILLOT CIRAD-Biotrop TA 40/03 Avenue d'Agropolis F-34398 Montpellier Cedex 5 France

Tel : (33) 4 67 61 58 58 Fax : (33) 4 67 61 56 05 e-mail: claire.billot@cirad.fr <http://www.cirad.fr/presentation/programmes/biotrop.shtml>

Rice cell types

I'm looking for a reference for the number of different cell types that can be found in Rice, *Oryza sativa*. I am conducting a pilot study comparing number of cell types and numbers of genes in Eukaryotes with sequenced genomes. Any estimates, and/or referrals to references that might contain an estimate would be greatly appreciated.

Thanks, Jeff

Dr. Jeffrey M. Marcus Assistant Professor Department of Biology 1 Big Red Way Western Kentucky University Bowling Green, KY 42101 -3576 USA 716-908-1461 jeffrey.marcus@wku.edu

RoyalInstLondon Lecture

L'Oréal-Royal Institution Science Graduate of the Year Award 2003 3 July, 7.30pm This year's winner of the L'Oréal-Royal Institution Science Graduate of the Year 2003, has recently been announced as Araxi Urrutia Odabachian and as part of the prize, Araxi will be presenting a lecture here at the Ri about her research on Thursday 3rd of July at 7.30pm. She will be talking about the organisation and the function of most genes contained in the human genome sequence. Araxi will show that understanding gene control is crucial. She will discuss the adaptations found in those genes with high levels of activity and how her research is changing our understanding of human genome organisation. Not only will this be a timely discussion with the newly completed mapping of the human genome, but it will also be a chance to see an enthusiastic young researcher talking passionately about her work. For details of the event, please go to <http://www.rigb.org/rimain/calendarDisplay.jsp?&cat=9&mnth=6&yr=2003> and for details of the news release about Araxi's prize winning research please visit <http://www.rigb.org/rimain/newsdetail.jsp?cat=1&nid=46> To book your tickets please call the events team on 020 7409 2992 or e-mail events@ri.ac.uk, giving details of the event you wish to attend and quoting "EvolDir" to ensure you receive £5 concessionary tickets. Bookings can also be made online at www.rigb.org

Daniela Queen Events Assistant The Royal Institution 21 Albemarle Street London W1S 4BS Tel: 020 7670 2903 Fax: 020 7670 2920 Email: dqueen@ri.ac.uk www.rigb.org Registered Charity No 227938

Daniela Queen <DQueen@ri.ac.uk>

Sloan Research Fellowships

SLOAN RESEARCH FELLOWSHIPS IN COMPUTATIONAL AND EVOLUTIONARY MOLECULAR BIOLOGY

The Alfred P. Sloan Foundation is pleased to invite nominations for Sloan Research Fellowships in Computational and Evolutionary Biology.

The Sloan Research Fellowships are awarded each year to a select number of scientists in the early stages of their careers, usually in their first appointment to university faculties. Since the program was initiated in 1955 in only three scientific fields, some 28 former Sloan Research Fellows have won Nobel Prizes, and hundreds have received other honors.

The deadline for receipt of nominations is September 15, 2003. Candidates must be members of the regular faculty (i.e. tenure track) of a college or university in appointments in United States or Canada, and be nominated by a senior scientist. Direct applications are not accepted. The eligibility criteria are quite specific, and are described in appropriate detail in the enclosed brochure, and at www.sloan.org under "Fellowships."

I invite you to consider nominating any outstanding young scientists who meet the eligibility criteria.

Further information may be obtained from: Dr. Michael S. Teitelbaum Alfred P. Sloan Foundation 630 Fifth Avenue, Suite 2550 New York, NY 10111 teitelbaum@sloan.org

Knowles <Knowles@sloan.org>

Software NexusBuilder

Hi,

For those of you who do parsimony searches, I'd like to announce the NexusBuilder Website (<http://www.donnasaxby.com/nexus.htm>).

This site builds PAUP command file to run advanced heuristic search strategies (the parsimony ratchet and 'new strategy'). These are very effective at searching large, 'noisy' data sets.

You set the parameters, and the PAUP command file is e-mailed to you.

For details of the advanced search strategies see: Kevin C. Nixon. The Parsimony Ratchet, a New Method for Rapid Parsimony Analysis. *Cladistics* 15: 407-414 (1999) and Donald L.J. Quicke, Jason Taylor and Andy Purvis. Changing the Landscape: A New Strategy for Estimating Large Phylogenies. *Systematic Biology* 50: 60-66 (2001)

I've just been learning website design, so I'd appreciate comments and bug-reports.

Cheers,

J.

Dr Jon Jeffery Maresingel 29 2316 HB Leiden Nederland

+31 (0)71 521 7885 (home) +31 (0)641 272 960 (mobile) +31 (0)71 527 4900 (fax) jon@donnasaxby.com

Software Structure 2.1

We have now released the newest version of the software package Structure (version 2.1) for analyzing genetic population structure. The new version includes some updates to the basic algorithm, as well as a user-friendly graphical front-end.

The software can be downloaded from <http://pritch.bsd.uchicago.edu> (click on "software").

Structure is designed for studying population structure using multilocus genotype data from each of a sample of individuals. The program implements a model-based clustering method for identifying the presence of distinct populations represented in the sample. Individuals in the sample are assigned (probabilistically) to populations, or jointly to two or more populations if their genotypes indicate that they are admixed. Applications include detecting the presence of population structure, assigning individuals to populations, studying hybrid zones, identifying migrants and admixed individuals, and association mapping in the presence of population structure.

Users may also be interested in the program 'distruct' written by Noah Rosenberg for plotting Structure results (see Science 298:2381). Distruct is available at www-hto.usc.edu/~noahr/diversity.html.

What's new in this release? Version 2 (Beta) introduced a user-friendly graphical interface that makes using Structure much easier, and provides various tools for visualizing the MCMC output and results and organizing the output data.

Version 2 (Beta) also introduced some algorithmic extensions, including a new model that allows loci to be linked (though still not tightly linked). Among other changes, it also improved the model of correlated allele frequencies, often leading to better performance on problems with weak population structure. The details are in a paper by Falush, Stephens and Pritchard (Genetics, in Press; available from the Structure website).

Version 2.1 corrects some minor bugs in the Beta release (see web page), and adds a few small features.

Contributors to the Structure project include Peter Donnelly, Daniel Falush, Matthew Stephens, William Wen and myself.

Sincerely, Jonathan Pritchard

Department of Human Genetics University of Chicago
<http://pritch.bsd.uchicago.edu> Please direct software-related email to structure_help@genetics.uchicago.edu

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Tel. France 04 6714 3732 - International 33 4 6714 3732 Fax. France 04 6714 3719 - International 33 4 6714 3719 <<http://www.univ-montp2.fr/serveurs/-ecolag.html>> berrebi@srvmail.univ-montp2.fr

Up Down Lines

Dear all,

investigating the realized heritability for nectar production in *Echium vulgare* I established high and low nec-

tar production lines. However, for the low line contrary to expectation nectar production increased rather than decreased. To control for this shift in nectar production I thus combined the two lines for calculation of heritability, since no proper control lines were included in this experiment. Does anybody know about other studies in which the calculation of realized heritability is based on the combination of up and down lines after bi-directional selection?

Kirsten Dr. Kirsten Leiss Institute of Biology,
University Leiden Kaiserstraat 63, 2311 GP Leiden
P.O.Box 9516,2300 RA Leiden The Netherlands Phone:
+31 (0)71 5275158 Fax: +31 90)71 5274900 e-mail:
Leiss@RULSFB.LeidenUniv.nl

I have two equipment questions.

1) We (Walt Eanes' Lab) are looking to scale up to using a UV/visible wavelength microplate reader for Vmax and various metabolite concentration measurements. Does anyone have suggestions as to a good (or bad for that matter) spec. that we should look into?

2) I'm looking to purchase a cellulose acetate electrophoresis rig on which to run allozymes for a teaching lab. I'm having a hard time locating the old Gelman (now Pall) rig that I have used in the past. Does anyone know of a good, currently available, set up?

Thanks in advance for any help that can be offered.

Thomas Merritt Dept of ecology and Evolution SUNY-Stony Brook

thomas merritt <merritt@life.bio.sunysb.edu>

equipment questions

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Antibes INRA InsectPopGenet

A two-years postdoctoral position is available in the area of insect population genetics of invasive species in the National Institute of Agricultural Research (INRA) of Antibes, France.

The postdoctoral associate will participate in research that combines experimental and molecular data analysis to study the invasion and geographic expansion of the Western Corn Rootworm (WCR) *Diabrotica virgifera virgifera* (Coleoptera: Chrysomelidae) in the USA and Europe. The main objectives of the program will be to retrace the routes of introduction of WCR in western America and in Europe and to describe the general dynamics of spread of recently founded populations. The applicant must have a good expertise in theoretical and/or empirical population genetics analysis and more generally in evolutionary biology. Some experience in the use of microsatellite markers and data analysis of such markers (including simulations) will be appreciated.

This position is funded by the INRA institute which is the major French state funded institute of agricultural research. Funding will start 1 January 2004 until 31 December 2005. The successful applicant will receive a one-year appointment with good chances for a one-year renewal.

Job location: INRA-UNSA Research Center of Antibes, Sophia-Antipolis (Provence-Côte d'Azur, France). The successful applicant will work in= close collaboration with a group of four scientists: - Thomas Guillemaud: population genetics of neutral markers and of markers under selection, UMR ROSE INRA-University of Nice. - Laurent Lapchin: coevolution and population dynamics, UMR ROSE INRA-University of Nice. - Arnaud Estoup: population genetics of neutral markers. CBGP, INRA Montpellier - Denis Bourguet: population genetics of neutral markers and of markers under selection. CBGP, INRA Montpellier

Application : a Ph.D. is required; to apply, submit electronically to Thomas Guillemaud (guillem@antibes.inra.fr): (1) a CV, (2) copies of recent publications (maximum of three), (3) a statement of research interests and

(4) the names and addresses of three scientists who may be contacted. Applications will be considered until fulfilled. French fellows cannot apply.

Thomas Guillemaud

Equipe Biologie des Population en Interaction UMR 1112 "ROSE", INRA-UNSA 123, boulevard Francis Meilland - BP 2078 - F-06606 ANTIBES CEDEX FRANCE E-mail : guillem@antibes.inra.fr

ArizonaStateU Bioinformatics

Postdoctoral Position Bioinformatics and Computational Evolutionary Biology Arizona State University

A postdoctoral position is available in the areas of bioinformatics and computational evolutionary biology. There is considerable freedom in the choice of research topics, although spatial and comparative genomics and phylogenetics are areas of particular interest. Extensive collaborative opportunities exist between this position and the Arizona Bidesign Institute's Center for Evolutionary Functional Genomics (<http://www.azbio.org>) and the Translational Genomics Research Institute (<http://www.tgen.org>).

Doctoral degree in Biology or related area prior to appointment and not currently in a permanent faculty position is required. Background in evolutionary biology or theory; experience with computer programming, statistics or data analysis; and research interest in spatial comparative genomics and/or phylogenetics desired.

The position is for one year, renewable, with the earliest start date of August 16, 2003. Applications (including a CV, research statement, and names/contact info for three references) and questions must be submitted to msr@asu.edu (email preferred) or

Michael Rosenberg School of Life Sciences PO Box 874501 Arizona State University Tempe, AZ 85287-4501

Phone 480-965-1578 <http://lswb.la.asu.edu/rosenberg>
Applications will be reviewed beginning July 30, 2003; if not filled, weekly thereafter until the search is closed. AA/EOE

Arizona State University is an Equal Opportunity/Affirmative Action Employer.

Michael S. Rosenberg, Ph.D. Assistant Professor School of Life Sciences / Arizona State University msr@asu.edu <http://lswb.la.asu.edu/rosenberg>

CornellU TheoPopGenet

Postdoc in Theoretical Population Genetics

We are seeking a postdoctoral researcher in the area of theoretical population genetics of crop species evolution starting 9/1/03 or soon after. The chosen applicant is expected to work on the development of population genetic models of crop species evolution and applications of these models in data analysis of population genetic data from rice (*Oryza*). Funding for the postdoc comes from a large scale genotyping project in rice. The postdoc is supervised directly by theoretical population geneticists, but is also expected to interact with plant biologists and plant breeders. The major aim of the project is to examine the extent of linkage disequilibrium in rice, but the data generated from the project might also be appropriate for other types of population genetic analysis. The applicant should have a Ph.D. in a field related to theoretical population genetics, experience in population genetic theory/modelling or statistical genetics and a desire to work on data analysis

Please contact either Carlos Bustamante (cdb28@cornell.edu) or Rasmus Nielsen (rn28@cornell.edu) for more information. Applicants should send a CV, list of publications and the names and addresses of three references electronically to both CDB and RN.

“Carlos D. Bustamante” <cdb28@cornell.edu>

DalhousieU ComputationalGenomics

Post-doctoral position in computational Protein Science / Genomics

The Statistical Evolutionary Bioinformatics group (SEB) is a team of research laboratories based at Dalhousie University, Halifax, Nova-Scotia, Canada. We have members in the faculty of computer science (C. Blouin), Dept. of biochemistry and molecular biology (A. Roger, FW Doolittle, J. Archibald), Dept. of biology (J Bielawski) and Dept. of statistics and applied mathematics (C Field, E Susko). We are pursuing lines

of research in phylogenetics, protein evolution and protein science as well as applied phylogeny. These researches are conducted in a multidisciplinary and collaborative environment that proved to be very productive.

We are seeking candidates for a post-doctoral position in the computational fields of protein biophysics, protein evolution or functional genomics. The research is funded by Genome Atlantic and will be hosted in the faculty of Computer Science, Dalhousie University. The duration of this position is for 2 years with the possibility to extend to a third year. There is a possibility to have access to a wet bench for limited experimental work. We are working amongst many projects on realistic evolutionary models, protein folding, functional divergence, prediction of function and evolution of protein structures.

The candidates must hold a Ph.D. in any of the following background: statistics, computer science, theoretical and/or experimental biochemistry and similar fields. The candidate must be familiar with issues in protein science (folding and structure/function) and ideally with some/all of the current issues in functional genomics, structure prediction, molecular simulation and phylogenetics.

Most of our in-house re-usable code is written in C++ for Unix/Linux platform, a familiarity with this environment would be useful. Numerical computing and software engineering skills would be valued.

Please submit a CV with reference and publication list as well as a description of your research interest to C. Blouin, ideally in the PDF format or by mail at the address provided below.

Christian Blouin Fac. of Computer Science Dept. of biochemistry and molecular biology Genome Atlantic Dalhousie University Halifax, NS, Canada B3H 1X5 ph: (902)494-2881 fx: (902)494-1355 bongo@hades.biochem.dal.ca

Selected publications

Inagaki, Y., Blouin, C. Doolittle, F.W. and Roger, A.J. Convergence and constraint in eukaryotic release factor 1 (eRF1) domain 1: the evolution of stop codon specificity. *Nucleic Acids Res*, 2002. 30(2): p. 532-44.

Blouin, C., Y. Boucher, and A.J. Roger, Inferring functional constraints and divergence in protein families using 3D mapping of phylogenetic information. *Nucleic Acids Res*, 2003. 31(2): p. 790-7.

Archibald, J.M., C. Blouin, and W.F. Doolittle, Gene duplication and the evolution of group II chaperonins: implications for structure and function. *J Struct Biol*,

2001. 135(2): p. 157-69.

Inagaki, Y., Blouin, C., Susko, E. and Roger, A.J. Assessing functional divergence in EF-1alpha and its paralogues in eukaryotes and archaeobacteria. *Nucleic Acids Res*, 2003: p. in press.

DijonFrance CropGeneFlow

Dear colleague

Please find below the offer for a postdoctorate position at INRA Dijon, France, on Crop/Weed gene flow. Thank you very much.

POSTDOCTORATE POSITION IN CROP/WEED GENE FLOW

We are currently looking for a postdoctorate candidate to be involved in our ongoing research project on the assessment of gene flow between a cereal, the foxtail millet, and its wild relative, the green foxtail. This project is the continuation of a European contract and has French-Chinese funding, and the one-year postdoctorate position is funded by the Council of the Burgundy Region. It is part of the activity of our team working on herbicide resistance in weed and gene flow between transgenic crops and wild relatives.

Genetic resources were used to breed for herbicide resistant millet. Since green foxtail, the putative ancestor, is distributed in the same areas, there is a risk of spread of the resistance trait from the crop to the weed, which could jeopardize the benefits. The question is similar to that raised with transgenic crops and their impact on the genetic structure and diversity of populations of wild relatives. Contrary to maize, oilseed rape and beet that have outcrossing (and even self-incompatible) wild relatives, the originality and interest of millet is that both the crop and the wild relative are mainly autogamous. However, evidence of gene flow has been already provided. We investigate the speed of gene dispersal in three cases: a cytoplasmic inherited, a nuclear dominant, and a nuclear recessive resistance. Point mutations have been described (the last one in press) and PCR allelic tests allow recognizing hetero and homozygous plants. Sampling of the weed within and around experimental resistant millet fields in France and China provides the material to check resistance alleles frequency evolution under different selection pressures. At the same time, neutral marker genes and domestication alleles flow toward the weed and offer the way to study

the impact of gene flow onto the genetic structure of populations. Study and link to past introgression could be approached using the genetic resources. Recent references of our group on that topic are listed below.

We are primarily looking for a candidate with laboratory expertise in molecular biology applied to population genetics tools and evolutionary biology. The position is available now and must start before the end of December 2003. The candidate must have obtained a PhD within 5 years (no more) and never get a salary in France. The grant is 1850 per month (the same as for a young scientist) offered for 1 year (with little chance of extending to a second year). Language is not a problem at the laboratory. The INRA Institute is located on the University campus (30000 students) in the city of Dijon, the capital of Burgundy wine...

To apply, please send a cover letter describing your research interests, a complete CV and names of three references by e-mail to darmency@dijon.inra.fr

Recent references of our group on the millet story: - Benabdelmouna A., Shi Y., Abirached-Darmency M., Darmency H., (2001). Genomic in situ hybridization (GISH) discriminates between the A and B genomes in diploid and tetraploid *Setaria* species. *Genomes*, 44 : 685 - 690. - Benabdelmouna A., Abirached-Darmency M., Darmency H., (2001). Phylogenetic and genomic relationships in *Setaria italica* and its close relatives based on the molecular diversity and chromosomal organization of

5S and 18S-5.8S-25S rDNA genes. *Theoretical and Applied Genetics*, 103 : 668 - 677. - Délye C., Wang T., Darmency H., (2002). An isoleucine-leucine substitution in chloroplastic acetyl-CoA carboxylase from green foxtail (*Setaria viridis* L. Beauv.) is responsible for resistance to the cyclohexanedione herbicide sethoxydim. *Planta*, 214 : 421 - 427. - Benabdelmouna A., Darmency H., (2003). Copia-like retrotransposon in the genus *Setaria*: Sequence heterogeneity, species distribution and chromosomal organization. *Plant Systematics and Evolution*, 237 : 127-136. - Wang T., Li Y., Shi Y., Reboud X., Darmency H., Gressel J., (2003). Low frequency transmission of a plastid encoded trait in *Setaria italica*. *Theoretical and Applied Genetics*, in press.

To learn more about our laboratory: <http://www.dijon.inra.fr/malherbo/AccueilE.htm>

Henri Darmency Unité de Malherbiologie et Agronomie INRA, 17 rue Sully BP 86510, 21065, Dijon, France Tel. 33 380 693186 Fax. 33 380 693262 Fax. 33 380 693262

GreensboroNC PlantEvol

PostDoc in Plant Evolutionary/Physiology Ecology

Description: I am looking for a post-doctoral associate to help with research addressing fundamental questions about the evolution of phenotypic plasticity, parental effects, and thermoregulation in plants. The research project includes examining multigenerational fitness effects of plasticity in reflectance/color pattern in reproductive spikes of *Plantago lanceolata*, and assessing geographic variation in reflectance/color pattern. The post-doc will be expected to help direct field and laboratory experiments, analyze data, write papers, and direct students. For more information, contact Dr. Lacey, e-mail address: eplacey@uncg.edu. (Personal web page is under construction.)

Desired qualifications: Ph.D. and research experience in the area of plant evolutionary or physiological ecology, ability to work independently and as part of a team, competence in statistics, ability to direct undergraduate and Master's level students, and ability to work outdoors during all seasons in North Carolina.

To Apply: Interested persons should send a cover letter outlining qualifications and research interests, CV, reprints or preprints, and names, phone numbers, and e-mail addresses of at least 2 references to Dr. Elizabeth P. Lacey, Department of Biology, 312 Eberhart Building, University of North Carolina, Greensboro, NC, 27402, USA. These items can be sent via email.

Dates: Starting as soon as possible. The position is for one year initially, with the possibility of yearly extensions for three additional years.

Starting Salary: \$30,000 with benefits

Closing Date: when a suitable candidate is identified.

The University of North Carolina is an affirmative action/equal opportunity employer.

– Elizabeth P. Lacey Professor of Biology Department of Biology Eberhart Bldg. P.O. Box 26170 University of North Carolina Greensboro, NC 27402-6174 USA Phone: 336-334-4955 e-mail: eplacey@uncg.edu fax: 336-334-5839

Elizabeth Lacey <eplacey@uncg.edu>

HullYorkMedicalSchool Cercopithecine models

JOB ADVERT

Post Title: Postdoctoral Research Assistant

Location: Hull York Medical School

Cercopithecine models as a contextual framework for human evolution

Applications are invited for a Postdoctoral Research Assistant in Anatomy on a 3-year collaborative project with the Universities of Durham and Liverpool funded by the Leverhulme Trust, starting on October 1st 2003. This is an interdisciplinary project that will integrate behavioural and morphological aspects of cercopithecine biology in order to illuminate human evolutionary history.

The primary responsibilities of this position will be to collect, collate and analyse cercopithecine morphological data. Applicants should have a relevant PhD and experience in primate/mammalian morphometrics.

Salary on the RA1A Grade Point 6 - 20,311 per annum

Informal enquiries should be addressed to Dr Sarah Elton (University of Kent: s.e.elton@ukc.ac.uk)

PLEASE NOTE: THIS POSITION WAS PREVIOUSLY ADVERTISED AS BEING BASED AT THE UNIVERSITY OF KENT.

Reference: PG24

Closing date: 14/07/2003

There are no restrictions on who may apply

For further information and details of how to apply, please contact the Personnel Office quoting the vacancy reference. See contact details below.

Address: The H R Office The Postgraduate Medical Institute The Cohen Building The University of Hull Cottingham Road Hull, HU6 7RX Tel: 01482 466734 Fax: 01482 466672 Email: D.Mann@hull.ac.uk

Dr Sarah Elton Lecturer in Biological Anthropology Department of Anthropology University of Kent at Canterbury Canterbury Kent CT2 7NS U.K.

Tel: 01227 823232 Fax: 01227 827289 Email: S.E.Elton@ukc.ac.uk

Sarah Elton <S.E.Elton@kent.ac.uk>

ICAPBEdinburgh Speciation

Postdoctoral research position: Theoretical analysis of speciation

The aim of this project is to develop a general theoretical framework for modelling the origin of new species. This will be based on a new technique for analysing the evolution of multiple genetic loci, which leads to simple approximations. Particular attention will be paid to the genetic basis of reproductive isolation; the relation between parapatric and sympatric models; and understanding how divergence is maintained in mosaic hybrid zones.

The PDRA would develop population genetic models of speciation, using computer simulation and the symbolic algebra package Mathematica. The successful candidate would either be a biologist with strong quantitative skills, or someone with a background in mathematics/physics/statistics who is keen to work in evolutionary genetics. Previous experience with computer simulation/numerical methods, together with some mathematical ability, are required.

The project is a collaboration between Nick Barton and Mark Kirkpatrick (Univ. of Texas at Austin). It is funded by the Natural Environment Research Council for three years; the starting salary is £22,191 p.a. The postdoc would be based at Edinburgh, but would involve short visits to work in Austin.

The Institute of Cell, Animal and Population Biology at the University of Edinburgh has an exceptionally strong group of evolutionary geneticists. Details of ICAPB research can be found at <http://www.icapb.ed.ac.uk>, and the multilocus software is at <http://helios.bto.ed.ac.uk/evolgen/>. To find out more, contact n.barton@ed.ac.uk. To apply for the post, please email a CV, together with the names of at least two referees, and a brief statement of your research interests. The closing date is August 15th 2003, with a starting date as early as possible.

References:

Kirkpatrick, M., T. Johnson, and N. H. Barton. 2002. General models of multilocus evolution. *Genetics* 161:1727-1750. Kirkpatrick, M., and V. Ravigné. 2002. Speciation by natural and sexual selection: models and experiments. *American Naturalist* 159(S):22-35.

Turelli, M., N. H. Barton, and J. A. Coyne. 2001. Theory and speciation. *Trends in Ecology and Evolution* speciation. *Trends in Ecology and Evolution*

Marseille Phylogeography

POSITION AVAILABLE IN PHYLOGEOGRAPHY AND GENETIC STRUCTURE IN A CONTEXT OF PLANT SPECIES INVASION

A post-doc position is available in the research institute IMEP (Institut Méditerranéen d'Ecologie et de Paléoécologie) team EPBC (Ecologie du Paysage et Biologie de la Conservation) from November 2003 to April 2004 (six months) in the city of Marseille (Provence France). The candidate must be a non-french person due to our financial sources (approximately 1750 eue per month) from EGIDE dedicated to non-french salary. * Research themes The candidate will participate in a research project on invasive plant species in Mediterranean Basin based on two scientific programs: an european program, EPIDEMIE (Exotic Plant Invasions: Deleterious Effects on Mediterranean Ecosystems; see <http://www.ceh.ac.uk/epidemie/>) and one from the French Ministry of Ecology (INVABIO). The main objectives of these research programs consist in evaluating the dynamics of invasive plant species (particularly, *Oxalis pes caprae*, *Carpobrotus* spp., and *Ailanthus altissima*) and their consequences for the biodiversity and dynamics of native Mediterranean ecosystems. The precise research work of the candidate will investigate (i) at a regional scale, the phylogeography of *Oxalis pes caprae* across the Mediterranean Basin and (ii) at a local scale, the comparative genetic structure of insular and continental populations of *Carpobrotus* spp. * Ability Strong molecular skills in plant genetic diversity screening (plant DNA extraction, PCR-based markers such as AFLP, Acrylamid-gel electrophoresis, screening of CpDNA diversity by genome wllaking) and also a relevant experience in plant phylogeography and population genetic analysis are essential. As the candidate will participate in collaboration with population biologists and community ecologists a good knowledge of evolutionary ecology and interest for plant systematic will be appreciated. The candidate could participate in the supervising of students from our university and coordinating the functioning of the molecular laboratory. * Applications Candidates have to send a CV, a statement of research interests and past research projects, and two names, addresses and letters of refer-

ence to laurence.affre@univ.u-3mrs.fr IMEP institute is constituted of 60 scientist members working in interdepartmental research on Ecology and Evolutionary Biology. For more information on IMEP Institute, see the web site <http://www.imep-cnrs.com/pages/imep1.htm>
Yours sincerely, Laurence AFFRE

AFFRE Laurence Faculté de St Jérôme - IMEP - case 461 Av Escadrille N. Niemen 13391 Marseille cédex 20 tel St Jé : 04.91.28.83.39 tel Arbois : 04.42.90.84.52 mail : laurence.affre@univ.u-3mrs.fr <http://www.imep-cnrs.com/>

Laurence Affre <ms461a15@univ.u-3mrs.fr>

Montpellier TheoPopGenet

Post-Doctoral position in theoretical population genetics

A one year Post-Doctoral position (with good chances for a one-year renewal) will be open in January 2004 at the C.B.G.P. (Center for Biology and Management of Populations) in Montpellier (France) to work on the coupling of coalescence theory and geographic information. The work will focus on theoretical developments and computer programming. It will be done in close collaboration with two researchers of the C.B.G.P., Jean-Marie Cornuet and Arnaud Estoup. Coalescent based approaches will be evaluated on simulated data, and compared to more conventional approaches. If they provide positive results, these coalescent based approaches will be applied to relevant questions on endangered or invasive species currently studied in the C.B.G.P.

Required experience: We are looking for candidates with strong potential in theoretical population genetics, and with good knowledge on modern statistical methods (e.g. M.C.M.C.). The candidates must also be familiar with computer programming. A good background in evolutionary biology would be an advantage.

Job location: Center for Biology and Management of Populations (C.B.G.P.), Montpellier (France). The successful candidate will join the Genetics and Ecology of Populations (Gene & Pop) team which includes 10 researchers in evolutionary biology. For more information on the C.B.G.P. and on the team, please visit the web site at <http://www.ensam.inra.fr/-CBGP/>. Application: a Ph.D. is required; to apply, submit electronically (1) CV, (2) copies of re-

cent publications (maximum of three), (3) a statement of research interests,(4) the names and addresses of three persons that could provide a letter of support to Jean-Marie Cornuet (cornuet@ensam.inra.fr), Arnaud Estoup (estoup@ensam.inra.fr) and Denis Bourguet (bourguet@jouy.inra.fr). These documents can be send also by regular mail to : Jean-Marie Cornuet C.B.G.P., Campus International de Baillarguet, CS 30 016, 34988 Montferrier / Lez cedex France Review of applications will start on the 1st of September 2003 and will continue until the position is filled. French people cannot apply.

Denis Bourguet Unité Génétique Microbienne et Environnement INRA La Minière 78 285 Guyancourt Mail: bourguet@jouy.inra.fr Phone: (33) 130 833 655 Fax: (33) 130 438 097

Denis Bourguet <bourguet@jouy.inra.fr>

OregonStateU ConservGenet

POSTDOC POSITION: PACIFIC NORTHWEST FOREST SALAMANDER CONSERVATION GENETICS

There are a number of Pacific Northwest Forest salamander species of concern with unknown taxonomic identity or population status. Thus, we undertook a study using a diversity of molecular markers (mtDNA, allozymes, etc) to address these concerns. As a result, 5 molecular papers were submitted for publication and the reviews have been returned. The papers now require revision and re-submission (most were accepted with revision). At this point, we would like to hire someone with proven capabilities in preparing molecular population data for publication to revise the papers. The person who deals with publication of the papers will be first author in each paper they revise. USGS FRESC will pay for all publication costs.

Contractor must have experience analyzing mtDNA sequence data as well as allozyme and RAPD data for population genetic papers. Understanding of nested clade analyses and other phylogenetic methods will be required. Contractor must also have a proven record of efficiently and effectively producing molecular population genetic manuscripts in a timely fashion. It is assumed that this contract will most likely require that the contractor have a Ph.D. in an appropriate field. However, others with appropriate qualifications will be considered. **Contractor must be a U.S. citizen.

Contractor will be paid after completion of each manuscript is submitted. Contract will begin on or before 1 November 2003 and will extend to 1 July 2004. For further information, contact Dr. Susan Haig at Oregon State University (address below).

Susan Haig USGS Forest and Rangeland Ecosystem Science Center 3200 SW Jefferson Way Corvallis, OR 97331 541-750-7482 (o), 541-758-8806 (fax)

PurdueU SnailPops

Post-doctoral researcher to be part of a NIH-funded study investigating the genetic structure of schistosome/snail populations in Brazil. The project will determine the extent of genetic subdivision in host and parasite populations based on multilocus microsatellite data, and will assess the relationship between microsatellite diversity and biomarkers for schistosome virulence and snail resistance. Applicants should be experienced with current tools and techniques used in molecular epidemiology and/or landscape genetics. The position can begin August 1st and can last 1-2 years. Contact Dennis J. Minchella, Department of Biological Sciences, Purdue University (dennisM@purdue.edu)

Seattle RockfishMolEcol

POSTDOCTORAL FELLOWSHIP, NATIONAL RESEARCH COUNCIL: MOLECULAR ECOLOGY, POPULATION GENETICS, AND SYSTEMATICS OF ROCKFISH

A postdoctoral fellowship is available in our laboratory to pursue a variety of potential studies in rockfish of the North Pacific. Proposals will be considered that address one or more issues related to the genetics, demographics, life history, and ecology of this highly speciose and evolutionarily interesting group. The Sebastes rockfish complex of the North Pacific has been compared to the East African cichlid species flock as a laboratory for the study of speciation and ecological diversification. Research opportunities range from

higher-order systematics and evolutionary history to fine scale population structure relevant to, for example, Marine Protected Areas. Of particular interest will be proposals that target species of conservation concern (or appropriate surrogates) and provide a combination of basic descriptive information as well as exploration of more general biological phenomena. We're looking for creative applications using varied molecular techniques, different scales of temporal divergence, and various ecological life-history classes (e.g., sedentary to pelagic).

The Genetics and Evolution Program is the oldest fish genetics laboratory in the country. Initiated in the late 1970s, this complex of lab facilities provides state-of-the-art genotyping and DNA sequencing capabilities. Current research includes a wide range of evolutionary and population genetic studies, genome mapping, and quantitative genetics (both traditional breeding designs and molecular studies). For more information see the NWFSC website (<http://www.nwfsc.noaa.gov/>).

The successful candidate will participate in collaborations with geneticists and ecologists at the Northwest Fisheries Science Center (Montlake campus and Newport Research Station) as well as with colleagues from the Southwest Fisheries Science Center, Oregon State University, Oregon Department of Fish and Wildlife, University of Puget Sound, University of Washington, Washington Department of Fish and Wildlife, Canadian Department of Fisheries and Oceans, and other Pacific Rim laboratories.

We are seeking a candidate with both strong molecular skills and a firm grasp of evolutionary and population genetic theory. Current funding is available for 1 year with likely extension for a second year. Please send to <mailto:paul.moran@noaa.gov>paul.moran@noaa.gov a cover letter describing your research interests with possible ideas for this proposal, a complete CV, and names of three references. The fellowships are funded by NOAA and administered through the National Research Council. A short list of candidates will be asked for full proposals to be submitted to the NRC before 15 August 2003.

Paul Moran Conservation Biology Division Northwest Fisheries Science Center 2725 Montlake Boulevard East Seattle, Washington USA 98112-2097 Voice 206-860-3245 Fax 206-860-3335 Email <mailto:paul.moran@noaa.gov>paul.moran@noaa.gov

Tony Wilson Genetics and Evolution Conservation Biology Division Northwest Fisheries Science Center 2725 Montlake Blvd. E. Seattle, WA 98112, USA Tel: (206) 302-2428 / (425) 743-3307 x234 Fax: (206) 860-3335 tony.wilson@noaa.gov

Tony Wilson <tony.wilson@noaa.gov>

Seattle Salmon

NOAA/NRC POSTDOCTORAL RESEARCH ASSOCIATESHIP PROGRAM 2003 at the Northwest Fisheries Science Center, Seattle, WA 98112

Two Post Doctoral Fellowships at the Northwest Fisheries Science Center are offered on the several possible topics related to Pacific salmonids population biology and its relationships to habitat, hatchery and harvest impacts.

We are offering two postdoctoral research fellowships at the Northwest Fisheries Science Center (NMFS) in Seattle. A primary focus of research at the Science Center is the conservation and recovery of wild populations of anadromous Pacific salmonids. The postdoctoral fellows will have the opportunity to interact with over 200 scientists from several Divisions at the Northwest Fisheries Science Center. Research interests include general fish ecology, physiology, population biology, interactions between wild and hatchery fish, ocean and estuarine ecology, and evolutionary biology. More details about specific research foci at the Center and potential collaborators for this project can be found at the NWFSCs web site (<http://www.nwfsc.noaa.gov/>) and through contacts below.

The postdoctoral positions are part of the National Research Council Research Associateship program; salary is \$42,000 U.S. per year. Requirements: you must have received a PhD, ScD, or MD degree (or foreign equivalent) within the last five years, or you must be able to present evidence of having completed all formal requirements for the degree before tenure begins. U.S. citizenship is not required. Deadlines for postdoctoral applications is August 1 (email or postmark date) or November 1. Awards will be announced in September or October 2003 for the August deadline and in January 2004 for the November deadline, and tenure could begin soon thereafter.

As described below, we have identified two general areas of emphasis for the two postdoctoral research positions and expect that the successful candidates will work in one of these areas:

1. The effects of the characteristics of freshwater/estuarine habitat, hatchery management and harvest effects on salmon population dynamics and pro-

ductivity.

Successful recovery of listed Pacific salmon in the Pacific Northwest will depend in part on our ability to quantify the relative effects of different habitat, hatchery and harvest management changes on salmon populations. Population dynamic models that can integrate the effects of different management actions on salmonid population status are in their infancy. We are seeking candidates with quantitative skills who can further develop population models to relate effects of habitat, hatchery and harvest on salmon populations across the Pacific Northwest. Modeling approaches that take advantage of life-stage-specific data are encouraged.

2. Effects of climate change on Pacific salmonids.

Climate effects on populations occur on time scales from years to decades to global climate change. Retrospective analyses help us understand past anthropogenic impacts on anadromous fish species. Forecasts can help us understand rates of recovery of threatened salmonids. We are seeking a postdoctoral candidate who can propose novel approaches to investigation of climate impacts on the terrestrial and marine environments associated with anadromous salmonid species along the U. S. West coast.

For more information about these postdoctoral positions, contact Mary Ruckelshaus (mary.ruckelshaus@noaa.gov) or Michelle McClure (michelle.mcclure@noaa.gov).

JJ Westfall <JJ.Westfall@noaa.gov>

StanfordU MaizeDuplicatedGenes

Postdoctoral position: evolutionary and functional analysis of duplicated genes in maize

The maize genome is the result of a fairly recent polyploidization event (~20 MYA) that left behind a very large number of duplicated genes. Many of these duplicated genes are functional, and initial analysis has shown that many duplicates have evolved non-redundant regions of expression. Maize provides a nearly perfect system to answer the key evolutionary questions about the fates of duplicated genes. The genome duplication is recent enough that the data are not hopelessly saturated with multiple hits, yet old enough that there is enough information to carry out most evolutionary analyses. The recently finished genome sequence of Rice provides a convenient out-

group.

The project builds on the success of the maize gene discovery project (<http://www.zmdb.iastate.edu>) spearheaded by the PI Virginia Walbot. The project has generated a large number of EST sequences from different tissues and strains of maize. These sequences are being used to generate oligo microarrays to investigate gene expression of genes throughout maize development. The design of the oligo arrays will allow the measurement of duplicate-specific gene expression for even very similar duplicated genes.

The current project is a collaboration between the PI Virginia Walbot (maize genetics and molecular biology) and co-PI Dmitri Petrov (molecular evolution) (both at Stanford). Volker Brendel (bioinformatics) at the Iowa State University is a collaborator on the project. The position is advertised in anticipation of funding from the NSF.

We are looking specifically for a molecular evolutionary biologist or a population geneticist with strong quantitative skills. The postdoctoral fellow will be based at Stanford University and will interact closely with both Dmitri Petrov and Virginia Walbot. The project will involve annual trips to Iowa State University to consult with Volker Brendel who will be maintaining the main databases.

For additional information please e-mail Dmitri Petrov (dpetrov@stanford.edu). To apply please email a CV, together with the names of at least two referees, and a brief statement of your research interests and accomplishments. The position will be opened until filled. The starting date is negotiable. until filled. The starting date is negotiable.

UArizona BactGenomeEvol

BACTERIAL GENOME EVOLUTION UNIVERSITY OF ARIZONA

A Postdoctoral Research position is available to study the processes of gene transfer and degradation on the evolution of bacterial genomes. Potential projects include both bioinformatic and experimental approaches. Applicants could have skills in molecular genetic or microbiological procedures, and/or in computational or phylogenetic analysis. Candidates trained in the fields of Evolutionary Biology, Microbiology, Computational Biology, Molecular Biology or Genetics are encouraged

to apply. The position is available immediately; however, the starting date is very flexible. Salary (in the range of \$35K to \$40K, plus benefits) will be commensurate with experience.

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

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

UBurgundy SeaUrchinOntogeny

A postdoctoral position is available to study the ontogeny of developmental instability on sea urchins at the University of Burgundy (France). The project will be primarily conducted on a bilaterally symmetrical spatangoid (*Abatus cordatus*) for which complete ontogenetic series are available, and also on a pentaradial "classical" sea urchin (e.g. *Paracentrotus lividus*). Most of the specimens have been already collected, but complementary field trips on the Mediterranean sea shore should be necessary. The focus of the lab is on the relationships between differentiation and speciation. This includes the consideration of the mechanisms of control of morphological variability and hence the study of developmental instability. For more information on our current research projects see <http://www.u-bourgogne.fr/BIOGEOSCIENCE/P1T.html> The University of Burgundy (one and half an hour from Paris and two hours from Lyon) is a vibrant academic community of roughly 25,000 students. This one-year position, funded by the "Region Bourgogne", will be available as early as october 1, 2003 (but will remain open until filled). The fellow cannot be a French citizen. Salary (1850 euros per month), and benefits (healthcare) are competitive. Candidates should have a strong background in evolutionary biology with skills in morphometrics and statistics. He (she) should be highly motivated and able to work independently in the lab. Informal inquiries are encouraged. To apply, please submit electronically your CV, a statement of research interests, letters from three references and relevant reprints (maximum to three) to Paul Alibert (alibert@u-bourgogne.fr) or Bruno David (bruno.david@u-bourgogne.fr).

Paul Alibert Biogeosciences, UMR CNRS 5561 Université de Bourgogne 6, Bd Gabriel 21 000 DIJON

FRANCE tel.: + 33 380 39 63 45 fax.: +33 380 39 62 31 e-mail: alibert@u-bourgogne.fr <http://www.u-bourgogne.fr/BIOGEOSCIENCE/>

UCBerkeley Seals

Postdoctoral Position: Isolation and characterization of SNPs in ringed seals

A Postdoctoral Researcher position is available at the University of California, Berkeley to participate in NSF funded research aimed at isolating and developing 96 SNP markers to study test the micro-evolutionary effects of annual sea-ice dynamics upon the effective population size, population structure and dispersal in Greenland Ring Seal,

Phoca hispidae. The salary range is \$31,044-\$38,652 annually depending on qualifications; appointments are initially for one year. Experience in

cloning of random nuclear DNA sequences, primer design and subsequent amplification and sequencing PCR products for the identification of SNPs. Once 96 reasonably polymorphic SNPs have been identified a multiplexed SNP genotyping procedure need be developed and tested on a small number of ringed seal sample. Extensive experience in cloning and characterization of nuclear DNA sequences (preferably for SNP detection) as

well as experience with SNP genotyping methods. Please send a CV, research

statement and the names of 3 potential references to (pdf attachments preferred) to:

Per J. Palsb, University of California, Ecosystem Sciences, 151 Hilgard Hall, Berkeley, CA 94720-3110, USA, Phone (510) 643-8225, Fax (510) 643-5098, email <<mailto:palsboll@nature.berkeley.edu>>palsboll@nature.berkeley.edu

Applications should be received by August 17,2003

The University of California is an Equal Opportunity/Affirmative Action Employer

Postdoctoral Position - Parasitoid Wasp - Virus Coevol
Postdoctoral Position - Parasitoid Wasp- Virus Coevolution

A 2-year position for a Postdoctoral Associate is available starting August 2003 in the laboratory of Dr. Jim Whitfield at the University of Illinois. The position is associated with an NSF -funded project, "Origin and Evolution of the Bracovirus/braconid Wasp Symbiosis", and will involve the acquisition and phylogenetic analysis of DNA sequence data from both wasp and viral genes. Goals are to discover the extent of wasp/virus co-phylogeny and to test possible origins of the symbiosis. The successful candidate will have experience in DNA extraction, amplification and sequencing, and some combination of experience with phylogenetic analysis of sequence data, co-phylogenetic analysis, and/or molecular biology of polydnviruses. The laboratory currently also contains 4 graduate students pursuing projects on systematic and evolution of parasitoid wasps, and is closely associated with several other systematic entomology laboratories, including those of Drs. Sydney Cameron (corbiculate bees), Chris Dietrich (leafhoppers and treehoppers), Kevin Johnson (parasitic lice and birds), and Mike Irwin (brachyceran flies). Excellent facilities for DNA analysis, micro- and supercomputer-based phylogenetic analysis, electron microscopy, etc. are available.

Those interested in applying should send a letter of interest, a current CV, copies of up to 3 relevant publications, and arrange to have 3 letters of reference sent to (by e-mail is acceptable):

Dr. James B. Whitfield Department of Entomology 320 Morrill Hall 505 S. Goodwin Avenue University of Illinois Urbana, IL 61821 Tel 217-333-2567 FAX 244-3499 Email jwhitfie@life.uiuc.edu (e-mail inquiries welcome)

Consideration of applications will begin 10 July 2003 and continue until a suitable candidate is identified.

- Sydney A. Cameron Department of Entomology and Program in Ecology and Evolutionary Biology 320 Morrill Hall 505 S. Goodwin Ave. University of Illinois Urbana, IL 61801

Ph: 217-333-2340 Fax:217-244-3499 e-mail: scameron@life.uiuc.edu <http://www.life.uiuc.edu/~scameron>

UKansas Drosophila courtship

Uillinois Parasitoid Virus Coevol

A post-doctoral research associate position is available to examine the genetic architecture of *Drosophila* courtship song, an important trait involved in species recognition. The work will involve selection experiments on courtship song in *Drosophila simulans* and also quantitative trait loci (QTL) mapping of song. The lab is well versed in quantitative trait loci mapping, molecular techniques and behavioral analyses. Required qualifications are 1) a PhD. in Biology, Genetics, Evolutionary Biology, or related field. 2) Experience in one of the following areas: a) molecular biology, b) quantitative genetics, c) *Drosophila* genetics, d) behavioral genetics. 3) Good organizational and statistical skills. 4) Demonstrated verbal and written communication skills. 5) An ability to work independently, as well as to collaborate productively with other laboratory members. A complete application will include a letter of application stating the research and career interests of the applicant, a curriculum vitae and three letters of reference. Application materials should be sent to Dr. Jennifer Gleason, Dept. of Ecology and Evolutionary Biology, Univ. of Kansas, 1200 Sunnyside Road, Lawrence, KS 66045-7534, or via email at jgleason@ku.edu. Phone: 785-864-5858. Review of applications begins July 15, 2003, and will continue until the position is filled. Lawrence is a fun and historic town located ~ 25 miles west of Kansas City. The city offers art museums, restaurants and clubs, bookstores, etc., and there are nearby hiking and fishing areas. KU is a large research university. Within the Division of Biology are several dynamic and collegial labs studying fly genetics, quantitative genetics, and evolution that meet regularly for seminars and discussions. The project is part of the new initiative on Ecological Genomics in Kansas (<http://www.ksu.edu/ecogen/>). KU is an EO/AA employer.

— Jennifer Gleason Assistant professor The University of Kansas Department of Ecology and Evolutionary Biology 1200 Sunnyside Ave, Rm 6006 Lawrence, KS 66045 phone: 785-864-5858 FAX: 785-864-5860 email: jgleason@ku.edu <http://www.ku.edu/~eeb/faculty/gleason.htm>

ULausanne EvoGenomics

POSTDOCTORAL POSITION IN EVOLUTIONARY GENOMICS

A Postdoctoral position is available beginning September 1 (2003) in the group of Henrik Kaessmann at

the Center of Integrative Genomics, University of Lausanne, Switzerland.

I am interested in the origin, evolution, and polymorphism of genes and noncoding DNA sequences in the human genome. We will explore available data from genomic databases and generate complementary data by large-scale experimental analysis. My current research focuses on the origin and evolution of primate genes and gene architectures. For more information see the web site: <http://home.uchicago.edu/~kaessm/> I am seeking highly qualified and motivated applicants with computational experience and a strong interest in one or several of the following fields: bioinformatics, data mining, molecular evolution, population genetics, and/or statistics. Alternatively, I welcome applications from researchers with an experimental background in molecular evolution and/or related fields, but who also have a strong commitment to analyze evolutionary data and are eager to acquire or deepen programming skills for large-scale evolutionary analyses.

Although living costs in Switzerland are relatively high, the salary still is attractive: ~60.000 CHF (~40.000 Euro, ~\$45.000) per year is the starting salary.

The position is available for at least 2 years with possible extensions.

The Center of Integrative Genomics (CIG) is a new (starting September, 2003) interdisciplinary research and training institute of the University of Lausanne covering all aspects of genome evolution and functional genomics. It is set up in collaboration with the University of Geneva and the Swiss Federal Institute of Technology in Lausanne. The CIG is also supported by the Swiss Institute for Experimental Cancer Research, the Ludwig Institute for Cancer Research, the Swiss Institute for Bioinformatics and the University Hospitals at both Geneva and Lausanne.

The Lausanne region is known for its excellent public schools, an attractive cultural atmosphere, a growing economy, and its beautiful environment next to Lake Geneva.

Informal inquiries may be addressed to Henrik Kaessmann kaessm@uchicago.edu. Applications including a CV, statement of research interest, copies of relevant publications, and two letters of recommendation should be emailed or mailed to me at the address below. Review of applications will begin immediately. Starting dates after 1 September 2003 are flexible.

until August 1, 2003: Dr. Henrik Kaessmann Department of Ecology and Evolution University of Chicago 1101 East 57th Street Chicago, IL 60637 USA Phone: +1-773-834-3965 Fax: +1-773-702-9740 E-mail:

kaessm@uchicago.edu

After August 1, 2003: Dr. Henrik Kaessmann, Assistant Professor Center for Integrative Genomics BEP University of Lausanne Phone: +41-21-692-2054 Note: please use my Chicago email address until further notice on my webpage!

ULaval SalmonidGenomics

POSTDOCTORATE POSITION IN SALMONID EVOLUTIONARY FUNCTIONAL GENOMICS

We are currently looking for a postdoctorate candidate to be involved in our ongoing research project on the elucidation of genetic and ecological processes of adaptive radiation. This multidisciplinary project is funded by NSERC (Canada) and part of the research program of the Chair in conservation genetics of aquatic organisms.

The originality and interest of this project is based upon a multidisciplinary approach integrating genomics, systematics and ecology. The use of coregonine fishes (salmonidae) as a model system also offers particular interest for investigating the interactions of evolutionary forces in shaping population divergence and reproductive isolation. Namely,

the whitefish species complex is characterized by the occurrence of sympatric forms that are highly differentiated in life history traits, metabolism, morphological and ecological characteristics. Yet these populations remains partially reproductively isolated despite potential for gene flow.

The specific objective of the proposed research will be to apply microarray

technology for quantifying gene expression profiles between dwarf and normal whitefish ecotypes. The general hypothesis to be tested is that these forms exhibit adaptive differential gene expression patterns that have been shaped by natural selection. A 4000 gene microarray developed in

salmonids is already available to achieve this work.

We are primarily looking for a candidate with strong laboratory expertise in functional genomics, a solid theoretical background in evolutionary biology, as well as expertise in management and analysis of large data bases. The position is available now and will be offered for 2 years with a

possibility of extending to a third year.

To apply, please send a cover letter describing your research interests, a

complete CV and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca

To learn more about

Quebec city : <http://www.quebecweb.com/tourisme/-quebec/villequebec/introang.html> Laval University : <http://www.ulaval.ca/> The Biology department and our research programs: <http://www.bio.ulaval.ca/index-alt.html>

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 Courriel: Louis.Bernatchez@bio.ulaval.ca Toile: <http://www.bio.ulaval.ca/index-alt.html> Chaires de recherche du Canada: www.chaires.gc.ca

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 Courriel: Louis.Bernatchez@bio.ulaval.ca Toile: <http://www.bio.ulaval.ca/index-alt.html>

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

ULaval SalmonidGenomics 2

UMichigan Phylogeography

University of Michigan: Postdoctoral in Plant and Insect Phylogeography

Applications are solicited for a one-year postdoctoral position in the Department of Ecology and Evolutionary Biology at the University of Michigan, for analysis of the phylogeography of plants and associated host-specific insects. Proficiency with methods of obtaining sequence and microsatellite data, experience with phylogeographic or phylogenetic analysis, and a background in evolutionary biology are expected. Aid in learning methods specific for either plant or insect material is available if needed. The successful applicant will help to complete the setup of a new lab. The salary level will be \$28,000 per year. The position will start as soon as a suitable candidate can arrive.

Applicants should send a curriculum vitae, statement of research interests, and publications or manuscripts, and arrange to have three letters of recommendation sent to Douglas Futuyma, Dept. of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI 48109-1048; or email dfutuyma@umich.edu. Applications will be accepted until a suitable candidate is found. The University of Michigan is a nondiscriminatory affirmative-action employer.

Douglas J. Futuyma Professor Department of Ecology and Evolutionary Biology University of Michigan Natural Science Building 830 North University Avenue Ann Arbor, MI 48109-1048

tel. (734) 936-0549 fax (734) 763-0544 dfutuyma@umich.edu

US EPA EcolAssessment

A unique postgraduate research fellowship opportunity is available to work with two national EPA research laboratories to improve the science of ecological assessment. The Population Ecology Branch of the National Health and Environmental Effects Laboratory (NHEERL) in Narragansett, RI develops population models to study the effects of anthropogenic contaminants on fish and wildlife. The Molecular Ecology Research Branch of that National Exposure Research Laboratory (NERL) in Cincinnati, OH uses molecular genetic methods to assess the condition and vulnerability of fish and wildlife populations. The postdoctoral researcher will receive mentorship from researchers in both programs to develop sophisticated population models that make use of population genetic data, such as the distribution and dynamics of neutral and fitness-linked genetic markers. It is expected that

these models will lead to new insights in the assessment of ecological condition and projected short- and long-term population vulnerabilities. The postdoctoral researcher will be allowed a high degree of autonomy to develop and pursue an original plan of research that addresses this overall objective.

The researcher will reside at Narragansett, RI or Cincinnati, OH, depending on the requirements of the proposed project plan. Some travel to/from Narragansett and Cincinnati is expected.

Qualifications: The ideal candidate will have a mastery of theoretical population biology and a familiarity with quantitative genetics, population genetics and viability methods and models. Experience with modern molecular biology/genetics methodologies and their applications to ecological and environmental issues would be advantageous. He/she will be able to conceptualize and execute an original plan of research, establish research priorities and deadlines, judge the completeness and accuracy of research results and present his/her research findings to diverse audiences, both orally and in writing.

The appointment is for one year and may be renewed upon recommendation of NERL and subject to availability of funds.

The Postgraduate Research Participation Program is administered by the Oak Ridge Institute for Science and Education (ORISE). Potential applicants are strongly encouraged to contact Dr. Diane Nacci (nacci.diane@epa.gov, 401-782-3143) or Dr. Mark Bagley (bagley.mark@epa.gov, 513-569-7455) for details about this research opportunity. For application materials and information about the ORISE program, contact Betty Bowling (bowlingb@ornl.gov, Phone: 865-576-8503, Fax: 865-241-5219. Mail: Postgraduate Research Program-EPA, Science and Engineering Education - MS36, Oak Ridge Institute for Science and Education, P.O. Box 117, Oak Ridge, TN 37381-0117. Please reference project number NERL 03-05 when inquiring about the project.

UToronto MaleInfertility

Postdoctoral Position - Population Genetics of Human Male Infertility

A postdoctoral position is available immediately to study the genetic underpinnings of male infertility in

the human population. The study will entail both SNP mining and SNP discovery in infertile patients, using a candidate gene approach. Postdoctoral trainees with interests in either bioinformatics or population genetics are especially encouraged to apply. Please address inquiries to: Dr. Sue Varmuza, Department of Zoology, University of Toronto, M5S 3G5, tel 416-9782759, FAX 416-9788532, email: svarmuza@zoo.utoronto.ca.

Susannah Varmuza, PhD, Associate Professor, Department of Zoology, University of Toronto, 25 Harbord St., Toronto, Ontario, CANADA, M5S 3G5

tel. 416-978-2759 FAX 416-978-8532

UVirginia PlantEcoGenet

POSTDOCTORAL POSITION: PLANT ECOLOGICAL GENETICS A post-doctoral position is available in the Galloway lab at the University of Virginia to work on an NSF-funded project to evaluate the role of maternal effects in the evolution of life history. The study will focus on the herbaceous plant *Campanula americana*. The research will use environmental and genetic manipulations to alter maternal effects and the results will be used to fit evolutionary genetic models (see website below for further details). The project uses a quantitative genetics approach and will include both greenhouse and field work. In addition to collaborating on the project, the post-doc will have the opportunity to independently develop related research and to interact with the population biology and evolution communities at the University of Virginia and at the Mountain Lake Biological Station. Candidates should have a background in population biology. Knowledge of quantitative genetics and an interest in polyploidy is a plus! Start Date: January 2004 (delay through spring is fine) Duration: 2-3 years To apply: Send a CV, a statement of research interests and experience, and the names and contact information for two references to either the e-mail or postal address below. Review of applications will begin September 15. Informal inquiries are welcome. Laura F. Galloway e-mail: lgalloway@virginia.edu

Department of Biology Gilmer Hall, P.O. Box 400328 University of Virginia Charlottesville, VA 22904-4328 For further information on the position and Galloway lab see: <http://www.people.virginia.edu/~lg8b/>

Laura Galloway <lgalloway@virginia.edu>

UWashington ComputationalBiol

The Felsenstein/Kuhner Lab is seeking a Senior Fellow to work with Mary Kuhner on development of algorithms to estimate evolutionary parameters from molecular sequence data. This position is funded by the NIH for two years with the option of a third year.

Our approach involves Markov Chain Monte Carlo sampling of genealogies, a computer-intensive approach that attempts to take into account our inability to be certain about the genealogy of a population. Our lab's central goal is to develop, test, and distribute computer programs in the LAMARC package so that these methods will become available to biologists.

The successful applicant will work on one or more of our three current areas of interest: * Estimation of selection coefficients * Estimation of recombination rate and detection of recombination hotspots * Mapping of trait loci via linkage disequilibrium patterns

We are looking for someone who can take up one of our subprojects and pursue it, managing both design and coding, though with ample support and collaboration from the group as a whole. The applicant will be expected to help design as well as implement new algorithms.

This is a small, tight-knit working group with good computer support resources. The University of Washington is developing interdisciplinary strengths in computational biology and this is an exciting time to work here. Our lab's previous work can be found at: <http://evolution.gs.washington.edu/lamarc.html> Applicants should hold a Ph.D. in biology, computer science, or statistics. Statistical experience is needed; phylogenetics or population genetics will be particularly helpful. C++ programming experience is preferred, although candidates familiar with other object-oriented languages will be considered. Experience with large programming projects is desirable.

Applications will be considered beginning September 1, 2003 and continuing until the position is filled. Please send a letter of application, CV, and arrange for three letters of reference to be sent to:

Gretchen Smith University of Washington Department of Genome Sciences Box 357730 Seattle, WA 98195-7730

Applications may be emailed to ghsmith@u.washington.edu. The University of Washington is building a culturally diverse department and strongly encourages applications from women and minority candidates. The University of Washington is an Affirmative Action/Equal Opportunity Employer.

mkkuhner <mkkuhner@kingman.gs.washington.edu>

Virginia MolEvol

Postdoctoral Position in Molecular Evolution and Bioinformatics

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

A postdoctoral position is available starting as early as in September, 2003. The primary focus of this position will be, but not restricted, to study DNA polymorphisms in populations and to analyze SNP patterns in the genomes. The candidate may also involve in the bioinformatics part in a project for studying nicotine dependence. For more information, please visit later the website <http://www.cs.uh.edu/~zzhao/job.html>. Qualified candidate should have background in molecular biology and/or computational biology. Training in the molecular evolution will be a plus but not required. Experience in one of the programming languages (C/C++, Perl, SQL) is desirable, and experience in database management is a plus. Applicants should send a CV, brief statement of research interests, and reference to: Zhongming Zhao (zzhao@cs.uh.edu).

Zhongming Zhao, Ph.D. Human Genetics Center University of Texas Houston Health Science Center 1200 Herman Pressler E435 Houston, TX, 77030 Phone: 713-500-9817 FAX: 713-500-0900 Email: zzhao@sph.uth.tmc.edu Web: <http://www.cs.uh.edu/~zzhao>

New address after September 1, 2003

Dept Psychiatry MCV Virginia Commonwealth University PO Box 980126 Richmond VA 23298 Fax: 804-828-1471 Email: zzhao@cs.uh.edu

“Zhao, Zhongming” <zzhao@sph.uth.tmc.edu>

WalnutCreekCA CoralGenomics

POST-DOCTORAL POSITION IN CORAL REEF GENOMICS
POST-DOCTORAL POSITION IN CORAL REEF GENOMICS

Global warming has impacted coral reefs worldwide by causing the disruption of coral-zooxanthella symbioses (coral bleaching), causing many corals to subsequently die. This project aims to gain a better understanding of the molecular and cellular interactions that are critical to the functional integrity of these symbioses. This is an interdisciplinary project that will integrate ecology and genome biology to study gene expression in a tropical marine reef ecosystem. Research will be conducted in the Florida Keys and at the Joint Genome Institute in Walnut Creek (JGI), California, starting on September 1st 2003. A postdoctoral scientist position is available to study the molecular mechanisms involved in coral-zooxanthellae symbiotic interactions by using genomic approaches.

The primary responsibilities of this position will be to develop EST data from the coral host and the algal symbiont, and participate in microarray development and expression profile analyses. There will be possibilities to interact with a wide array of genome scientists at the JGI as well as with coral reef biologists in the field. Applicants should have a relevant Ph.D. and experience in functional genomics. Experience with management and analysis of microarray datasets, symbiotic systems and/or coral reef biology would be desired. The position will be offered for one year with the possibility of extension.

The JGI, established on January 1, 1997, is a consortium of scientists, engineers and support staff from the U.S. Department of Energy's Lawrence Berkeley, Lawrence Livermore and Los Alamos National Laboratories. The Evolutionary Genomics Department is one of several at the JGI (<http://www.jgi.doe.gov/-programs/comparative/>). We have active interactions with scientists, post-docs and students from the San Francisco Bay Area universities.

Walnut Creek is a nice community located approximately 25 miles from San Francisco, 20 miles from Berkeley with easy access to many locations in the Bay Area.

To apply, please send a cover letter describing your re-

search interests, a CV and names of three references by e-mail to m.medina@lbl.gov

Mónica Medina Research Scientist Department of Evolutionary Genomics Joint Genome Institute 2800 Mitchell Drive B400 Walnut Creek, CA 94598 Email: M.Medina@lbl.gov

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Mónica Medina Ph.D. Department of Evolutionary Genomics Research Scientist Joint Genome Institute 2800 Mitchell Drive, B400 Walnut Creek, CA 94598

925-296-5633 Phone 925-296-5666 Fax

Monica Medina <M.Medina@lbl.gov>

YaleU MolEvolHoxGenes

NSF funded post-doctoral position for up to three years is available in the laboratory of Gunter Wagner at Yale University

Starting date: ASAP

Area of research: molecular evolution of duplicated Hox genes

Summary: This research is part of a collaborative effort to understand the role of developmental gene duplication in the evolution of chordates. The participating labs are that of Dr Frank Ruddle at Yale's Department of Molecular, Cell and Developmental Biology (responsible for the mammalian transgenic work), Dr Chris Amemiya from the Virginia Mason Research Institute in Seattle, WA (responsible for the zebrafish transgenic work and genomic analysis) and the Wagner lab at Yale's Department of Ecology and Evolutionary Biology (responsible for molecular evolution). The goal of this continuing project is to understand the role that Hox cluster duplications have played in the evolution of the vertebrate body plan. The most recent Hox cluster duplication happened in the ray finned fish lineage, leading to the seven Hox clusters found in zebrafish, and other teleosts. Surprisingly Hox clusters duplications do not seem to have played a prominent role in the evolution of other metazoan phyla.

The specific objectives of the research in the Wagner lab during the current funding cycle are: 1) to determine exactly when in ray finned fish phylogeny the most recent Hox cluster duplication happened. 2) Determine what the evolutionary forces were that acted on Hox genes after duplication, both at the coding as well as the cis-regulatory sequences. The latter objective will closely interact with the experimental work determining the functional differences between teleost genes and their unduplicated outgroups done in the Ruddle and Amemiya labs. 3) Isolate and analyze the Hox clusters of the basal ray finned paddlefish, *Polyodon spathula*. This part of the project will establish an appropriate out-group model species for the analysis of teleost gene function.

Required skills and expectations: Skill in standard molecular techniques is required (cloning, PCR, sequencing and sequence assembly), as is familiarity with the standard molecular evolution analysis techniques such as sequence alignment, phylogenetic analysis, analysis of rates and patterns of sequence evolution. The post-doctoral researcher is expected to integrate into a highly interactive and diverse group of researchers. The Wagner lab consists of geneticists, paleontologists and theorists working on various aspects of the developmental evolution of vertebrates. See <http://pantheon.yale.edu/~gpwagner/index.html>

Applications: please email a CV and at least three references to <gunter.wagner@yale.edu>

Some recent publications from the lab: Prohaska, S. J., C. Fried, C. Flamm, G. P. Wagner, and P. F. Stadler 2003 Surveying phylogenetic footprints in large gene clusters: applications to Hox cluster duplications. *Mol. Phylog. Evol.* Submitted. Hermisson, J., T. Hansen and G. P. Wagner 2003. Epistasis in polygenic traits and the evolution of genetic architecture. *Am. Nat.* 161:708-734. Larsson, C. E., and G. P. Wagner 2002 The pentadactyl ground state of the avian wing. *J Exp Zool (Mol & Dev Evol)* 294: 146-151. Carter, A. J. R. and G. P. Wagner 2002 Evolution of functionally conserved enhancers can be accelerated in large populations: a population genetic model. *Proc. Roy Soc., Biol.* 169: 953-960. Chiu, C.-h., C. Amemiya, K. Dewar, C.-B. Kim, F. Ruddle and G. P. Wagner 2002. Molecular evolution of the HoxA cluster in the three major gnathostome lineages. *PNAS*, 99:5492-5497.

WorkshopsCourses

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ColdSpringHarbor ComputationalGenomics Nov5-11

I encourage Evolutionary Biologists to apply to this course. We do not cover phylogeny reconstruction methods, but the steps before tree-building - establishing homology. This year, we will also place considerable emphasis on comparative genomics.

Bill Pearson

Course announcement - Application deadline, July 15,

Cold Spring Harbor COMPUTATIONAL GENOMICS
NOVEMBER 5 - 11, 2003

INSTRUCTORS:

Pearson, William, Ph.D., University of Virginia, Charlottesville, VA
Smith, Randall, Ph.D., SmithKline Beecham Pharmaceuticals, King of Prussia, PA

Beyond BLAST and FASTA - This course presents a comprehensive overview of the theory and practice of computational methods for gene identification and characterization from DNA sequence data. The course focuses on approaches for extracting the maximum amount of information from protein and DNA sequence similarity through sequence database searches, statistical analysis, and multiple sequence alignment. Additional topics include gene recognition (exon/intron prediction), identifying signals in unaligned sequences, and integration of genetic and sequence information in biological databases. The course combines lectures with hands-on exercises; students are encouraged to pose challenging sequence analysis problems using their own data. The course makes extensive use of local WWW pages to present problem sets and the computing tools to solve them. Students use Windows and Mac workstations attached to a UNIX server; participants should be comfortable using the Unix operating system and a Unix text editor.

The course is designed for biologists seeking advanced training in biological sequence analysis, computational biology core resource directors and staff, and for scientists in other disciplines, such as computer science, who wish to survey current research problems in biological sequence analysis.

The primary focus of the Computational Genomics Course is the theory and practice of algorithms used in computational biology, with the goal of using current methods more effectively and developing new algorithms. Students more interested in the practical aspects of software development are encouraged to apply to the Cold Spring Harbor Bioinformatics - Writing Software for Genome Research Course.

For additional information and the lecture schedule and problem sets for the 2002 course, see:

<http://www.med.virginia.edu/~wrp/cshl02>

To apply to the course, fill out the form at:

http://meetings.cshl.org/course_app.htm

NCStateUniv QTLMapping Fall

North Carolina State University currently offers an internet course in Fall 2003 on QTL Mapping. This is a distance learning course, designed for geneticists who need to analyze and interpret QTL mapping data. The course systematically introduces statistical methods for genetic linkage map construction, for mapping quantitative trait loci and for estimating the genetic architecture of multiple quantitative traits in experimental populations.

The course currently receives registration. For more information, look at the web site <http://distance.ncsu.edu/> and <http://statgen.ncsu.edu/zeng/i-st610e.htm>

Fall 2003, COURSE BY INTERNET NCSU Office of Instructional Telecommunications ST 610E: SPECIAL TOPICS: QTL MAPPING

COURSE DESCRIPTION: This course systematically introduces statistical methods for genetic linkage map construction, for mapping quantitative trait loci and for estimating the genetic architecture of multiple quantitative traits. Topics include: Molecular marker data; Linkage map estimation;

Quantitative genetic models; Experimental designs for mapping QTL; One marker analysis; Interval mapping; Composite interval mapping; Multiple interval mapping; Testing epistasis; Multiple trait analysis;

Testing genotype by environment interaction; QTL CARTOGRAPHER.

Dr. Zhao-Bang Zeng Professor of Statistics and Genetics Bioinformatics Research Center Departments of Statistics and Genetics North Carolina State University 1521 Partners II Building, 840 Main Campus Drive Raleigh, NC 27695-7566, USA Tel: 919 515-1942; FAX: 919 515-7315 (Attn: Zeng) Email: zeng@stat.ncsu.edu; Home page: <http://statgen.ncsu.edu/zeng/>

UMinnesota ComparativeGenomics Oct20-24

Call for participation/poster-abstracts

IMA/RECOMB Satellite Workshop on Comparative Genomics

Dates: October 20-24, 2003 Location: Institute for Mathematics and its Applications (IMA), University of Minnesota, 207 Church Street S.E., Minneapolis

Organizers: Jens Lagergren, Royal Institute of Technology, jensl@nada.kth.se Bernard M.E. Moret, University of New Mexico, moret@cs.unm.edu David Sankoff, University of Ottawa, sankoff@uottawa.ca

Jointly sponsored by RECOMB and IMA.

REGISTRATION FEES: There are no registration fees. An invitation can be requested from IMA.

Three poster-abstracts will be selected for 20 minutes presentations. The abstracts will be published in LNBI Springer Verlag. Poster abstracts should be 1 to 2 pages and submitted no later than August 27, 2003. More information concerning the submission will in early August be available at:

<http://www.ima.umn.edu/complex/fall/c2.html> This cite already contains information on participation, registration, accommodations, and travel.

Confirmed speakers include: Andersson, Siv; Brinkman, Fiona S.; Durand, Dannie; El-Mabrouk, Nadia; Eichler, Evan; Guigo, Roderic; Housworth, Elizabeth; Kaessman, Henrik; Lagergren, Jens; Lanfranco, Luisa; Larget, Bret; Lerat, Emmanuelle; Lynch, Michael; Martin, William; Mclysaght, Aoife; O'Brien, Steve; Pevzner, Pavel; Wang, Li-San; Wolfe, Ken

The increasing availability of complete genomes from diverse organisms offers unprecedented opportunities. Exploitation of the full power intergenomic comparative maps for all types of genomic events will be central in biological, medical and bioinformatics research in the post-genomic era. Several areas are crucial to the success of this enterprise, for instance: understanding patterns and processes of genome evolutionary change, mapping genomic mutational events, and the utilization of such maps as bioinformatics tools. Genomic data also facilitates phylogeny reconstruction based on genomic mutational events rather than nucleotide substitution.

The kernel of comparative genome analysis is the establishment of the correspondence (orthology analysis) between genes in different genomes. It is such intergenomic maps that make it possible to translate information from one organism to another. Genome evolution is shaped by a multitude of evolutionary events acting at various organizational levels. On a low level point mutations affect individual nucleotides. On a higher level genome segments are affected by processes such as duplication, lateral transfer, inversion, transposition, deletion and insertion. Finally, the whole genome is influenced by speciation and hybridization of organism lineages. The complexity of genome evolution poses a serious challenge in developing mathematical models and algorithms. Fortunately, there is a spectra of algorithmic techniques that can be applied to problems from this domain, ranging from exact, heuristic, fixed parameter and approximation algorithms for problems based on parsimony models to Monte Carlo Markov Chain algorithms for Bayesian analysis of problems based on probabilistic models.

Wageningen AsexualReprod Nov19-23

Second announcement: Call for Expressions of Interest for PARTNER-1, Nov. 2003

A first Workshop in a series of four on the Ecology and Evolution of Asexual reproduction

Wageningen, The Netherlands, November 19-23, 2003

The PARThenogenesis NETwoRk (PARTNER) is a network on the ecology and evolution of asexual reproduction, funded by the European Science Foundation (ESF). It aims to join European empiricists and theoreticians in a total of four workshops during the period of 2003-2005. See also: (<http://www.nioo.knaw.nl/NETWORKS/PARTNER> and <http://www.nioo.knaw.nl/NETWORKS/-PARTNER>)=20

The subject of the First Workshop is Asexuality and Time-scales

Topics of the first workshop are: (1) ancient asexuals (2) ancient asexual genes (3) methods of ageing in asexuals (4) pests in agriculture

Each topic will include a morning or afternoon session with 2-3 lectures of invited speakers and a few contributed papers. Two evening sessions will be held with discussions, and a plenary summary of the outcomes.

Organizers are: Kitty Vijverberg (Netherlands institute of Ecology) Koen Martens (Royal Belgian institute of Natural Sciences),

Confirmed speakers: Bengt O. Bengtsson, Sweden C. W. (Bill) Birky Jr., Tucson, USA Hugh D. Loxdale, England Michael Heethoff, Germany David Mark Welch, Woods Hole, USA Koen Martens, Belgium Matthew Meselson, Cambridge, USA Claudia Ricci, Italy W. L. (Bill) Rice, Santa Barbara, USA Isa Schön, Belgium Tim Sharbel, France Peter Van Dijk, The Netherlands

Expression of interest: The number of participants is limited. Please send an expression of interest with a brief CV, and a maximum of one page summary with your thoughts about what you can gain from and contribute to the workshop. Students are also invited to apply. In case of approval, you will be invited to participate. Meals and accommodation will be provided by the ESF. Travel costs will NOT be reimbursed

Submission deadline is August 15, 2003

For further information about the first workshop and submission of expression of interest, please contact Kitty Vijverberg Netherlands institute of Ecology PO Box 40 NL-6666 ZG Heteren The Netherlands k.vijverberg@nioo.knaw.nl

Instructions

Instructions: To be added to the EvoDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvoDir 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 EvoDir direct them to the email evodir@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 preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.