E v o l D i r

May 31, 2005

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

Forward

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

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

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

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Conferences

KansasCity EcolGenomics Nov4-6 swp

Plan now to attend the 3rd Annual Genes in Ecology, Ecology in Genes Symposium on November 4 - 6, 2005, in Kansas City at the Radisson Hotel in Lenexa-Overland Park, Kansas. The Symposium will begin on Friday at 7:00 pm and conclude on Sunday at noon. Registration and hotel reservation information will be available soon on our website, www.ksu.edu/ecogen <http://www.ksu.edu/ecogen> .

Ecological Genomics is an emerging field at the interface of ecology, evolution, and genomics that seeks to place the functional significance of genes and genomes into an ecological and evolutionary context. The Symposium will feature lectures by scientists at the forefront of Ecological and Evolutionary Functional Genomics. Participants will also learn about the Ecological Genomics research initiative in Kansas that includes 37 faculty members in 10 departments from three Kansas universities. A partial list of speakers follows: Toby Bradshaw, University of Washington, The genetic basis of adaptive evolution in natural plant populations John Kenneth Colbourne, Indiana University, Finding genes linked to the ecological success of Daphnia Edward F. DeLong, Massachusetts Institute of Technology, Exploring the natural microbial world, from genomes to biomes Martin E. Feder, The University

of Chicago, Transposition and heat-shock genes: a genomic scan for evolvability of transcription Trudy F. C. Mackay, North Carolina State University, The genetic architecture of complex traits: Lessons from Drosophila Thomas Mitchell-Olds, Max-Planck Institute of Chemical Ecology, Functional evolutionary genomics of ecologically important variation Johanna Schmitt, Brown University, Ecological genomics of seasonal timing in Arabidopsis thaliana Charles W. Whitfield, University of Illinois, Genomic dissection of naturally occurring behavioral maturation in the honey bee"

Our slate of speakers continues to grow. Please watch our website, www.ksu.edu/ecogen <http://www.ksu.edu/ecogen> , for announcements of additional speakers.

Participants can share their own research with the group through a poster session on Friday night and Saturday. Poster topics should be related to the field of Ecological Genomics. Poster dimensions are not to exceed 4' w x 3' h. Please submit poster title with authors and affiliations directly to ECOGEN@ksu.edu <mailto:ECOGEN@ksu.edu> before September 20, 2005.

Please share this announcement with colleagues and students who are interested in learning more about the emerging field of Ecological Genomics. For information about this interdisciplinary research initiative and Symposium, please see: www.ksu.edu/ecogen <http://www.ksu.edu/ecogen> Project Directors include: Dr. Loretta Johnson, Kansas State University Ecosystem Biology Dr. Mike Herman, Kansas State University

Developmental Genetics Dr. Robert Cohen, University of Kansas Molecular Biosciences Dr. Daniel Crawford, University of Kansas Ecology and Evolutionary Biology

Funding for this symposium is provided by Kansas NSF EPSCoR and the Kansas Technology Enterprise Corporation.

Doris Merrill Ecological Genomics in Kansas KSU Division of Biology 231 Ackert Hall Manhattan, KS 66506-4901 Phone: (785) 532-3482 FAX: (785) 532-6653 E-mail: ECOGEN@ksu.edu

Australia AphidEvolution

<http://www.aphidsymposium.org/index.php>

The organizing committee for the 7th International Symposium on Aphids is now accepting registrations, and calling for abstract submissions. All details can be found on the website (www.aphidsymposium.org <http://www.aphidsymposium.org/>) - abstract submission information can be found on the Program page, and the deadline for abstract submissions is 1 July 2005.

Please note that an International Phylloxera Symposium will be held in conjunction with this Aphid Symposium. See the website for more details.

Best regards,

Owain Edwards

Chair, Local Organizing Committee 7th International Symposium on Aphids, Esplanade Hotel, Fremantle, WA AUSTRALIA

Owain.Edwards@csiro.au

France Conservation Sep29-Oct2

International Symposium

*****Mediterranean plant conservation in a changing world*****

29 September - 2 October 2005 Hyeres, Var, France

NEW

Abstract submission :

proposal before 10th July 2005, to: f.medail@univ.u-3mrs.fr

Please, indicate if you would like to present an oral communication or a poster. Only proposals in french or english will be accepted, english contributions are prefered.

Guidelines for abstract submission

-The text (arial 10) cannot exceed 1500 characters (space included), excluding title, names and adresses of authors.

- Authors and adress format : Stéphane Marin1, Franoise Provence2 & Yong-Ming Yuen 1 Institution 1. Adress, Email. 2 Institution 2. Adress, Email. 3 Institution 3. Adress, Email. Etc

- No tables, no graphics are allowed. - No literature cited. - Include 4-5 key-words.

Please select and indicate the topic number concerning your communication :

 Session 1 Evaluation of conservation strategies in different regions around the Mediterranean basin

 Session 2 Consequences of the major threats to the Mediterranean flora

 Session 3 New advances in biological and ecological plant conservation

 Session 4 Experimental programmes of conservation and restoration

****Website: http://www.colloquemed.tk****   Alex BAUMEL <alex.baumel@univ.u-3mrs.fr>

France PlantConservation Sep29-Oct2

International Symposium

*****Mediterranean plant conservation in a changing world*****

29 September - 2 October 2005 Hyeres, Var, France

Organizers :

Institut Méditerranéen dEcologie et de Paléoécologie (IMEP, UMR CNRS 6116), Université Paul Cézanne (Aix-Marseille III) & Conservatoire Botanique National Méditerranéen de Porquerolles

Program

29th September : - Session 1 Evaluation of conservation strategies in different regions around of the Mediterranean basin

- Session 2 Major threats and their consequences for the Mediterranean flora

30th September : - Session 3 New advances in the biological and ecological plant conservation

1rst October : - Session 4 Experimental programmes of conservation and restoration

2nd October : Field excursion.

Scientific committee:

Responsable : Dr Frédéric Médail, email: f.medail@univ.u-3mrs.fr

Dr Laurence Affre, Dr Alex Baumel, Prof. Dr Franois Bretagnolle, Dr Max Debussche, Prof. Dr. Mohammed Fennane, Dr Daniel Jeanmonod, Prof. Dr. Vernon Heywood, Prof. Dr José M. Iriondo, Dr Joël Mathez, Dr Frédéric Médail, Prof. Dr. Neriman Ozhatay, Prof. Dr. Pierre Quézel, Dr Jamie Skinner, Dr John D. Thompson, Dr Régine Verlaque.

***** DEADLINE FOR REGISTRATION : the 15 of june 2005*****

Further details on registration : ****http:/-/www.colloquemed.tk/***** Alex BAUMEL <alex.baumel@univ.u-3mrs.fr>

FremantleAust Evolution Sep27-30

Second Announcement 4th Meeting of the Australasian Evolution Society

27th-30th September 2005

Esplanade Hotel Fremantle Western Australia

Plenary Speakers

Geoff A. Parker FRS, University of Liverpool, UK H. Carl Gerhardt, University of Missouri, USA Mark Blows, University of Queensland, Australia Russell D. Gray, University of Auckland, NZ

Registration Closes July 31st

Members Full Registration $350.00 Student $250.00

Non Member Full Registration $425.00 Student $325.00

Registration fees include welcome reception 1800-2000 on 27th September, Abstract book and delegate pack-

age, entrance to the meeting, and tea/coffee & lunches on 28th to 30th September. There will be an optional conference dinner on the evening of 30th September priced at $95.00 or $75.00 for students. The cost includes 5h access to beverages. Download and complete the registration form, and e-mail to wjk@cyllene.uwa.edu.au

Accommodation at the venue is available at a cost of $180.00 per room single/double/twin share. Details of the venue can be found on the Hotels fact sheet (pdf). A variety of other options, ranging from Hotels to Apartments and Units, from B&B to Backpackers, are available and can be booked using the Fremantle Tourist Information web site @ http://-www.FremantleWA.com.au –

Professor Leigh W. Simmons Zoology Building School of Animal Biology (M092) The University of Western Australia Nedlands Tel: +61 8 6488 2221 WA 6009 FAX: +61 8 6488 1029 Australia

http://www.lwsimmons.org UWA CRICOS Provider Code 00126G

Leigh Simmons <lsimmons@cyllene.uwa.edu.au>

Fribourg ParasiteResistance Oct3-4

EVOLUTIONARY ECOLOGY OF PARASITE RESISTANCE AND TOLERANCE IN PLANTS AND ANIMALS

Symposium organised by Thomas Steinger, Dieter Ebert, and Heinz Müller-Schärer 3-4 October 2005, Fribourg/Switzerland

http://www.unifr.ch/biol/ecology/resistevoeco We are organising an international symposium to discuss recent progress in the study of the evolution of resistance and tolerance to parasites (herbivores, fungal and bacterial pathogens, arthropods etc.) in both plants and animals.

We have invited a number of internationally renowned scientists to give plenary lectures, but we also have time for approximately 15 talks by younger researchers (PhD students & post-docs).

Invited speakers: - Janis Antonovics (University of Virginia, USA) - Yannis Michalakis (CNRS, Montpellier, France) - Paul Schmid-Hempel (ETH Zurich, Switzerland) - Michael Siva-Jothy (University of Sheffield, UK) - Peter Tiffin (University of Minnesota, USA)

The symposium will be free, but registration is necessary.

Deadline for abstract submission: July 8 Deadline for registration: September 2

The symposium is generously funded by the "Troisième Cycle" Program of the Conférence Universitaire de Suisse Occidentale (CUSO).

Best regards,

Thomas Steinger (thomas.steinger@unifr.ch) Dieter Ebert (dieter.ebert@unibas.ch) Heinz Müller-Schärer (heinz.mueller@unifr.ch)

thomas.steinger@unifr.ch thomas.steinger@unifr.ch

GhentU StatGenetics May17

The Center for Statistics of Ghent University is organizing a one-day symposium on Statistical Genetics to be held in Ghent (Belgium) on May 17, 2005. The goal of this symposium is to bring together statisticians, data analysts, bio-information scientists and computational biologists from universities, research institutes and industry and to bring them in contact with the newest developments in statistical genetics. Leading experts in this field will discuss different themes, including pharmacogenetics, genetic association analysis, marker-assisted plant breeding and micro-array analysis.

REGISTRATION IS STILL OPEN, but now excludes lunch (prices are discounted to exclude lunch expenses).

Invited speakers: Balding, David (Imperial College London, U.K.) Goldstein, David (University College London, U.K.) Hospital, Frederic (INRA, UMR de Genetique Vegetale, France) Lange, Christoph (Harvard School of Public Health, U.S.A.) Storey, John (University of Washington, U.S.A.) van Eeuwijk, Fred (Wageningen University & Research Centre, The Netherlands) Moerkerke, Beatrijs (Ghent University, Belgium) Vuylsteke, Marnik (Flanders Institute for Biotechnology, Belgium)

Details of the scientific program, as well as guidelines for registration are available on the symposium web site: http://www.cvstat.ugent.be . –

Stijn Vansteelandt Phone. ++32 9 2644776 Ghent University Fax. ++32 9 2644995 Dept. Applied Mathematics and Computer Science Krijgslaan 281, S9 B-9000 Gent, Belgium

Center for Statistics: http://cvstat.ugent.be Master in Statistical Data Analysis: http://www.mastat.ugent.be

Stijn Vansteelandt <Stijn.Vansteelandt@ugent.be>

Gottingen EvoDevoTribolium Aug3-4

2. International Tribolium Meeting in Göttingen/Germany

It is time to talk about a beetle! The Tribolium castaneum genome has been sequenced, RNAi proves to be a powerful tool and the first insertional mutagenesis screen is on its way. Because of these and other advances, Tribolium has evolved from a comparative to a full model system that provides answers to novel questions.

Therefore we invite you to join the discussion on recent findings regarding segmentation, oogenesis, head and leg development and other issues. We are especially happy to announce Guillaume Balavoines talk about segmentation in the annelid Platynereis dumerilii. Some talks will also cover topics in millipeds and spiders. Furthermore, we will discuss technical advances and joint efforts to develop new tools. Finally we will coordinate our annotation efforts and have a workshop "How to annotate your favourite gene". There will be plenty of time for informal discussion and a poster session.

We would be especially happy to welcome people that are not yet working with the beetle but are considering doing so. This meeting will be a perfect start to make contacts and initiate cooperations.

Date: august 3-4, 2005

We hope to see you in Göttingen,

Gregor Bucher, Ernst Wimmer

Dr. Gregor Bucher

Institute for Zoology, Anthropology and Dev. Biology Dpt. for Developmental Biology Georg August University Göttingen Justus-von-Liebig-Weg-11 37077 Göttingen

Fon: +49-551-395426 Fax: +49-551-395416 Email: gbucher1(a)uni-goettingen.de Web: http://bucher.tribolium.net Gregor Bucher <gbucher1@uni-goettingen.de>

ics, bio-informatics, and ethical dimensions. Attendance is limited to 100 individuals selected on the basis of compulsory submitted abstracts. Abstract deadline 10th June 2005. Organizers; SJ Chanock, P-Y Kwok, I Gut, A Jeffreys, and AJ Brookes. See http://snp2005.nci.nih.gov/home.cfm for further details and registration.

Thank you With kindest regards, Ivo Gut

Ivo Gut <ivogut@cng.fr>

HarvardU PlantBiol May25

Everyone is welcome to attend a one-day, Inaugural Symposium for the Harvard Initiative in Plant Biology on Wednesday, May 25, 2005

Location: Fairchild Biochemistry Building Harvard University Main Auditorium, Room 102 7 Divinity Avenue, Cambridge, MA

For more information, see http://www.oeb.harvard.edu/faculty/holbrook/symposium/ Schedule of events 8:50 am Welcome 9:00 am Eliott M. Meyerowitz, Caltech, "Dynamic development: real-time analysis and computational modeling of cell division and gene expression in the growing shoot" 9:40 am Jiri Friml, University of Tubingen, "Cell polarity-dependent auxin gradients as a general mechanism in plant development" 10:40 am Xuemei Chen, Rutgers University, "Flowers show and tell: cell fate specification and micro-RNA biogenesis" 11:20 am Jen Sheen, Harvard University, "Molecular signaling networks: probing creativity and adaptability in plants" 1:30 pm Jeffrey D. Palmer, Indiana University, "The highly promiscuous genome of plant mitochondria: bacterial levels of horizontal gene transfer in a eukaryotic genome, with some unusual twists" 2:10 pm Ian Baldwin, Max Planck Institute for Chemical Ecology, "Using genetically modified plants to study ecological interactions" 3:10 pm Howard Stone, Harvard University, "Physical lessons adduced from plants by thinking across scales - transport, optimization, flexibility and function" 3:50 pm Christopher B. Field, Carnegie Institution of Washington, "Terrestrial ecosystems and the carbon cycle" –

npierce@oeb.harvard.edu npierce@oeb.harvard.edu

HinckleyUK SNPs Sep22-24

7th International Meeting on Single Nucleotide Polymorphism and Complex Genome Analysis Hinckley Island Hotel, Hinckley, Leicestershire, UK on September 22 to 24, 2005 Topics include association studies, haplotypes, methods/strategies, population genet-

KansasCity EcolGenomics Nov4-6

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Doris Merrill Ecological Genomics in Kansas KSU Division of Biology 231 Ackert Hall Manhattan, KS 66506-4901 Phone: (785) 532-3482 FAX: (785) 532-6653 E-mail: ECOGEN@ksu.edu

Marseilles 6 EvolBiol Sep21-23 Preprogram

Dear Colleagues,

The pre program for the 9th Evolutionary Biology Meeting at Marseilles is available on our website www.up.univ-mrs.fr/evol/congres/ from Thursday May 12th . The following topics will be discussed : systematic biodiversity comparative genomics and post-genomics (at all the taxonomic levels) functional phylogeny environment and evolution

Few spots are available for oral presentations or posters.

We look forward to hearing from you soon.

Oumou Ba for the Evolutionary Biology Meeting at Marseilles.

egee@up.univ-mrs.fr

McMasterU 2 Astrobiology May24-Jun4

2nd Announcement

Origins Institute conference/workshop on:

"Astrobiology and the Origins of Life" conference: May 24-28/2005 workshop: May 30-June4/2005 McMaster Univerity, Hamilton, Ontario

http://origins.mcmaster.ca/conferences.html It is a great pleasure to announce the full programme for the Origins Institute conference and workshop on astrobiology and the origins of life, being held this spring at McMaster University (please see website for all of the details). The conference will provide both authoritative, interdisciplinary reviews as well as the latest results in a number of areas of interest to astrobiology. The workshop that follows will explore a number of these areas through informal discussion, with time to work and begin collaborative projects. The venue features the latest in lecture theatres and interactive facilities on the pleasant campus of McMaster University.

The programme for the ONE WEEK workshop is also available. NOTE: in order to concentrate the workshop into a very effective programme, the organizers have decided to shorten it to 6 days, rather than the original advertised length of 2 weeks.

This will be an international meeting with more than 120 participants from many countries already registered. We encourage anyone interested in this programme, which ranges over a number of areas in planetary science and evolutionary biology, to please register as soon as possible in order to take advantage of the reduced hotel rates.

You may still present a poster in the conference, or apply for some remaining openings in our workshop. Please use the registration form available on the website.

To assist us in organizing the conference, please inform Rosemary McNeice, via email at mcneicer@mcmaster.ca, of the following:

1) If you have special dietary requirements. 2) If you are planning to attend the Barbeque on Saturday, May 28. 3) If you are interested in taking the city bus for transportation to and from the University, tickets and

a bus route map will be available at the front desk of your hotel. 4) If you would like to adventure on the Maid of the Mist during the Niagara excursion. The organizers will lead all interested parties on a cruise in the Niagara River beneath the falls on the famous Maid of the Mist, tickets are $13.00 and can be purchased at the booth.

Please monitor the website for updates

We hope to welcome you at McMaster University to participate in this exciting and forefront area of contemporary science.

With best regards, Ralph Pudritz, Director, OI

For the organizing committee.

Ralph E Pudritz | Office: Bourns Bldg (ABB 318) | Telphone/voicemail: (905) 525-9140 x23180 Physics & Astronomy | Secretary: Cheryl Johnston(905) 525-9140 x27356 McMaster University | FAX: (905) 546-1252 Hamilton, Ontario | Canada L8S 4M1 | E-mail: pudritz@physics.mcmaster.ca

Rosemary McNeice, Origins Secretary McMaster University ABB-241, 1280 Main Street West, Hamilton, ON L8S 4M1 905-525-9140 X23531

"J. R. Stone" <jstoner@mcmaster.ca>

MurciaSpain Carabidologists Sep19-22

Dear Colleagues,

The second circular of the XII Carabidologists Meeting to be held in Murcia (Spain), 19-22 September 2005, is found at http://www.um.es/eurmecar/ Please have a look on it. Note that there are new deadlines to send the registration form. Best regards.

– Prof. José Serrano. Departamento de Zoología. Facultad de Veterinaria. Universidad de Murcia. Campus de Espinardo. 30071. Murcia (Spain)

Jose Serrano <jserrano@um.es>

Oslo HennigSociety July25-29 2ndCall Presentations

24th MEETING of the WILLI HENNIG SOCIETY

25-29 July 2005 in the mountains north of Oslo, Norway

2nd CALL FOR PRESENTATIONS

- Oral and poster; can fit in topically with preliminary symposia, or be on other topics of phylogenetic interest. All effort will be made to include non-symposium oral presentations: first-come, first-served.

- Oral presentations: when registering (see below), please suggest amount of time requested, and every effort will be made to accomodate.

PRELIMINARY SYMPOSIUM PROGRAM

- Phylogenomics (organized by David Liberles and Jens Lagergren)

- Ancient DNA (organized by Lutz Bachmann)

- Lower-level Phylogenetics of Angiosperms (organized by Victor Albert)

The Willi Hennig Society strongly encourages participation from students and postdocs on their developing research, either theoretical or empirical. There are several cash student prizes that will be awarded.

REGISTRATION AND ABSTRACT SUBMISSION

http://folk.uio.no/victoraa/Frontpage_files/-slide0003htm   **DEADLINE for REGISTRATION and ABSTRACT SUBMISSION is 1 July 2005**

victor.albert@nhm.uio.no

PennStateU Genomics July20-23

You are invited to the Symposium

"Comparative and Functional Genomics" to be held at the

Pennsylvania State University July 20-23, 2005

Keynote Address by: Dr. Robert Waterston "The genome revolution: At the barricades"

Five sessions of invited talks from top researchers from around the world will cover topics in:

"Evolutionary and Population Genomics" "Genome Function from Comparisons" "Genome Structure and Dynamics" "Genome Function from Experiments" "From Genomes to Mechanisms"

An additional session will feature oral presentations se-

lected from submitted abstracts. A complete schedule with lists of speakers and titles, along with information about housing and registration, is at:

http://www.symposium.psu.edu/ Registration fees are modest, but capacity is limited so please register today!

Thanks,

Ross Hardison, Kateryna Makova and Anton Nekrutenko Co-conveners Center for Comparative Genomics and Bioinformatics, Huck Institutes of Life Sciences

and

James L. McDonel Symposium Director

Betsy R. King Symposium Coordinator

Department of Biochemistry and Molecular Biology and Department of Biology Penn State University

Kateryna Makova <kmakova@bx.psu.edu>

RutgerU DFairbrothers Jun4

A Symposium and Banquet Honoring the Legacy of David E. Fairbrothers

"The Future of Plant Research"

at Rutgers University, NJ, USA

June 4, 2005

This event is organized to honor David Fairbrothers' work during his 40+ years career at Rutgers University as a researcher, academic advisor, teacher, administrator, and colleague. David Fairbrothers' historic influence over plant research, conservation of plants on both a local and nationwide scale, as well as protection of habitats in the NJ Pinelands cannot be overestimated. He will be honored by former students, colleagues and his friends in a Mini-Symposium discussing his influence over plant research and conservation in the United States, with personal anecdotes from students and colleagues, and presentations of current cutting-edge plant research at Rutgers. This is also the kick-off for the fundraising campaign for the David E. Fairbrothers Plant Resources Center (FPRC), an umbrella organization envisioned to consist of the Chrysler Herbarium, the Rutgers' Mycological Herbarium, Online Herbarium, Molecular and Plant Extract Archive and a K-12 Stakeholder outreach program. The endowment for the FPRC would secure funding for staff and

activities that would benefit both New Jersey plant and citizens, as well as nationwide plant research.

Speakers for Mini-Symposium:

Richard Triemer, Michigan State University Ilya Raskin, Rutgers University

Steven Handel, Rutgers University David Lee, Florida International University

Jim White, Rutgers University

Steven Clements, Brooklyn Botanic Garden Dennis Stevenson, The New York Botanical Garden

Art Tucker, Delaware State University

Lena Struwe, Rutgers University

David Fairbrothers and his family will of course attend the symposium. If you can't attend but would like to send your regards or anecdotes to be read at the symposium, please e-mail Lena Struwe (struwe@aesop.rutgers.edu).

Registration fee: $20 for symposium, $50 for banquet

Time: 2-5 PM (symposium), 6-9 PM (banquet), you can attend either or both.

Place: Winants Hall, College Avenue Campus, New Brunswick, Rutgers University, NJ, USA

Registration forms are enclosed and are also available on-line at http://aesop.rutgers.edu/˜herbarium/-fprc.htm For hotel suggestions see website.

Due date for registration: May 22, 2005 (we have a limited number of seats available so please respond early!).

Dr. Lena Struwe Dept. of Ecology, Evolution, and Natural Resources/ Dept. of Plant Biology and Pathology Rutgers University - Cook College 237 Foran Hall, 59 Dudley Road New Brunswick, NJ 08901-8551, USA phone: (732) 932-9711 ext. 235, fax: (732) 932-9441 e-mail: struwe@aesop.rutgers.edu home page: www.rci.rutgers.edu/˜struwe GENTIAN RESEARCH NETWORK: www.rci.rutgers.edu/-˜struwe/gentnet Director, CHRYSLER HERBARIUM: aesop.rutgers.edu/˜herbarium D. E. Fairbrothers Plant Resource Center: http://aesop.rutgers.edu/-˜ herbarium/fprc.htm Biodiversity and Training Program, ICBG CENTRAL ASIA: icbg.rutgers.edu <http://icbg..rutgers.edu/>

struwe@AESOP.Rutgers.edu

UMontpellier PhDStudents2

11th Meeting of PhD Students in Evolutionary Biology

Pre-registration for the 11th Meeting of PHD Students in Evolutionary Biology will be closed on friday 13th of may.

After this deadline, registration will still be possible at http://kimura.univ-montp2.fr/mpseb but candidates will automatically be put on the complementary list.

Best regards,

The organizing committee:

Eric Bazin<bazin@univ-montp2.fr> Emmanuelle Billard <billard@sb-roscoff.fr> Stéphane De Mita <demita@ensam.inra.fr> Julien Dutheil <Julien.Dutheil@univ-montp2.fr> Emmanuelle Eveno <eveno@pierroton.inra.fr> Baptiste Faure <bfaure@sb-roscoff.fr> Matthieu Faure <matthieu.faure@univ-montp2.fr> Olivier Lepais <Lepais@pierroton.inra.fr> Delphine Muths <muths@sb-roscoff.fr>

Julien.Dutheil@univ-montp2.fr   Julien.Dutheil@univ-montp2.fr

VictoriaAust HumanGeneMapping Nov23-25

1st Announcement

5th Australasian Human Gene Mapping Conference Incorporating the 9th Australasian Twin Registry Conference 23-25th of November 2005 Mt Buller, Victoria, Australia.

This conference is the 5th in a series of conferences on the genetics of common, complex disorders. We will discuss the traditional topics of linkage and association, technological developments, and statistical approaches. This year's GeneMapper's conference will focus on modern approaches to linkage and association mapping with a mix of methodological, technological and applied talks in the field of gene mapping, hopefully providing something for everyone!

For more information go to: http://bioinf.wehi.edu.au/folders/melanie/genemappers/ and bookmark for further updates.

Melanie Bahlo Ph.D. Special Fellow Division of Genetics and Bioinformatics The Walter and Eliza Hall Institute of Medical Research The Royal Melbourne Hospital Post Office Parkville 3050 VIC Australia

bahlo@wehi.edu.au Phone: +613 9345 2630 Fax: +613 9347 0852 http://bioinf.wehi.edu.au/ Melanie Bahlo <bahlo@wehi.edu.au>

GradStudentPositions

MaxPlanck HIVBioinformatics

Ph.D. position, statistical/computational analysis of HIV/AIDS data, MPII, Saarbruecken

A Ph.D position is available in the field of HIV Bioinformatics at the Computational Biology department of the Max-Planck-Institute for Informatics in Saarbruecken. The research project focuses on the development and application of statistical and computational methods for the analysis of HIV/AIDS data. The project is part of a large and well-established collaboration with several virological and medical research groups in Germany, Italy, and the USA. Further information is available at http://www.mpi-sb.mpg.de/units/ag3/hiv.html . The candidate should have a Masters or Diploma degree in computer science, bioinformatics, theoretical biology, mathematics, or physics, with background in statistical learning and/or theory of evolution. Interest in interdisciplinary research, computational skills and programming experience are important for the position.

The Max-Planck-Institute for Computer Science is a leading international research institute hosting 91 Ph.D. students. The Institute is part of the "Center for Bioinformatics, Saar", which is one of the 5 Centers for Bioinformatics in Germany funded by the German Science Foundation and provides excellent research opportunities in the field. On the European scale, the institute is partner in the EU Network of Excellence BioSapiens.

The Max Planck Society is committed to increasing the number of handicapped employees and of women in areas where they are underrepresented and therefore explicitly encourages such individuals to apply.

Interested candidates should send their application (preferably via email and in PDF-format), including motivation letter and CV to:

Prof. Dr. Thomas Lengauer, Ph.D. Max-Planck-Institut fuer Informatik Stuhlsatzenhausweg 85 D-66123 Saarbruecken Germany Phone: ++49 681 9325 300 http://www.mpi-sb.mpg.de/units/ag3/ Tobias Sing <tobias.sing@gmail.com>

MaxPlanckInst StatAnalysis

Max Planck Institute for Demographic Research Directors: Prof. James W. Vaupel, Prof. Jan M. Hoem

National Centre for Statistical Ecology Director: Prof. Byron J. T. Morgan

The Max Planck Institute for Demographic Research (MPIDR) and The National Centre for Statistical Ecology (NCSE) are seeking to appoint to a PhD position in the Statistical Analysis of Age-specific Survival Rates

The National Centre for Statistical Ecology (NCSE) is a new joint venture between the Universities of Cambridge, Kent and St Andrews, funded under the EPSRC multidisciplinary critical mass in Mathematics initiative. It links the research groups in statistical ecology at the three Universities. This particular position will principally involve collaboration between the University of Kent and the Biodemography research programme of the MPIDR. It will involve spending time both in Germany (Rostock) and in the United Kingdom (Canterbury). In Rostock, the successful candidate will complement an existing research team of 19 staff, including a number of recently recruited evolutionary ecologists. The team aims to gain a fundamental understanding of how age-specific demographic processes are shaped by evolution. In Canterbury, the student will form part of a thriving group, working on many different aspects of statistical ecology, biometry in general, and other areas of applied and theoretical statistics. The group involves PhD students and post-doctoral research workers. As a member of the National Centre for Statistical Ecology, the student will also come into close contact with related work in the universities of Cambridge and St. Andrews, which host similar research groups. The successful candidate will work towards their doctorate through structured coursework, focused workshops and seminar programmes as well as through their main research project on new statistical methods for modeling how survival rates of organisms change with age. We anticipate that mark-recapture data, mostly from bird and mammal populations, will be the main material used in the development of these methods.

We are seeking able graduate scientists with strong academic track records in quantitative disciplines. Applications should be addressed to Director MPIDR, Prof. James W. Vaupel and Director NCSE, Prof. Byron J.T. Morgan, and should include a CV with a statement of academic interests and relevant experience, qualifications (details of all grades for exams, projects, and coursework), and the contact details of 3 referees. Details of any publications should be listed. Material should be e-mailed to: MPIDR-NCSE-Age-Models@demogr.mpg.de by latest 15th June 2005. See www.demogr.mpg.de , http://www.ncse.org.uk/ and http://www.kent.ac.uk/ims/groups/statistics/index.htm for more information.

The Max Planck Society and the University of Kent wish to increase the share of women in areas where they are underrepresented, and strongly encourage women to apply.

The Max Planck Society and the University of Kent are committed to employing more handicapped individuals and especially encourage them to apply.

Dr. David L. Thomson Max Planck Institute for Demographic Research Konrad-Zuse Str. 1 D-18057 ROSTOCK Germany

Tel. +49 (0)381 2081 229 Fax. +49 (0)381 2081 529 E-mail: thomson@demogr.mpg.de Website: www.demogr.mpg.de "Thomson, David" <Thomson@demogr.mpg.de>

NorwichUK HostParasite Coevol

I have a Ph.D. studentship available to study 'Coevolution of One Host with Several Parasites'. This is a theoretical project, based on computer modelling. Please could you forward the attached advert to prospective Ph.D. students who might be interested. http://www.jic.ac.uk/staff/james-brown/Brown_MultiPathogens_advert.pdf Please note that the terms of the studentship mean that it's open to applicants from any EU/EEA country but the stipend can only be paid to a UK student (sorry - I don't make the rules!)

James Brown

Dr James K M Brown Dept of Disease & Stress Biology, John Innes Centre, Colney Lane, Norwich, NR4 7UH, England Phone 01603 450615 Fax 01603 450045 http://www.jic.bbsrc.ac.uk/staff/james-brown

UAlgarve MarineEvolution

Applicants for a PhD fellowship:

Applicants are invited to apply for an FCT (Portuguese Science Foundation) Doctoral fellowship. The successful candidate will join an established program of research between the Center for Marine Sciences (CCMAR, Universidade do Algarve, Portugal) and the University of Groningen, Netherlands (RUG), in association with the Marine Genomics Europe (MGE) Network of Excellence. The PhD will be co-supervised by Dr. Gareth Pearson (CCMAR) and Dr. Jeanine Olsen (RUG).

The program of research will make use of various expressed sequence tag (EST) databases from Fucus spp, as well as MGE technical platforms, bioinformatic support and training resources. The project will focus on the development and application of molecular markers for genes involved in stress responses in closely related benthic marine brown algae of the genus Fucus, to test hypotheses related to the evolution of stress-tolerance and local adaptation within the genus.

A strong interest in evolutionary biology is essential. Experience in basic laboratory molecular biology techniques, computer literacy and exposure to bioinformatic/phylogenetic methods is highly desirable.

Interested applicants should send by: email (gpearson@ualg.pt) or fax (+351-289-818353) a photocopy of their degree certificate and transcripts, a short CV and three letters of of recommendation including the address, phone and e-mail of the three referees. Deadline for receipt of applications May 30, 2005.

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MAREE-Marine Ecology and Evolution (http://www.ualg.pt/ccmar/maree) CCMAR - Centre of Marine Sciences, and CIMAR -Laboratório Associado Faculdade de Ciências do Mar e Ambiente, Universidade do Algarve

Mailing address: F.C.M.A., Univ. Algarve, Gambelas, 8005-139 Faro, Portugal Fax: 351-289-818353, Phone: 351-289-800928

eserrao@ualg.pt

UCollegeDublin BeeBat PopGenetics

PhD Studenship-

Bumble-bee bat population genetics

A funded three year PhD studentship is available in the Zoology Department, University College Dublin, Ireland, starting September 2005. This project plans to extensively describe and characterize the only two populations of bumble-bee bat, Craseonycteris thonglongyai in both Myanmar and Thailand. The two populations exhibit a large echolocation difference, but on initial genetic investigation appear to be the same species. Usually in bats, a large echolocation divergence between two populations of the same species in geographic proximity, indicates a species level divergence. The populations will be studied at the morphological, ecological, acoustic, and genomic level (mitochondrial and nuclear DNA), to examine the role that sensory ecology plays in bat speciation.

This project will involve both field and laboratory research in Ireland, Thailand and Myanmar. The student will learn modern molecular techniques; population genetic and phylogenetic analyses methods; bat identification and field methods.

Successful candidates most hold at least a 2:1 honours biology degree by September 2005. Field and molecular laboratory skills are desirable.

If interested please e-mail your CV, areas of research interest and contact details of two referees to Emma Teeling (emma.teeling@ucd.ie). The closing date is June 15th 2005.

Candidates must hold EU citizenship for full funding.

For further details contact:

Dr. Emma Teeling Department of Zoology University College Dublin Ireland + 353 1 716 2263 emma.teeling@ucd.ie   http://www.ucd.ie/zoology Emma Teeling <Emma.Teeling@ucd.ie>

UCopenhagen InsectSocieties

A 3-year PhD position will be available from August 2005 at Faculty of Sciences, University of Copenhagen, Denmark.

The position is funded by the European Community via a Marie Curie Excellence Grant. The successful candidate will work in a new research group leaded by Dr. Patrizia D'Ettorre, which will be integrated in the centre for Social Evolution and Symbiosis (http://www.zi.ku.dk/cses/) directed by Prof. JJ (Koos) Boomsma.

The research project will focus on Chemical Communication Code of Insect Societies, with a multidisciplinary approach (behavioural, chemical, electro- and neurophysiological analyses and genetics). Part of the field work will be carried out in the tropics.

Applicants should be highly motivated and have a Master degree in Biology or related disciplines, and a good background in Evolutionary Biology. Familiarity with general molecular evolutionary techniques, with chemical ecology techniques and neurophysiology is desirable but not compulsory. The position is NOT restricted to EU-citizens.

Applications should include CV, list of publications, research interests, name and email address of one referee, and be sent by email to Patrizia D'Ettorre at pdettorre@bi.ku.dk as soon as possible, latest by May 31st 2005.

Patrizia D'Ettorre Institute of Biology Department of Population biology University of Copenhagen DK-2100 Copenhagen, Denmark Phone +45 3532 1239 fax +45 3532 1250

http://www.biologie.uni-regensburg.de/Zoologie/Heinze/en/staff/dep/dep_e .html

"D'Ettorre, Patrizia" <PDEttorre@bi.ku.dk>

UDublin Host-Parasite

PhD Position studying the Evolution and Ecology of a Host-Parasite System

Abstract: Many host-parasite systems consists of a single parasite species in multiple host species. However, little is known about how such systems are structured in evolutionary and ecological time. This project will investigate the interaction between the parasitic nematode, Sphaerularia bombi and its bumble bee host species. Molecular, ecological and parasitological tech-

niques will be used to understand this complex relationship.

Host institution: The research will be conducted within the Department of Zoology (www.tcd.ie/zoology), University of Dublin Trinity College. The Department is well-supplied with modern molecular and parasitological labs, and has a thriving research community.

Applicants: Should have undergraduate or, exceptionally, post-graduate training in one or, preferably, more of the following areas: (i) evolutionary theory, particularly as it pertains to host-parasite systems; (ii) parasitology; (iii) ecological theory; (iv) molecular techniques, particularly PCR and sequencing (v) phylogenetic theory and techniques In addition, applicants must hold an EU passport (or equivalent) and would ideally hold a valid driving licence.

For further information, and to apply for this position, please contact:

Dr Mark Brown, Department of Zoology, Trinity College Dublin, Dublin 2 Ireland, email: mabrown@tcd.ie

Closing date: end of June 2005

This position is funded by the SFI Research Frontiers Programme 2005

Mark Brown <mabrown@tcd.ie>

UEastAnglia Phylogeography

PhD Studentship

Phylogeography School of Computing Sciences

New analytical tools for phylogeography and understanding biodiversity

In this project, we will develop new analytical tools within the recent and rapidly developing field of phylogeography. Phylogeography is concerned with the analysis of the geographical distribution of genealogical lineages, with application to understanding the structure of biodiversity. While current tools for quantifying biodiversity typically measure the relative distributions of species within a region, phylogeography seeks to assess the geographical distribution of genetic variation within each species. Given the clear link between genetic variation and the potential for adaptive response, such assessments are critical for the long-term maintenance of individual species and species assemblages.

A current challenge in phylogeography is that the ease

of obtaining genetic data has far outpaced the development of the analytical methods necessary to make full use of the data. It is becoming increasingly easier to obtain data from different DNA sequence regions from the same organism, and from different organisms with the same geographic distribution. However, to analyze them in concert it is now time to follow the lead taken by the field of molecular phylogenetics that has progressed from single marker studies to more rigorous studies of multiple independent genetic markers. In particular, some specific gaps in our analytical ability include: (1) How can we critically assess the degree to which two or more gene genealogies are concordant with one another? (2) How can we critically assess the degree to which demographic inferences from a gene genealogy/genealogies are concordant with non-DNA sequence genetic data (e.g. microsatellites, AFLPs, SNPs)? (3) How do we bridge the gap between phylogenetic trees and genealogical networks to deal with data sets spanning both temporal frames?

In this project we will address problems such as these using contemporary methods for inferring phylogenetic trees and networks. Such structures are well suited to the analysis of biodiversity at the species level. For example, the Cyberinfrastructure for Phylogenetic Research (CIPRes) project (www.phylo.org/index.html), is a US led project that aims to build the Tree of Life based on phylogenetic tree reconstructions from DNA data from hundreds of thousands of species. Projects such as this have great potential for categorizing and prioritizing species for conservation. Even so, as currently configured, present methods for phylogenetic inference are not well suited to quantify how genetic diversity is distributed across a landscape at the level of an individual species. This project will involve adapting phylogenetic methodology to address such issues.

Closing date for applications: 3 June 2005

This project will be supervised by Prof. Vincent Moulton (www.cmp.uea.ac.uk/people/faculty/vlm), School of Computing Sciences, and Dr. Brent Emerson (www.uea.ac.uk/bio/people/faculty/Brent.html), School of Biological Sciences.

Students interested in this PhD-studentship should have excellent programming skills, a good background in theoretical computer science and/or mathematics, and preferably a strong interest in biology.

The studentship is open to all UK and non-UK applicants, and application forms are available on www.cmp.uea.ac.uk/admissions/researchdegree.jsp .–

b.emerson@uea.ac.uk

tems across species.

UGlasgow MatingSystemsPathogens

PhD Studentship, University of Glasgow

A 3-year PhD studentship is available to study potential interactions between plant mating systems and pathogen response, using natural populations of Arabidopsis lyrata (Brassicaceae) that vary in their degree of outcrossing.

Many flowering plants have genetic mechanisms to reduce detrimental effects associated with inbreeding (i.e. inbreeding depression) that work by preventing fertilization of ovules by self-related pollen (i.e., self-incompatibility or SI systems). These systems tend to be under the control of complex signal transduction pathways that are activated when proteins expressed on the surface of pollen are recognized as matching the specificity of those on the surface of the stigma. The reproductive advantages of being different (in terms of number of available mating partners) result in exceptionally high levels of diversity at the loci controlling the recognition part of the reaction. Plants with a long history of outcrossing as a result of such processes are expected to accumulate high genetic loads due to the increased levels of heterozygosity expected for loci that are subject to this type of balancing selection. Despite this expectation, we have identified populations of A. lyrata that differ in their degree of outcrossing, presumably due to failure or relaxation of the SI system. An important issue in conservation biology is whether inbreeding always has negative consequences for adaptation and survivorship of small populations or whether negative deleterious mutations are purged following an initial change from outcrossing to inbreeding.

Immune tolerance, or the ability to adapt to pathogens, is often assumed to vary with overall host fitness but is itself an important selective force contributing to biodiversity and adaptation that is likely mediated by mating strategies. Although it has been suggested that inbreeding should decrease the available spectrum of responses to pathogens and therefore that inbred populations should be more susceptible to pathogens, this hypothesis has rarely been explicitly tested in natural populations. The variation in strength of SI among populations within a single species found here allows testing of ideas about both inbreeding depression and pathogen response without complications associated with comparing populations with different mating sys-

The main focus of the PhD project would be to examine the interaction between mating system variation and pathogen response, through controlled pollination experiments within and between populations that vary in their strength of SI in relation to the degree of colonization by powdery mildew and/or other biotrophic pathogens. The project is centred on a research question that draws techniques and underlying theories from molecular ecology, conservation genetics, evolution of sexual reproductive systems, population genetics, molecular biology; classical Mendelian genetics and host-pathogen co-evolution.

The project would be based in the Division of Environmental and Evolutionary Biology at the University of Glasgow. Interested individuals should send their CV and a brief statement of their research background and interests to b.mable@bio.gla.ac.uk. Review of applications will begin immediately and will continue until a suitable candidate is found. Additional background information can be found at http://www.gla.ac.uk:443/-ibls/staff/staff.php?who=PQdGnd . – Dr. Barbara Mable NERC Advanced Research Fellow Rm 404, Graham Kerr Bldg Division of Environmental and Evolutionary Biology University of Glasgow Glasgow, Scotland U.K. G12 8QQ Phone: +44 (0)141 330 3532 Fax: +44 (0)141 330 5971 email: b.mable@bio.gla.ac.uk

UHelsinki Sticklebacks

PhD position in Evolutionary Ecology The effects of eutrophication on sexual selection and viability of stickleback populations

A 3-year PhD project is available in the research group of Ulrika Candolin in the Department of Biology and Environmental Sciences of the University of Helsinki, Finland.

Environmental heterogeneity can cause the intensity and direction of selection to vary in time and space. Yet, the effects of human-induced environmental changes on selection and evolution are poorly known. Currently, the breeding habitats of the three-spine stickleback Gasterosteus aculeatus are changing in the Baltic Sea due to eutrophication and increased growth of filamentous algae and phytoplankton. The aim of the project is to investigate the effects of increased algae growth and water turbidity on sexual signalling, mate preferences and the intensity and di-

rection of selection on different traits in sticklebacks. The work will be realised through field and laboratory experiments, both at a field station by the sea (Tvärminne Zoological Station) and in the lab in the city. Molecular genetic techniques will be applied to determine the paternity of eggs. For further information, see http://www.mv.helsinki.fi/home/ucandoli/ or contact ulrika.candolin@helsinki.fi.

Starting date would be August 1st at the earliest. The salary is approximately 1900 EUR/month. Experience of working with fish as experimental animals and of molecular techniques is an advantage, but not necessary. Interested candidates should send a curriculum vitae, a brief summary of research experience and interests, and contact details of two referees to ulrika.candolin@helsinki.fi, or Ulrika Candolin, Dept of Biological & Environmental Sciences, PO Box 65, FI-00014 University of Helsinki, Finland. The review of applicants will start on June 24th.

Ulrika Candolin Div of Ecology and Evolutionary Biology Dept of Biological & Environmental Sciences PO Box 65 (Biocenter 3, Viikinkaari 1) FI-00014 University of Helsinki Finland

Phone: +358-(0)9-191 57815 Fax: +358-(0)9-191 57694 Mobile: +358-(0)40-767 7072 Email: ulrika.candolin@helsinki.fi http://www.mv.helsinki.fi/home/ucandoli/

skills and should develop a research programme for his/her PhD-thesis in collaboration with the head of the unit. Some teaching obligations are part of the job (c. 2 h per week during the semester).

The main research interests of the Unit of Plant Ecology are:

- Demographic and genetic effects of habitat fragmentation on plants - Population biology of hemiparasitic plants - The effects of global environmental change on plant populations - Plant reproductive ecology

Applicants should give the name and addresses of two referees and briefly explain their plans for a PhD-thesis.

Please send your application as soon as possible to:

Prof. Diethart Matthies Plant Ecology Department of Biology Philipps-University D-35032 Marburg Germany

For further information contact D. Matthies (matthies@staff.uni-marburg.de)

Prof. Diethart Matthies Plant Ecology Department of Biology University of Marburg D-35032 Marburg Germany Tel. +49-6421-282 2085 Fax. +49-6421-282 2093 matthies@staff.uni-marburg.de

Diethart Matthies <matthies@staff.uni-marburg.de>

UMarburg PlantPopBiol

Dear colleagues,

a PhD-position in plant population biology is available at the University of Marburg, starting as soon as possible (for details see below; in addition the German original of the advertisement is attached). I would appreciate it very much if you could bring this job opportunity to the attention of potential candidates.

Yours sincerely,

Diethart Matthies

—— PhD-position in plant population biology

At the Philipps-University Marburg (Unit of Plant Ecology, Prof. Diethart Matthies) a PhD-position (VergGr. BAT II a/2) is available for 3 years.

The successful applicant is expected to have a background in plant population biology, good statistical

UMassAmherst MolEvolInfectDis

Several graduate student positions will be open in my lab at the University of Massachusetts Amherst in Fall 2005. Work in the lab centers on Molecular Evolution and Population Genomic/Genetic studies of the agents and arthropod vectors of infectious disease. Particular foci at present are tick borne borrelioses (Lyme et al.) and human malaria. Students with interest in study of evolution and ecology as applied to our better understanding of disease transmission are encouraged to apply. Several Teaching and Research assistantships are available.

The lab is part of the Division of Entomology which comprises a strong research faculty with diverse interests in field and laboratory entomology/zoology.

For more information, see our web pages:

http://www.umass.edu/ent/ http://www.tufts.edu/vet/richlab or, contact

Stephen Rich Tufts University 200 Westborough Rd.

North Grafton, MA 01604

508.887.4749 stephen.rich@tufts.edu

N.B. Our lab is moving from Tufts University to UMass-Amherst effective 1 September 2005.

"Dr. Stephen M. Rich" <stephen.rich@tufts.edu>

University of Newcastle, School of Biology Ridley Building, room 461, Newcastle NE1 7RU, UK phone: (+44) 0191 222 5626 fax: (+44) 0191 222 5229 Plants have fingerprints too! Check it out: http://-www.ncl.ac.uk/biol/about/news.htm?type=3D1&id=-3D2782   http://www.staff.ncl.ac.uk/kirsten.wolff/ http://www.bioprofiles.co.uk/ http://www.ncl.ac.uk/-biol/ Kirsten.Wolff@newcastle.ac.uk

UNewcastle MolEvolPlantago

A NERC PhD studentship has become available in the research group of Dr Kirsten Wolff at the University of Newcastle, UK

Title: Genetical Ecology and Molecular Evolution in the genus Plantago.

Eligibility: Applicants must be eligible according to NERC criteria which can be found at http://-www.nerc.ac.uk/students/eligible/ (UK students only, sorry)

The genus Plantago has been studied for a wide range of questions, from ecology, via genetics to physiology. The species in the genus have mating systems from obligate outcrossing to highly selfing, diploids as well as polyploids can be found in the genus and many species are gynodioecious. This makes the genus very interesting from an evolutionary genetics point of view. The Plantago species that are most common in the UK have been studied for their variation at the morphological as well as the molecular level, for example, for allozymes, RAPDs, minisatellite DNA fingerprinting and cp RFLP variation. Studies describing variation at microsatellite loci are underway. Of particular interest is the reproductive isolation of taxa in the P. major group.

Many aspects of the genetics of Plantago have already been studied, but even more questions have not been answered. Therefore, there are opportunities for developing the project in a number of directions depending on the interests of the student appointed.

You will join an active research group, interested in a broad range of aspects of population genetics and evolutionary biology, in both animals and plants. The group is housed in a well equipped molecular laboratory, including DNA sequencer. For further information on the project, requirements and how to apply: http://www.ncl.ac.uk/biol/postgrad/kw_phd.htm Best wishes, Kirsten

Dr. Kirsten Wolff Reader in Evolutionary Genetics

UOxford WoodFungi

Do ancient woods have ancient fungi, and are they necessary for reestablishment of broadleaf woodland in the UK?

3 year DPhil (=PhD) CASE studentship supervised by Dr Nick Brown in the Department of Plant Sciences, University of Oxford, starting October 2005.

DEADLINE 27 MAY 2005

Many soil fungi are symbiotic with trees and other woodland plants, enhancing the capacity of seedlings to establish on resource-poor sites or in competition with other vegetation. However, we do not yet have adequate descriptions of the patterns and diversity of ectomycorrhizal (ECM) fungi in temperate woodland.

A combination of fieldwork and molecular biology can offer new insights into the ecology of fungal colonization. We are interested in practical questions which arise from some of the patterns of distribution revealed so far: can ancient woodland fungi be successfully established in newly created woodlands in order to add a key functional component of the woodland ecosystem? Have ancient woodland fungi survived in plantations on ancient woodland sites (PAWS)? The answers to these questions are important in developing protocols for PAWS restoration and the creation of new native woodlands.

Aims 1. To inventory, using molecular probes and genetic analysis of ECM samples taken from the field, the fungi of ancient semi natural woodland and secondary woodland sites, controlling for soil type, tree species composition and woodland size. We will compare this with 'fungal foray' (sporophore) data where available. 2. To identify ECM species specific to native tree species that are restricted to ancient woodlands. We will determine how long fungal colonies have been in a site by mapping the size of single clones using genetic fingerprinting techniques. 3. To identify

the mode of root colonization used by widespread early successional ECM species and species restricted to ancient woodlands. 4. To detect if ancient woodland fungi have survived in the soils of PAWS sites. To develop a practical protocol for introducing ancient woodland fungi to newly created woodlands.

HOW TO APPLY Deadline 27 May 2005

In the first instance, contact Dr Nick Brown by email: Nick.brown@plants.ox.ac.uk Telephone 01865 275077

Open to UK citizens and to EU residents having or about to obtain a good first degree in an appropriate field. Non-UK residents are eligible for fees only, not living expenses.

David Bass <david.bass@st-catherines.oxford.ac.uk>

UPierreMarieCurie MarineEvolution

PhD student fellowships are available for short term training in the marine biological laboratory of Banyuls-sur-Mer in France.

Period: June to September 2005

Fellowships are funded by the European programme "Human resources and mobility - Marie curie training sites"

Project title: Molecular and Cell Biology of marine organisms,

specific focus on: i) analysis of cell proliferation and differentiation, ii) environmental genomics of microalgae, iii) sea urchin genomics.

For further information, please contact: Anne-Marie Geneviere e-mail: amg@arago.obs-banyuls.fr Phone: 33 (0)4 68 88 73 14 Fax: 33 (0)4 68 88 73 98 Observatoire Oceanologique de Banyuls CNRS/Universite Pierre et Marie Curie (Paris VI) Laboratoire Arago,66651, Banyuls-sur-Mer cedex, FRANCE http://www.obs-banyuls.fr desdevises@obs-banyuls.fr

URennes IsolatedSystems

PhD fellowship in

ADAPTATION AND FUNCTIONING OF SPECIES IN ECOLOGICALLY ISOLATED SYSTEMS

available at University of Rennes 1, France.

Scientific background: Most of ecology is implicitly based on the evolutionary assumption that species respond to environmental change by adaptation. Recent studies, however, indicate that this is not necessarily true. Under climate change, for instance, species tend to migrate with their climate and sedentary species tend to be replaced by immigrating invaders. Adaptation is thus replaced by migration and invasion. It has therefore recently been suggested that adaptation may occur only under very particular conditions such as ecological isolation of species within niche space (Ackerly 2003). The major goal of this thesis will be to test the importance of ecological isolation for phenotypic and genotypic responses of species to environmental change, and for the way how species interact with their environment. Approaches include meta-analyses of recent databases on the phylogeny, biology, ecology and sociology of plant species and on their genotypic differentiation. Application to various model systems in the field is possible.

Organizational background: A PhD fellowship by the Ecole Doctorale Vie, Agro, Sante (http://-www.vas.univ-rennes1.fr/scripts/index.php, allocations 2005 on the left) for three years, approx. 1040 Euros/month (which can luckily be backed by teaching assistance). Please note that a certain proficiency of French is expected at the end of the thesis. In fact, the introductory and concluding parts of the thesis have to be in French. Such proficiency is indeed useful to more easily integrate. At the same time, everybody is capable and willing to communicate in English with a foreigner, and French students are obliged to take courses in English. For formal reasons, the application has to contain a one-page summary of your MSc thesis, and a half-page summary of earlier theses or reports; and this also has to be in French. The rest of the application (c.v., expertise, list of all kinds of scientific communications, research interests and outlook, letters of reference, transcripts) as well as the presentation can be in English. Candidates are invited to submit their English versions to Andreas Prinzing (see below), who can also suggest low-price translation services that may help in the preparation of the French versions.

Qualification of the candidate: French DEA / Master II or equivalent (MSc, Diplom.) in biology or related field from a country of the European Union or the numerous European countries that have signed the Accord relatif à lEspace Europeen de lEnseignement Superieur (see http://www.dr.education.fr/Alloc_doc/-

alloc_2.html) Broad interest and experience in ecology and evolution, particularly the interface between macroevolution and microevolution; experience in advanced classical statistical concepts (e.g., multivariate techniques, generalized linear models, null modeling), phylogenetic, morphometric or population genetic statistics. Writing and communication skills, stress tolerance and single mindedness; possibly programming capabilities.

Application from beginning of June to July-4 (deadline) online at http://www.vas.univ-rennes1.fr/-scripts/index.php. Please send a *copy* to andreas.prinzing@univ-rennes1.fr. Presentations of short-listed candidates on July-11 and 12.

For further information please contact: Andreas Prinzing, Prof. Université de Rennes 1 Unité Mixte de Recherche CNRS 6553 ≪ Ecobio ≫ : Ecosystèmes - Biodiversité - Evolution Campus de Beaulieu, Batiment 14A 263 Avenue du General Leclerc 35042 Rennes Cedex, France andreas.prinzing@univ-rennes1.fr http://ecobio.univ-rennes1.fr/Fiches_perso/-Fiche.asp?pseudo=APrinzing andreas.prinzing@univ-rennes1.fr

UWindsor SalmonMateChoice

We are recruiting PhD students to work on a collaborative research project involving labs at the University of Windsor, Waterloo, Western Ontario, and Guelph and the BC salmon aquaculture industry targetting Chinook salmon mate choice. We arelooking for students interested in quantitative genetics and performance as well as immunogenetics and disease resistance to complement doctoral studies in parental and offspring behaviour and feeding physiology. A project decsription follows:Mate choice in Chinook salmon: performance comparisons with hatchery-bred stock (PhD): Offspring of Chinook salmon will be produced from parents allowed to breed in semi-natural spawning channels (sexual selection) or from parents artificially spawned using current aquaculture practices (no sexual selection). All offspring will be followed through to adulthood in the aquaculture environment. Behavioural, immunological, physiological and genetic analyses will be used to partition differences in growth performance and productivity into additive genetic, environmental and genotype-by-environmental interaction components, and ultimately to assess the economics of the breeding strategies for aquaculture production. Work

in the Heath lab (Windsor) will focus on using microsatellite parentage assignment to partition offspring trait variance into genetic, environmental and interaction components. The project will involve considerable field work at our salmon farm partner in BC. Information on the Heath lab and the Great Lakes Institute for Environmental Research (U Windsor) can be viewed at; www.uwindsor.ca/glier Contact Dr. Heath at dheath@uwindsor.ca Daniel Heath Presently at Queensland Department of Primary Industries & Fisheries Southern Fisheries Centre 13 Beach Rd Deception Bay 4508 Queensland, Australia 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

UWyoming ComputBiol

M.S. research assistantship (2 years) Evolutionary genetics of sunflower domestication University of Wyoming, USA

An M.S. research assistantship is available to work in the area of evolutionary genetics and computational biology. The position will begin in late August 2005 and is funded for two years.

The goal of the research is to estimate parameters of the population bottleneck that sunflowers experienced in the process of domestication and to identify genes that experienced selection during domestication. This is a collaborative project that is led by John Burke at Vanderbilt University; empirical data are being gathered by the Burke group and the statistical and computational analyses are done in the Buerkle lab at the University of Wyoming.

This M.S. research assistantship is a good opportunity for a student to gain skills in computational biology and statistical genetics in the context of interesting evolutionary questions. The central tasks for the assistantship are computational, and applicants with experience in computer programming, modeling and statistical analysis (R/S-Plus, Perl, C/C++, Maple/Mathematica, etc.), or a demonstrated aptitude for and an interest in learning skills of this type, will be preferred.

Preliminary inquiries are encouraged and should be directed to Alex Buerkle (buerkle@uwyo.edu). Addi-

tional information about the University and the position is available on-line:

<http://www.uwyo.edu/buerkle/misc/-ms_pos_2005.asp> Review of applications will begin 6 June 2005.

Alex Buerkle <buerkle@uwyo.edu>

microbial dispersal

Testing the theory of microbial ubiquitous dispersal: molecular and ultrastructural studies of the evolution, biodiversity and ecology of unicellular eukaryotes

3 year DPhil (=PhD) studentship

Application deadline Friday 27 May 2005

Supervisors: Professor T. Cavalier-Smith FRS, Department of Zoology University of Oxford and Dr G. Novarino, Natural History Museum, London

Some argue that microbial populations are so huge that global dispersal is inevitable, so species should be globally distributed, and uninfluenced by intercontinental barriers that cause striking historical biogeographic patterns in animals, e.g. kangaroos only in Australia. Paraphysomonas, with morphospecies distinguished by surface scale ultrastructure, was used to argue that virtually all global species regularly disperse into one English pond. This has two potential flaws. First, most ?species? were defined from studies in Europe. Most of the world has never been sampled, especially the tropics and southern hemisphere; maybe hundreds of un-

described species never get to Europe. Secondly, morphospecies may not be true species; 18S rRNA genes show huge genetic diversity. This project will:

1. Use 18S rDNA sequencing of hundreds of freshwater Paraphysomonas strains from all continents to establish whether genotypes are cosmopolitan or not.

2. Use electron microscopy to test whether global sampling at the morphological level is relatively complete or grossly biased geographically.

3. Use DNA sequencing of selected protein genes to detect linkage disequilibrium and show whether population structure is clonal or sexual. If the latter, this will establish boundaries between biological species.

Students? own ideas or enquiries about other protist biodiversity projects are also invited.

Finlay BJ (2002) Global dispersal of free-living microbial eukaryote species. Science 296:1061-3 Finlay BJ, Clarke KJ (1999) Apparent global ubiquity of species in the protist genus Paraphysomonas. Protist 150:419-30 von der Heyden S, Chao EE, Vickerman K, Cavalier-Smith T (2004) Ribosomal RNA phylogeny of bodonid and diplonemid flagellates and the evolution of Euglenozoa. J. Euk. Microbiol. 51:402-416

HOW TO APPLY Deadline 27 May 2005

In the first instance, contact Prof. Cavalier-Smith FRS, preferably by email: tom.cavalier-smith@zoo.ox.ac.uk, or telephone 01865 271286 / 281322.

Open to UK citizens and to EU residents having or about to obtain a good first degree in an appropriate field. Non-UK residents are eligible for fees only, not living expenses.

David Bass <david.bass@st-catherines.oxford.ac.uk>

Jobs

CollegeWilliamMary ConservBiol

VISITING ASSISTANT PROFESSOR OF CONSERVATION BIOLOGY

College of William and Mary

The Department of Biology invites applications for a one-year visiting faculty position in Conservation Biology, beginning in August 2005. The successful candidate will teach one upper division conservation biology course with two laboratory sections in the fall of 2005 and one upper division lecture/seminar course in ecological, evolutionary, or organismal biology in the spring of 2006. Applicants must have a Ph.D. in an appropriate field. Postdoctoral experience is preferred. Candidates should have a demonstrated commitment to excellence in teaching and are encouraged, but not required, to engage in collaborative research projects with our current faculty members (http://www.wm.edu/-biology).

Please send a letter of application, curriculum vitae, statement of teaching interests and philosophy, description of research interests, and three letters of reference to: Dr. George W. Gilchrist, Dept. of Biology, College of William and Mary, PO Box 8795, Williamsburg, VA 23187. Review of application materials will begin on May 15th and will continue until the position is filled. The College of William and Mary is an EEO/AA Employer. Informal inquiries can be made to Dr. Gilchrist: gwgilc@wm.edu.

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

CornellU LabTechnician

Ecology & Evolutionary Biology Cornell University Lab Technician IV - Job # 03926

Job Description

Research position in evolutionary biology/herpetology lab. Provide tech support for molecular systematics and population genetics research. Specific responsibilities include DNA isolation, PCR, construction and cloning of gene libraries, sample preparation for automated sequencing, editing sequence data, using genomic database and searching tools, running phylogenetic and population genetic software, and data interpretation. General responsibilities include maintaining and purchasing laboratory supplies, assisting with grant proposal and manuscript preparation, and assisting with student training. This is a one-year term position; renewable for second year contingent upon availability of funding. Endowed college employee benefits apply.

Qualifications

BS in biology-related field strongly preferred with at least one year of experience in a molecular biology or molecular systematics environment. Working knowledge of standard molecular lab protocols and basic field biology techniques. Neatness, attention to detail, good organizational skills and ability to manage people. Some weekend/evening hours necessary.

Applications will be accepted through June 20, 2005.

Informal inquiries can be directed to Dr. Kelly Zamudio at krz2@cornell.edu.

Located in Ithaca, NY, Cornell University is an equal opportunity, affirmative action educator and employer.

To apply please visit: http://www.ohr.cornell.edu/jobs Job Number 03926

krz2@cornell.edu krz2@cornell.edu

Dublin SummerResearch

Dear all,

Full funding is available for 8 international students to attend a new summer research programme in Dublin (10 week course). Apologies for cross-postings; please circulate widely and note the fast-approaching deadline!!

Collections-based Biology in Dubin (CoBiD) provides an exciting research environment, with experience both in high quality laboratories in the science departments in University College Dublin, and important international research centre in the National Musuem of Ireland (Natural History) collections in Dublin city centre. Diverse research projects are offered, with topics ranging from systematic biology including traditional and molecular techniques to ecology and population genetics. Students will work side-by-side with curators and senior scientists and will be involved in all aspects of collections-based research including collection and curation of specimens, experiments and analysis, participation in field expeditions, and dissemination of scientific results through oral presentation and publication.

The CoBiD summer school programme is funded by Science Foundation Ireland

Term dates: July 4th to September 5th 2005

Requirements * completion of the third (junior) year of an undergraduate biosciences degree * proficiency in English (written and spoken) * willingness to work hard, and ability to work independently * strong interest in the project of choice * career goals in organismal biology

Your application must include a total of three documents recieved as e-mail attachments in MS-Word format. Two documents (CV and letter of interest) in an email recieved from the applicant, and a seperate letter of recommendation in an e-mail recieved directly from your reference.

All materials must be recieved by: Sunday 29 May

Research Projects feather histology of galliforms | evolution of fossil crocodiles | mayflies and climate change | evolution of cation-independent receptors | carboniferous coral "reefs" | evolution in mammalian sensory perception | resource partitioning in inshore fish | distribution and metapopulation structure of cockles

For more information, including project descriptions see http://www.ucd.ie/ureka/ or e-mail ureka@ucd.ie

Collections-based Biology in Dublin The UREKA Summer Research programme is funded by Science Foundation Ireland (w) http://www.ucd.ie/ureka/ (e) ureka@ucd.ie

ureka@ucd.ie

Darwin Initiative Project Officer

Two year fixed-term contract

The Darwin Initiative Project will help Costa Rica implement the Convention on Biological Diversity through research and training in orchid conservation. Your main role will include assisting with the day-to-day management of the Project, including field work, and producing orchid DNA barcodes for species identification. You will also help with the herbarium digitalisation of Meso-American orchid types and the running of the MolSys laboratory.

With excellent communication and organisational skills, you will have a good degree in a relevant subject area and basic knowledge of molecular techniques, including PCR and DNA sequencing. You will have the ability to plan and organise work schedules and have some proven project management experience. Basic computer skills and a full, clean driving licence, for the field work, are essential, with a fluency in Molecular Biology, Computing and Phylogenetics being desirable. The ability to speak Spanish would also be an advantage.

Salary is GBP 17,505 per annum and benefits include a choice of final salary or stakeholder pension, generous annual leave and a stunning work environment.

Application packs are available from our website at www.kew.org (click on the 'about us' icon). Alternatively, please contact the HR Department, RBG Kew, on 020 8332 5184/5150 (24 hour answerphone). Please quote Ref DO. Closing date: 20 May 2005.

Committed to equality through diversity. Selection is on merit alone. INVESTOR IN PEOPLE ROYAL BOTANIC GARDENS KEW WORLD HERITAGE SITE

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

Join the Society of Systematic Biologists at //syst-biol.org/

v.savolainen@rbgkew.org.uk

NorthCarolinaStateU ResearchTech

London DarwinProjectOfficer

We are anticipating of hiring a full time research technician/lab manager in the laboratory of Dr. Astrid Groot

at the Department of Entomology at North Carolina State University. The succesful candidate will be lab manager in a laboratory of population and evolutionary genetics, focusing on geographic variation in the sexual communication of two heliothine moth species (Lepidoptera, Noctuidae).

The responsibilities include breeding lines from different regions, green house experiments, occasional field work, and after the first year molecular analysis of the different lines. Responsibilities will also include data analysis, ordering lab supplies, supervising undergraduates, and assistance in preparing manuscripts for publication.

The successful candidate will have a minimum of a bachelors degree in biology or related field and some laboratory research experience. Additional knowledge favorable but not required: chemical ecology, evolutionary genetics, experience with breeding moths, experience with molecular biology protocols, experience with supervising others.

Starting salary: $26,000+ (depending on experience) and benefits.

Anticipated starting date: July 15, 2005. Application deadline: June 15, 2005, or until position is filled. To apply, please send a letter of your interests and qualifications, a CV, and a list of three references including telephone number and email address to: Astrid Groot, astrid_groot@ncsu.edu. North Carolina State University is an Equal Opportunity/Affirmative Action Employer.

astrid_groot@ncsu.edu

OxfordU EvolLecturer

A Departmental Lectureship in Evolutionary Ecology is available from October 2005 for a period of four years, possibly renewable for another two years. The successful candidate, who should have completed a Ph.D. in a subject related to evolutionary ecology, will be expected to develop and run an active research group within the Department, and will be required to teach and examine in their field of expertise. Further particulars are available from Lisa Harris in the Department of Zoology, (Tel: 01865 271259; E-mail: lisa.harris@zoo.ox.ac.uk). Applicants should provide a covering letter explaining their suitability for the post, a full curriculum vitae and the contact details of two academic references. There

are no applications forms. Address e-mail applications to (E-mail: paul.Harvey@zoo.ox.ac.uk) and postal applications (six copies or one from overseas) to Professor Paul Harvey, FRS, Head of Department, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS. Please quote reference number AT05029. The closing date for the above posts is Friday, 10 June 2005.

http://www.admin.ox.ac.uk/ps/gp/current/-http009.shtml oliver.pybus@zoology.oxford.ac.uk

PurdueU GenomicsProgrammer

Job Posting for a Database Programmer at Purdue University

Department of Agronomy, Purdue University has a full-time Database Programmer position. We are looking for a self-motivated individual with considerable initiative. The successful applicant will develop understanding of faculty research programs in genomics and Proteomics, design novel software applications; train students of Genomics computing facilities; keep abreast of new technology, identify novel technological solutions, and interface with the larger research computing environment at Purdue University. A B.S. in Computer Science, Math, Engineering, or related is required with three years experience programming Perl or Java and systems administration and maintenance. Will also consider a MS and one year experience. The position has special requirements including knowing software design principles, scripting languages, Perl or Java and the Unix/Linux system. Must be able to lift and carry 10-25 pounds frequently and 40 pounds occasionally. For consideration submit resume and apply online at: http://www.adpc.purdue.edu/hr/referral.htm. Reference the posting number 1150.264.0504. Purdue University is an equal opportunity, equal access, affirmative action employer.

Lisa Bono Research Associate in the Genomics Center 2-371 Lilly Hall Phone: (765) 496-3385 Fax: (765) 496-2926 915 W. State Street Purdue University West Lafayette,IN 47907-2054

QueensU EnvGenomics

Research Associate, Ecological and Environmental Genomics

Biology, Queen's University

The incumbent will manage a core, high through-put sequencing and genotyping facility, including overseeing use of core equipment and completion of work-orders. He/she will train faculty, junior technicians, and graduate and undergraduate students on use of core equipment (most notably, automated sequencers), and help trouble-shoot problems with equipment and analyses. He/she will help to develop new laboratory and analytical methods of molecular analyses. He/she will assist with the instruction of the molecular components of undergraduate courses in evolution, ecology, behaviour and conservation, including (but not restricted to) Biol325, Biol404, Biol439, Biol440 (approx. 25% time). The position includes maintaining databases, account administration, providing direction to junior staff and students, liaising with faculty/staff/students at Queen's and elsewhere, using computers for data entry/analysis/interpretation, ensuring compliance with safety and ethical guidelines, and preparation of protocol guides, proposals and reports. Work may include handling animals and hazardous materials or equipment. The incumbent may participate in other special projects.

The candidate must have an M.Sc. with previous experience in DNA sequencing and genotyping, ideally on non-model systems. Full details are posted at <http://www.hr.queensu.ca/job/externalposition.php>http://www.hr.queensu.ca/job/externalposition.php. The annual salary will be $42,589. Application deadline is June 2, 2005. Please contact Dr. Vicki Friesen (friesenv@biology.queensu.ca) with any questions/concerns.

Vicki Friesen <friesenv@biology.queensu.ca>

SimonFraserU EvolBiol

Limited-term Lecturer

The Department of Biological Sciences is seeking to fill a Limited-term Lecturer position starting in September 2005 for a two year period. The successful candidate should possess skills and experience in phylogenetics, insect evolution, and plant-insect interactions, and should be able to teach undergraduate and graduate courses in introductory bilogy, evolution and insect biology. In addition, the position will involve some supervision of graduate students in Dr. Bernard Crespi's research group (http://www.sfu.ca/biology/faculty/crespi/). A PhD is preferred and previous teaching experience is required. Review of applications will begin on May 1st 2005, and the search will remain active until the position is filled. Applicants should send a curriculum vita, statement of teaching experience, and three letters of reference to:

Dr. Tony D Williams, Chair Biological Sciences Simon Fraser University Burnaby BC, V5A 1S6 FAX. 604-291-4312

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

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

Dr. Bernie Crespi Professor Behavioral Ecology Research Group Department of Biosciences Simon Fraser University Burnaby BC V5A 1S6 Canada ph 604 291-3533 fax 604 291-3496 http://www.sfu.ca/biology/faculty/crespi/ This email should not be forwarded to anyone without my permission, thank you

Bernard Crespi <crespi@sfu.ca>

UBern EvolBehavEcol

A 3 year PhD position is available for a behavioural ecologist to work with Dik Heg and Michael Taborsky (University of Berne, Zoological Institute, Department of Behavioural Ecology) to study the behavioural ecology of cooperative breeding in Lake Tanganyika cichlids. The PhD is part of a project financed by the Swiss National Science Foundation, involving both field experiments at Lake Tanganyika (Zambia) and laboratory

experiments, to study causes of variation in helping behaviour and dispersal, and the benefits of sociality. For information on our work see:

http://www.zoology.unibe.ch/behav/index_e.php
Starting date of the project will be August 2005. We shall start to scrutinize applications by 25 May, but later applications will be considered until the position is filled.

The successful applicant will have training in animal behaviour and ecology, with good abilities in statistical data analysis and computer skills, diving license (PADI or equivalent), and preferably some experience in scientific diving. Application material should be sent by email to dik.heg@esh.unibe.ch and lesley.roth@esh.unibe.ch. Please send with your application a CV (pdf format) and publications (pdf format), and names and contact information of two people who can provide references.

Dr. D. Heg Department of Behavioural Ecology Zoological Institute University of Bern Wohlenstrasse 50a CH-3032 Hinterkappelen Switzerland Email: <mailto:dik.heg@esh.unibe.ch> dik.heg@esh.unibe.ch Tel: +41 31 631 9151 Fax: +41 31 6319141

Dik Heg <dik.heg@esh.unibe.ch>

and experience in molecular biology and genomics research, is required. Background in computer science is desirable. We offer a competitive salary plus excellent benefits. Review of applications will begin May 20, 2005. Position will remain open until suitable candidate is found. Complete the faculty/administrative form at the web site http://employment.unl.edu then submit curriculum vitae and the names and addresses of three references to Search Committee Chair, Bioinformatics Specialist, Center for Biotechnology, University of Nebraska-Lincoln, 1901 Vine Street, Lincoln, NE 68588-0665. Fax: 402-472-3139.

The University of Nebraska is committed to a pluralistic, campus community through affirmative action and equal opportunity. We assure reasonable accommodation under the Americans with Disabilities Act; contact the Center for Biotechnology at (402) 472-2635 for assistance.

Candace Ristow Program Assistant University of Nebraska-Lincoln N300 Beadle Research Center Lincoln, NE 68588-0660

402.472.0748 (direct) 402.472.2635 (main) 402.472.3139 (fax) cristow@unlnotes.unl.edu

"Candace K. Ristow" <cristow@unlnotes.unl.edu>

UNebraskaLincoln Bioinformatics

The Center for Biotechnology of the University of Nebraska-Lincoln seeks a Manager for its Bioinformatics Core Research Facility. The Facility cooperates with the UNL faculty to develop and exploit state of the art bioinformatic tools; e.g., molecular modeling, mining genomic and proteomic databases, as well as microarray and complex systems data. The Manager will support life sciences research and act as a liaison among UNL computational biology groups in the State to foster bioinformatics program development. Excellent computer laboratory facilities will be available for conducting collaborative extramurally funded research. The manager also has primary responsibility for team-teaching a senior undergraduate/graduate level laboratory course in Bioinformatics and for training and service of existing UNL licensed software including VectorNTI, GCG (SeqLab), Affymetrix software. The manager is also expected to share system administration of the Facility???s Linux cluster with an existing staff. A doctoral degree and demonstrated expertise in computational biology and sound, practical knowledge

USheffield EvolBiol

Senior Lecturer / Reader / Professor Department of Animal and Plant Sciences The University of Sheffield

Ref No R3677

Closing Date: 30th June, 2005

Salary: UKpound37,558 - 42,573 per annum (Senior Lecturer/Reader), By agreement (Professor)

Summary The Department has an outstanding international reputation for research (5* RAE 2001) and teaching (QAA 24/24) and now seeks to appoint an outstanding individual to complement one or more of our key five research themes: evolution and behaviour; population and community ecology; biodiversity and conservation; global change biology; and plant molecular science. Informal enquiries may be addressed to the Head of Department, Professor Malcolm Press (m.c.press@sheffield.ac.uk).

See http://www.sheffield.ac.uk/jobs/academic.html
Roger Butlin Professor of Evolutionary Biology

Department of Animal and Plant Sciences The University of Sheffield Western Bank Sheffield S10 2TN UK

r.k.butlin@sheffield.ac.uk

UWisconsinMilwaukee FishGenetics

The position described below is currently being advertised and I thought might be of interest to certain members of this group. This USDA-funded Center has just been established at the University of Wisconsin-Milwaukee Great Lakes WATER Institute (www.glwi.uwm.edu). Feel free to distribute. Thank you for your help in identifying qualified candidates.

The U.S. Department of Agriculture, Agricultural Research Service, is accepting applications for an Interdisciplinary: Research Geneticist (Fish)/Research Physiologist (Fish)/Research Biologist (Fish), GS-440/413/482-12/13/14 at the Great Lakes Wisconsin Aquatic Technology and Environmental Research (WATER) Institute on the University of Wisconsin-Milwaukee campus. Salary is commensurate with experience ($60,576 - $110,662 per annum) plus benefits. U.S. citizenship is required. Incumbent will be lead scientist to identify high-priority, researchable problems in the development of state-of-the-art technologies using yellow perch and other species that may be integrated into cool and cold-water aquaculture production systems. Research objectives are to develop: 1) genetically improved broodstocks of yellow perch with traits for year-round production; 2) optimal culture technology for year-round fingerling production and one-year grow out; and 3) environmentally compatible and sustainable aquaculture systems for year-round viable production of Great Lakes species. For program information, contact Neal Martin, 608-890-0050, npmartin@wisc.edu. Candidates must request the vacancy announcement (ARS-X5W-0246) by calling 301-504-1482 or via the ARS Homepage at www.ars.usda.gov/careers. Location contact: Jean Weinbrenner 608-890-0044, jweinbr@wisc.edu. Candidates must submit specific information as outlined in the vacancy announcement. Applications must be postmarked by May 31, 2005. USDA/ARS is an Equal Opportunity Provider and Employer. Best Regards, Mike. Michael J. Carvan III, Ph.D Phone: (414) 382-1706 Lab: (414) 382-1712 Fax: (414) 382-1705 Email:

carvanmj@uwm.edu Great Lakes WATER Institute University of Wisconsin-Milwaukee 600 E. Greenfield Avenue Milwaukee, Wisconsin 53204 It is a miracle that curiosity survives formal education. - Albert Einstein The most exciting phrase to hear in science, the one that heralds new discoveries, is not "Eureka!" ("I have found it!"), but "That's funny..." - Isaac Asimov

Yukon RedSquirrels

Summer Field Assistants Needed - Red Squirrels, Kluane Lake, Yukon

Two field assistants are needed to work as part of a long-term project studying the ecology and evolution of red squirrels near Kluane Lake, Yukon, Canada. Details on the project and area can be found at www.redsquirrel.msu.edu. Assistants will be responsible for establishing three new study areas. Duties will include grid surveying as well as live-trapping, handling and tagging of red squirrels. Successful applicants will have a biology or wildlife background and will be prepared to live in or near our remote northern field camp. Previous field experience with small mammals is an asset. Exact employment dates are to be determined but could range from July 1 to September 30, 2005. Transportation to and from the field site, food and accommodation will be provided. Wages start at $7/hr. Applicants should send a resume and cover letter, including references and available dates for employment to Dr. Andrew McAdam, 13 Natural Resources Building, Department of Fisheries and Wildlife, Michigan State University, East Lansing, MI, 48824 (mcadama@msu.edu). Electronic applications are preferred. Applicants must be eligible for employment in the United States. Underrepresented groups are particularly encouraged to apply.

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

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

Other

Ambystoma sample

I'm looking for some "Ambystoma jeffersonianum" specimens from any places in Canada or United-States, for genetical purposes. It would be highly appreciated if a contact person could help me to obtain them.

Kind regards,

Jeanne Dumoulin Université de Montréal, Québec, Canada

jeanne.dumoulin@umontreal.ca

AmerGenetAssoc Award

Colleagues,

The American Genetics Association invites applications for Special Events Awards as described below. If you are not a member of AGA, you would need to join to submit an application, but there are other benefits from membership, notably a membership to Journal of Heredity, and membership cost is modest. The application is due May 15.

– Mary V. Ashley, AGA Special Events Committee Chair Professor, Department of Biological Sciences University of Illinois at Chicago 845 W. Taylor St., M/C 066 Chicago, IL 60607

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

SPECIAL EVENT AWARDS FROM THE AMERICAN GENETICS ASSOCIATION

The Council of the American Genetics Association invites applications from members of the Association for support of special events that further the purposes of the Association. The Association expects to make one award of approximately $10,000-15,000 each year. Eligible events include specialized workshops open to Association members in areas of great current interest and short courses in some aspect of organismal genetics, but any event that would advance the purposes of the Association is eligible for support. We encourage members to think creatively about the types of events they could offer with support from the Association. All applications received will be carefully reviewed.

An application for a Special Event Award should include the following items of information:

1. The name(s) and title(s) of the individual(s) who will be responsible for organizing the event and overseeing the expenditure of any funds awarded. 2. The institution to which an award should be made, including the complete address of the relevant institutional department and the signature of an authorized institutional representative indicating the institution's willingnness to administer the award if granted. 3. The title of the event for which an award is requested. 4. A rationale for the event explaining (a) why the event is timely or needed, (b) how the planned event will address the perceived need, and (c) how support from the American Genetics Association will improve the event, e.g., by making it possible or by making it more affordable for graduate students and post-doctoral research associates. The rationale need not be longer than 1 page. 5. A description of the event including (if available): a list of primary participants (e.g., workshop leaders, course instructors), dates and location of the event, a preliminary schedule for the event, and a plan for how participants will be selected. The description need not be longer than 2 pages. 6. A budget for the event showing how funds provided by an award from the Association would be used to support event activities. If funds are also being sought from other sources, the budget should show both how funds from the Association will be used and how funds from other sources will be used. (The sources of other funds need not be identified, but the application should indicate whether the funds are in hand.)

Applications for a Special Event Award should be sent to the Editorial office (American Genetic Association, P.O. Box 257, Buckeystown, MD 21717-0257). The Council will review all applications received before 15 May 2005 and will decide on an award at its annual meeting in June 2005.

ashley@uic.edu

Arlequin AFLP data

In attempting to use Arlequin for an AMOVA analysis of AFLP data, I am unable to get my input file to work. The following error message appears: 1 #[ERROR # 1] from function "Population::read_gametic_data() (Hapl NFCC1)" : missing haplotype definition 2 #[ERROR # 2] from function "Samples::Read()" : unable to read sample data Unable to read the specified number of populations.

I do not currently have a haplotype list subsection because the manual states that it is optional and I don't know of an easy way to create one (I have 200 samples and 154 loci). Does anyone know 1) if the haplotype definition section is truly optional for AFLP (RFLP) data? 2) Is there a program that will facilitate the creation of a haplotype list?

Thanks in advance for troubleshooting assistance.

Molly Stephens Graduate Group in Ecology Genomic Variation Lab University of California, Davis mrstephens@ucdavis.edu http://genome-lab.ucdavis.edu 530-752-6351

mrstephens@ucdavis.edu

Biodiversity library

Dear Friends,The Trinidad campus of the University of the West Indies (UWI) is in the process of strengthening and consolidating its expertise in biodiversity studies as a major thrust of this department. As part of this, we areinterested in improving our campus library's holdings in this area. The campus has about 9000 students, the majority undergraduate, with about 300 studying one or another part of the life sciences. Of this department's 21 academic staffers, seven include some area of biodiversity studies as part of their research.Ifyou have had occasion to come up witha list of books in biodi-

versity studies – by which I mean the assessment, analysis and conservation of biological diversity at all levels – that facilitate my task of formulatingaset of recommendations to our acquisitions librarians, I would very much like to hear from you. This is not at all to suggest that we are starting from scratch, far from it.I expect that we have most or all of the obvious titles, among others, but the time has come to go beyond the obvious. The most valuable language, for our purposes, is English, with Spanish in second place.

While I am at it, I should mention that Trinidad & Tobago are increasingly favoured as a field destination for ecological and biodiversity studies. These are continental islands close to the South American mainland, semi-industrialized but with substantial good habitat, harbouring an estimated 2-4% of the world's land and fresh-water biota. Our government's Wildlife Section(with authority overboth animals and plants) regulates the collection and export of specimens in a sensible, non-bureaucratic fashion that serves the interests of science well. These remarks are made in the selfish consciousness that thoseforeign biologists who work in-Trinidad & Tobago are providing new knowledge that benefits all of us.

Yours for Wild Nature, Chris Starr

Christopher K. Starr Dep't of Life Sciences University of the West Indies St Augustine, Trinidad & Tobago tel (868) 645-3232 ext 3096 or 662-2002 ext 3096 fax (868) 663-5241or 663-9684 http://www.uwi.tt:8081/lifesci-index.htm Consigue aquílas mejores y mas recientes ofertas de trabajo en América Latina y USA: Haz clic aquí

"Christopher K. Starr" <ckstarr99@hotmail.com>

Biogeography teaching

Dear Evoldir Members,

I am looking for people who teach classes in biogeography from a phylogenetics perspective.

Can you please send write to me if you teach such a class? If anyone else would like the list, please let me know.

Thanks very much,

Chris

– Chris Simon Professor, Ecology & Evolutionary Biol-

ogy 75 North Eagleville Road, University of Connecticut Storrs, CT 06269-3043

chris.simon@uconn.edu Office (860) 486-4640; Lab (860) 486-3947; Fax (860) 486-6364

Home page: http://www.eeb.uconn.edu/faculty/-simon/simon.htm with links to Student research opportunities in the Simon lab; the periodical cicada web-searchable data base; Cicada Central with New Zealand cicada and periodical cicada information

Reprints: http://collections2.eeb.uconn.edu/-collections/cicadacentral/resources/reprints.html

Brassicaceae MatingSystem

Dear all I am studying a brassicacea endemic in the sub-antarctic Islands, which seems to be closely related to the south american Thelypodieae (Sisymbrium magellanicum, S. foliosum, S. andinum, S. tortuosus, Caulanthus amplexicaulis...). I would like to know more about the mating systemes known for these species : evidences for insect or wind pollination, existence of self incompatibility... Please let me know if you have any source of information. Thank you in advance

Agnès Schermann Legionnet Maître de Conférences Université de Rennes 1 UMR 6553 Ecobio, équipe Ecologie du Paysage http://ecobio.univ-rennes1.fr/ http://ecobio.univ-rennes1.fr/Fiches_perso/-Fiche.asp?pseudo=ASchermann Campus de Beaulieu bât. 14B, porte 120 35042 Rennes Cedex tel : (33)(0)2 23 23 51 21

agnes.schermann@univ-rennes1.fr

Contig editors

Dear Colleagues,

After years of searching, I am still unable to find a good sequence editor and contig builder for automated DNA sequence data that fulfills my needs as an evolutionary geneticist. I've used Sequencher, Codoncode Aligner, and ABI's Seqscape. These all have great features, but none of them has all the best features.

Beyond the standard base calling, trimming, contig

assembly, and chromatogram display for proofreading purposes, Seqscape has the neatest feature: it allows users to align all of their contigs (using Clustal) and compare them, calling up the chromatograms as needed with a simple click of the mouse. This is fantastic feature that can save many hours of time. The downsides to Seqscape are that the program is cumbersome, slow, expensive ($7000?) and only works with ABI generated sequences (I haven't found software to export sequences from my Beckman sequencer in a format Seqscape will read).

The other two programs are faster and easier to use, and Codoncode Aligner is only about $1000 (compared to Sequencher's absurdly high price). But neither will make an overall alignment of many different contigs (with chromatograms accessible), and I find workaround solutions waste many hours.

Does anyone know of a program that is inexpensive, fast, easy to use, and that will allow correction of data from a screen showing an alignment of contigs with easy access to the chromatograms?

Are any programmers seeking the fame and glory (if not wealth) that would come from finally writing a practical sequence correction program for the evolutionary geneticist?

Thanks,

Steve

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

sdjordan@bucknell.edu sdjordan@bucknell.edu

Coral DNA degradation

Hello evoldir people!

Our lab is now working on coral DNA for evolution studies. Extractions are being made with zooxanthellae, as corals are hosts for those. We just started, and we have serious DNA degradation problem. Surprisingly, DNA extraction done 2 weeks ago and stored in -20C freezer, which looked great at that moment, is now already degraded. Has anyone of you already experienced that sort of problem before??

Catherine Lippe Lab technician University of Hawaii at Manoa

lippe@hawaii.edu

Creationist cartoon

For your amusement:

"News of the Times: Creationists Challenge the Teaching of Water's Freezing Point" http://www.ucomics.com/tomthedancingbug/ dave.ardell@lcb.uu.se dave.ardell@lcb.uu.se

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DNA outsourcing answers

Thank you all for you replies regarding the outsourcing services you use for DNA sequencing. A very special thanks to Brian Golding for all his efforts in maintaining this wonderful list that is Evoldir. I have compiled extracts from the mails sent to me, in some cases indicating in square brackets [] how many mails I recieved recommending a given service. In some cases I followed the provided links and added price information.The order of the facilities has to do with the order in which I recieved emails, and is no way sorted by price, quality, or preference. Hope this is helpful for others as well.

1.MWG [2] "Nowadays we send the purifed ethanol precipitated PCR products to MWG biotech (in Germany).I use MWG in Germany and they are very fast and produce excellent sequences!" http://www.mwg-biotech.com 2. Macrogen [6] "they are extremely cheap, and so far, we have been very happy with the results." http://www.macrogen.com/eng/macrogen/-macrogen_main.jsp 3. GATC - "I am using GATC Biotech in Germany for eight years now for various projects and samples. I am very satisfied with them. They can offer you special conditions to be negotiated and are very customer-friendly, have excellent service and great monitoring options for the order and easy download of your chromatograms. " one or two sequencing reactions incl. DNA quality check up to 1000 nt in Phred20 quality 1-2 days 27.00 / read http:/-/www.gatc.de/en/index_en.php e-mail to Ms. Magdalena Surina (m.surina@gatc-biotech.com).

4. Prokaria [2] - I know a very good company in Ice-

land that could help you. My lab is very satisfied with their services. "We at Prokaria have been offering DNA sequencing services for several years. Our customers seem to be quite satisfied with our services as they keep coming back! PROCEDURE : The customer delivers the samples as PCR products or plasmids. You can send them on dry ice by DHL, FEDEX etc. The client also provides the sequencing primers OR info on the primers sequences (we can provide them but it takes a few days) . All sequencing is done in duplicates without any extra charge. We are using the ABI 3730 DNA Analyser. After sequencing we edit the sequences using the Sequencher 4.05 software. The client receives the sequences in word format by E-mail. We can also provide the sequences as chromatographs. TIME: The process takes 2-3 days after delivery of the samples, if sequencing primers are provided. PRICE: DNA sequencing (Fewer than 94 sequences) 36 pr sequence. Please check our homepage http://-www.prokaria.com/default.asp?cat_id=105. For bigger projects we are willing to negotiate on the price. Contact: Sólveig K. Pétursdóttir, MSc , Prokaria ltd, Gylfaflöt 5 , 112-Keldnaholt-Reykjavík, Iceland, Tel: +354 570 7922 Fax: +354 570 7901 www.prokaria.com E-mail: solveigp@prokaria.com http://www.prokaria.is 5. "The Paleo-DNA Laboratory at Lakehead University Canada is where I work and it provides sequencing services. I find them very efficient and capable at this task particularly for difficult to sequence samples as they are trained in ancient DNA and sequencing those types of templates. However the Canadian turnaround time is short, it is same day as delivery." http:/-/www.ancientdna.com/molecular.html 6. TCAG - "There is a not-for-profit DNA sequencing facility at The Centre for Applied Genomics in Toronto (TCAG; www.tcag.ca), which has two ABI 3730XL instruments for sequencing of PCR products, plasmids and genomic clone ends using custom or standard primers. You can find more information at: TCAG also has other services that might be of interest to EvolDir members, such as run and analysis of user-generated microsatellite fragments (for population genetics studies). " *The cost for sequencing is:* $10 per successful reaction for all users. http://www.tcag.ca/index.php?pagename=-sequencingSynthesis.php 7. Yale - Cost for any number of sequencing reactions is for now $4.5 per reaction, but it will go down when we get our new large capacity sequencer up and running (Fall 2006). We also provide troubleshooting help to improve the quality of the products. For large projects when the client provides 96 or 384 plates and reactions with only one or two primers the cost is lower and project based. For microsatellites we run them for $1.5 per lane, so the more you can multiplex the better. AFLP can also be run at the same cost per lane as microsats. Future service

— / —

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

DNAeasy answers

Qiagen dnaeasy kits costs about $1.70 per specimen: how can costs be reduced?

(1) Has anyone re-used the column with experimental confirmation that the column has no dna "carryover" between specimens?

(2) Has anyone used a column several times for the same specimen (to make more dna than the specified 25mg tissue per dnaeasy column)?

(3) What other ways can costs be reduced?

AEM Baker 101 Morgan Bio University of KY Lexington KY 40506 mouse@lamar.colostate.edu

I am grateful to all who responded (below). Some responses were about RNA but the ideas might be useful for DNA. One caveat on cheap quick protocols for purifying DNA: I wasted much time/ $$ / tissue using "quick and dirty" purification methods: later I found my "clean dna" failed to PCR-amplify, which was the main reason I switched to dnaeasy. I will try some other brands including ones listed below; none below mentioned "genepure" (ca. $1/sample), which someone recently said worked fine for horse and dog blood. I think none tried to reuse the qiagen column with a different individual (PCR may amplify the contaminating dna leftover from the first column use); many reused the column multiple times for the same individual as a way to harvest more dna. =====

>===== Original Message From "ma wheel" <wheel_mlc@hotmail.com> ==== > we develop a similar protocles and use cb3 column instead. Actually only >the membrane in the column matters. You can visit web sites about patent >and find something alike. I mean in the collection step, when you use >solutions like TE to wash the membrane and collect it, after 4-times wash, >you may still have DNA that is detectable by PCR. >Wish it will be helpful. > >> >>Ma, >>I am happy to correspond with you, but I don't understand what you wrote.

>>What do you mean by 4th collection? and how is this helping to save \$\$? >>How can we get CB3 column? DNAeasy comes as a kit (all reagents included): >>you buy the columns separately and then also buy all reagent separately? >>Respectfully, >>Ann >> >===== Original Message From "ma wheel" <wheel_mlc@hotmail.com> ==== >> >hellow, I've used anthoer kit from Qiagen for stool samples. the column >> >will surely carry DNA since even the 4th collection solution will cary >DNA >> >that can be detected by PCR. Here in China, we use some column named CB3 >> >cost \$0.2, hope you can find something of the same price. >> >good luck.

>===== Original Message From Anne Genissel <amgenissel@ucdavis.edu> ==== >Hi Ann, >so here is my protocol, it worked fine with me, and it is cheap.I try to >work in very clean conditions (autoclaved buffer and tips, filter >sterilized water etc.. and DNA can be stored at least a couple of years). >Good luck, >Anne > >DNA isolation Protocol For Single Fly > > >- Squeeze the fly with a potter in 100ul of cell lysis buffer on ice in >1.5ml tube >- heat for 15min at 65C >- cool sample at RT >- RNase treatment: add 1ul RNase solution at 2mg/ml >- leave 15-60min at 37C >- cool down at RT >- add 33ul of 5M KAc >- vortex vigorously at high speed for 20sec >- put sample on ice for 5min >- centrifuge at 14,000g for 3min (pellet=precipitated proteins) >- pour the supernatant containing the DNA into a new 1.5ml tube containing >100ul of isopropanol >- mix sample by inverting gently 50times >- centrifuge at 14,000g for 5min >- pour off supernatant and drain tube on clean paper >- add 100ul of 70% ethanol and invert tube several times to wash the DNA pellet >- centrifuge 1min >- pour off ethanol -watch pellet!- >- let it dry ˜ 15min >- add 100ul of low TE buffer or sterilized dd water >- allow DNA to rehydrate overnight at RT or heat at 65C for an hour and >tap tube to disperse DNA > >Cell Lysis Buffer >5mM PIPES pH8.0 >85mM KCl > >Low TE buffer (0.1X) >1mM Tris-HCl pH7.4 >0.1mM EDTA pH8.0 > > >At 05:29 PM 5/16/2005, you wrote: >>Anne, >>Pls provide, stating advantages. I got burned using cheap/dirty way of >>dna prep: later the dna was degraded: I need a way to prep dna which will >>stay "good" (amplify/rflp) for long periods. >>Respectfully, >>Ann >> >===== Original Message From Anne Genissel <amgenissel@ucdavis.edu> ==== >> >hello, >> >the cheapest is to use no kit -have a receipe if you are interested, >> >Anne >> > >> > >> > >> >Anne Genissel >> >University of California >> >Evolution and Ecology Department >> >3322 Storer Hall >> >One Shields Avenue >> >95616, Davis, CA, USA >> >tel. 530 752 9322 >> >fax. 530 752 1449

Dear Ann,

try this website:

— / —

DamselflyHybridZone

Dear all,

I am trying to do a nuclear genetic analysis of an Ischnura damsefly hybrid zone in the SF Bay Area, and I am trying to find good, informative nuclear markers for this population level study. I have been using Ef1-alpha and ITS so far, but I would really like to try Cpnl-1 (which has been used in a similar study in grasshoppers), as it seems most promising, but I am struggling with find the appropriate primers for this gene. I am also open to any suggestions for other nuclear markers, though at this point I am not looking for microsatellites.

Thank you,

Vicki Moore

Dept. of Biology San Francisco State University nilechile@hotmail.com

nilechile@hotmail.com

Dog phylogeny

Dear Evoldir members,

I am studying microsatellite evolution in purebred dogs for which I need to construct a phylogenetic tree for the different dog breeds based on markers other than microsatellites (SNPs, mtDNA or maybe SINEs). Does anyone know about a dog breed phylogeny (besides of Wayne or Parkers work) that has been constructed or is in the way to be obtained?

Many thanks for any responses,

Iris

– Iris M. Vargas Jentzsch Ph.D. Student School of Biological Sciences University of Canterbury Private Bag 4800 Christchurch - New Zealand

Mobile: 0064   021   1623853   Email: imj15@student.canterbury.ac.nz

Drosophila willistoni lines

Drosophila willistoni isofemale lines

The Tucson Drosophila Species Stock center has 120 new isofemale lines of Drosophila willistoni, one of the species for which 8X whole genome sequencing is being completed and BAC libraries are under construction. The new strains are from the Caribbean, collected in spring 2005. They will be available until July 15, 2005.

To order, contact Sergio Castrezana at the Tucson Stock Center castreza@email.arizona.edu

Therese Ann Markow Regents' Professor of Ecology and Evolutionary Biology Director, Center for Insect Science University of Arizona Tucson, AZ 85721 Office: 520-621-3323 Lab: 520-626-2772 tmarkow@arl.arizona.edu http://cis.arl.arizona.edu/-markow_lab/

Teri Markow <tmarkow@public.arl.arizona.edu>

EvolBioinformatics OnLine

ANNOUNCING EVOLUTIONARY BIOINFORMATICS ON-LINE

Libertas Academica announces a new open-access journal Evolutionary Bioinformatics Online*, with Professor Mark Pagel as editor-in-chief and a distinguished editorial board of leading academics (http:-//www.libertasacademica.com/EBO-edboard.htm).

Evolutionary Bioinformatics Online is an international peer-reviewed Open Access journal focusing on evolutionary bioinformatics (http://www.libertasacademica.com/ebo-CFP.htm). There is growing awareness that to understand organismal form and function, through the use of molecular, genetic, genomic, and proteomic data, due consideration must be given to an organism's evolutionary context: history constrains the path an organism is obliged to take, and leaves an indelible mark on its component parts.

Being an Open Access journal means that the papers published are freely available to everyone via the Internet. Authors retain copyright of their work. The publishers, Libertas Academica, do not charge readers any form of sub scription, instead asking authors of accepted papers to make an article-processing payment. A number of fee waivers are available and are intended to facilitate publication by individuals irrespective of their individual or institutional means.

I write to you as the Editor-in Chief to invite you to submit an article for publication. To meet publishing commitments we would need to receive a manuscript from you by the end of August 2005 to be considered for the next issue.   To submit a paper, go to www.libertasacademica.com/-evolbio.htm.   For detailed author instructions, go to www.libertasacademica.com/Instructions.htm.   To apply for an article processing fee waiver, go to www.libertasacademica.com/waiver.htm.   Questions can be directed to the EBO website, following the links to ?contact us?.

Institutions can also support Evolutionary Bioinformatics Online and the other Libertas Academica Open Access journals by becoming a member institution. An unlimited number of authors from member institutions can publish papers without paying the article-processing fee. Details are available at the Libertas Academica website (www.libertasacademica.com).

Yours sincerely,

Mark Pagel Editor-in-Chief Evolutionary Bioinformatics Online www.libertasacademica.com/ebo.htm * This is a new title and is the official journal of The Bioinformatics Institute of the Universty of Auckland.

Mark Pagel <m.pagel@reading.ac.uk>

Flow cytometry technique

Hello,

I'm a grad student majoring in EEB in Iowa State University. I appreciate your advice on my problem with flow cytometry technique.

I'm trying to measure ploidy level of purple loosestrife, using flow cytometry facility. Here is our protocol. The initial step of common sample preperation is to chop

and homogenize the leaf tissue with lysis buffer. Then the sample is filtered two times and centrifuged in 200g to remove other things in supernatants and preserve nuclei in pellets.

This technique applied very well to other species. Though, for purple loosestrife sample, chopped tissue usually become sticky and mucosy, probably because of lots of polysaccharides in cytoplasm. And it doen't work at all in flow cytometry machine.

I searched over all resources that I can use to find better protocol for this kind of species, But I couldn't find how to prepare sample removing mucosy contaminants. I appreciate your advice and better idea. Thank you.

Young Jin Chun Ph. D. Candidate President of Korean Student Association (2005) at ISU Department of Ecology, Evolution, and Organismal Biology Interdepartmental Program in Ecology and Evolutionary Biology 339 Bessey Hall Iowa State University Ames, IA 50011 USA

Phone : 515-450-4270 (cellular) Email : yjchun@iastate.edu Official webpage of Korean Student Association: http://www.stuorg.iastate.edu/korean/ yjchun@iastate.edu

theta are not genuinely independent parameters in the sense that an under-estimated theta can be easily compensated by a smaller alpha and vice versa. It is very difficult to distinguish invariable sites, which are described by theta, from the slow-evolving sites in the discrete gamma distribution, which are described by alpha. The good news is that the "I+Gamma" gives higher likelihoods compared with each of the two simpler models and is therefore often preferred. The bad news is that parameter estimates do not mean much as there may exist several combinations of theta and alpha that appear almost equally probable.

What is the best way to deal with the "I+Gamma"? Should we

(1) not use it at all?

(2) use it, but ignore the parameter estimates?

(3) optimize only the alpha and determine theta empirically, i. e. by counting the invariable sites?

(4) introduce some constraint between alpha and theta, which turns the "I+Gamma" effectively into an one-parameter model?

Any suggestions?

Gangolf Jobb

Gangolf Jobb <gangolf@treefinder.de>

GammaI model

Hi all,

just some questions.

The "I+Gamma" is very popular model of sequence evolution with rate heterogeneity among sites. It is a superposition of two simpler models, which are both able to account for invariable sites in a sequence alignment. The first distinguishes two classes of sites, of which one may evolve while the other is invariable. The other part is Yang's discrete gamma model, which is used for the variable sites. The "I+Gamma" has two parameters, namely the fraction of invariable sites (theta) and the shape parameter of the discrete gamma distribution (alpha).

When I simulate sequences under the "I+Gamma" and try to re-estimate the two heterogeneity parameters by maximum likelihood optimization afterwards, it turns out that the estimated parameters often differ severely from the original parameters that were previously used in the simulation. This indicates to me that the "I+Gamma" is over-parameterized, that alpha and

GammaI model answers

Hi all,

with your help, I was able to solve my little optimization problem and, thereby, to save the I+Gamma (at least for me): The trick is to bound alpha > 1. Smaller alphas should not be used. This avoids a situation where both parameters have nearly the same effect on the distribution shape and, as a consequence, 'fight' to explain the data. On the other hand, this constrained I+Gamma has still the advantages it was made for: It can produce two-peaked rate distributions as well as one-peaked ones, ranging from homogeneity to extremely L-shaped and anything between. However, it is better not to the interpret the heterogeneity parameters.

Thanks to all who contributed valuable information. As this might be useful to others, I have included the most informative answers below.

Best,

Gangolf Jobb

———————————————-

Hi all,

just some questions.

The "I+Gamma" is very popular model of sequence evolution with rate heterogeneity among sites. It is a superposition of two simpler models, which are both able to account for invariable sites in a sequence alignment. The first distinguishes two classes of sites, of which one may evolve while the other is invariable. The other part is Yang's discrete gamma model, which is used for the variable sites. The "I+Gamma" has two parameters, namely the fraction of invariable sites (theta) and the shape parameter of the discrete gamma distribution (alpha).

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What is the best way to deal with the "I+Gamma"? Should we

(1) not use it at all?

(2) use it, but ignore the parameter estimates?

(3) optimize only the alpha and determine theta empirically, i. e. by counting the invariable sites?

(4) introduce some constraint between alpha and theta, which turns the "I+Gamma" effectively into an one-parameter model?

Any suggestions?

Gangolf Jobb

———————————————-

Hi Gangolf,

The two parameters are clearly confounded to some ex-

tent. It seems that there is little information in the data, without large number of sequences for determining whether a constant site is "invariable" or "slowly evolving". You might want to look at these two papers by Jack Sullivan, in case you haven't already.

Regards,

Thomas

Sullivan, J. and D. L. Swofford. 2001. Should we use model-based methods for phylogenetic inference when we know assumptions about among-site rate variation and nucleotide substitution pattern are violated? Systematic Biology, 50:723-729

Sullivan, J., D. L. Swofford, and G. J. P. Naylor. 1999. The effect of taxon sampling on estimating rate-heterogeneity parameters of maximum-likelihood models. Molecular Biology and Evolution. 16:1347-1356.

———————————————-

I think this is an interesting question. I too have been concerned about the use of I+Gamma and the interpretation of estimated parameters. I would be interested to hear what other responses you get, and I encourage you to post summaries to the EVOLDIR list.

> When I simulate sequences under the "I+Gamma" and try to re-estimate the > two heterogeneity parameters by maximum likelihood optimization > afterwards, it turns out that the estimated parameters often differ > severely from the original parameters that were previously used in the > simulation.

I too have observed this.

I recall Ziheng Yang telling me something similar; he performed experiments sub-sampling sequences from a multiple alignment, and estimated the parameter you are calling theta (he was not using +Gamma then, I think). He found that as you included more and more of the sequences, the parameter you are calling theta got lower and lower. Evidently the +I part of the model has some trouble distinguishing sites that never vary, and sites which may vary but happen not to have in the tree under consideration. But you should check with Ziheng if you are

—— / ——

Gradients SexualSelection

Dear colleages,

I recently came across this interesting quote:

"In other words, the fact that, for example, many tropical bird species are more colourful and have more intricate song patterns than birds from colder environments, does not necessarily result from selection, but may simply be the result of random addition of species (Rohde 2005)"

Rohde, K. 2005. Cellular automata and ecology. Oikos 110: 203-207.

I thought this hypothesis is indeed intriguing, but I was wondering: are you aware of any hypothesis to explain consistent differences in the degree mating signal complexity according to the environment or latitude? (in addition to the one I just listed.

Any hints will be greatly appreciated. Please respond to my email: mike_lotar@yahoo.com

Mark

mike_lotar@yahoo.com

Haploid Ne

Hey everybody, I have haploid allelic data (Y-chromosome microsats) for one set of organisms, and other set of mitochondrial D-loop sequences. Is there any program that allowed me to handle both set of data to estimate Ne? Thanks a lot,

Marina S. Ascunce University of Florida e-mail: ascunce@ufl.edu

"Ascunce, Marina S." <ascunce@ufl.edu>

HelpAttending GordonConf

Financial assistance for attending the EEFG Gordon Conference Evolutionary & Ecological Functional Genomics 31 July - 5 August 2005, Oxford, UK

A limited amount of funding is available to help graduate students and post-docs offset the cost of attending the upcoming Gordon Conference on Evolutionary & Ecological Functional Genomics. To see the schedule and list of speakers, please visit www.grc.uri.edu/ programs/2005/evolut.htm. Information about registration, transportation, etc. can be found by clicking buttons at the bottom of the web page. If you are interested in applying for funding to attend this conference, please contact Greg Wray by email (gwray@duke.edu). Preference will be given to those who plan to present a poster at the conference.

Greg Wray <gwray@duke.edu>

Hermatipic coral tissue preservation

Dear Evoldir

I am new to coral genetics and I wonder if someone has a ambient temperature preservation method for hermatipic coral tissue samples that works well with subsequent specific DNA extraction protocols required for these organisms. Any help will be appreciated, as usual, I will post a summary of the information received. (BTW, any pointers to a Coral Reef science bulletin board will also be appreciated).

Best regards,

Axayacatl Rocha-Olivares, Ph.D. Chair Biological Oceanography Department CICESE P. O. Box 434844 San Diego, CA, 92143-4844

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Email: arocha@cicese.mx http://dob.cicese.mx/pag/-arocha.htm

Axayacatl Rocha <arocha@cicese.mx>

Hyfrecator advice

Hi, I need advice on selecting a hyfrecator. It will be used primarily for small tissue ablations in insects. I am considering buying the Conmed Hyfrecator 2000, and was wondering if anyone might have had experience with this or other models. Many thanks!!

Armin

Armin P. Moczek Assistant Professor Department of Biology & Indiana Molecular Biology Institute

Mailing address: Armin P. Moczek Department of Biology Indiana University 915 E. Third Street Myers Hall 150 Bloomington, IN 47405-7107

email: armin@indiana.edu phone: (812) 856-1468 (office) phone: (812) 856-1783 (lab) fax: (812) 855-6082 http://www.bio.indiana.edu/facultyresearch/-faculty/Moczek.html http://www.bio.indiana.edu/-~moczeklab/index.html armin@indiana.edu armin@indiana.edu

ID minister

The Dutch minister of Education and Science, Maria van der Hoeven (Christian Democrat) has said that she would like to organize a broad debate about evolutionary theory and religion. (Saturday 21 May in an interview in the paper Volkskrant). She said that she would like to promote a dialogue between scientists and people favouring creation (in a wide sense). Minister Maria van der Hoeven said that she herself is an adherent of Intelligent Design. She said that "it should be recognized that evolutionary theory is not complete, as we are still discovering new things". Parliament is having nothing of it. In the Netherlands, less than half of the population has connections to a church. The minister seems badly suited for her job. Minister Maria van der Hoeven did not think it necessary that prospective primary school teachers have any math in their background training.

dr Gerdien de Jong Evolutionaire Populatiebiologie Universiteit Utrecht

tot 1 augustus 2005: University of California Riverside, CA 95207

g.dejong@bio.uu.nl

IUMS meeting roommate

Dear All,

I am looking for one or more roommate(s) for the IUMS/ICM meeting in San Francisco (July 23 to 29). http://www.iums2005.org/ Please, let me know if you are interested.

Cheers,

József

József Geml, Ph.D.

Institute of Arctic Biology 311 Irving I Building 902 N. Koyukuk Drive P.O. Box 757000 University of Alaska Fairbanks Phone: 907-474-7957 (lab) Fairbanks, AK 99775-7000 907-474-1140 (office) U.S.A. Fax: 907-474-6967 E-mail: jgeml@iab.alaska.edu Web: http://www.iab.uaf.edu/ ~ jozsef_geml/ József Geml <jgeml@iab.alaska.edu>

IntelligentDesign film at Smithsonian

To the evolution community:

Many of you may be aware from recent newspaper articles (for example, the New York Times article available at http://www.nytimes.com/2005/05/28/-national/28smithsonian), that the NationalMuseum of Natural History at the Smithsonian Institution is about to show a film that was co-written and co-produced by members of the creationist Discovery Institute. (The showing is on June 23.) This film, called "The Privileged Planet", the Search for Purpose in the Universe". It is an attempt to use geology, climatology, and physics to show that the earth was designed by an intelligent designer, and of course is part of the latest strategy of "intelligent design" creationists to worm their way into the public consciousness and school curriculum. You can read about the film at its website http://www.privilegedplanet.com/, and see the Discovery Institute's announcement of the co-sponsorship at http://www.discovery.org/-scripts/viewDB/index.php?command=view&id=-

133&program=CSC&isEvent=true

Although the Smithsonian must give non-profit organizations (of which the Discovery Institute is apparently one) the right to present films in its facilities, it seems wrong for the Smithsonian to also co-sponsor such films. The Smithsonian has a history of supporting the fact of evolution, and in fact has a wonderful Hall of Evolution in the NMNH to present the data. Why, then, is it co-sponsoring this film? The effect of this is to give a U.S. government imprimatur to the activities of the Discovery Institute. The Discovery Institute is of course playing up this co-sponsorship on its website.

The director of the National Museum of Natual History, which is co-sponsoring the film, is Christian Samper, whose email address is SamperC@si.edu . I would urge you to consider emailing him and expressing your feelings about this event.

I am sure that Dr. Samper is not very happy with this event (apparently the Discovery Institute sneaked in the film under the Museum's radar), but perhaps a series of emails from evolutionists could get the Smithsonian re-examine its policy of cosponsoring events like this. Needless to say, we should all be polite in our emails.

Thanks. Jerry Coyne

Jerry Coyne <j-coyne@uchicago.edu>

Large Allele Dropout

Hello, we are running microsatellites on leaves and seeds and have two primers where some of the large fragment size alleles are much reduced in amplification as compared to the smaller fragment size allele in the same individual. At times, amplification of the large allele is so low in comparison to the small allele as to make the large allele barely noticeable, and it may be dropping out entirely sometimes.

I've tried suggestions from various sources to bring up the large allele including: Increasing MgCl2, Increasing KCl, decreasing annealing temperature, decreasing DNA concentration, increasing and decreasing extension time, decreasing cycle #, and increasing taq. Increasing KCl brought up the large allele slightly, so I'm going to try higher concentrations. While some of the others increased amplification overall, none brought up the large allele relative to the small allele. Increasing amplification overall is not helpful as I would need to

overamplify the small allele to make the large allele more visible, and overamplification will cause fluorescence to be picked up by nearby sample capillaries.

Has anyone tried other methods that have been successful in bringing up the large allele relative to the small allele?

Thanks, Christy Stewart

– Christy Stewart USDA, ARS Vegetable Crops Dept. of Horticulture University of Wisconsin 1575 Linden Dr. Madison, WI 53706 Phn 608-263-1129 Fax 608-262-4743 cstewart1@wisc.edu

Micro bias

Dear All,

I tested a microsatellite set for cross-utilty among species within a genus. I detected that microsatellites of the original species are longer as in cross-amplified species. This is known to occur, when ascertainment bias is present. But is there is a statistical test to test for acertainment bias?

Thanks a lot for your answers!

Ill post the collected answers on this site.

Best regards,

Cornelya–Cornelya KlütschZFMK- Zoologisches Forschungsinstitut und Museum Alexander KoenigAdenauerallee 160 53113 BonnGermanyTel.: 49-228-9122-242Fax: 49- 228-9122-212Mail: cornelya@freenet.de

cornelya@freenet.de cornelya@freenet.de

Mountain range population data

Dear EvolDir,

I am working on a method of estimating 'distance' across mountain ranges. Although this is still in the preliminary stage, I am now at a point where I wish to test this method. I am looking for any published or unpublished datasets where populations have been studied along mountain systems (on either side of mountains and across the system) and

where genetic, morphological or linguistic distance have been calculated (or I can calculate from raw data). To test my method I would need locations of the populations (or latitude/longitude) and either genetic/morphological/linguistic distance as a matrix or as a raw file. If you have any data such as these, I would be very grateful.

Please contact me if you have any concerns about how the data would be used or if you have data you may be able to contribute.

Kind regards, Gabriela Ibarguchi

Gabriela Ibarguchi Department of Biology, Queen's University Kingston, Ontario, Canada, K7L 3N6 ibarguch@biology.queensu.ca or gibarguchi@biology.ca NEW: tel (613) 533-6000 ext. 75539, fax (613) 533-6617

Gabriela Ibarguchi <ibarguch@biology.queensu.ca>

MultiGene phylogenies

Dear all, I would like to ask for pdfs or references to molecular systematic studies that use more than 9 gene partitions and that use both maximum parsimony and model-based methods of analysis (Bayesian and/or maximum likelihood). Specifically, I am interested in whether the different methods give the same answer when the amount of data is large. This information will be used in a review I am co-authoring. Please contact me at niklas.wahlberg@zoologi.su.se if you can help. Thanks!

Best regards, Niklas

– Niklas Wahlberg Department of Zoology Stockholm University S-106 91 Stockholm SWEDEN

Phone: +46 8 164024 Fax: +46 8 167715

Nymphalidae Home Page: http://www.zoologi.su.se/research/wahlberg/   niklas.wahlberg@zoologi.su.se niklas.wahlberg@zoologi.su.se

Netherlands ID

Dear All,

Unfortunately more ID news. The Dutch minister of Education, Culture & Science wants to call for a meeting with scientists and religious leaders in the Netherlands to discuss ID. This, because 'the evolution theory is not complete'. She envisages an intercultural discussion which should be embedded in science...

Best wishes, Mark

– Dr. Mark van der Giezen Lecturer in Microbiology School of Biological Sciences Queen Mary, University of London Mile End Road, London E1 4NS, UK tel.: +44 207 8823057/e-fax: +44 870 1629212 e-mail: m.vandergiezen@qmul.ac.uk   http://web.onetel.com/˜vandergiezen mark.vandergiezen@rhul.ac.uk

Outsourcing Sequencing

Hello I have a number of samples I am going to send out for DNA sequencing, but due to some recents problems with the company I usually sent samples too, I thought it might be safest to try an alternative service. I was hoping evoldir-ers could inform me of the companies/services they use for outsourcing DNA sequencing, and whether they have been satisfied with their work. (I'll post a summary of replies, a yellow-pages of sequencing services). Thanks

– André Levy, PhD in Ecology and Evolution Unidade Eco-Etologica Instituto Superior de Psicologia Aplicada (ISPA) R. do Jardim do Tabaco, 34 1149-041 Lisbon PORTUGAL

http://pwp.netcabo.pt/andrelevy/ andre_levy@ispa.pt

PHT test

Dear all,

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

(good) method to test data homogeneity, with an associate software or PAUP routine?

Many thanks in advance.

Yves

Yves Desdevises Laboratoire Arago, Universite Pierre et Marie Curie UMR CNRS 7628: Modeles en biologie cellulaire et evolutive BP 44, 66651 Banyuls-sur-Mer Cedex, France http://www.obs-banyuls.fr Phone: (33) (0)4 68 88 73 13 / (33) (0)6 17 27 17 97 Fax: (33) (0)4 68 88 73 98 Email: desdevises@obs-banyuls.fr Web: http://desdevises.free.fr

PartitionHomogeneityTest answers

Dear all,

A few days ago, I posted the following query:

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

Many people seem to have the same problem. Here are the putative solutions I received:

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

Rob Cruickshank

- The test was made for and justified based on the parsimony criterion, of course. To make it tractable for a large dataset, you can use an abbreviated heuristic search to speed up the analysis of the random partitions if necessary (i.e., limit the number of trees swapped using nchuck command, for instance, or use a smaller number of repetitions using the nrep=5 command, or even using the parsimony ratchet, though implementing that might be a chore). This app[roach risks not finding the very best tree for each random replicate, which would have the effect of increasing the variance of your p-value from its "true" value that you would find using exact searches. However, this approach shouldn't intro-

duce a strong bias that would drive the p-value strongly up or down, because the failure to find the best tree would be equally likely to affect the partitioned and unpartitioned length estimates for each replicate, giving the ILD for each replicate a more-or-less equal chance of increasing or decreasing.

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

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

Joe Thornton

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

Sophie Quérouil

[My translation]

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

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

John Harshman

- The attached paper by Waddell, Kishino and Ota [2000. Rapid Evaluation of the Phylogenetic Congruence of Sequence Data Using Likelihood Ratio Tests.

Mol Biol Evol 17(12): 1988-1992] describes a homogeneity test that can use RELL. RELL is, in this sort of application, very fast. The required parts are available in PAUP (the site likelihoods or probabilities of data patterns) but an R script would be best to put it all together.

Peter Waddell

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

Yves

Yves Desdevises Laboratoire Arago, Université Pierre et Marie Curie UMR CNRS 7628 : Modèles en biologie cellulaire et évolutive BP 44, 66651 Banyuls-sur-Mer Cedex, France http://www.obs-banyuls.fr Tél. : (33) (0)4 68 88 73 13 / (33) (0)6 17 27 17 97 Fax : (33) (0)4 68 88 73 98 Email : desdevises@obs-banyuls.fr Web : http://desdevises.free.fr Web : http://desdevises.free.fr

Polyploidy

Other: Polyploidy question

Hello all,

I'm looking for an easy, inexpensive, and fast method to check whether the plants I'm studying are polyploid. Because my study species is well protected and endangered, I'm looking in particular for a method that can be used without destroying the root system.

Are there any suggestions (references, methods, protocols, labs that have experiences with this) on how to do this?

Philippe Helsen philippe.helsen@ua.ac.be Universiteit Antwerpen Departement Biologie - Campus Middelheim Onderzoeksgroep Evolutionaire Biologie Groenenborgerlaan 171 B-2020 Antwerpen Belgium

Reducing Qiagen costs

Qiagen dnaeasy kits costs about \$1.70 per specimen: how can costs be reduced?

(1) Has anyone re-used the column with experimental confirmation that the column has no dna "carryover" between specimens? (2) Has anyone used a column several times for the same specimen (to make more dna than the specified 25mg tissue per dnaeasy column)? (3) What other ways can costs be reduced?

AEM Baker 101 Morgan Bio University of KY Lexington KY 40506 mouse@lamar.colostate.edu

mouse <mouse@lamar.colostate.edu>

Reptile genomes

The Reptile Genome Working Group is proud to announce the introduction of a web site for Reptilian Genomics – http://www.reptilegenome.com/ .We have developed a short list of reptilian species for possible genome sequencing. We now seek comments that will help us choose the best species and to justify sequencing the entire genome of one or more reptiles. We welcome your input to ensure that the species recommended for sequencing will benefit the largest possible community of scientists who will make use of the data. Please visit http://www.reptilegenome.com/-white_paper/survey.shtml by Friday 3 June, 2005 to help select the species that will be proposed for full genome sequencing.

Please see the website for additional information, to join our e-mail list-serve, or to join our working group. Please also forward this e-mail to anyone who may find this of interest

The Reptile Genome Working Group

Scott Edwards Harvard Avian & Reptilian Genomics Travis Glenn SREL, UGA, USC Reptilian (Alligator) & Peromyscus genetics/genomics Ed Braun University of Florida Avian & Reptilian Genomics & Systematics Wes Warren WUSTL Genomics Pat Minx WUSTL Reptilian Genomics Sandy Clifton WUSTL ESTs Dorrie Main BioInformatics Clemson University Jonathan Losos WUSTL Anolis Genomics Jeremy Gibson-Brown WUSTL Anolis Genomics William Modi NIH - NCI Genomics David Pollock LSU Genomics - Modelling Lisa Davis AB (SREL) Alligators - Contacts Dan Brown University of Florida Host/Microbe Gene co-expression in infected reptiles Lou Guillette University of Florida Alligators, Ecotoxicology, Immunology Andy Shedlock Harvard Reptilian Genomics David Ray LSU Repetitive elements, crocodilians

sedwards@fas.harvard.edu

SSR null alleles

Hello, EvolDir,

My lab is increasingly using SSR markers (microsatellites) to address population and conservation questions for a variety of plant species, and null alleles appear to be present in the data with some frequency. I am not familiar with how to account for a null allele in SSR data, especially when the analysis software requires alleles to be designated as number of repeats for a step-wise mutation model.

Is there a convention for coding or accounting for null alleles observed in microsatellite data collected for wild populations? Can you recommend literature that addresses this subject?

Thanks for your help in advance, Jenn

Jennifer DeWoody, Biologist USDA Forest Service, NFGEL 2480 Carson Road, Placerville, CA 95667 530-295-3028 (voice), 530-622-2633 (fax)

jdewoody@fs.fed.us

SSR null alleles responses

Hello again, EvolDir,

Below you can find the compiled responses on my question regarding null alleles in SSR data. Thank you to everyone who responded - the information and citations are most helpful.

Cheers, Jenn

original message:

———————————————————————

Hello, EvolDir,

My lab is increasingly using SSR markers (microsatellites) to address population and conservation questions for a variety of plant species, and null alleles appear to be present in the data with some frequency. I am not familiar with how to account for a null allele in SSR data, especially when the analysis software requires alleles to be designated as number of repeats for a step-wise mutation model.

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Thanks for your help in advance, Jenn

Jennifer DeWoody, Biologist USDA Forest Service, NFGEL 2480 Carson Road, Placerville, CA 95667 530-295-3028 (voice), 530-622-2633 (fax) jdewoody@fs.fed.us

Responses:

Yes, nulls are a pain in the neck, and they seem to be very common in organisms with large Ne –> long coalescence times.

The ideal is to detect them asap and get technical fixes to avoid them:

- as a first approach, using the least stringent conditions that give you interpretable results should minimize your problems

- change PCR conditions

- redesign primers even if you have to sequence some alleles to find suitable primer regions

- drop the locus

The coding of nulls depends on what you are trying to do. Of course it is important to note the difference between a 'definite' homozygous null and a failed PCR: a null homozygote is an individual that gives nothing when it should have worked (you will know the DNA is fine at other loci and the locus is reliable, or even better than loci are scored in multiplexes that are reliable). GENEPOP will estimate null allele frequencies as long as you identify null homozygotes, which must be coded as the largest allele (so we call them 9999999).

Often there is little justification for assuming SMM, and it is even less likely to apply in taxa with high frequencies of nulls because these may have a lot of indels in the flanking regions.

The champion 'null' species of which I am aware (and we have stumbled over several in my group!) is Scaptodrosophila hibisci with an impressive 17/20 loci affected (admittedly in part owing to Stuart Barker's high standards of demanding proof that loci do NOT have nulls).

See

Wilson, A.C.C., Sunnucks, P. & Barker, J.S.F. (2002) Isolation and characterization of twenty polymorphic microsatellite loci for Scaptodrosophila hibisci and endemic Australian Drosophilidae. Molecular Ecology Notes. 2, 242-244.

and

Barker JSF (2005). Population structure and host-plant specialization in two Scaptodrosophila flower-breeding species. Heredity 94, 129-138.

————————————————————

I can help you with some references that either talk about null alleles or they mention how they treated null alleles, as well as one that has information on genotyping errors. These are:

Goodman SJ. 1998 Molecular Biology and Evolution 15(2):104-118. Patterns of extensive genetic differentiation and variation among European harbor seals (Phoca vitulina vitulina) revealed using microsatellite DNA polymorphisms

Dakin EE, Avise JC. 2004 Heredity 93(5):504-509 Microsatellite null alleles in parentage analysis

Hoffman JI, Amos W. 2005 Molecular Ecology 14:599-612 Microsatellite genotyping errors: detection approaches, common sources and consequences for paternal exclusion

Sorry they are mostly in terms of parentage analysis but I'm sure they will help to bring some answers.

——————————————————-

We developed a software program Micro-Checker which helps you deal with nulls. Please follow this link http://www.microchecker.hull.ac.uk .

The Programme Note is there too as PDF. If you have any more questions, just drop us an email!

————————————————————

I've recently read a journal that deals (somewhat) with your problem. Here is the citation:

Molecular Ecology 2005 Vol.14, 885-890 "Standardizing for microsatellite length in comparisons of genetic diversity"

Hope this helps out a little.

I just came across these...they might help too:

Genetics (April 2003) Vol. 163, 1467-1482 "Microsatellite allele sizes: A simple test to assess their significance on genetic differentiation"

Mol. Biol. Evol. (1995) Vol.12(6), 1074-1084 "Size homoplasy and mutational processes of interrupted microsatellites in two bee species, Apis mellifera and Bombus terrestris (apidae)

——————————————————-

Pls make answers available to the whole list; see Josephine Pemberton's

— / —

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

———————————————

Serum vs plasma

Evoldir:

I have several samples for which all the components of the blood were separated (i.e. RBC, WBC, Serum, and Plasma). However, some of the samples have lost their identifying information over the years stating what part of the blood the sample came from. I am wondering if there is a test which can identify plasma vs serum vs WBC? Additionally, has anyone extracted DNA from serum or plasma? What was the quantity/quality of the DNA obtained? I am wondering if it is good enough quality to perform a multilocus scan.

Thanks in advance

Melissa Gray

PhD Graduate Student UCLA Dept. EEB/Wayne Lab 621 Charles E. Young Dr. South Los Angeles, Ca 90095 Phone: 310-825-5014 Fax: 310-206-3987 Homepage: www.bol.ucla.edu/~mgray9 email: mgray9@ucla.edu

Melissa <mgray9@ucla.edu>

———————————————

Software Migrate

MIGRATE NEWS: May 2005

New versions and macosx graphical-user interface: http:// popgen.csit.fsu.edu

(1) Migrate has now a graphical user interface for Apple Macintosh OS 10.2+ systems. We call the interface Miggui. The name is spoken Miggi (for english speakers: meeggy), of course it means migrate-graphical-user interface, but reminds me of a cat we had long time ago in Switzerland. Carl McIntosh programmed the Graphical User Interface, it is written in Objective-C and is an independent program that calls the command-line version of migrate.

Once you downloaded the package, a short guide to miggui can be found in the directory miggui-short-

documentation, double click index.html or in the help menu of the miggui application. Currently miggui does not support all possible options in migrate-2.0.6: the Bayesian portion is currently not implemented and will come at a later time. This is the first release of miggui and so it will have rough edges and we would like to hear about these. If you find errors, problems, or have suggestions please email us at miggui@csit.fsu.edu.

(2) A new maintenance release of migrate (now version 2.0.6) that removes a few memory leaks (if your dataset crashed towards after running for a while you might want to retry with this version)

(3) Because of system-security issues, it gets more and more difficult for me to maintain migrate on evolution.gs.washington.edu. As of now if you go to http://evolution.gs.washington.edu/lamarc/-migrate.html you will be forwarded to my own site http://popgen.csit.fsu.edu . Carl McIntosh (cmcintosh@mac.com) Peter Beerli (beerli@csit.fsu.edu)

P.S. I send you this email because you registered on the migrate download page. If you think you should not receive this email, send me a note and I will remove you from the list (this is a low-traffic moderated list (only I can send messages to the list) to announce changes and news about migrate)

—- Peter Beerli, Computational Evolutionary Biology Group School of Computational Science (SCS) and Biological Sciences Department 150-T Dirac Science Library Florida State University Tallahassee, Florida 32306-4120 USA Webpage: http://www.csit.fsu.edu/-˜beerli Peter Beerli <beerli@csit.fsu.edu>

Software WinPop 2 5

Hello EvolDir

I have just released a new version of the Population Genetics simulation program WinPop. This new version, 2.5, corrects bugs present in previous releases and includes a new module and new features in the old ones.

This new release is available at

http://www.genedrift.org/winpop.php Also the help file has been rewritten and it is included with WinPop installation package and also available online at

http://www.genedrift.org/winpophelp I am making available a forum to discuss subjects on Population Genetics and WinPop on the website too. It is free and easy to register, so please do so. The forum is at

http://www.genedrift.org/winpopforum Thanks for you attention

Paulo Nuin

pnuin@terra.com.br

Stationarity tests

One more question about stationarity tests.

Note: I will post the collected answers to help those with similar questions. This is as per common practice and as listed on the EvolDir website.

And now the question.

Stationarity of nucleotide frequencies is an important assumption of most sequence evolution models. Although ML tree reconstrucion is to some extent robust against the violation of underlying assumptions, one never knows how much violation is actually tolerated before the method produces wrong results. It is therefore good practice to exclude sequences from the analysis whose base compositions deviate too much from the average.

A popular method to facilitate this decision is a simple chi-square test which compares the nucleotide distribution of each sequence with that of the whole data set: It rejects a sequence if it becomes improbable that the two distributions are equal. Many people have been using this test over years and I too have implemented it in my own software - whithout thinking too much about it.

The problem is that p-values produced by this method depend strongly on the sequence lengths. Any naturally evolving sequence which is to some extent off the equilibirium will pass the test if it is only short enough, and any sequence that is long enough will fail - no matter how good or bad it is. Especially the punishment of long sequences is bad because ML tree reconstruction is known to become more and more reliable the longer the sequences are.

Take a small sequence alignment whose sequences have passed the chi-square test and concatenate it several times with itself. You will be surprised that very likely some of the sequences are being rejected now, though the phylogenetic information can not have changed.

I am looking for alternatives. Any ideas? Is there a sim-

ple way to check that the base composition in a data set is or was suitable for tree reconstruction?

Gangolf

Gangolf Jobb <gangolf@treefinder.de>

Stationarity tests answers

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I am looking for alternatives. Any ideas? Is there a simple way to check that the base composition in a data set is or was suitable for tree reconstruction?

Gangolf

Hi Gangolf

Perhaps one way to do this is to use parametric boot-strapping, as follows:

1. Estimate the best (i.e., ML) model of evolution, stationary frequencies, and tree for a given dataset. 2. Use the estimated model, frequencies and tree to generate simulated datasets. 3. Now estimate the distribution of your Chi-squared statistics using the simulated sequences.

You can now assess how each sequence fits against this distribution.

Of course, this approach is predicated on your choice of the model that best describes the evolution of the sequences. The ML rate/tree/frequency estimates of a less-than-satisfactory model will give an inappropriate chi-squared distribution.

Be interested to know how this works. Cheers

Allen Rodrigo

Dear Jobb

We developed a Disparity Index test that is more powerful than the Chi-square test for this purpose. This method can also be used to compute the disparity index per site, as well. It is implemented in the software MEGA (www.megasoftware.net) for DNA and protein sequences and it has been used for analysis of mammalian DNA and proteins. Relevant references are given below (note that all pdfs at available at www.kumarlab.net/publications):

Kumar S & Gadagkar SR (2001) Disparity Index: A Simple Statistic to Measure and Test the Homogeneity of Substitution Pattern Between Molecular Sequences. Genetics 158:1321-1327.

Tamura K & Kumar S (2002) Evolutionary Distance Estimation Under Heterogeneous Substitution Pattern Among Lineages Molecular Biology and Evolution 19:1727-1736.

I hope this is helpful.

Sudhir   Kumar   www.biodesign.org/efg www.kumarlab.net

Dear Gandolf,

We recently published a paper (Systematic Biology 53, 638-643 [2004]) in which we reviewed methods for assessing compositional heterogeneity.

All the best,

Lars

Hi,

My view on how to think about this is as a model selection problem: We have to choose between a model M0 under which all sequences have the same base composition, and models M1,... under which some sequences have different base compostions.

It is well known that many classical (p-value/likelihood/LRT/AIC) model selection methods are asymptotically inconsistent, meaning that as the number of i.i.d. observations goes to infinity the probability of selecting the the right model does not go to one. In contrast, the Bayes factor and BIC (a.k.a. Schwarz criterion) are asymptotically consistent. Note that consistency is an entirely classical concept, referring to probabilities in repeated sampling under the same true model. In this sense, Bayesian methods perform better by a classical criterion.

The BIC is like a LRT/AIC model selection criterion, but is

BIC = 2 x (lnL(M1) - lnL(M0)) - k ln(n)

where k is the difference in degrees of freedom of the two models, and n is the number of i.i.d. observations. Thus as n gets large we

— / —

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

Substitutes for ABIreagents

What companies make inexpensive reliable reagents for ABI machines genotyping microsatellites? Please provide contact info (email/phone) for company; I will post a summary on evoldir. Thanks.

AEM Baker 101 Morgan Bio University of KY Lexington KY 40506 0225 mouse@lamar.colostate.edu

mouse <mouse@lamar.colostate.edu>

TOTALML questions

Hi there,

Is anybody familiar with the TOTALML program in MOLPHY? Could anybody please kindly tutor me how to compare topologies from separate ML analyses of individual proteins? What's the LLS files input for?

Your attention will be highly appreciated!

Tuo

Tuo Shi Institute of Marine and Coastal Sciences Rutgers University 71 Dudley Road, New Brunswick, NJ 08901 Phone: (732)-932-6555 ext. 332 Fax: (732)-932-4083 Email: tuoshi@imcs.rutgers.edu

Tuo Shi <tuoshi@imcs.marine.rutgers.edu>

Volvox cultures

Hello, I am looking for Volvox cultures for a phylogenetic project. I have found several in culture collections (UTEX, NIES, SAG, etc.), but still haven't located the ones in the list below. If anyone has any of these, or can put me in touch with someone who might, I would love to hear from you. Live algae would be ideal; DNA and frozen algae are fine too. Thanks!

V. amoeboensis V. aureus var. hemisphaericus V. capensis V. carteri f. hazenii V. carteri f. iyengarii V. carteri f. Stein V. globator var. australis V. globator var. maderaspatiensis V. lismorensis V. maderaspatiensis V. merrillii V. perglobator V. pocockiae V. prolificus V. tertius var. godwardensis V. tertius var. guttulosa V. tertius var. ovalis V. tertius var. tessellate Also, Gonium dispersum Eudorina minodii

Matthew D. Herron Department of Ecology and Evolutionary Biology University of Arizona 1041 E. Lowell St. Tucson, AZ 85721-0088 520-621-1844 mherron@email.arizona.edu http://www.u.arizona.edu/~mherron/

Wolbachia

I am looking for samples of arthropods of all types that are maintained as laboratory cultures. I will be testing them for the presence of Wolbachia. Wolbachia is an endosymbiotic bacteria that infects somewhere between 20-75% of all arthropod species and manipulates their

hosts in a number of ways, most notably by manipulating reproduction.

If anyone has any arthropods (other than Drosophila in the melanogaster subgroup) that they maintain and would be willing to let me test them for Wolbachia, please write to me at mclark11@mail.rochester.edu. We can then arrange for easy shipping of material (5-10 female insects in 95% ethanol is prefered). I will be able to let you know if your organisms are infected, and if so, with which Wolbachia strain.

If interested, please email me and I will send you shipping information.

Thanks, Michael Clark

Department of Biology University of Rochester Rochester, NY 14627

mclark11@mail.rochester.edu

cDNA library subtraction

Does anybody has a protocol for cDNA library subtraction. We have a directional Lambda-Zap (Stratagene) library and are in the middle of a moderately large project to identify all genes expressed during wing development in Heliconius butterflies. Our goal is to subtract out those genes that we have sequenced multiple times before beginning the next round of sequencing. The technical support team at Stratagene is of no help, and I would love to start a dialogue with anyone that has experience with subtractive hybridization. Please contact me at wmcmilla@rrpac.upr.clu.edu. As I think that this information may be generally useful, I will distill any correspondence and keep people abreast of our progress. Many thanks, Owen

W. Owen McMillan Associate Professor Department of Biology University of Puerto Rico- Rio Piedras P.O. Box 23360 San Juan, PR 00931-3360

wmcmilla@rrpac.upr.clu.edu   http://zephyr.hpcf.upr.edu/ ˜ mcmi-lab/ phone (office): 787-764-0000 [(1)2909] phone (lab): 787-764-0000 [(1)2902, (1)2853] phone (home): 787-764-3564 fax: 787-764-3875

wmcmilla@rrpac.upr.clu.edu

PostDocs

CornellU TheoPopGenet

Theoretical / Computational Population Genetics Post-doctoral position Cornell University

A postdoctoral research position is available in Carlos D. Bustamante?s lab at Cornell. The lab focuses on statistical inference in population genetics and molecular evolution with emphasis on developing novel methods for detecting evidence of natural selection from comparative sequence data. Successful applicants will have expertise in one of the following areas: theoretical population genetics, comparative genomics and bioinformatics, computational statistics, and/or biophysics. The position is initially for one year, with the option for renewal for up to 3 years. For more details on current research visit http://www.bscb.cornell.edu/ Homepages/Carlos_Bustamante/.

The ideal start date for the position is 9/1/2005, but negotiable. Review of applicants will start 6/15/2005. If interested in applying, please send a current cv, statement of research interest, and the contact information of three references to cdb28 AT cornell DOT edu. Your cv and statement must be in PDF format and the email subject should read ?Post-Doctoral Position Application ? <LAST NAME>,<FIRST NAME>?. Please include your contact details and those of your references in the email.

Carlos D. Bustamante Assistant Professor, Biological Statistics and Computational Biology 101A Biotechnology Building Ithaca, NY 14853 (607) 266-1640

Carlos Bustamante <cdb28@cornell.edu>

DalhousieU FishDNABarcodes

Postdoctoral position: DNA Barcodes for the Marine Fishes of Atlantic Canada

A postdoctoral position is available immediately (May or June 2005). The term of the position is initially for one year, but may be extended for a second year, depending on availability of funding. Starting salary is approximately $40,000 (Can).

The postdoctoral research will carry out a project aimed at DNA barcoding the approximately 350 species of fishes that known from Atlantic Canada. In addition to DNA barcoding, this will entail assembling voucher specimens for all of these species. This work will contribute to an international research program that will gather DNA barcodes for all fishes.

Candidates for this position must possess a Ph.D. in the biological sciences. Past experience in fish or fisheries biology, particularly involvement in faunal surveys and/or taxonomy, is desirable. Prior experience in molecular techniques and phylogenetic analysis are also desirable, but not essential.

This project will be coordinated by Dr. Paul Bentzen (Dalhousie University) and Dr. Ellen Kenchington (Bedford Institute of Oceanography and Dalhousie University).

This position will be based at the Gene Probe Laboratory, Dalhousie University, Halifax, Nova Scotia.

Application Procedure: Send your curriculum vitae and contact details for 3 references to Paul Bentzen at Paul.Bentzen@dal.ca.

DeakinU MolPhylogenetics

Postdoctoral Position: Academic in Molecular Phylogenetics Molecular Ecology and Biodiversity Laboratory, School of Ecology and Environment, Deakin University, Warrnambool, Victoria, Australia.

A full-time post-doctoral position is available for three years, starting immediately (June 2005 or ASAP). The appointee will be required to undertake research and support research activities in the field of molecular ecology and phylogenetics. Specifically, the job will involve the utilization of various molecular tools for population genetic research, management or genetic improvement of commercial fish and invertebrate species, conservation genetics, and the taxonomy, evolution and biogeography of aquatic species.

Principal accountabilities include undertaking research and publishing findings in refereed international journals, making contributions to existing research programs and the development of grant applications, developing teaching materials, field work participation, supervising honours and higher degree students, management of a molecular genetics laboratory, and the acquisition and subsequent analysis of molecular and morphological data.

We are seeking a person with a PhD in molecular phylogenetics or population genetics or similar field. Highly developed laboratory skills in PCR-based molecular genetic techniques and a demonstrated ability to collect and analyse large molecular data sets is essential. Applicants should have high-level communication and inter-personal skills, and must be prepared to work as a member of a collaborative team. In depth knowledge of the theory and practice of phylogenetic analysis as applied to molecular data, and knowledge of either macroecology, biogeography or systematics is required.

Please refer to http://www.deakin.edu.au/hrs/employment/ for application details including selection criteria. Applications close May 27.

Dr Christopher Austin, Associate Professor, Campus Coordinator - Warrnambool, HDR-Student Coordinator - Warrnambool School of Ecology and Environment, Deakin University, PO Box 423 Warrnambool, 3280 Victoria, Australia Phone: +61 35563 3518 chris_austin@deakin.edu.au.

– Adam Miller Postgraduate Research School of Ecology and Environment, Deakin University, PO Box 423 Warrnambool, 3280 Victoria, Australia Phone: +61-35563-3059 Fax: +61-35563-3462

Adam Miller <admiller@deakin.edu.au>

ErasmusU CompBiol

POST-DOCTORAL RESEARCH SCIENTIST or PH.D. STUDENT

In Computational Biology / Theoretical Genetics

The Department of Forensic Molecular Biology (FMB) at the Erasmus University Medical Centre Rotterdam (Netherlands) is looking for a post-doctoral research scientist or PhD student in the area of computational biology / theoretical genetics. The FMB department is housed within the interactive medical-genetic cluster of Erasmus MC, comprising strong research departments of genetics, cell biology, clinical genetics, biochemistry (www.erasmusmc.nl/medical_genetics/) with tight links to departments of bioinformatics and genetic epidemiology. Erasmus MC is the leading medical research centre in the Netherlands and well recognized internationally and Rotterdam is a lively and highly international city closely located to many highlights of Europe. The focus of the FMB department is in identification and characterization of human individual and population differences (e.g. visible traits) with the future aim of applications in forensics for which we use genomics, transcriptomics and computational approaches (www.erasmusmc.nl/fmb) . The successful candidate is expected to develop independent research applying computational algorithms to questions of neutral and non-neutral human individual and population differentiation using SNP and gene expression data. This will include evolutionary genetic and functional genetic perspectives. The candidate will enhance the theoretical group within the FMB department (currently 1 post-doc) with close interactions with EMC departments of bioinformatics, and genetic epidemiology. Candidates should hold a PhD in computational biology, statistical / theoretical genetics, or related fields. Outstanding students holding a M.Sc. / Diploma degree are also encouraged to apply. Programming skills are required. Experience in medical-genetic statistics (e.g. genetic association studies) is a plus. The successful candidate is highly motivated to built-up an independent research line and has demonstrated (post-doc) or envisions (PhD student) a strong interest in a research career in this area. If applicable a PhD degree from the Erasmus University can be obtained within the Postgraduate School Medical-Genetic Centre Southwest Netherlands (MGC). The Post-doc position is available for 2.5 years with likely possibilities for elongation; gross monthly salary is depending on experience with a max. of 4483 Euro plus all benefits of governmental employment The PhD position is for max. 4 years and gross monthly salary will be 1.702 Euro in the first year up to 2.283 in the fourth year. CV including publication list and three references should be submitted to Prof. Manfred Kayser, Department of Forensic Molecular Biology, Erasmus University Medical Centre, Medical-Genetic Cluster, PO Box 1738, NL-3000 DR Rotterdam, The Netherlands, preferentially via e-mail: m.kayser@erasmusmc.nl Closing date of application is June 1, 2005.

– Manfred Kayser, Ph.D., Professor Head, Department of Forensic Molecular Biology Erasmus University Medical Centre Rotterdam Medical-Genetic Cluster PO Box 1738, NL-3000 DR Rotterdam phone: ++31-10-4638073 fax: ++31-10-4089300 e-mail: m.kayser@erasmusmc.nl website: http://www.erasmusmc.nl/fmb/ m.kayser@erasmusmc.nl

ErasmusU EvolGeneExpression

POST-DOCTORAL RESEARCH SCIENTIST

In Molecular Biology / Gene Expression

The Department of Forensic Molecular Biology (FMB) at the Erasmus University Medical Centre Rotterdam (Netherlands) is looking for a post-doctoral research scientist in the area of molecular biology / gene expression. The FMB department is housed within the interactive medical-genetic cluster of Erasmus MC, comprising strong research departments of genetics, cell biology, clinical genetics, biochemistry as well as a biomics facility (www.erasmusmc.nl/medical_genetics/-) . Erasmus MC is the leading medical research centre in the Netherlands and well recognized internationally and Rotterdam is a lively and highly international city closely located to many highlights of Europe. The focus of the FMB department is in identification and characterization of human individual and population differences (e.g. visible traits) with the future aim of applications in forensics for which we use genomics, transcriptomics and computational approaches (www.erasmusmc.nl/fmb) . The successful candidate is expected to develop independent research applying gene expression analyses to questions of human individual and population differentiation, (e.g. externally visible characteristics), and biodegradation. The candidate will enhance the molecular genetic / biology group within FMB (currently 2 Post-docs and 3 technicians) with close interactions to the department of clinical genetics, bioinformatics, and genetic epidemiology. Candidates should hold a PhD in molecular biology, genetics, biochemistry or related fields with a strong background in gene expression analysis including both data generation (including array-based technology and RT-PCR) and interpretation. Experiences in proteomics will be a plus as well as with animal experiments. The successful candidate is highly motivated to built-up an independent research line and has demonstrated a strong interest in a research career in this area. The position is available for 2.5 years with a likely possibility for elongation. Salary is depending on experience with a max. of 4483 Euro (gross / month) with all benefits of governmental employment. CV including publication list and three references should be submitted to Prof. Manfred Kayser, Department of Forensic Molecular Biology, Erasmus University Medical Centre, Medical-Genetic Cluster, PO Box 1738, NL-3000 DR Rotterdam, The Netherlands, preferentially via e-mail: m.kayser@erasmusmc.nl Closing date of application is June 1, 2005.

– Manfred Kayser, Ph.D., Professor Head, Department of Forensic Molecular Biology Erasmus University Medical Centre Rotterdam Medical-Genetic Cluster PO Box 1738, NL-3000 DR Rotterdam

phone: ++31-10-4638073 fax: ++31-10-4089300 e-mail: m.kayser@erasmusmc.nl website: http://-www.erasmusmc.nl/fmb/ m.kayser@erasmusmc.nl

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Human Diversity

Genographic Postdoctoral Fellowship in Human Population Genetics

We are seeking postdoctoral researchers in the area of human population genetics starting June 1st, 2005 or soon thereafter. Successful applicants will be expected to oversee a 5-year project comprising field sampling and laboratory analyses to reconstruct historical human population events. The position will be funded by The Genographic Project, a research partnership of the National Geographic Society and IBM, with field research support provided by the Waitt Family Foundation. This position will be supervised by the principal investigator heading one of our regional centers (for list see http://www3.nationalgeographic.com/-genographic/faqs_about.html#Q1), and the individual will be expected to lead a group of laboratory technicians and field support staff necessary for the completion of the project at that regional center. The aim of the project is to reconstruct the ancient migration events that led to the peopling of the world and to assess regional patterns of human genetic diversity. The applicant should have a Ph.D. in a field related to human population genetics, some fieldwork experience, and a working knowledge of molecular laboratory techniques. Ability to speak English and at least one other language, and a certificate in phlebotomy or willingness to obtain one, are highly recommended. Please send CV, 3 letters of reference, and the desired regional affiliation electronically to The Genographic Project: genographic@ngs.org Closing date is 30 May 2005.

Fabrício Rodrigues dos Santos <fsantos@mono.icb.ufmg.br>

Iraklio Crete EvoDevo

POST-DOCTORAL POSITION AVAILABLE

Michalis Averof / Development and Evolution lab Insti-

tute of Molecular Biology and Biotechnology (IMBB) Iraklio Crete, Greece

Marie Curie Research Training Network"Zoonet" Development and evolution of animal form: Training modern comparative zoologists

A postdoctoral position is available for 30 months, from 1 May 2006, funded by the Marie Curie Research Training Network "ZOONET", to study the evolution of developmental processes in crustaceans and insects using comparative gene expression and functional studies (for a summary of our lab's interests see: http://www.imbb.forth.gr/people/averof/).

Applicants should have a doctorate and relevant experience in molecular biology; experience in developmental biology, genetics and/or bioinformatics would be an advantage. Training will be given in the full range of approaches relevant to Evolutionary Developmental Biology (e.g. comparative studies of gene expression, functional studies by RNAi and transgenesis), and may require exchanges between laboratories in the ZOONET Network, as well as participation in network meetings.

In the selection process, the sponsor stipulates that:

 Candidates must have at least four and no more than ten years (full time equivalent) of post-graduate research experience; At the start of their fellowship, researchers may not have resided or carried out their main activity (work, studies, etc) in Greece for more than 12 months in the 3 years immediately prior to the appointment. Greek nationals may apply only if they can provide evidence that they have legally resided and have had their principal activity (work, studies, etc) in a third country for at least four of the last five years immediately prior to the reference deadline.

The salary will be approximately 25,000 Euro per annum (net), plus contributions for social security and income tax. Researchers will also be eligible for an annual travel allowance and a one-off Career exploration allowance of 2,000 Euro.

Applicants should send their CV and publication list to Michalis Averof (please send electronically to averof@imbb.forth.gr). They should also ask two referees to send letters of recommendation to the same electronic address.

The closing date for applications is 15 July 2005.

m.telford@ucl.ac.uk m.telford@ucl.ac.uk

LausanneU TheoPopBiol

University of Lausanne, Switzerland

Post-doc in theoretical population biology

I am seeking a biologist with strong background in theoretical population biology (demography and/or genetics) and excellent mathematical skills (or alternatively a mathematician with strong interests in population biology) to join a team project on the demogenetics of metapopulations funded by the Swiss National Science Foundation.

We aim at combining demographic and genetic approaches to understand and characterize the effects of landscape structures and species traits (fecundity, dispersal?) on key metapopulation features (such as ability to resist demographic extinction or genetic drift). Theoretical analyses will be coupled with individual-based simulations and empirical investigations aimed at parameterizing models. This project has relevance to conservation biology. The successful candidate will also have the opportunity to develop his/her research along own lines.

Duration: 2 years with a possible one year extension Salary according to the Swiss FNRS standards

Details on the research group at http://www.unil.ch/dee/page6761.html. The Department of Ecology and Evolution (http://www.unil.ch/dee/) hosts about 15 faculty members with wide-ranging interests in evolutionary biology, ecology and conservation biology. The campus of Lausanne University (http://www.unil.ch/central/) is beautifully situated on the shore of Lake Geneva, just in front of the Alps. Lausanne (http://www.lausanne.ch/; http://www.lausanne.ch/;) is a cosmopolitan and lively city in western, French-speaking Switzerland, with an active cultural life and nice natural surroundings.

Deadline for sending CVs 31May 2005 For further information nicolas.perrin@unil.ch

Nicolas Perrin Dept. Ecology & Evolution University of Lausanne (Switzerland) http://www.unil.ch/dee/page5090_en.html Tel (0041) 21 692 41 84 new mail: nicolas.perrin@unil.ch

Nicolas Perrin <Nicolas.Perrin@unil.ch>

Massachusetts EvolEnv

MASSACHUSETTS ENVIRONMENTAL FELLOW POST DOCTORAL POSITIONS available for a unique program at The Environmental Institute, University of Massachusetts Amherst. Three Massachusetts Environmental Fellows will be hired, one in each of three thematic areas. 1) Climate Change - Areas of particular interest include environmental and social impacts of climate change; mitigation and response approaches; science/policy interface; and energy and water resources. 2) Environmental Contaminants - Areas of particular interest include environmental and aquatic chemistry; environmental toxicology; bioremediation; and biological water or air pollution control. 3) Environmental Modeling and Monitoring - Areas of particular interest include fate and transport of environmental contaminants; social/ economic correlates of environmental quality and hazards; remote sensing and GIS; sustainable landscape and forest management; transportation/environment interface; and human ecology and biodiversity.

Each Massachusetts Environmental Fellow will coordinate and provide leadership for an Interdisciplinary Faculty Working Group (50 percent time) in the thematic area and will function as a Post-Doctoral Research Fellow (50 percent time) working on related research. Minimum qualifications are a Ph.D. in a field relevant to the thematic area. Positions are available for one year with the possibility of reappointment.

Each Environmental Fellow will have several major responsibilities: 1) to develop an area of research expertise within the thematic area of environmental excellence, working in cooperation with a Faculty Mentor; 2) to play a leadership role in the interdisciplinary Faculty Working Group; and 3) to facilitate the activities of the working group with TEI staff providing support for these activities. The Environmental Fellow will work with both a Faculty Mentor and TEI Senior Staff. The Fellows will function in dual positions ? they will develop their own specific area of research expertise within a strategic area of environmental excellence (this activity will be sponsored by the faculty mentor who will provide the Fellow access to research facilities as appropriate), and they will play a leadership role within a thematic interdisciplinary Faculty Working Group as the group meets to discuss and respond to research needs and opportunities.

Salary will be commensurate with experience. Please submit cover letter, curriculum vitae and the names of three references to Richard Taupier, Associate Director, The Environmental Institute, Blaisdell House, University of Massachusetts Amherst, MA 01002 or Email: taupier@ tei.umass.edu. Review of applications will begin on July 1 and continue until the positions are filled. Desired start date is September 1. UMass is an Equal Opportunity / Affirmative Action Employer. Women and members of minority groups are encouraged to apply.

I think this is a pretty cool opportunity for a postdoc as papers and grant proposals are likely to develop from the working groups. It is advisable to first contact a potential Faculty Mentor before sending in a proposal.

Cheers,

Jeff Blanchard

Jeffrey L. Blanchard Assistant Professor Department of Microbiology University of Massachusetts Amherst, MA 01003 Office and Lab: Morrill I N330 Tel: 413-577-2130 Fax: 413-545-1578 http://www.bio.umass.edu/-micro/blanchard/Lab_About.html Jeffrey Blanchard <blanchard@microbio.umass.edu>

NorthCarolinaStateU PopGenetics

The Department of Entomology at North Carolina State University is seeking a postdoctoral associate to investigate genetic structure in urban and agricultural populations of the German cockroach, Blatella germanica, using microsatellite markers. This USDA-NRI funded position is for up to 3 years with an anticipated start date of September 1, 2005. Candidates should have experience in the use of molecular markers to analyze the genetic structure of natural populations. Knowledge and interest in invasive species biology would be advantageous. For more information and application procedures contact Ed Vargo (ed_vargo@ncsu.edu; http://www.cals.ncsu.edu/entomology/vargo/-) or Coby Schal (coby_schal@ncsu.edu; http://-www.cals.ncsu.edu:8050/entomology/schal/program/).

Edward Vargo Department of Entomology Box 7613 North Carolina State University Raleigh, NC 27695-7613

Tel. (919) 513-2743 Fax (919) 515-7746 Email: ed_vargo@ncsu.edu http://www.cals.ncsu.edu/-

entomology/vargo/ ed_vargo@ncsu.edu

Portugal Drosophila Wolbachia

Hi Everybody,

We have a one-year Post-Doctoral Research Fellowship on the project Vertical transmission of Wolbachia bacteria in Drosophila available. The project has been financed for 3 years and will be developed at the Evolution and Development Group at Instituto Gulbenkian de Ciência (http://www.igc.gulbenkian.pt).

We aim at identifying the mechanisms by which the vertically transmitted bacteria Wolbachia colonizes the reproductive tissues of adult Drosophila females, assuring its transmission to new hosts.

The fellowship will be financed for 12 months and a fellowship contract will be celebrated. The fellowship may be extended pending on the financing entities approving a new scholarship. The successful candidate should have defended his/her PhD, or have his/her PhD scheduled for no later than the 30th of September, 2005. He or she should be available to start research at IGC no later than November 1st 2005; should be familiar with Molecular techniques and/or Confocal microscopy, and/or have experience in research with Drosophila; and should also be fluent in spoken and written English. Applications should be submitted until the 30th of June, 2005. Applications - motivation letter, two recommendation letters, CV, and copy of PhD diploma (or proof of a scheduled PhD), should be sent (e- or snail-mail) to the address bellow.

All candidates with the appropriate profile will be invited for an interview. All candidates will be informed of the result of their application within two weeks of the interview. For more info on this please contact me. Best regards, Filipa Vala, Instituto Gulbenkian de Ciência, Grupo de Investigaão de Evoluão e Desenvolvimento, Apartado 14, 2781-901 Oeiras, Portugal. fvala@igc.gulbenkian.pt

F Vala <fvala@igc.gulbenkian.pt>

STRI AvianColonizationGenetics

Postdoc: Genetic variation, divergence, and differentiation in land bird populations in the West Indies

Smithsonian Tropical Research Institute

Eldredge Bermingham (Smithsonian Tropical Research Institute, Panama) and Robert Ricklefs (University of Missouri St. Louis) are seeking a postdoctoral researcher to collaborate on a molecular population genetic analysis of dispersal, genetic variation, and differentiation of land bird populations in the West Indies. Our previous molecular phylogeographic work (see list of publications below) has characterized the history of the distributions of birds in these islands, and has related geography and age to habitat distribution and abundance of individual island bird populations. In the proposed study, we shall explore genetic variation in West Indian island bird populations in relation to history, distribution, and ecology to determine factors that augment and reduce genetic diversity.

The processes of primary concern are colonization, migration between islands, and maintenance of genetic diversity. We address these processes by a combination of population genetic and phylogeographic approaches. The contemporary distribution of genetic variation within a taxon provides clues to important features of its history: colonization, including the temporal and spatial pattern of a taxon[1]s spread through an island chain; evidence of founder effects and population bottlenecks in the erosion of the genetic variation held by the source population; genetic differentiation between island populations when migration is too infrequent to homogenize the gene pool across islands; accumulation of new diversity within island populations through mutation; and attainment of evolutionary independence, ultimately revealed by fixed genetic differences between island populations. Laboratory analyses will be based primarily on nearly 12,000 DNA samples obtained since 1991 from most of the major islands in the West Indies and continental sites around the Caribbean Basin. Fieldwork will include additional sampling in northern Venezuela or Trinidad to characterize genetic variation in source populations more thoroughly; on St. Lucia to increase population samples of uncommon birds and to estimate population densities; and in the northern Lesser Antilles to sample populations on very small islands.

We are interested in addressing the following questions:

(1) How much genetic diversity is carried to the islands from continental source populations? Comparisons of the genetic diversity between source populations and undifferentiated (recent) island populations in the Lesser Antilles would permit estimation of the size of founder populations. Suitable taxa include

Columbina passerina, Elaenia flavogaster, Turdus nudigenis, Mimus gilvus, Tiaris bicolor, Quiscalus lugubris. Molecular markers are likely to include the mitochondrial cytochrome B and ATPase 6,8 genes and nuclear introns (ACO1-I10, FGB-15, MUSK-14, RHO-I, and TGFB2). Mitochondrial genes have a relatively rapid nucleotide substitution rate, whereas nuclear genes permit increased power of tests afforded by multiple, unlinked loci and the 4-fold increase in the effective population size of nuclear compared to mitochondrial loci.

(2) How isolated are island populations? The extent of migration between island populations can be assessed by genetic variation within and between populations using population genetic statistics. Genetic variance in isolated populations at mutation-drift equilibrium is proportional to effective population size. A high rate of migration increases local variance and homogenizes genetic variation among island populations. Low migration in recently founded populations is accompanied by low genetic variance. We aim to compare genetic diversity between weakly and strongly differentiated populations in an analysis of variance with island size and relative abundance as covariates (see 3 below). In addition to the undifferentiated species listed in objective 1, taxa with significant quantitative genetic differentiation of mitochondrial genes within the Lesser Antilles include Orthorhynchus cristatus, Elaenia martinica, Myiarchus [stolidus] oberi, Margarops fuscus, Vireo altiloquus, Dendroica petechia, Coereba flaveola, and Loxigilla noctis.

(3) How does genetic variation reflect the size and ecology of populations? Theory developed for mutation-drift equilibrium predicts a direct relationship between genetic diversity and effective population size. Populations that fluctuate greatly in size might exhibit more (contracting) or less (expanding) genetic variation than predicted from present size. We have sampled bird populations in the West Indies on islands ranging in size from Little Cayman to Hispaniola. We shall compare genetic diversity in genetically differentiated island populations (to ensure sufficient time is allowed for equilibrium under constant conditions) to island size and

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SanFranciscoStateU MarinePopBiol

Research associate/postdoc OR technician position

Position in a marine population biology/genetics and molecular evolution lab at the Romberg Tiburon Center for Environmental Studies (http://rtc.sfsu.edu/) of SFSU (http://www.sfsu.edu/~biology/). The lab uses molecular techniques to characterize patterns and investigate mechanisms of population differentiation.

Projects in the lab currently include immunogenetic (Mhc) and detoxification genetic variation in estuarine fish, connectivity between onshore and offshore invertebrate populations, population structure and restoration genetics of seagrasses in SF Bay, and invasion biology and evolution of allorecognition in colonial tunicates.

Must be capable of working independently and also with a diverse lab group, including some mentoring of students. Must have a car and be able to travel to the main campus in SF occasionally. Might involve assisting with field sampling or wetlab experiments from time to time, but funded position is for laboratory genetics.

Duties include running an ABI 3730 Avant capillary sequencer in sequencing and fragment sizing modes. Training provided, but experience with fragment sizing on any platform much appreciated.

Other duties consist of molecular lab procedures (including, but not limited to, nucleic acid extraction, PCR, cloning, and sequencing) and data manipulation and analysis (e.g., sequence alignments, phylogenetic, and population genetic analysis). General lab maintenance (e.g., ordering, keeping track of supplies, collection maintenance) will also be expected.

Minimum qualifications are an undergraduate college degree and laboratory experience. Good organizational and communication skills are essential. The position might be flexibly configured as a postdoctoral position, alternatively.

Please contact me by email and include a statement of interest and CV:

Sarah Cohen Romberg Tiburon Center for Environmental Studies and the Biology Department San Francisco State University 3152 Paradise Drive Tiburon, CA 94920

sarahcoh@sfsu.edu   http://rtc.sfsu.edu/   http://online.sfsu.edu/~sarahcoh/   – Sarah Cohen Assistant Professor in Biology Romberg Tiburon Center for Environmental Studies San Francisco State University

3152 Paradise Drive Tiburon, CA 94920

sarahcoh@sfsu.edu phone 415-338-3750 (office) http://rtc.sfsu.edu/ http://online.sfsu.edu/˜sarahcoh/ Sarah Cohen <sarahcoh@sfsu.edu>

UArizona BacterialGenomeEvol

BACTERIAL GENOME EVOLUTION UNIVERSITY OF ARIZONA

A Postdoctoral Research position is available to study the origins and functions of novel genes in bacterial genomes. Potential projects include both bioinformatic and experimental studies centering on the evolution of bacterial gene repertoires. 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 $36K to $42K, plus benefits) will be commensurate with experience.

If interested, please see: Howard Ochman

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

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

Howard Ochman <hochman@email.arizona.edu>

UCaliforniaIrvine Viral Phylogenetics

Department of Ecology and Evolutionary Biology

Open Position: POSTDOCTORAL SCHOLAR

A postdoctoral scholar position in the Lab of Dr. Walter M. Fitch is available at U.C. Irvine. The laboratory studies the conclusions one can derive from viral phylogenetic analysis. These include new methods for determining the migrations around the world of the human influenza virus. We also study how to predict the future evolution of the human influenza virus.

The successful candidate will have had several courses in Biology and know several programming languages. Funding for this position is available for two years. Review of applicants will begin July 1, 2005 and position will remain open until filled. Salary to be commensurate with experience. To apply, send your name, CV, address, and phone numbers to the address below along with the names and addresses of two referees along with their phone numbers.

Applications or queries can also be sent to: wfitch@uci.edu

URL: ecoevo.bio.uci.edu/Faculty/Fitch/Fitch.html

The Department of Ecology and Evolutionary Biology at UC Irvine houses a dynamic group of faculty in evolutionary genetics, including Professors Long, Clegg, Bush, Ayala, Wallace, and Fitch, among others. Information about the department and the campus is available at ecoevo.bio.uci.edu

Applications due by: 07/01/05

Contact information:

Dr. Walter M. Fitch Department of Ecology and Evolutionary Biology 321 Steinhaus Hall University of California, Irvine Irvine, CA 92697-2525 e-mail: wfitch@uci.edu

The University of California, Irvine has an active career partner program, is an equal opportunity employer committed to excellence through diversity, and has a National Science Foundation Advance Gender Equity Program. Posted: May 24, 2005

wfitch <wfitch@uci.edu>

UCaliforniaSanDiego ViralEvolutionDynamics

Postdoctoral positions VIRAL EVOLUTION AND DYNAMICS Department of Pathology University of California San Diego

DESCRIPTION: Up to two fully funded postdoctoral

position (up to two years in the first instance) will be available starting immediately to work on the evolution and dynamics of human immunodeficiency virus (HIV).

RESEARCH GROUP: The position is based in the laboratory of Dr. Simon Frost (http://-www.hivevolution.org, http://www.hivevolution.org,). In this group, the successful candidate(s) will interact with Dr. Sergei Kosakovsky Pond (http://-www.hyphy.org/sergei/) in developing, implementing and applying cutting edge statistical methods for the analysis of viral sequence data (e.g. using the HyPhy package) and the dynamics of escape of HIV from neutralizing antibodies. There is the potential to develop and co-supervise undergraduate and graduate research projects.

LOCATION: University of California, San Diego. The position is based at the Antiviral Research Center (http://www.avrctrials.org), situated in the Hillcrest area (http://www.hillquest.com) near downtown San Diego.

REQUIREMENTS: A Ph.D. in statistics, population genetics, mathematical or computational biology, or similar. Evidence of research productivity as indicated by scholarly publications is required. Sound skills in C/C++ programming, algorithms and methods and the analysis of sequence and/or population dynamic data are a prerequisite. Familiarity with parallel (SMP) and distributed (MPI) computing environments are preferred. Experience in advanced statistics (random effects models, Markov Chain Monte Carlo approaches) a plus. Evidence of strong communication and teamwork skills is highly desired.

APPLICATION: Please send letter of interest, C.V., and the names and contact details of three referees by June 15th, 2005 to: Postdoctoral Position in Viral Evolution and Dynamics, Dr. Simon Frost, UCSD Antiviral Research Center, 150 W. Washington St., San Diego CA 92103, USA. Electronic application materials (PDF, Word) are preferred - please email to sdfrost at ucsd.edu. Review of applications will begin immediately, and continue until the positions are filled.

sdfrost@ucsd.edu sdfrost@ucsd.edu

UCambridge ViralPhylodynamics

Postdoctoral Research Associate, Center for Infectious Disease Dynamics, Penn State University and Depart-ment of Zoology, University of Cambridge.

Phylodynamics of avian influenza

Supervisors, Drs Bryan Grenfell and Eddie Holmes Further particulars

A Postdoctoral Research Associate is required to work on a project funded by the UK Biotechnology and Biological Sciences Research Council. The RA will use mathematical and statistical approaches to study the epidemiological and evolutionary dynamics of avian influenza, at within-host and population levels. Work will be divided between Pennsylvania State University and Cambridge. Collaborative partners also include the Institute of Animal Health, Compton, and the Veterinary Laboratories Agency, Weybridge, where novel experimental infection data are being collected.

Candidates should have a PhD in a quantitative subject; a strong background in one or more of the following would be desirable: stochastic dynamical systems, phylogenetics, virology.

Salary will be on the RA1A scale (£19,460- £29,127 pa). The appointment will be for up to four years, subject to satisfactory completion of a six month probationary period. Two emailed references will be required.

Please email a letter of interest and CV by June 15, 2005 to: Grenfell@psu.edu Short-listed candidates will be contacted for further details. Short-listed candidates will be contacted for further details.

UCorkIreland PlantEvoGenomics

UCorkIreland.PlantEvoGenomics

SFI Post Doctoral Fellow : Functional evolutionary genomics (Arabidopsis)

We are seeking an enthusiastic & highly motivated Postdoctoral Fellow to join our research team working on epigenetics and reproduction. Our lab employs a combination of molecular biology, functional genomics, evolutionary bioinformatics and genetics to study basic and applied aspects of reproduction. (www.ucc.ie/-spillane). The successful applicant will work on a 3 year SFI-funded project on elucidating processes of evolutionary birth & death of plant genes, using Arabidopsis as a model for functional evolutionary genomics. The project is funded by Science Foundation Ireland and involves collaboration with Karl Schmid

(Max Planck ICE, Jena), Ken Wolfe (Trinity College Dublin) and Dolores Cahill (National Centre for Proteomics, Dublin). The starting gross salary for the SFI Postdoctoral Fellow will 33,000 euros per annum. We are seeking candidates that can effectively combine molecular evolutionary analysis with wet lab functional genomics approaches in Arabidopsis. Candidates with proven experience in molecular evolution, bioinformatics (e.g. programming in C, Perl, Python), Arabidopsis developmental genetics & evolutionary genetics are particularly encouraged to apply. Applicants should send an e-mail outlining your research interest and motivations, including; (a) your C.V. (please list publications and experimental skills) & (b) contact details and e-mail addresses for 3 referees to:

Dr. Charles Spillane, Biochemistry Dept & Biosciences Institute, University College Cork, Cork, Ireland. E-mail: c.spillane@ucc.ie

Deadline: 10th June 2005 UCC is an equal opportunities employer

Dr. Charlie SPILLANE, SFI Investigator, Dept of Biochemistry & Biosciences Institute, University College Cork (UCC), 2.10, Lee Maltings, Cork, IRELAND

[T] 00-353-21-4904124 (office) [E] c.spillane@ucc.ie [W] www.ucc.ie/ucc/depts/biochemistry/-staff/cspillane.html "Spillane, Charles" <C.Spillane@ucc.ie>

UGeorgia EvolBiol

Postdoc: Evolution Biology, Univ. Georgia

A post-doctoral position is available in the Promislow lab at the University of Georgia. Current projects include empirical work on the impact of gene interactions on fitness in Drosophila, computational studies of yeast networks, and theoretical models (for more information on the lab, see http://mango.ctegd.uga.edu/-PromislowLab/homepage.html). Funding is available for at least two years. The ideal candidate will have a background in evolutionary biology, with research experience in population or quantitative genetics, molecular evolution and/or mathematical modeling. Start date is flexible, with salary depending on qualifications.

Interested applicants should send a CV, the names of three references, and an informal cover letter (preferably via email) to Daniel Promislow, promislow@uga.edu, no later than May 27, 2005 (by snail mail:

Department of Genetics, University of Georgia, Athens GA 30602-7223).

UGA has an outstanding group of evolutionary biologists (http://www.genetics.uga.edu/evolution/-evoluga.html). Athens is an attractive, inexpensive place to live, with the thriving culture of a 200-year-old university town, and Atlanta, the mountains and the coast are all within driving distance. For more info on life in Athens, see http://www.flagpole.com . Daniel Promislow <promislow@uga.edu>

ULaval DNABarcodes Fish

Postdoctorate position: DNA Barcodes for the Freshwater Fishes of Canada

We are currently looking for a postdoctorate candidate to get involved in our research contribution to the Canadian Barcode of Life Network (BOL.ca) that has recently launched efforts to assemble a DNA barcode library for all Canadian eukaryotes. Involving more than 50 researchers, BOL.ca represents the world's first national barcode network.

The candidate will be responsible for collecting (through both field sampling and collaborations) and DNA barcoding representative specimens of all Canadian freshwater species. Depending on the candidate's interest and expertise, the project may potentially extend to several ramifications, including the coverage of all North American freshwater species, the comparative phylogeography of multiple taxa, the comparison of evolutionary rates among genes and species, etc.

Candidates for this position must possess a Ph.D. in the biological sciences. We are primarily interested in finding a strong candidate with experience in fish biology, particularly involvement in faunal surveys and/or taxonomy, as well as experience in molecular systematics. Additional skills and expertise in molecular evolution and bioinformatics would also be advantageous assets.

The position is available now and will be offered for one year with a possibility of extending to two more years, depending on availability of funding.

To apply, please send a cover letter describing your research interests, a complete CV and names of three references by e-mail to <mailto:Louis.Bernatchez@bio.ulaval.ca>Louis.Bernatchez@bio.ulava

To learn more about Québec city : <http:/-

/www.quebecregion.com/e/index.asp>http:/-
/www.quebecregion.com/e/index.asp Laval
University <http://www.ulaval.ca/>http://-
www.ulaval.ca/ and its Biology department :
<http://www.bio.ulaval.ca/index-alt.html>http:/-
/www.bio.ulaval.ca/index-alt.html The Cana-
dian Research Chair in Conservation Genetics of
Aquatic Resources: <http://www.bio.ulaval.ca/-
louisbernatchez/>http://www.bio.ulaval.ca/-
louisbernatchez/ Canadian Barcode of Life Net-
work (BOL.ca): <http://www.barcodinglife.com/-
>http://www.barcodinglife.com/ Consortium for the
Barcode of Life (CBOL) <http://barcoding.si.edu/-
index_detail.htm>http://barcoding.si.edu/-
index_detail.htm Louis Bernatchez, Titulaire de
la Chaire de recherche du Canada en conservation
génétique des ressources aquatiques Département
de biologie, Pavillon Vachon, Université Laval,
Sainte-Foy, QC G1K 7P4 Canada Phone: 1 418
656-3402 Fax: 1 418 656-2043 E-mail : Couriel:
<mailto:Louis.Bernatchez@bio.ulaval.ca>Louis.Bernatchez@bio.ulaval.ca
Web: <http://www.bio.ulaval.ca/louisbernatchez/-
>http://www.bio.ulaval.ca/louisbernatchez/
louis.bernatchez@bio.ulaval.ca

UMontreal Hybridization

Hybridization and reticulation in phylogenetic analyses

Project summary: Hybridization is recognized as a fre-
quent and important phenomenon in the evolution of
angiosperms, but also is thought to have played an im-
portant role in the evolution of animals. The methods
of phylogeny reconstruction commonly used in system-
atics represent evolution as strictly dichotomous and
thus do not permit a reliable reconstruction of the phy-
logeny of taxa of hybrid origin. New methods have been
developed to integrate and better represent the position
of hybrid taxa, but these are not commonly used by
biologists and their effectiveness remains to be tested.
In a collaborative project between botanists and zool-
ogists, we are examining the effect of including hybrids
in phylogenetic analyses of plants and animals through
an experimental and theoretical approach.

Objectives: As part of this project, we are searching for
a postdoctoral fellow to participate actively in the fol-
lowing objectives: 1, evaluate the relative performance
of different reticulistic methods for detecting hybrids; 2,
compare through simulations methods for representing
reticulations; 3, establish criteria that will allow the

selection of the best methods for either detection or
representation and for the type of data available (mor-
phological or molecular, characters or distances, uni-
parental or biparental markers, etc.); and 4, develop
new and effective reticulistic methods for detecting and
representing hybrid taxa.

Research team: Bernard Angers, Luc Brouillet, Anne
Bruneau, Franois-Joseph Lapointe, Pierre Legendre of
the Département de sciences biologiques and the Insti-
tut de recherche en biologie végétale at the Université
de Montréal.

For more information, contact Anne Bruneau
(anne.bruneau@umontreal.ca, 514-872-
7301) or Franois-Joseph Lapointe (francois-
joseph.lapointe@umontreal.ca, 514-343-7999).

bernard.angers@umontreal.ca

UNeuchatel GrapeGenetics

Post Doctoral position: grape genetics, microsatellites,
database

A postdoctoral position (duration: 12 months) is avail-
able at University of Neuchâtel to carry out the Swiss
Vitis Microsatellite Database project. The aim is to
set up a harmonised database containing microsatel-
lite data of all grape varieties, rootstocks and wild
grapevines present in Switzerland. Nearly 150 varieties
will be genotyped using at least 6 microsatellite mark-
ers. Allele sizes will be standardised according to re-
cent recommendations of the international community.
These data will be made available to the public via a
searchable internet database.

We are seeking a highly motivated candidate with a
Ph.D. in biology, having good experience in microsatel-
lite genotyping and database development. Good
knowledge of data processing and informatics is rec-
ommended.

Applications including letter of motivation, CV, list
of publications, and contact details of three referees
should be submitted by June 17, 2005 to the address
below. Starting date is July 1 or later, 2005 for 12
months. Salary according to Swiss SNF standards.

Dr. Claire Arnold, Coordinator University of Neucha-
tel National Centre of Competence in Research "Plant
Survival" Rue Emile Argand 11 CH - 2007 Neuchatel,
Switzerland

Tel.: +41 (0)32 718 2503 Fax: +41 (0)32 718 2501 email: claire.arnold@unine.ch; website: http://-www.unine.ch/nccr <http://www.unine.ch/nccr> Dr. Claire Arnold, Coordinator University of Neuchatel National Centre of Competence in Research "Plant Survival" Rue Emile Argand 11 CH - 2007 Neuchatel, Switzerland

Tel.: +41 (0)32 718 2503 Fax: +41 (0)32 718 2501 email: claire.arnold@unine.ch; website: http://www.unine.ch/nccr Arnold Claire <Claire.Arnold@unine.ch>

UOxford EvolRNAViruses

POSTDOC IN VIRAL EVOLUTION, DEPARTMENT OF ZOOLOGY, UNIVERSITY OF OXFORD

Postdoctoral Research Assistant, Academic-Related Research Staff Grade 1A Salary range: £19,460 - £29,128 p.a.

Applications are invited for a postdoctoral research assistant, funded by the Wellcome Trust, to work on the evolutionary genetics of RNA viruses.The project represents a collaboration between Dr. Andrew Rambaut, University of Oxford, and Dr. Andrés Moya, University of Valencia, and will combine both phylogenetic and experimental approaches to the study of RNA virus evolution.This postdoctoral position will involve large-scale phylogenetic and population genetic analyses of a wide range of RNA viruses and willbe based in the Department of Zoology, Oxford.Experience in phylogenetics, simulation and computer programming are highly desirable.This position will run for 18 months and will start as soon as possible after the 1st September 2005.

Further particulars are available from general.office@zoo.ox.ac.uk or from the website: http://evolve.zoo.ox.ac.uk/jobs.html.Applications should be addressed to the Administrator, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS, enclosing contact details of three referees and quoting reference: AT05027.Informal enquiries to Dr. Andrew Rambaut, e-mail: andrew.rambaut@zoo.ox.ac.uk.The closing date for applications is Friday 27th May 2005.

– Andrew Rambaut, EMAIL - andrew.rambaut@zoo.ox.ac.uk Zoology Department, WWW - http://evolve.zoo.ox.ac.uk/ University of Oxford, TEL - +44 1865 271261 South Parks Road, Oxford, UK FAX - +44 1865 271249

andrew.rambaut@zoology.oxford.ac.uk

USouthernCalifornia OysterQuantGenetics

Postdoctoral Position: Quantitative Trait Loci Mapping in Oysters University of Southern California, Department of Biological Science, Marine Environmental Biology Section, Los Angeles, California

A post-doctoral position is available for two years, starting immediately (May 2005). Starting salary is approximately $38,500 (U.S.) per annum, depending on experience; USC offers an excellent benefits package.

The post-doctoral researcher will participate in a multi-disciplinary project funded by the NSF Biocomplexity in the Environment Initiative, "Genomic approaches to understanding variation in marine larval recruitment." This project combines the tools of physiological genomics and population modeling to investigate the complexity of biological factors affecting marine recruitment. Three hypothesis-driven research activities – gene mapping, gene-expression analysis, and mathematical population modeling – are each expected to advance knowledge of the endogenous and exogenous sources of variation in marine recruitment. The research of this post-doctoral researcher will focus on the first of these activities, utilizing existing F2 families and mapped microsatellite DNA markers (e.g. Launey & Hedgecock 2001 Genetics 159:255-265; Hubert & Hedgecock 2004 Genetics 168:351-362). Genetic variation in key physiological processes, such as larval growth and resistance to starvation, has previously been identified, and genes responsible for this variation are being revealed through comprehensive gene-expression profiling (Hedgecock et al. 2002. http://www.intl-pag.org/pag/10/abstracts/-PAGX_W15.html). Candidate genes regulating physiological processes will be mapped to verify their co-location with QTL.

Candidates should have a Ph.D. in population, quantitative, or statistical genetics, experience in high-throughput genotyping, and facility with bioinformatics. Review of applications will begin as they are received and continue until the position is filled. To apply, please first send a short e-mail to Dennis Hedgecock (dhedge@usc.edu), stating your interest and summa-

rizing your research experience and publication record (please do not send attachments). A subset of applicants will be invited to submit full CV's and the names of three references.

USC is an equal opportunity/ affirmative action employer.

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

dhedge@usc.edu

UTulsa ViralEvol

POSTDOCTORAL POSITION

Ecology and Evolution of a Bird-Borne Alphavirus

An NIH-funded postdoctoral position is available 15 August 2005 to study the population dynamics of Buggy Creek virus, an alphavirus associated with cliff swallows and their cimicid ectoparasites (see Proc. R. Soc. Lond. B 268, 1833, 2001). The position includes both field- and laboratory-based work and requires travel to and from performance sites in Nebraska and Oklahoma. Applicants should have a Ph.D. and background in phylogenetics. To apply, send a curriculum vita and names and addresses of three references to: Charles R. Brown, Department of Biological Sciences, University of Tulsa, 600 S. College Ave., Tulsa, OK. 74104, email: charles-brown@utulsa.edu

UWalesBangor MolEvolEcol2

Dear All

Please note that the initial posting of the below job advert contained an incorrect e-mail address for Prof. G.R. Carvalho. The following advert includes the correct e-mail address. Apologies for any confusion.

UNIVERSITY OF WALES, BANGOR

SCHOOL OF BIOLOGICAL SCIENCES

Postdoctoral Researcher in Molecular Ecology

R&A Grade 1A: £19,460 - £29,128 p.a.

Applications are invited for a Postdoctoral University-funded three-year post in the School of Biological Sciences, University of Wales, Bangor, working with Professor G. R. Carvalho and members of a newly established Group focusing on the molecular ecology of aquatic animals and fisheries genetics. The appointee will join a team using molecular markers to investigate the origins and significance of population and species biodiversity. In 2006 the Group will transfer to the new Environment Centre whose remit will be to provide a high-profile hub for co-ordinating strategic research and training in the environmental sciences sector in Wales. In addition to independent research, the appointee will assist in the development of the new Group including submission of research grant applications and the management of projects and research students.

Applicants should possess a PhD in molecular ecology or associated areas, with some postdoctoral experience, together with a strong commitment to timely publication and collaborative research. Although applications are welcomed from those working in any area of molecular ecology, research interests and experience in environmental genomics and/or quantitative genetics within an evolutionary context are especially encouraged.

Application forms and further particulars should be obtained by contacting Human Resources, University of Wales, Bangor, Gwynedd LL57 2DG; tel: (01248) 382926/388132; e-mail: personnel@bangor.ac.uk

Please quote reference number 05-4/180 when applying.

Closing date for applications: Friday 3rd June, 2005.

Informal enquiries can be made by contacting Professor Gary Carvalho, e-mail: g.r.carvalho@bangor.ac.uk or tel: +44 (0)1248382100.

Committed To Equal Opportunities

"S.Creer" <bssa0d@bangor.ac.uk>

UppsalaU 5 EvolGenomics

5 POST-DOCS TO CENTRE OF EXCELLENCE IN EVOLUTIONARY GENOMICS

The Swedish Research Council has recently funded a Centre of Excellence in Evolutionary Genomics, headed by Siv Andersson and Hans Ellegren, at the Evolutionary Biology Centre of Uppsala University (Department of Evolution, Genomics and Systematics). The Centre combines research at the prokaryotic as well as the

eukaryotic level on general topics such as molecular evolution, genome evolution and transcriptome evolution. The Centre will now recruit five enthusiastic and competitive post-docs broadly within the two areas indicated below.

1. The research group of Siv Andersson studies how microbial genomes evolve, using the alpha-proteobacteria as the main model system. The current research focus is on comparative genome analyses of bacteria that are endosymbionts of insects or pathogens of humans, animals and plants. In one project, we use microarray hybridizations to study clinical and environmental isolates of Bartonella. In another project, we study Wolbachia, a manipulator of sex ratios in insect populations. Metagenomic studies of environmental samples will also be initiated. The overall aim is to determine the flow of genes within and among lineages so as to develop models describing microbial genome evolution. Suitable background may be in microbial genomics, bioinformatics, or molecular evolution.

Informal inquiries and applications relating to this research should be addressed to Prof. Siv Andersson (Siv.Andersson@ebc.uu.se) See also http://www.egs.uu.se/molev/staff/siv.html 2. The research group of Hans Ellegren studies how evolutionary forces such as mutation and selection shape DNA sequence evolution in higher organisms. Planned research, mainly focusing on birds (chicken as well as natural populations of wild species) include studies of male-biased mutation, the rate and pattern of insertion-deletion mutations, biased gene conversion and isochore evolution, microsatellite evolution, sex chromosome evolution, studies of the efficacy of selection in different parts of the genome, linkage disequilibrium and linkage mapping in natural populations, and analysis of chicken expression data. The precise projects are flexible and will depend on the interests and skills of the successful candidates. Suitable background may be in molecular evolution, bioinformatics, or population genetics.

Informal inquires and applications relating to this research should be addressed to Prof. Hans Ellegren (Hans.Ellegren@ebc.uu.se) See also http://www.egs.uu.se/evbiol/ The Evolutionary Biology Centre (www.ebc.uu.se) is situated in recently-built localities in central Uppsala and is equipped with facilities for large-scale sequencing, genotyping and expression analysis. The working atmosphere is international with a regular recruitment of post-docs from abroad. The Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 400 scientists and graduate students, with research programs in ecology, systematics,

genetics, genomics, functional genomics and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated close to Stockholm.

Please include with the application a full CV, a statement of research interests and the name and address of at least two referees. The positions are initially for two years, with possibilities for prolongation after this period.

– Professor Hans Ellegren Dept of Evolutionary Biology Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

Email: Hans.Ellegren@ebc.uu.se Phone: +46-18-4716460 Fax: +46-18-4716310

Lab home page: http://www.egs.uu.se/evbiol/index.html My home page: http://www.egs.uu.se/evbiol/Persons/Hans.html My home page: http://www.egs.uu.se/evbiol/Persons/Hans.html

UppsalaU 5 EvolGenomics 2

The somewhat weird format of the first posting of this ad meant that it did not read well - sorry. Here's a new try. / Hans

5 POST-DOCTORAL POSITIONS IN EVOLUTIONARY GENOMICS

The Swedish Research Council has recently funded a Centre of Excellence in Evolutionary Genomics, headed by Siv Andersson and Hans Ellegren, at the Evolutionary Biology Centre of Uppsala University (Department of Evolution, Genomics and Systematics). The Centre combines research at the prokaryotic as well as the eukaryotic level on general topics such as molecular evolution, genome evolution and transcriptome evolution. The Centre will now recruit five enthusiastic and competitive post-docs broadly within the two areas indicated below.

MICROBIAL GENOMICS

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Informal inquiries and applications relating to this research should be addressed to Prof. Siv Andersson (Siv.Andersson@ebc.uu.se). See also http:/-/www.egs.uu.se/molev/staff/siv.html   AVIAN GENOMICS

2. The research group of Hans Ellegren studies how evolutionary forces such as mutation and selection shape DNA sequence evolution in higher organisms. Planned research, mainly focusing on birds (chicken as well as natural populations of wild species) include studies of male-biased mutation, the rate and pattern of insertion-deletion mutations, biased gene conversion and isochore evolution, microsatellite evolution, sex chromosome evolution, studies of the efficacy of selection in different parts of the genome, linkage disequilibrium and linkage mapping in natural populations, and analysis of chicken expression data. The precise projects are flexible and will depend on the interests and skills of the successful candidates. Suitable background may be in molecular evolution, bioinformatics or population genetics.

Information inquiries and applications relating to this research should be addressed to Prof Hans Ellegren (Hans.Ellegren@ebc.uu.se). See also http://-www.egs.uu.se/evbiol/ The Evolutionary Biology Centre (http://www.ebc.uu.se) is situated in recently-built localities in central Uppsala and is equipped with facilities for large-scale sequencing, genotyping and expression analysis. The working atmosphere is international with a regular recruitment of post-docs from abroad. The Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 400 scientists and graduate students, and with research programs in ecology, systematics, genetics, genomics, functional genomics, and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated close to Stockholm.

Please include with the application a full CV, a statement of research interests and the name and address of at least two referees. The positions are initially for two years, with possibilities for prolongation after this period. – Professor Hans Ellegren Dept of Evolutionary

Biology Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

Email: Hans.Ellegren@ebc.uu.se Phone: +46-18-4716460 Fax: +46-18-4716310

Lab   home   page: http://www.egs.uu.se/evbiol/-index.html My home page: http://www.egs.uu.se/-evbiol/Persons/Hans.html   Hans.Ellegren@ebc.uu.se Hans.Ellegren@ebc.uu.se

UppsalaU EvolPopGenet

A Post Doctoral researcher position is immediately available at the Linnaeus Center for Bioinformatics in Uppsala, Sweden (http://www.lcb.uu.se). The post is initially for one year but with a possibility for a prolongation to two years.

The successful applicant will join a multidiciplinary research team focusing on dissection of the genetic architecture of complex traits. We have been able to show that epistasis is important in the regulation of complex traits. Our future goal is to improve our understanding of epistasis and to understand the consequences of different kinds of genetic architecture on selection response and evolution. We are therefore looking for a Post-doctoral researcher to join our group in a project where we are investigating the population genetic impact of the epistatic interactions.

In our previous research we have developed methodology for large scale screening for epistatic QTL involved in regulating complex trait expression. These tools have been used to study the importance of epistasis in phenotypic evolution using data from divergent crosses between domesticated animals. We have e.g. explored the role of epistasis in domestication using a cross between wild and domesticated species and in directional selection using data from an intercross between two divergent selection lines resulting from a long term bi-directional selection experiment. Further information and references can be found on http://-www.orjancarlborg.com . A successful applicant should have relevant scientific education (Ph.D. degree or similar) and an interest in Quantitative-, Population- and Evolutionary Genetics. A strong mathematical / statistical background and programming experience is an advantage.

Salary and conditions of employment are under the terms of the current agreement for academic scientists

employed in the public sector.

Application: The position remains open until a successful candidate has been selected. Submit a letter of interest by email including CV, experience, qualifications, list of publications, and names, addresses and telephone numbers of two references to: Orjan.Carlborg@lcb.uu.se

WellingtonNZ PlantMolSyst

PLANT MOLECULAR SYSTEMATIST

The Museum of New Zealand Te Papa Tongarewa is seeking a plant molecular systematist to undertake research on New Zealand and Australian species of the flowering plant genus Chionohebe. The successful applicant will be expected to conduct molecular biological investigations, specifically DNA sequencing and AFLP, on existing collections of this genus. The aim is to determine the phylogenetic and biogeographic relationships of the different species, and provide a basis for future taxonomic revision.

The position will be based at Te Papa in Wellington, but will use facilities at Victoria University to conduct the research. The work is funded by the Foundation for Research Science and Technology as part of the OBI Defining New Zealand's Land Biota being conducted in partnership by Landcare Research and Te Papa.

The position is for a one-year fixed term agreement.

Visit   http://www.tepapa.govt.nz/TePapa/English/-AboutTePapa/CareersAtTePapa/   to   view   a   job description and to apply online for this position.

Applications close 3 June 2005.

Leon Perrie, Curator of Botany, leonp@tepapa.govt.nz

LeonP@tepapa.govt.nz LeonP@tepapa.govt.nz

WorkshopsCourses

Berlin EvolNetworksRegulation Aug26-Sep4

Dear colleague,

we are happy to announce the

Otto Warburg International Summer School and Workshop on Networks and Regulation.

August 26 to September 4, 2005

Berlin, Germany

The aim of this program is to bring together researchers and students from different backgrounds (including molecular biology, bioinformatics, biological physics) to discuss Networks and Regulation, a topic of high current interest on the interface between statistical physics and biology. We plan an integrated program, which is focused on high-level training during the first days and leads to topical research seminars in the second part.

We will discuss ideas and approaches both from physics and biology. The goal is to promote a joint effort and establish a common ground to approach problems in this emerging field of research. The schedule will leave sufficient time for discussion and interaction among students and lecturers.

Confirmed speakers:

David Arnosti - East Lansing Alvis Brazma - Hinxton Harmen Bussemaker - New York Wolfgang Huber - Hinxton Terence Hwa - San Diego Eric van Nimwegen - Basel Luca Peliti - Napoli Nikolaus Rajewski - New York Roded Sharan - Berkeley Denis Thieffry - Marseille Michael Zhang - Cold Spring Harbor

Scientific Coordinators:

Peter Arndt - Berlin Michael Lässig - Cologne Martin Vingron - Berlin

The deadline for applications is June 5, 2005. The registration fee of 600 EUR includes costs for accommodation and meals. The registration fee for PhD and Masters students is 400 EUR (or 100 EUR without accomodation).

Application forms can be filled in online on the workshop's website at

http://ows.molgen.mpg.de   The announcement as a printable poster is available from

http://ows.molgen.mpg.de/poster.pdf   For further questions please contact

Hannes Luz c/o Max Planck Institute for Molecular Genetics Computational Molecular Biology Ihnestrasse 73 D-14195 Berlin, Germany Tel: +49 30 8413 - 1154 Fax: +49 30 8413 - 1152 Email: luz@molgen.mpg.de

Best regards,

the Otto Warburg Summer School team

luz@molgen.mpg.de

MBL TIGR GenomeTechnologyBioinformatics Oct4-30

Advances in Genome Technology and Bioinformatics Course Marine Biological Laboratory & The Institute for Genome Research October 4 - October 30, 2005

http://www.mbl.edu/education/courses/-special_topics/genome.html   A comprehensive, four-week course in Genome Science that will integrate Bioinformatics with the latest laboratory techniques for genome sequencing, genome analysis, and high throughput gene expression (DNA microarrays). A distinguished faculty from major universities, bioinformatic centers, The Institute for Genomic Research and

the Marine Biological Laboratory will train students including postdoctoral students, graduate students and established PI's. This cutting-edge course will integrate a series of lectures with laboratory exercises both at the computer and in a high technology, high throughput facility. Limited to 24 students.

The major instructional modules include (1) Genome Sequencing (vector development, library construction, high throughput sequencing technologies, principles of automation using advanced robotic liquid handlers, genome assembly algorithms and closure strategies); (2) Bioinformatics (Gene prediction algorithms,annotation, database construction and searching, phylogenetics and molecular evolution); and (3) Functional Genomics (DNA microarrays, data analysis). In addition, we will sponsor symposia in topical areas in genome science. Examples of symposia to be offered include: Advances in genome assembly; Genomes and development; Genome science and environmental biology; Genome evolution; Impact of genome science on Drug design; etc. The breadth of topics in genome science and the advanced training based upon advanced laboratory technology, distinguish this course from all other offerings.

Directors: Claire M. Fraser, The Institute for Genomic Research Mitchell L. Sogin, The Marine Biological Laboratory, Woods Hole.

2004 Course Faculty: Tove Andersson, The Institute for Genomic Research Claudia Bertonati, Columbia University Nirmal Bhagabati, The Institute for Genomic Research Shanda Birkeland, The Marine Biological Laboratory Gary Churchill, The Jackson Laboratory Michael Cipriano, The Marine Biological Laboratory Jonathan Eisen, The Institute for Genomic Research Tamara Feldblyum, J. Craig Venter Science Foundation Rich Fox, The Marine Biological Laboratory Claire Fraser, The Institute for Genomic Research Renee Gaspard, The Institute for Genomic Research Robert Gentleman, Harvard School of Public Health John Gill, J. Craig Venter Science Foundation Steve Gill, The Institute for Genomic Research Leslie Graham, The Marine Biological Laboratory Kasia Hammar, The Marine Biological Laboratory Eric P. Hoffman, Children's National Medical Center David Jaffe, Broad Institute Patrick Keeling, University of British Columbia Ewen Kirkness, The Institute for Genomic Research Norman Lee, The Institute for Genomic Research Wei Liang, The Institute for Genomic Research William Majoros, The Institute for Genomic Research Andrew McArthur, The Marine Biological Laboratory Hilary Morrison, The Marine Biological Laboratory William Nierman, The Institute for Genomic Research Gary J. Olsen, University of Illinois Bert Olsson, The Marine Biologi-

cal Laboratory William Pearson, University of Virginia Scott Peterson, The Institute for Genomic Research Mihai Pop, The Institute for Genomic Research Marco Punta, Columbia University John Quackenbush, The Institute for Genomic Research Alexander Saeed, The Institute for Genomic Research Steven Salzberg, The Institute for Genomic Research Vasily Sharov, The Institute for Genomic Research Mitchell Sogin, The Marine Biological Laboratory Luke Tallon, The Institute for Genomic Research Herve Tettelin, The Institute for Genomic Research Andy Tolonen, Massachusetts Institute of Technology Joseph White, The Institute for Genomic Research Owen White, The Institute for Genomic Research

mcarthur@mbl.edu mcarthur@mbl.edu

Roscoff EnvironmentalGenomics Sep3-9

Please, could you post the following:

You can still register (deadline extended) at http://-/genomique-environnementale.univ-rennes1.fr/ at the Course in Residence "Hight Throughput Methods of Molecular Biology in Environmental Sciences" that will take place in Roscoff (western Brittany, France) 3 - 9 september 2005. The program includes seminars, discussions and workshops on ENVIRONMENTAL GENOMICS, COMPARATIVE AND EVOLUTIONARY GENOMICS, FUNCTIONAL GENOMICS AND ECOSYSTEM FUNCTIONING, FUNCTIONAL GENOMICS AND ADAPTATION, POPULATION GENOMICS AND HIGH-THROUGHPUT GENETICS

Invited speakers: Thierry Heulin (CNRS/CEA, Cadarache, France) Francis Martin (INRA, Nancy, France) Rama Singh (McMaster, Hamilton, Canada) Olivier Poch (CNRS, Strasbourg France) Peter Young (University of York, UK) Eric Allen (Berkeley, USA) Pierre Pontarotti (Univ. de Provence, France) Jonathan Wendel (Iowa State University, USA) Malika Ainouche (UMR Ecobio, CNRS Univ. Rennes, France) Jean Weissenbach, Abdelghany Sghir or Denis Le Paslier (Génoscope & CNRS, Evry France) Oded Beja (Technion, Haifa, Israel) Virginie Chapon (CNRS/CEA, Cadarache, France) Yutaka Kawarabayasi (Tsukuba, Japan) Jean-Michel Danger (Univ. du Havre, France) Vincent Colot (CNRS, Evry, France) Frédérique Viard or Didier Jollivet (CNRS Roscoff, France)

Pierre Taberlet (CNRS, Grenoble, France) Ana Caicedo (North Carolina State University, Raleigh)

A provisional program is presented in the attached pdf file

M. L. AINOUCHE Evolution des Genomes et Speciation, Dpt Ecologie Evolutive UMR CNRS 6553 Ecobio, Universite de Rennes 1 Campus Scientifique de Beaulieu, Bat. 14A 35 042 Rennes Cedex France Ph. 33 (0)2 23 23 51 11 Fax 33 (0)2 23 23 50 47

malika.ainouche@univ-rennes1.fr

Instructions

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LATEX files, Excel files, etc. ...plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LATEX do not try to embed LATEX or TEX in your message (or other formats) since my program will strip these from the message.