
E v o l D i r

July 1, 2006

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

Forward

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

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

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



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Halifax SMBE June24-28 2007

SMBE ANNUAL MEETING—June 24-28, 2007

You are invited to attend the 2007 Annual Meeting of the Society for Molecular Biology and Evolution (SMBE), to be held at Dalhousie University in Halifax, Nova Scotia, Canada, June 24-28. The meeting will be held in conjunction with the Evolutionary Biology Program of the Canadian Institute for Advanced Research.

Meeting Organizers:

John Archibald, Ford Doolittle & Wanda Danilchuk
Department of Biochemistry and Molecular Biology,
Dalhousie University

Information about speakers, registration, travel, accommodation, etc. will be available shortly at the SMBE website:

<http://www.smbc.org/> — John M. Archibald, Ph.D.
Genome Atlantic and CIAR Evolutionary Biology Program
Department of Biochemistry and Molecular Biology
Dalhousie University Sir Charles Tupper Medical
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(902) 494-1355 Archibald Lab Webpage: <<http://myweb.dal.ca/jmarchib/>> —

John Archibald <jmarchib@dal.ca>

Hinxton GenomeInformatics Sept13-17

The next Genome Informatics meeting will be held in the United Kingdom at the Wellcome Trust Genome Campus in Hinxton. It will begin on Wednesday evening, September 13, and conclude after lunch on Sunday, September 17. More information can be found at <http://meetings.cshl.edu/meetings/infouk06.shtml>

At this meeting, Jeffrey Boore and Nick Goldman will be leading a session on “Comparative and Evolutionary Genomics” that may be of interest to evolutionary biologists. Abstracts can be submitted at the website with a deadline of June 21.

Jeffrey L. Boore, Ph.D. Evolutionary Genomics Program
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Drive Walnut Creek, CA 94598

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Associate Adjunct Professor Department of Integrative
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of California Berkeley, CA 94720

jllboore@calmail.berkeley.edu

HongKong Bioinformatics Jan15-17

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SECOND CALL FOR PAPERS (APBC 2007) Asia-Pacific Bioinformatics Conference, APBC2007, will be held in Hong Kong during 15 - 17 January 2007. See <http://www.cs.hku.hk/apbc2007> . The Asia-Pacific Bioinformatics Conference series is an annual forum for exploring research, development, and novel applications in bioinformatics. The aim of this conference is to bring together researchers, professionals, and industrial practitioners for interaction and exchange of knowledge and ideas. We invite submissions that address conceptual and practical issues of bioinformatics.

TOPICS OF INTEREST Typical, but not exclusive, topics of interest include:

Sequence analysis Motif Finding Recognition of Genes RNA Analysis Population genetics/SNP/Haplotyping Physical and Genetic Mapping Comparative Genomics, Genome rearrangements Evolution and Phylogeny Protein structure analysis Microarray design Proteomics Transcriptome, Gene Expression Pathways, Networks and Systems Databases and Data Integration Ontologies Text Mining Applications

IMPORTANT DATES Submission of papers: Jul 15, 2006 Notification of paper acceptance: Sep 15, 2006 Submission of posters: Sep 30, 2006 Camera-ready copy & Author registration: Oct 10, 2006 Notification of poster acceptance: Oct 20, 2006 Conference: Jan 15 - 17, 2007

CONFERENCE CHAIR Francis YL Chin, The University of Hong Kong, Hong Kong PROGRAM CHAIRS David Sankoff, The University of Ottawa Lusheng Wang, The City University of Hong Kong

PROGRAM COMMITTEE Tatsuya Akutsu, Miguel Andrade, Stephane Aris-Brosou, Joel Bader, Serafim Batzoglou, David Bryan, Jeremy Buhler, Peter Donnelly, Dannie Durand, Nadia El-Mabrouk, Robert Giegerich, Carole Goble, Concettina Guerra, Dan Gusfield, Michael Hallett, Sridhar Hannenhalli, Daniel Huson, Gavin Huttley, Jenn-Kang Hwang, Tao Jiang, Uri Keich, Anand Kumar, Tak Wah Lam, Doheon Lee, Jinyan Lim, Wentian Li, Guohui Lin, Michal Linial, Zhijie Liu, Bin Ma, Satoru Miyano, Laxmi Parida, Mark Ragan, Marie-France Sagot, Akinori Sarai, Vincent Schachter, Steven Skiena, Yun Song,

Robert Stevens, Alfonso Valencia, Michael Waterman, Ken Wolfe, Stacia Wyman, Hong Yan, Qiang Yang, Kaizhong Zhang, Liqing Zhang, Louxin Zhang

SUBMISSION GUIDELINES APBC2007 invites high-quality original papers on any topic related to Bioinformatics. Papers should be no more than 10 pages in length conforming to the formatting instructions for the series *Advances in Bioinformatics & Computational Biology* (instructions available at the APBC2007 website). Papers will be judged on originality, significance, correctness, and clarity. Authors should submit a PDF file according to the instructions on the APBC2007 Paper Submission Website. The full paper must be submitted by 15 July 2006. The proceedings will be published as a volume in the series *Advances in Bioinformatics & Computational Biology* by Imperial College Press. Expanded version of the selected papers will be invited for publication in the *Journal of Bioinformatics and Computational Biology*. Inclusion of a paper in the proceedings is contingent on one of the authors registering and presenting at the conference.

David Sankoff <sankoff@uottawa.ca>

InstZoolLondon Evol Sept8

LONDON EVOLUTIONARY RESEARCH NETWORK 4th ANNUAL CONFERENCE

8TH SEPTEMBER 2006 ZOOLOGY MEETING ROOMS INSTITUTE OF ZOOLOGY

****CALL FOR TALKS AND POSTERS****

If you are a post-graduate or post-doctoral student, working on any aspect of evolutionary research, you are welcome at our FREE, one day conference. If you would like to present a talk or poster, please submit a title and abstract (100-150 words) by 31st July 2006. Talk slots are usually booked, so early submission will increase chance of success. Contact Victoria Herridge (<<mailto:v.herridge@ucl.ac.uk>>v.herridge@ucl.ac.uk) or Emily Hornett (<<mailto:e.hornett@ucl.ac.uk>>e.hornett@ucl.ac.uk) to register and submit abstracts.

This years keynote speakers are Georgina Mace (Director, Institute of Zoology) and Steve Mithen (Head of the School of Human and Environmental Science, University of Reading).

Georgina Mace's research is in conservation biology, emphasising evolutionary, ecological and genetic as-

pects, for the formulation of conservation policy. She is particularly interested in the assessment and management of populations of threatened species, and in the dynamics of extinction pressures.

Professor Steven Mithen's research interests cover from the origin of Homo c.2 million years ago to the invention and spread of agriculture up to 5000 BC. His projects fall into three areas: Late Pleistocene and Early Holocene hunter-gatherers and early farmers, the evolution of the human mind, and computational archaeology. He has directed fieldwork in Western Scotland and is currently co-directing excavations in Wadi Faynan, southern Jordan. His authored books include *The Prehistory of the Mind* (1996) and *After the Ice* (2003), and he has edited volumes on *Human Creativity* (1998) and *Hunter-Gatherer Landscape Archaeology* (2001). Steve's latest publication is *The Singing Neanderthals: The Origins of Music, Language, Mind and Body*.

The conference is funded through the support of University College London, the Centre for Ecology and Evolution, Queen Mary University of London, The AHRC Centre for the Evolution of Cultural Diversity, and the Institute of Zoology. —

Nehal Saleh PhD Candidate School of Biological and Chemical Sciences Queen Mary- University of London London E1 4NS UK

<http://www.biology.qmul.ac.uk/research/staff/-chittka/chittkalab/Team/Nehal/Webpage-Nehal.htm>

Tel: 44 (0) 207 882 5555 Ext. 4169

n.saleh@qmul.ac.uk

JWGoetheU Hybridization Oct12-15

This is the first announcement of the symposium:

“Hybridization in Animals - Extent, Processes and Evolutionary Impact”

at the J.W. Goethe University, Frankfurt am Main, Germany, between Thursday, October 12 and Sunday, October 15, 2006.

In order to exchange ideas covering novel research approaches, new experimental and analytical techniques and results of empirical and theoretical studies on interspecific hybridization we invite you to contribute to the symposium. Our aim is to stimulate a broad and interdisciplinary discussion among ecologists, geneticists

and bioinformatic scientists, we invited a number of leading scientists in the field of interspecific hybridization.

Confirmed key-note lectures:

Michael L. Arnold - University of Atlanta

Eric C. Anderson - Southwest Fisheries Science Center, USA

Because of the limited size of the symposium we will only accept participants that contribute a poster or oral presentation. In total we will be able to host around 70 participants.

Please submit an abstract of maximum 250 words before July 24, 2006. Symposium fee will be EUR 200. For further information please check: www.hybridization.uni-frankfurt.de

Organization:

Klaus Schwenk Bruno Streit Nora Brede

Contact: n.brede@zoology.uni-frankfurt.de

Department of Ecology and Evolution Institute of Ecology, Evolution and Diversity Johann Wolfgang Goethe University Siesmayerstr. 70 D - 60323 Frankfurt Germany

n.brede@zoology.uni-frankfurt.de n.brede@zoology.uni-frankfurt.de

London PlantEvol Aug4

Plants, People and Evolution 4 August 2006 London

On 4 August 2006 the Linnean Society of London is hosting a one- day conference in honour of Dr Barbara Pickersgill, the geneticist and expert on Capsicum at Reading University, who retired in September 2005 after over 30 years teaching and research.

It's a rare opportunity to hear an international range of specialists in plant domestication, cytogenetics and taxonomy, reflecting Barbara's wide interests:

*Bruce Smith (USA) *Lagenaria siceraria*: Genetic and archaeological evidence for the early history of domesticated bottle gourd. *Duncan Vaughan (Japan) Rice, people & evolution: From prehistory to the biotechnology era *Giles Waines (USA) Domestication and Crop Physiology: Roots of a Green Revolution *Mark Nesbitt (Kew) Wheat domestication: a critical re-evaluation of its archaeology and genetics

*Jonathan Wendel (USA) Genes, jeans, and genomes: plant exploration and the wonders of cotton *Daniel Zohary (Israel) The impact of self-pollination on early crop domestication in the Near East *Alejandro Casas (Mexico) Evolutionary ecology of columnar cacti under domestication in Mesoamerica *Colin Hughes (Oxford) Backyard sympatry, spontaneous hybridisation and crop domestication in pre-Columbian Mexico insights from *Leucaena* (Leguminosae) *Spencer Barrett (Canada) The evolution of sexual diversity in Daffodils (*Narcissus*)

Registration fees are low (£25/£15) and include lunch and an evening reception. As it will be summer, cheap accommodation will be available at university halls of residence (details on reg. form).

Registration form and details at the Linnean Society website:

<http://pixbox.co.uk/linnean/-eventdetails.php?eventID=51> or <http://www.rbgekew.org.uk/scihort/ecbot/index.html> Contact: Mark Nesbitt (m.nesbitt@kew.org)

Dr Mark Nesbitt Jodrell Laboratory Royal Botanic Gardens Kew Richmond, Surrey TW9 3AE

Tel (direct): +44 (0)20 8332 5386 Fax: +44 (0)20 8332 5310

www.kew.org/scihort/ecbot www.plantcultures.org.uk
Mark Nesbitt <m.nesbitt@rbgekew.org.uk>

Lund Speciation Sept27-28

Dear all:

To honour the memory of the late animal ecologist Hans Kristiansson from Lund University, we invite members of the evolutionary biology community to a scientific symposium that will take place between September 27 (Wednesday) and September 28 (Thursday) 2006. The symposium will take place at the "Blue Hall" in the Ecology Building.

The theme of the symposium is Speciation: from diversification to reproductive isolation.

The symposium is intended to be a conceptually and taxonomically broad meeting, aimed to stimulate cross-disciplinary discussions. The target of the symposium will be the interface between genetic polymorphisms and ecological genetics at the intraspecific level and up

to the species level. We have invited a diverse group of speakers representing different research traditions, organisms and approaches (theoretical as well as empirical). This symposium is open also to researchers and PhD-students from universities in Sweden as well as those from other countries. For those who are interested, there will also be opportunities for short research presentations (15 minutes), in addition to the plenaries.

Invited speakers:

Scott Armbruster (University of Portsmouth, UK)

Ulf Dieckmann (Iiasa, Austria)

Kerstin Johannesson (Gothenburg University, Sweden)

Olle Leimar (Stockholm University, Sweden)

Ben C. Sheldon (Oxford University, UK)

Rhonda Snook (Sheffield University, UK)

Jon Ågren (Uppsala University, Sweden)

For more information see www.diversification.ecol.lu.se

Registration: gunilla.lindquist@zoekol.lu.se no later than August 31 2006. The symposium is cost-free, apart from an informal conference dinner on September 28, that will cost 100 SEK (to be paid upon arrival). Please indicate upon registration if you want to participate in the conference dinner, and/or if you would like to have a presentation.

Organizing committé: Roger Härdling, Åsa Lankinen, Jörgen Ripa, Erik Svensson

Symposium funding: "The Memory Fund of Hans Kristiansson" and the Sections for Animal Ecology, Theoretical Ecology and Plant Ecology and Systematics (Lund University).

Erik Svensson Associate Professor Section for Animal Ecology Ecology Building SE-223 62 Lund SWEDEN

Phone: +46 46 222 38 19 Mobile Phone: +46 0705 97 04 03 Fax: +46 46 222 47 16 erik.svensson@zoekol.lu.se

<http://www.biol.lu.se/zoekologi/epb/people-en/es-en/es-en.htm> "Nothing in biology makes sense, except in the light of evolution" (Theodosius Dobzhansky)

Erik Svensson <erik.svensson@zoekol.lu.se>

Lund Speciation Sept27-28 corrected

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For more information see www.diversification.ekol.lu.se

Registration: gunilla.lindquist@zoekol.lu.se no later than August 31 2006. The symposium is cost-free, apart from an informal conference dinner on September 28, that will cost 100 SEK (to be paid upon arrival). Please indicate upon registration if you want to participate in the conference dinner, and/or if you would like to have a presentation.

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Erik Svensson <erik.svensson@zoekol.lu.se>

Madrid ForestPopGenet Oct1-6 DeadlineExtended

Dear Friends and Colleagues,

We have extended the deadline for Abstract submission till 20th June. More information at the Conference web site at <http://www.genfor2006.fgua.es>. However, I encourage you to submit an Abstract as soon as possible: we have already received several communications and we might need to hire a bigger conference room, depending on the final number of attendants.

I hope to see you at Madrid in October,

Santiago

Santiago C. González-Martínez 'Ramón y Cajal' Research Fellow Unit of Forest Genetics Department of Forest Systems and Resources Center of Forest Research (CIFOR-INIA) Carretera de La Coruña km 7.5 28040 Madrid (Spain) Ph +34 913471499 Fax +34 913572293 e-mail santiago@inia.es

Personal: www.genpopevol.arrakis.es/scgonzalez.htm
INIA: www.inia.es GENFORED (Spanish Network on Forest Conservation Genetics): <http://www.inia.es/-gcont/redestem/centrosydep.jsp?idcentro=69&tema=relint>

"Santiago C. González Martínez" <santiago@inia.es>

Marseilles 10EvolBiol Sep20-22 Deadline

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

Deadlines registrations: 30th June, 2006! This is in 4 days!!

Registration form, Abstract and Payment are due before saturday (wednesday 24:00).

First round accepted abstracts are on line.

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

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

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

Nadège Bardiou Logistical Organisation Committee EA 3781 Evolution Biologique Université d'Aix Marseille I - case 19 Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 <http://www.up.univ-mrs.fr/evol> We are organizing the 10th Evolutionary Biology Meeting at Marseilles <http://www.up.univ-mrs.fr/evol-cgr/> egee@up.univ-mrs.fr

MissouriBotanicalGarden Systematics

50th Annual Systematics Symposium of the Missouri Botanical Garden, Species Reconsidered: Consequences for Biodiversity and Evolution.

<http://www.mbgpress.info/index.php?task=id&id=11001>

Thank you for your assistance,

Monica Anderson

MBG Press Assistant P.O. Box 299 St. Louis, MO 63166-0299 USA Ph:314-577-9547 Fax: 314-577-9594 Email:adele.niblack@mobot.org www.mbgpress.org
New title from MBG Press A Tour of the Flowering Plants Based on the Classification System of the Angiosperm Phylogeny Group by Priscilla Spears <http://www.mbgpress.info/index.php?task=id&id=06031>

Adele Niblack <adele.niblack@mobot.org>

Montreal RECOMB ComparativeGenomics Sep24-26 DeadlineExtension

Fourth Annual RECOMB Satellite Meeting on Comparative Genomics September 24-26, 2006, Montreal, Canada

EXTENSION OF SUBMISSION DEADLINE:

Due to numerous requests, we are extending the deadline for submissions until Friday June 9. Notification of acceptance or rejection delayed until June 28.

MEETING WEBSITE: <http://www.crm.umontreal.ca/Genomics06/> ORGANIZERS: Guillaume Bourque, Genome Institute of Singapore, Singapore Nadia El-Mabrouk, University of Montreal, Montreal, Canada Jens Lagergren (Stockholm Bioinformatics Centre & KTH) Aoife McLysaght (Trinity College Dublin) David Sankoff (University of Ottawa)

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

Expanded versions of conference papers will be invited for submission to a special issue of the Journal of Computational Biology.

Papers should be submitted via the EasyChair system. Submissions must be received in electronic form by 11:59pm (Montreal local time) of June 9th, 2006.

Submissions should be no more than 12 single-spaced A3 or A4 pages with 1.25-inch margins all around, everything included (title, authors, addresses, abstract, references, figures, tables), in at least a 10-point font. An optional short appendix may contain details or additional data to be consulted at the discretion of the program committee. Note that authors of accepted papers will have to reformat them for the proceedings using the Springer LNCS style, which has even wider margins. It may save the authors' some work if this format is used from the outset. The submission must include the corresponding author's email address.

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

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

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

PROGRAM COMMITTEE CO-CHAIRS: Guillaume Bourque, Genome Institute of Singapore, Singapore
Nadia El-Mabrouk, University of Montreal, Montreal, Canada

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

David Sankoff <sankoff@uottawa.ca>

SanJuanIsland MarineGenomics Sept9-12

We are organizing a “Genomics and the Life Aquatic” symposium at the beautiful Friday Harbor Labs on San Juan Island from September 9-12, 2006. We anticipate a small but interactive meeting that will bring together scientists who are really doing “functional genomics” in aquatic systems to address a diversity of questions, from the origins of multicellularity to the evolution of new species. We have invited a number of great speakers! For more information, please check the website:

<http://depts.washington.edu/fhl/centsymp/-2006genomics.html> We are currently soliciting applications from graduate students and postdocs to give them a chance to present their work as an oral presentation and to interact with leaders in the field. Please pass this information along to any grad students or postdocs you know who might be interested. If you would like to apply, please use the website and click on the application form for grad students and postdocs. You will need to submit a 250 word abstract, as well as a 250 word description of your research interests and why they are relevant to the symposium. Applications are due by July 15 and we will notify people by the end of July.

We plan to cover lodging and food while at the confer-

ence for all attendees. We are still working on soliciting more support for the meeting, but will try to cover at least some amount of travel expenses for all attendees.

If you would like any more information, please send either myself (cpeichel@fhcrc.org) or Chris Amemiya (camemiya@benaroyaresearch.org) an email.

We look forward to seeing you at Friday Harbor in September.

Katie Peichel and Chris Amemiya -- Katie Peichel, PhD Assistant Member, Division of Human Biology Fred Hutchinson Cancer Research Center 1100 Fairview Ave North Mailstop D4-100, PO Box 19024 Seattle, WA 98109-1024 (206) 667-1628 (206) 667-2917 (fax) <http://www.fhcrc.org/science/labs/peichel/wjs18@u.washington.edu>

UGlasgow EvolEnvChange

Dear Colleague, Please could you circulate details of this conference to your staff and students. Many thanks

Kathryn Arnold, Pat Monaghan and Ruedi Nager

Coping with environmental change: integrating avian ecology and endocrinology

17 - 19 November 2006 at University of Glasgow, Scotland, U.K.

This workshop will focus on birds and climate change, and the role of the endocrine systems in mediating responses or buffering birds against environmental challenges.

Plenary speakers include Martin Wikelski (Princeton), John Wingfield (University of Washington), Alistair Dawson (CEH, Monkswood), Marcel Visser (Netherlands Institute of Ecology) and Greg Ball (John Hopkins University).

Deadline for abstracts is 31st July 2006.

For registration details and more information: <<http://e-bird.cefe.cnrs.fr/final-workshop.htm>><http://e-bird.cefe.cnrs.fr/final-workshop.htm>

Dr. Kathryn Arnold

Royal Society University Research Fellow

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

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

UWollongong MolluscEvol Dec6-8

Molluscs 2006 - Molluscs in Research, Conservation and the Economy

Triennial meeting of the Malacological Society of Australasia

6 - 8 December 2006, University of Wollongong, NSW plus two day pre and post conference workshops (4-5th Dec, 9-10 Dec)

The objective of this meeting is to bring together students, established researchers, naturalists and members of government and NGO agencies that have an interest in molluscs. The meeting will focus on current research involving molluscs in the Australasian area.

Molluscs are the second largest animal phylum and many are ecologically and economically important. They are dominant organisms in marine environments and have suffered more human-induced extinctions on land and in freshwaters than seen in all tetrapod vertebrates.

Themes:

- * Applied studies (aquaculture, fisheries, parasitology, invasive species)
- * Conservation and ecology (including endangered species, indicator species, molluscs in experimental ecology, tracking environmental changes)
- * Systematics (including taxonomy, phylogeny, evolution, faunistics, biogeography)
- * Genetics and development (population genetics, evolution-development, larval development)

Venue: McKinnon Centre, University of Wollongong.

Wollongong is about 1.5 hrs by road or rail south of Sydney. Details on other options for travel to Wol-

longong from Sydney provided on the conference website: www.uow.edu.au/conferences/MOLLUSCS06/
Registration: on line at www.uow.edu.au/conferences/-MOLLUSCS06/ Preconference Workshop

Dr Mark Norman and Dr Mandy Reid - cephalopod identification and biology (two days 4th - 5th Dec)

Postconference Workshop

Dr John Staniscic and Mr Michael Shea - land snails their identification, diversity and conservation (two days 9th - 10th Dec)

For more information contact:

Mark Norman: mnorman@museum.vic.gov.au

or

Winston Ponder: wponder@bigpond.net.au

Please feel free to distribute this notice to other lists etc.

The Australian Museum. Australia's first - and leading - natural sciences and anthropology museum. Visit www.amonline.net.au Dr Don Colgan Research Branch The Australian Museum 6 College St. Sydney 2010 Australia

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

WroclawPoland IntSocEvolProtist Aug1-5

The deadline for early registration for the 16th meeting of the International Society of Evolutionary Protistology is fast approaching (June 15, 2006).

This year's meeting will be in the beautiful city of Wroclaw, Poland. 1-5 August, 2006.

Registration and housing information can be found at: <http://www.isep16.biol.uni.wroc.pl/> or by writing to: Andrzej Bodyl bodyl@biol.uni.wroc.pl

farmer@cb.uga.edu

GradStudentPositions

BrighamYoungU EvolBiol	56	UDurham RoeDeer PopGenet	16
DurhamU RoeDeerPopGenet 2	11	UHull EvolColonisation	16
Hawaii MolEcol	11	UHull EvolDominance	17
Leipzig CulturalEvol	12	UKonstanz MolEvolBiol	18
OhioU EvolPlantBiol	13	URennes EvolClimateChange	18
SouthernIllinoisU PineBeetle	13	UVermont BarberryEvol	19
TexasAM InvasivePlantEvolGenet	14	UmeaU EvolEcol	20
UCD Dublin MarinePopGenet 2	14	WrightStateU MidgeEvolEcol	20
UCollegeDublin EvolIGF2Receptor	14		
UDublin RyeGrassPhylogenomics	15		

BrighamYoungU EvolBiol

Graduate Student & Postdoctoral Positions in Evolutionary Biology at Brigham Young University

A. Graduate student positions in phylogeography, systematics, and evolutionary ecology. Several positions funded in part by NSF to pursue graduate work at both the Masters and Ph.D. levels with an emphasis on phylogeography in Patagonian systems are available with Jerry Johnson (Fishes), Keith Crandall (Crustaceans), or Leigh Johnson (Plants). This opportunity is part of a collaborative research study (<http://patagonia.byu.edu>) that includes colleagues from Chile, Argentina, and Canada. Students with some fluency in Spanish, or a willingness to learn as part of their graduate study, are preferred. Applications for graduate study beginning Fall semester 2007 are due by 31 January 2007. Interested students are encouraged to contact investigators much earlier, by 1 September 2006 or soon thereafter, to begin dialogue regarding opportunities and the graduate program at Brigham Young University.

B. Two postdoctoral positions in systematics/evolutionary biology are available in the Department of Integrative Biology at Brigham Young University in Provo, Utah, USA (<http://inbio.byu.edu>). For both positions, the ideal candidate would be an investigator interested in using this experience to further develop her/his own independent research program - there should be sufficient time for the successful candidate to complete dissertation manuscripts, mentor undergraduate students, and pursue side projects.

1). Assembling the Tree of Life: "The Deep Scaly

Project: Resolving Higher Level Squamate Phylogeny Using Genomic and Morphological Approaches" - An NSF-funded postdoctoral position is available in the Jack Sites' lab for molecular work on phylogenetic reconstruction of deep relationships of squamate reptiles. Support is available for up to two years pending satisfactory performance in the first year, with a starting salary of \$32k, plus benefits. The preferred start date will be 1 January 2007, with some flexibility, and the primary focus will be to generate a large molecular data set from multiple nuclear loci for a limited number of taxa. The project includes Co-PIs and collaborators from San Diego State Univ. (T. Reeder), SUNY at Stony Brook (J. Wiens), the Field Museum of Natural History (M. Kearney and O. Rieppel), Univ. of Texas - Austin (J. Maisano), and Yale Univ. (J. Gauthier), and will involve integration of molecular with fossil and morphological data from the same taxa. Applicants should have strong molecular skills in modern DNA, PCR, and sequencing technology, competence in development/optimization of primers for new genes for large-scale sequencing, and be thoroughly familiar with conceptual issues and methods of phylogenetic inference. If interested, contact: Jack.Sites@byu.edu on or before 30 June 2006 to be considered. Please send a CV and statements of career goals and research interests.

2). Species-level Plant Systematics. An NSF funded postdoc position to work with Leigh Johnson on phylogenetic reconstruction and evolutionary inference within the phlox family in a research environment emphasizing low-copy nuclear genes, character evolution, qualitative and quantitative analysis of morphology, and integration of diverse data sets. Support is available for up to 18 months, pending satisfactory performance in the first year, with a starting salary of 30K plus benefits. Starting date between 1 September 2006 and 1 January 2007 preferred. An enthusi-

astic, self-motivated candidate with moderate to advanced molecular biology skills, desire/ willingness to learn new techniques, and thorough familiarity with conceptual issues and methods of phylogenetic inference is sought. Primary responsibilities will include completion of nuclear gene data sets, data analysis, and help with coding morphological data and the preparation of manuscripts. Candidates with an interest in phylogeographic studies and capable of field work in Patagonia will be given highest priority, with the potential to transition the research focus in this direction and extend the post-doc beyond 18 months (via a separate NSF funded opportunity). Interested candidates should contact: leigh_johnson@byu.edu on or before 15 July 2006; applications will be considered until the position is filled. Please send a CV, a statement of career goals and interests, and contact information for 3 references.

The evolutionary biology group at Brigham Young University has substantial depth in molecular systematics, evolutionary ecology, population genetics, phylogenetics, coevolution, computational biology, and molecular evolution and includes, in addition to the above, Byron Adams, David McClellan, Duke Rogers, and Michael

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

DurhamU RoeDeerPopGenet 2

The deadline for the following studentship has been extended to 10 July, and further information is now available at:

<http://www.dur.ac.uk/a.r.hoelzel/megwebpageStud06.htm> Fully Funded PhD Studentship on the Temporal and Spatial Population Genetics of Roe Deer in the UK

The roe deer is one of only two deer species indigenous to the British Isles (the red deer is the other). Known roe deer remains in Britain date back to the late OIS 5 (about 100,000 years ago). They are numerous in archaeological sites throughout Roman and Saxon times, but suffered a steady decline during the mediaeval period. Protected by the Normans, they were declared beasts of the warren (unworthy of noble hunting) in 1338. This led to extensive hunting, and by the

late 16th century they had become scarce throughout England, and extinct in Wales, though populations survived in some areas of Scotland. The UK population remained small (though how small is not known) until a series of re-introductions into the Lake District, East Anglia and southern England re-established the species in England in the 19th century. The impact of re-introductions on native populations is poorly understood in mammals, however this species provides an excellent test case, given the long historical record and availability of samples from all relevant time periods.

The project will involve the application of population genetic analyses to modern and ancient roe deer samples to help address this question. The student should have at least a 2.1 undergraduate degree result, and preferably an MS degree in a related field. The stipend will be £12,000 per year, to cover tuition and living expenses (note that this would be sufficient to cover all expenses for UK and EU nationals, but not for overseas students). Consumables costs are also fully funded. Please send your c.v., a cover letter explaining why you are well suited to this project, your undergraduate and where relevant postgraduate course records, and arrange for three letters of reference to be sent to: Prof. A. R. Hoelzel, School of Biological and Biomedical Sciences, University of Durham, Durham, DH1 3LE, UK. These materials should be preferably sent by email to a.r.hoelzel@dur.ac.uk to arrive before 10 July (for a preferred starting date of Oct 2006). Applicants should also complete the application form for postgraduate studies, which can be downloaded from the Durham University website.

a.r.hoelzel@durham.ac.uk

Hawaii MolEcol

RESEARCH ASSISTANTSHIP (PhD) POSITION (50% RA) IN MOLECULAR ECOLOGY Funding for a 3-year Ph.D. project is available through the College of Tropical Agriculture and Human Resources (CTAHR) in the Department of Tropical Plant and Soil Sciences (<http://www.ctahr.hawaii.edu/-ctahr2001/TPSS/Index.html>), to work on the development of unique molecular markers for rapid identification of potentially invasive weeds in Hawaii. This project aims to develop molecular markers to identify invasive weeds from closely related and morphologically similar desirable species. The objective is not necessarily to identify species per se, but to develop procedures

to screen out certain samples of concerned species or eliminate potential invasive species. The project also presents an opportunity to use molecular population genetic methods to address questions related to dispersal and gene flow in invasive plants.

This is primarily a lab-based project, therefore, experience with molecular genetic methods and analyses (e.g. PCR, gel electrophoresis, automated sequencing/genotyping) is desirable but not essential. The candidate will work under supervision of Dr. Ania Wieczorek (<http://www.ctahr.hawaii.edu/ctahr2001/TPSS/facultystaff/profiles/wieczorekA.html>). The Faculty at CTAHR provides an active and interesting research environment housing number of active groups of ecologists, geneticists, plant and environmental management biologists (see: <http://www.ctahr.hawaii.edu/ctahr2001/> for an overview). Starting date is flexible, preferably in January 2007, and the salary is for a 50% RA and includes a tuition waiver and benefits. Applicants should provide a full CV, including details of laboratory experience, a list of undergraduate courses and grades, a maximum 1-page description of research interests, three letters of reference, and desired start date. There is no fixed application deadline, but position will be filled once a suitable candidate is found. Potential applicants are encouraged to submit their applications as soon as possible. Applications should be sent (preferably by e-mail) to Dr. Ania M Wieczorek, <ania@hawaii.edu>.

thanks

Jaco Le Roux

Department for Tropical Plant and Soil Sciences University of Hawai'i at Manoa Hawai'i tel (808) 956 0781 fax (808) 956 3894

<http://www.ctahr.hawaii.edu/rubinoffd/jaco.htm> Johannes J L Roux <roux@hawaii.edu>

Leipzig CulturalEvol

PhD Position: Modelling cultural transmission and evolution

Max Planck Institute for Evolutionary Anthropology, Department of Primatology, Leipzig, Germany

We seek a graduate student interested in modelling the spread of cultural traits using epidemiological and phylogenetic approaches, with the goal to investigate the

distribution of cultural variants in non-human primates and humans. Specific research aims will be decided based on the interests of the student, and could include any of the following: (1) developing an agent-based model to investigate how different social learning mechanisms impact the spread of cultural traits; (2) developing and testing statistical methods for differentiating transmission mechanisms in human cultural practices; (3) using phylogenetic comparative methods to examine the distribution of cultural traits in non-human primates and across human societies; and (4) developing models to compare and contrast cultural transmission in non-human primates, early humans and modern humans. The PhD project will include both theoretical and empirical components and will address fundamental questions in human evolution. The student should have some previous experience with modelling, computer programming, and statistics, with an interest in developing these skills further through a PhD program.

Research will be conducted with Dr. Charles Nunn and Prof. Christophe Boesch at MPI-EVA, and potentially also with their collaborators around the world. The successful applicant can start immediately and will have an opportunity to earn a degree through the Leipzig School of Human Origins (<http://www.leipzig-school.eva.mpg.de/>). The research will primarily take place in the Department of Primatology, and the Institute offers a unique opportunity for interaction with researchers in the Departments of Human Evolution, Linguistics, Evolutionary Genetics, and Developmental Psychology.

For further information, please contact Dr. Charles Nunn (nunn@eva.mpg.de, website: www.eva.mpg.de/-primat/staff/charles_nunn/index.htm). To apply, please submit a CV, a statement of research interests (1-2 pages), and the names and email addresses of three referees to nunn@eva.mpg.de. The start date is flexible, but should occur before January 1, 2007.

Charles L. Nunn personal site: www.eva.mpg.de/-primat/staff/charles_nunn/index.htm mammal parasites: www.mammalparasites.org phylogeny of sleep: www.bu.edu/phylogeny/index.html book just published! - <http://www.oup.com/uk/catalogue/?ci=9780198565857>

Max Planck Institute for Evolutionary Anthropology Deutscher Platz 6 04103 Leipzig, Germany email: nunn@eva.mpg.de tel.: ++49 (0) 341 3550 204 fax: ++49 (0) 341 3550 299

and

Department of Integrative Biology University of California Berkeley, CA USA tel.: ++1 510 643 2579

nunn@eva.mpg.de

OH 45701 USA

Stefan Gleissberg <gleissberg@uni-mainz.de>

OhioU EvolPlantBiol

PhD student position in Evolutionary Developmental Plant Biology, Athens, OH

A PhD student position is available at the Department of Environmental and Plant Biology, Ohio University, to study the genetic control of early events in leaf development in the basal eudicot plant *Eschscholzia*. The typical bifacial architecture of angiosperm leaves with their upper and lower surfaces is determined at early stages of leaf development. Evidence from the model plant *Arabidopsis* indicates that a network of genetic regulatory elements is responsible for this morphogenetic process. In other plants, some of these genes are also involved in leaf dissection, a process by which the leaf blade is subdivided into segments. To better understand the evolution of development of bifaciality and leaf dissection, this project addresses the role of relevant genes in the basal eudicot *Eschscholzia californica*, a plant with bifacial and dissected leaves.

The project involves (i) cloning and characterization of relevant candidate gene families, (ii) characterization of early stages of leaf development and associated gene expression patterns, and (iii) the study of phenotypic effects of modulated expression using a transgenic approach and virus-induced gene silencing. Candidates for this position should have a strong interest in plant development and evolution, and demonstrable experience in some of the methods mentioned. The ability to work independently and self-motivated is essential.

The student will join a new lab in a Department with vibrant research in plant development, systematics, and evolution.

Interested candidates should send a cover letter, a curriculum vitae, a statement of research experience, and the names and contact information of at least two scientists available for reference. Please send your application and informal inquiries to Dr. Stefan Gleissberg (gleissbe@ohio.edu). Review of applications will start July 15, 2006, and continue until the position is filled.

Present Address Institute of Systematic Botany Johannes-Gutenberg-University Mainz Bentzelweg 9a 55099 Mainz Germany

New Address (starting September 2006) Environmental and Plant Biology Ohio University Porter Hall Athens,

SouthernIllinoisU PineBeetle

Graduate position to study dispersal patterns of Southern Pine Beetles (*Dendroctonus frontalis*) using genetic markers, modeling and GIS.

The population dynamics of most organisms are influenced by landscape structure, including the size and arrangement of habitat patches, distance between patches, and the matrix (non-habitat areas) in which the habitat patches are embedded. This has been recognized for SPB, where attempts have been made to link risk of SPB infestation with features of the landscape, including the location of stands of suitable host pines, their arrangement in space, and possible corridors for dispersing beetles. As part of an ongoing research project we have developed a suite of polymorphic DNA microsatellite markers for the SPB and demonstrated that they exhibit heterogeneous allele frequencies across large geographic scales. This project extends the use of these genetic markers to measure SPB movement through fragmented habitat and on a hierarchy of spatial scales. The emphasis of this project will be population genetics and modeling based on microsatellite marker data as well as field estimates of SPB dispersal. Applications will be accepted at either a PhD level (for which applicants should have a Masters of Science and competitive GPA and GRE scores) or a Masters level. For Ph D candidates, previous experience in relevant lab work and GIS software would be a plus. The start date will be August, 2006.

Interested individuals should contact Drs: Kamal Ibrahim (kibrahim@zoology.siu.edu), John Reeve (jreeve@zoology.siu.edu) or Edward Heist (edheist@siu.edu) all at: Department of Zoology, SIU-C, Carbondale, IL 62901.

Kamal M. Ibrahim, Ph D Department of Zoology, Southern Illinois University, Carbondale, Illinois 62901-6501 Phone: 618-453-4120 Fax: 618-453-2806 E-mail: kibrahim@zoology.siu.edu Web: <http://www.science.siu.edu/zoology/ibrahim> kibrahim@zoology.siu.edu kibrahim@zoology.siu.edu

TexasAM InvasivePlantEvolGenet

Opportunity to study evolutionary genetics of the invasive grass *Bothriocloa ischaemum* var. *songarica*, King Ranch Bluestem. The main objectives of the study are to identify the original source (or sources) of introduction, to investigate the possibility of hybridization with native or other introduced relatives, and to investigate possible changes in chromosome number after introduction. I am looking for a Master's level student with an interest in using molecular markers to address evolutionary and population genetics questions and an interest in one or more of the above objectives.

Admission to our Master's program in Biology for Fall 2006 with a teaching assistantship is still possible – admission for Spring 2007 is also an option. In addition to teaching assistantships for the fall and spring semesters, a summer research assistantship is guaranteed for Summer 2007 and possible for Summer 2008.

Interested students please contact R. Deborah Overath at deborah.overath@tamucc.edu or (361) 825-2467.

Please pass this message on to any recent (or soon to be) graduates from your undergraduate programs who may be looking for graduate school opportunities.

Sincerely,

R. Deborah Overath

R. Deborah Overath, Ph.D. Assistant Professor of Biology Department of Physical and Life Sciences (ST 312) 6300 Ocean Drive, Unit 5800 Texas A&M - Corpus Christi Corpus Christi, TX 78412

Phone: (361) 825-2467 Fax: (361) 825-2742 email: deborah.overath@tamucc.edu

deborah.overath@tamucc.edu

UCD Dublin MarinePopGenet 2

PhD opportunity in marine population genetics at UCD, Dublin

With regard to the announcement posted yesterday, we would like to specify that non-EU applicants can still

apply, but they have to be aware that - due to the higher cost of university fees for non-EU students - their salary would be thinned down to around 960 EUR per month.

thanks

Dr Stefano Mariani MARine Biodiversity, Ecology & Evolution UCD School of Biological & Environmental Science Science and Education Research Centre (West) University College Dublin Belfield Dublin 4 Republic of Ireland tel. +353.1.716.2347 fax. +353.1.716.1152 <http://www.ucd.ie/zoology/marbee/> stefano.mariani@ucd.ie

UCollegeDublin EvolIGF2Receptor

Genomic imprinting in a novel mammalian order: the canine IGF2 receptor

A three-year PhD Studentship, funded by Science Foundation Ireland and commencing September 1 2006 is available in the UCD School of Biology and Environmental Science (Kay Nolan's lab). The studentship will examine genomic imprinting in the dog, *Canis familiaris*, and is for three years. It covers full Ph.D fees (for a student of EU origin) and a stipend of 16,000 per annum.

Background and project description

Imprinted genes are epigenetically modified in a parent of origin-dependent manner. This usually results in differential expression of maternally- and paternally-derived alleles. Imprinted genes are few in number but have important roles in growth, development and behaviour, and abnormal regulation of imprinted genes has been implicated in several human disorders. There are many unanswered questions regarding the biology and evolution of imprinting, and extending the study to novel mammalian orders should help to answer some of these, as to date most studies have focused on imprinting in mice and humans.

The dog (a member of the Carnivora) belongs to a different group of mammals than rodents and primates. This, together with the recent publication of the canine genome, means that the dog is an important animal for comparative genome studies. In addition the dog is fast becoming a valuable model of human disease. This studentship will investigate the imprint status of the canine IGF2 receptor.

The IGF2 receptor (IGF2R) is large multifunctional

protein that has an essential role in normal mammalian development and also acts as tumour suppressor. Its gene is imprinted in some mammals (including opossum, mice, cattle) but not in others (egg-laying mammals, tree shrews, lemurs, humans). In an effort to understand how the imprinted IGF2R evolved, we are studying the regulation of this gene in novel animal taxa and the investigation of the canine IGF2R represents an extension of this study. The student will be based in UCD's School of Biology and Environmental Science (Nolan lab). Our collaborators in this research include other research groups in Dublin and in Duke University (North Carolina).

Applications for this position are invited. Candidates should have an honours degree in a biological subject (minimum 2:1 grade; preferably with experience in molecular biology). We are seeking highly motivated individuals, with an interest in genomic imprinting and epigenetics, an enthusiasm for research and a determination to succeed.

Application process

Letter of application explaining your interest in this project, together with curriculum vitae and names and contact details of two referees, to:

Kay Nolan

UCD School of Biology and Environmental Science
Science Center West

Belfield

Dublin 4

Ireland

Tel: +353-1-716 2112

E-mail: Catherine.Nolan@ucd.ie

Further reading

Wilkins and Haig (2003) What good is genomic imprinting: the function of parent-specific gene expression. *Nature Reviews: Genetics* 4: 1-10

Killian, Nolan et al (2001) Divergent evolution in M6P/IGF2R imprinting from the Jurassic to the Quaternary. *Human Molecular Genetics* 2001 10: 1721-1728.

Killian, Nolan et al (2001) Monotreme IGF2 expression and ancestral origin of genomic imprinting. *Journal of Experimental Zoology* 291, 205-12.

Nolan et al (2001) Imprint status of M6P/IGF2R and IGF2 in chickens. *Development Genes and Evolution* 211: 179-83.

Nolan et al (2006) Mannose 6-phosphate receptors in

an ancient vertebrate, zebrafish. *Development Genes and Evolution* 216: 144-51.

Lindblad-Toh et al (2005) Genome sequence, comparative analysis and haplotype structure of the domestic dog. *Nature* 438: 803-19.

Ostrander and Wayne (2005) The canine genome. *Genome Research* 15: 1706-1716

Kay Nolan Senior Lecturer UCD School of Biology and Environmental Science Science Center West Belfield dublin 4 Ireland

Tel: +353 1 716 2112 Fax; +353 1 716 1152 E-mail: catherine.nolan@ucd.ie

catherine.nolan@ucd.ie

UDublin RyeGrassPhylogenomics

PhD fellowship Phylogenomics/bioinformatics of perennial ryegrass (*Lolium perenne*) organelle genomes (Funded by Teagasc Walsh Fellowship Scheme)

Department of Botany, University of Dublin, Trinity College, Ireland Teagasc, Oak Park Research Centre, Carlow, Ireland

We are looking for a suitable student with an interest in DNA bioinformatics to work on the phylogenomics of perennial ryegrass (*Lolium perenne*). *Lolium* is the most important forage grass species of Ireland and most temperate regions of the world. We have funding to sequence its entire mitochondrial and chloroplast genomes (outsourced to a private company) and investigate them in a phylogenomic context. More specifically we would like to investigate their sequence structure and variation in comparison to other sequenced grasses, compare them phylogenetically to other grasses, develop molecular markers for both genomes applicable in plant breeding, and to get first insights into the horizontal gene transfer between nuclear and organellar sequences of the species.

This project is a collaboration between molecular laboratories at the Department of Botany, Trinity College Dublin (TCD) and Teagasc and will be jointly supervised by Dr Trevor Hodkinson (TCD; www.tcd.ie/Botany/staff/THodkinson), Dr Susanne Barth (Teagasc Oak Park; <http://www.teagasc.ie/-oakpark/sbarth.htm>). The researcher will be based at Oak Park, Carlow and TCD and will benefit from interactions with both institutes. The student will receive an

annual tax free stipend of 17,000 Euro for maintenance and to cover university fees. Fees are approximately 4,000 Euro for EU students or 8,000 Euro for non-EU students. There will be opportunities to earn money teaching and demonstrating on undergraduate courses and invigilating examinations.

Applicants must have a first or second class (preferably upper) Bachelors, or Masters, degree in a biological science or relevant subject. To apply or to obtain further information, please send a CV including research interests and contact details of two referees and a letter of motivation to trevor.hodkinson@tcd.ie and susanne.barth@teagasc.ie by June 23 2006.

– Dr Trevor Hodkinson Department of Botany School of Natural Sciences University of Dublin, Trinity College D2, Ireland

Phone: 353-1-6081128 Fax: 353-1-6081147 Email: trevor.hodkinson@tcd.ie

Trevor Hodkinson <hodkinst@tcd.ie>

have at least a 2.1 undergraduate degree result, and preferably an MS degree in a related field. The stipend will be £12,000 per year, to cover tuition and living expenses (note that this would be sufficient to cover all expenses for UK and EU nationals, but not for overseas students). Consumables costs are also fully funded. Please send your c.v., a cover letter explaining why you are well suited to this project, your undergraduate and where relevant postgraduate course records, and arrange for three letters of reference to be sent to: Prof. A. R. Hoelzel, School of Biological and Biomedical Sciences, University of Durham, Durham, DH1 3LE, UK. These materials should be preferably sent by email to a.r.hoelzel@dur.ac.uk to arrive before the end of June (for a preferred starting date of Oct 2006). Applicants should also complete the application form for postgraduate studies, which can be downloaded from the Durham University website.

a.r.hoelzel@durham.ac.uk

UDurham RoeDeer PopGenet

Fully Funded PhD Studentship on the Temporal and Spatial Population Genetics of Roe Deer in the UK

The roe deer is one of only two deer species indigenous to the British Isles (the red deer is the other). Known roe deer remains in Britain date back to the late OIS 5 (about 100,000 years ago). They are numerous in archaeological sites throughout Roman and Saxon times, but suffered a steady decline during the mediaeval period. Protected by the Normans, they were declared beasts of the warren (unworthy of noble hunting) in 1338. This led to extensive hunting, and by the late 16th century they had become scarce throughout England, and extinct in Wales, though populations survived in some areas of Scotland. The UK population remained small (though how small is not known) until a series of re-introductions into the Lake District, East Anglia and southern England re-established the species in England in the 19th century. The impact of re-introductions on native populations is poorly understood in mammals, however this species provides an excellent test case, given the long historical record and availability of samples from all relevant time periods.

The project will involve the application of population genetic analyses to modern and ancient roe deer samples to help address this question. The student should

UHull EvolColonisation

Applications are invited for a fully-funded PhD studentship to be held at the University of Hull, UK. This studentship is supported by a scholarship from the Natural Environment Research Council (NERC: for details see www.nerc.ac.uk). Applicants must have at least a 2.1 Honours degree or equivalent in the Biological Sciences. UK students will receive an annual stipend, currently £12,000 pa, and tuition fees and other expenses will be covered. Students of other EU countries are eligible for a fees-only award, although they may be eligible for a full stipend if they have been resident in the UK for the past 3 years. Nationals of countries outside the EU are not normally eligible. Informal enquiries should be directed to Dr. Africa Gómez: a.gomez@hull.ac.uk. Completed applications should be sent to The Research Secretary, Department of Biological Science, University of Hull, HU6 7RX, UK, putting the name of the main project supervisor under previous contact. Application forms are on <http://www.hull.ac.uk/biosci/students/-apply.html>. Applicants should also send a covering letter outlining their relevant skills and experience and their motivation for applying. Closing Date 13th July 2006

Project summary: Colonisation is a crucial process, shaping almost all biological systems. Understanding the interaction of evolutionary forces during habitat

colonisation is key for many areas in biology from the applied - environmental research and management - to fundamental ones - population structure, phylogeography, biogeography, ecology and speciation. Despite its importance, colonisation is not well understood from an evolutionary point of view. Due to the fleeting nature of colonisation, evolutionary studies in the wild are difficult, labour intensive, and very rarely have colonising populations been followed from the initial stages. Few studies have been able to test experimentally the interaction of evolutionary forces in new populations, mostly due to challenges involved in the choice of model organism. Accelerated global climate change and other anthropogenic impacts are changing colonisation rates, increasingly affecting native species distribution ranges and facilitating biological invasions, making the understanding of colonization even more urgent. The PhD student will be closely associated to an ongoing NERC funded fellowship awarded to Africa Gómez to investigate the interplay of inbreeding, migration and local adaptation during colonisation in zooplankton populations. The PhD student, in a separate but complementary project, will investigate the interaction of evolutionary forces in recently established populations by using laboratory microcosms of the rotifer (*Brachionus plicatilis*). The early stages of population establishment will be examined experimentally to test for i) the effect of different numbers of founding individuals, ii) the dynamics of inbreeding, iii) the development of local adaptation, iv) the build-up of neutral genetic differentiation by using microsatellite loci and vi) the impact of migration. Therefore the student will gain a broad knowledge in ecology, genetics and evolution, as well as transferable skills in experimental design, statistics, molecular techniques and analysis.

Africa Gomez Advanced NERC Research Fellow Department of Biological Sciences University of Hull Cottingham Rd. Hull, HU6 7RX U.K.

Tel: +44 (0)1482 465505 Fax: +44 (0)1482 465458
e-mail: a.gomez@hull.ac.uk <http://www.hull.ac.uk/-molecol/Africa.html>
A.Gomez@hull.ac.uk

UHull EvolDominance

Fully funded PhD Studentship in Biological Sciences, University of Hull, UK

Project title: The behaviour and genetics of reproduc-

tive dominance

Applications are invited for a fully-funded PhD studentship to be held at the University of Hull. This studentship is supported by a scholarship from the Natural Environment Research Council (NERC: for details see www.nerc.ac.uk). Applicants must have at least a 2.1 Honours degree or equivalent in the Biological Sciences. UK students will receive an annual stipend, currently £12,000 pa, and tuition fees and other expenses will be covered. Students of other EU countries are eligible for a fees-only award, although they may be eligible for a full stipend if they have been resident in the UK for the past 3 years. Nationals of countries outside the EU are not normally eligible. Informal enquiries should be directed to the main project supervisor (Dr Rob Hammond: Rob.Hammond@unil.ch: <http://www.unil.ch/-dee/page7720.html>). Completed applications should be sent to The Research Secretary, Department of Biological Science, University of Hull, HU6 7RX, UK, putting the name of the main project supervisor under 'previous contact'.

Application forms are on <http://www.hull.ac.uk/-biosci/students/apply.html>. Applicants should also send a covering letter outlining their relevant skills and experience and their motivation for applying. Closing Date 23th June 2006

Brief project description: The behaviour and genetics of reproductive dominance

Much is known about the ultimate causes of social living (e.g. kin selection, reciprocity) but little about the genetic mechanisms underlying differences in social phenotype. Advances in genetics and genomics mean that such investigations are now possible. The common ant *Leptothorax acervorum* shows easily scoreable variation in social phenotype as in multiple queen nests either all queens reproduce equally (low skew) or only one queen reproduces (high skew). These social phenotypes are stable in the lab and are likely to have a genetic basis. The aim of this studentship will be to investigate the behavioural mechanisms that maintain high reproductive skew among queens in some colonies and to uncover genes that are differentially expressed between reproductive queens in high and low skew nests. The work will be highly diverse including fieldwork, behavioural observations and experiments, molecular genetic lab work and chemical ecology.

<<mailto:rob.hammond@unil.ch>>
<mailto:rob.hammond@unil.ch>

Rob Hammond Dept. Ecology & Evolution Université de Lausanne Lausanne 1015 Switzerland Tel: ++(0)21 692 41 82 / Fax: ++ (0)21 692 41

65 homepage: <http://www.unil.ch/dee/page7720.html>
 publications (inc. pdfs): <http://www.unil.ch/dee/-page9104.en.html> Rob.Hammond@unil.ch

UKonstanz MolEvolBiol

A Ph.D. position in molecular evolutionary biology is available in the lab of Axel Meyer in the Department of Biology at the University of Konstanz in Germany. The evolutionary biology group is an international group of students and postdocs that consists of about 20 people from 10 different countries. The language in the lab is English.

We are looking for an energetic Ph.D. student who is interested in speciation, molecular evolution, bioinformatics/genomics, or evolutionary developmental biology. The specific research projects we are recruiting for involve (1) research on the patterns of relationships and population genetics of cichlid fishes (2) as well as the discovery and functional characterization of (e.g. coloration) genes underlying the diversification of cichlids in Africa and in Nicaragua.

The great lakes in East Africa house some of the world's most diverse freshwater ecosystems. Lakes Victoria, Malawi and Tanganyika are particularly well-known for their adaptive radiations of hundreds of endemic species of cichlid fishes. We are interested in understanding speciation, phylogeography, molecular evolution and molecular phylogenetics of these cichlid fish assemblages. Also, we wish to identify and characterize the function of genes that are involved in the phenotypic diversification and presumably speciation of cichlid fishes. Several molecular biological, "devo-evo" and genomic approaches, including candidate gene approaches, DNA-chip technology, characterization of ESTs, in situ hybridization in cichlids and transgenics in zebrafish are used to address these questions. We are also interested in evolutionary genomic questions and the evolution of novel gene functions after gene and genome duplications.

Some recent publications of the lab include: Verheyen et al. (2003). The origin of the superflock of cichlid fishes from Lake Victoria, East Africa. *Science* 300: 325-329. Salzburger et al. (2005). Out of Tanganyika: Genesis, explosive speciation, key-innovations and phylogeography of the haplochromine cichlid fishes. *BMC Evolutionary Biology* 5: 17. Barluenga et al. (2006). Sympatric speciation in Nicaraguan crater lake cichlid

fish. *Nature* 439: 719-23 Braasch et al. (2006). Asymmetric evolution in two fish-specifically duplicated receptor tyrosine kinase paralogs involved in teleost coloration. *Molecular Biology and Evolution* 23:1192-1202.

Funding is available for at least 2 years. A Ph.D. thesis in Germany is supposed to be finished within about 3 years. Ph.D. salaries (50% BATII/a government pay scale) are approximately 20 to 25,000 Euros annually, (depending on marital status, age, etc.) before deductions for taxes, health insurance and retirement contributions.

The position is open immediately. The review and invitation of applicants will begin at the end of June 2006 and will continue until the position is filled. To apply, please email a curriculum vitae, including a list of publications, a statement of research interests, and the names and email addresses of two references to axel.meyer@uni-konstanz.de.

Prof. Axel Meyer, Ph.D. Department of Biology Konstanz University 78457 Konstanz, Germany Email: axel.meyer@uni-konstanz.de

For more information visit <http://www.evolutionbiologie.uni-konstanz.de/-index.php?section=10>

– Axel Meyer, Ph.D. Professor of Zoology and Evolutionary Biology Department of Biology University of Konstanz Universitätsstr. 10 D-78457 Konstanz Germany

email: axel.meyer@uni-konstanz.de

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

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

URennes EvolClimateChange

PhD theme in

Where do species respond to climate change? The role of endemism and of margins of environmental gradients. offered within the competition for PhD fellowships at University of Rennes 1, France.

!!! Deadline for inscription: 22 June 2006 !!!

Obligatory dates for presentations of short-listed candidates: 10 / 11 July 2006.

SCIENTIFIC BACKGROUND: Contemporary ecology is implicitly based on the hypothesis that phenotypes of species respond to changes of their environment. These responses happen on the level of differentiation of populations within species as well as on the level of macroevolution of traits across species. Recent studies, however, indicate that this fundamental hypothesis often lacks support. Species exposed to changing climates, for instance, usually redistribute in space, they migrate with their climate (Ackerly 2003, *Int. J. Plant Sci.*). Species that stay will often be displaced by species that immigrate and are already well adapted to the novel climate. Consequently, the climate niche of species usually remains very rigid even across time periods of millions of years (for instance Prinzing et al. 2001 *Proc. R. Soc. B*). Adaptive responses of phenotypes are thus replaced by migrations and invasions. Overall, it is not obvious how phenotypes of species can respond to new climates. Recently, several hypotheses have been proposed to resolve this paradox. These hypotheses propose that an adaptation or adaptive plasticity is likely to occur in particular situations: (A) At the margin of climatic gradients. Two scenarios have been suggested. First, phenotypic responses appear at the margin where living conditions of established species become increasingly extreme, provided that species that are already well adapted to these conditions cannot immigrate from outside or where preadapted invasive species are not available from the outside. Second, the response appears at the margin where species face increasingly favorable conditions and can thus expand their range, leading to founder effects and increased phenotypic variability. (B) As a function of endemism. Again, two scenarios have been suggested: First, endemics are more responsive as their genotypic adaptations to local conditions are not diluted by genotypes arriving from outside. Second, the endemics respond less, as they do not profit from an immigration of genotypes from regions with a climate resembling the novel conditions arising at the given locality. These hypotheses will be studied for plant species, at the level of intraspecific differentiation of populations, and at the level of macroevolution of traits of traits across species. For the first level, we will use a system that is currently going through major environmental changes, with a well known history of colonization and a number of endemic species: the subantarctic Kerguelen Islands. In the field, the student will characterize climate and soil gradients, will sample different species, and culture plants for two generations in order to verify the heritability of the phenotype. In the lab, the student will

measure vegetative and reproductive structure, characterize biochemical phenotypes and their response to environmental conditions (metabolomics, polyamines, growth regulators contributing to stress tolerance; e.g.; Hennion et al. 2006; Heat Shock Proteins will be studied in collaboration). For the second, macroevolutionary, level we will profit from the regional flora that is best known in terms of phylogenetic relationships, life history traits, and distribution along environmental gradients; the flora of central Europe. The student will reconstruct characters of ancestors, i.e. their positions along environmental gradients and their degree of endemism, within habitats and regions. The student will identify macroevolutionary changes of life histories and certain physiological traits. Finally (s)he will test whether endemism of ancestors, or their position along environmental gradients, influence the evolution of the life history and ecophysiology of the descendants.

SALARY / ORGANIZATIONAL BACKGROUND: A PhD fellowship by the Ecole Doctorale Vie, Agro, Santé (<http://www.vas.univ-rennes1.fr/>) for three years, approx. 1040 Euros/month (which can luckily be backed by teaching assistance). Please note that candidates are selected by a committee of the Doctoral School, not by the supervisors of the theses (they can, however, contribute their opinion). Moreover, the number of PhD fellowships available to be distributed is much smaller than the number of themes being offered. Finally, travel costs will not be reimbursed by the Ecole Doctorale, and it is not sure whether other funds will be available. If selected, supervision is guaranteed by the director and co-director of thesis, plus a committee of internal and external scientist evaluating the overall progress.

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

UVermont BarberryEvol

Graduate Student Research Assistantship Department of Plant Biology University of Vermont

I am looking for MS or PhD students for a newly funded project on the ecology and evolution of invasive Japanese barberry (*Berberis thunbergii*). Planned

studies include common garden studies of Japanese barberry collected from both invasive and native range along a geographical gradient. However, the successful student would have freedom to develop their own interests. Potential areas of study include evolutionary studies, genetic studies, demography, soil plant feedbacks, and spatial pattern analysis. Preference will be given to students who already have MS degrees. Funding is guaranteed for length of degree (2.5 years for MS, 5 years for PHD). Graduate stipends are \$21,000 and \$17,500 for PhD and MS students, respectively. Students receive health insurance and a tuition waiver. Interested students should send a letter of interest, CV and three letters of reference to Dr. Jane Molofsky, Department of Plant Biology, University of Vermont, Burlington, Vermont 05405. Email applications are welcomed (Jane.Molofsky@uvm.edu).

jmolofsk@uvm.edu

UmeaU EvolEcol

PHD POSITION IN EVOLUTIONARY ECOLOGY

One PhD position in evolutionary ecology is available at the department of Ecology and Environmental Science, Umea University, SWEDEN.

A PhD position for the project "Evolution of phenotypic plasticity in predator-prey systems" is available at the department of Ecology and Environmental Science, Umea University, Sweden. The aim of the project is to understand the evolution of phenotypic plasticity in characters important for the coexistence of predators and prey. The focus will be on evolutionary patterns within and among species of aquatic insects, and the goal is to understand phenotypic plasticity's role in diversification and adaptation of organisms. The project will centre on experimental and comparative studies, and quantitative genetics and behavioural ecology are key concepts.

To qualify for the position you need a Bachelor university degree, typically with a minimum of 120 ECTS in biology. Advanced courses in ecology, evolutionary biology or the equivalent are desirable. Proficiency in both written and spoken English is required. The procedure for recruitment for the position is in accordance with the Higher Education Ordinance (Högskoleförordningen chpts. 5 and 9). The position is available for a four-year period

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

Further information on ongoing projects of the research group can be found at http://www.emg.umu.se/-personal/frank_johansson.htm. Further information for the position can be obtained from Dr. Frank Johansson, frank.johansson@emg.umu.se.

Union-related information is available at SACO, phone +46 90-786 51 53, SEKO-civil, phone +46 90-786 52 96 and also ST, phone +46 90-786 54 31.

Applications will be discarded or, if the applicant so wishes, returned two years after the position has been filled.

Regards Frank

Frank Johansson Associate Professor Umea University
Department of Ecology and Environmental Science 901
87 UMEA

Telefon: +46 90 7866637 E-mail:
frank.johansson@emg.umu.se

frank.johansson@emg.umu.se

WrightStateU MidgeEvolEcol

Ph.D. research assistantship available at Wright State University in the interdisciplinary PhD program in Environmental Sciences.

Project Title: Collaborative Research: Adaptive radiation of a gall midge-fungus mutualism in a multitrophic context.

I am looking for a PhD student to work on an NSF funded collaborative project examining the ecology and evolution of an incipient adaptive radiation of gall midges (Cecidomyiidae) and their symbiotic fungi on goldenrods (Solidago). See the project summary below for a brief overview of the project. Admission into Wright State's ES PhD program will be required of the selected applicant. Click link for details of this program (<http://www.wright.edu/academics/>-

envsci/index.html). Anticipated start date for the position is September 1, 2006 or as soon as the position is filled. Salary is approximately \$19,000/year plus tuition remission. Send letter of interest, resume, GRE scores, transcripts, and names and contact information for 3 references to:

John O. Stireman III Department of Biological Sciences
3640 Colonel Glenn Highway 235A, BH, Wright State
University Dayton, OH 45435

Phone: 937-775-3192 email: john.stireman@wright.edu

See my Web page for publications and research interests in the Stireman lab <http://www.wright.edu/~john.stireman> Project summary

Adaptive radiation has long been a central theme in evolutionary biology and this selection driven process is thought to be a fundamental engine of biological diversification. Recent years have seen a tremendous growth in empirical studies and synthetic reviews of the subject. Our proposed work, however, addresses an important shortcoming: there are almost no studies of how species interactions other than competition promote or hinder adaptive radiation. In particular, there is a dearth of studies examining how trophic interactions among species spur or inhibit adaptive diversification. Given that most species are embedded in complex ecological networks encompassing multiple trophic and/or symbiotic interactions, the shortage of work in this area means we currently lack data of general significance, essential to ground-truth new theory and predictions concerning the causes and processes of adaptive radiation and biological diversification.

The focus of the proposed work is the pattern and process of adaptive radiation in a multi-trophic community context. Preliminary evidence suggests that the gall midge *Asteromyia carbonifera* and its fungal associate (*Botryosphaeria* sp.) are undergoing an incipient, rapid radiation on their goldenrod (*Solidago* spp.) hosts. Furthermore, the midges suffer extraordinarily high rates of parasitism by hymenopteran parasitoids, the distribution of which suggests that these enemies may influence adaptive divergence of their midge hosts. We will focus on understanding how adaptive radiation in this system is influenced by geography, interactions between mutualists, and interactions between trophic levels. We propose to employ genetic analyses (e.g., DNA sequencing, AFLPs, microsatellites) and laboratory/field studies to reconstruct the recent history and ongoing population genetic and ecological processes involved in radiation of the midge-fungus species complexes. Cecidomyiid gall midges have long attracted attention for their phenomenal taxonomic and ecological diversity, and the proposed work will enable a detailed dissection of the patterns and processes of gall midge diversification in its earliest stages. Most importantly, the work will provide a tractable model for exploring how adaptive divergence in complex ecological systems is influenced by hosts, mutualists, natural enemies, and their interactions.

John O. Stireman III Assistant Professor Department of Biological Sciences 3640 Colonel Glenn Highway 235A, BH, Wright State University Dayton, OH 45435

Phone: 937-775-3192 john.stireman@wright.edu
<http://www.wright.edu/~john.stireman>
john.stireman@wright.edu john.stireman@wright.edu

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CalAcademySci DirectorResearch

Director of Research Position California Academy of Sciences, San Francisco

Position Summary: The California Academy of Sciences is recruiting for Director of Research to help develop and implement a vision for the Academy's research departments, library, technical laboratories, and the training of students in systematic and evolutionary biology. As a member of the senior management team, the new Director will advance the Academy's research agenda and provide leadership in scientific research, biological collections and associated research data, research budgets, long-term planning, administration and integrated programming across the Academy.

Founded in 1853 and located in San Francisco, the Academy includes a natural history museum, aquarium, planetarium, research division and education programs. We are currently in an active building campaign - constructing a new public museum facility and planning our future research enterprises. The Academy will move from its current temporary space to a new facility in Golden Gate Park in late 2007. It is expected that the Director of Research will oversee and direct this important growth period that we hope will include several curator hires.

San Francisco and the Bay Area hosts an educated, active and engaged public that is very supportive of science and science education. Several area universities offer a vibrant academic community with potential for collaboration and co-sponsoring students.

Interested applicants should send a letter of interest,

curriculum vita and the names and contact information of three references to:

California Academy of Sciences Attn: HR#DirRA 875 Howard Street San Francisco, CA 94103-3098

To view the job ad, click here: http://calacademy.snaphire.com/safelink=JSJD&O_p=xv0f7

John P. Dumbacher (Jack) Chair and Curator Department of Ornithology and Mammalogy California Academy of Sciences 875 Howard Street San Francisco, CA 94103 USA Phone: 415 321-8369 Fax: 415 321-8637 jdumbacher@calacademy.org <http://www.calacademy.org/research/bmammals/-jdumbacher.html> jdumbacher@calacademy.org

ColoradoStateU ResAssoc EvolBiol

Research Associate. One year, non-tenure track. Renewal contingent upon availability of funds. Primary emphasis on molecular biology, genomic and microbiology techniques. Secondary responsibilities include lab organization and ordering. A Bachelors degree and at least three years lab experience in Molecular Biology or a related field. Experience in basic plant molecular biology techniques such as DNA extraction, cloning of PCR products, DNA sequencing, RT-PCR, and plant growth. Preference will be given to candidates with demonstrated experience in microbiology and high-throughput genetic techniques, specifically: growth and manipulation of bacterial strains and SNP genotyping.

Application deadline of July 15, 2006, however, ap-

lications will be considered until the position is filled. Salary is commensurate with experience. Send all application materials as a single pdf to: Frank.Peairs@Colostate.edu. or mail to Frank Peairs, Colorado State University, C129 Plant Sciences, Fort Collins, CO 80523-1177. Please include 1) a letter of interest including a brief summary outlining experience and qualifications for this position; 2) a C.V.; 3) names and contact information for three references. CSU is an EEO/AA employer.

The full job ad is posted at this (very long) url

http://www.colostate.edu/cgi-bin/cgiwrap/-cwis202/db.cgi?db=jobs&uid=faculty&college=-Agricultural%20Sciences&sb=10&so=-descend&view_records=1&nh=1&mh=1

Informal inquiries about this position can be directed to John McKay at

email jkmckay@colostate.edu

– John McKay Bioagricultural Sciences and Pest Management C129 Plant Sciences Building Fort Collins, CO 80523

office 530 754 5338 cell 970 402 4828 fax 970 491 3862
email jkmckay@colostate.edu

John McKay <jkmckay@lamar.colostate.edu>

ColoradoStateU ResAssoc EvolBiology

Research Associate. One year, non-tenure track. Renewal contingent upon availability of funds. Primary emphasis on molecular biology, genomic and microbiology techniques. Secondary responsibilities include lab organization and ordering. A Bachelors degree and at least three years lab experience in Molecular Biology or a related field. Experience in basic plant molecular biology techniques such as DNA extraction, cloning of PCR products, DNA sequencing, RT-PCR, and plant growth. Preference will be given to candidates with demonstrated experience in microbiology and high-throughput genetic techniques, specifically: growth and manipulation of bacterial strains and SNP genotyping.

Application deadline of July 15, 2006, however, applications will be considered until the position is filled. Salary is commensurate with experience. Send all application materials as a single pdf to:

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The full job ad is posted at this (very long) url

http://www.colostate.edu/cgi-bin/cgiwrap/-cwis202/db.cgi?db=jobs&uid=faculty&college=-Agricultural%20Sciences&sb=10&so=-descend&view_records=1&nh=1&mh=1

Informal inquiries about this position can be directed to John McKay at

email jkmckay@colostate.edu

jkmckay@lamar.colostate.edu

Europe ArabidopsisGrowth FieldResAssist

Field research assistants needed for Arabidopsis ecological genetics project in Europe

We are looking for field assistants to participate in a large-scale investigation of the evolution of flowering time in *Arabidopsis thaliana*. Our approach includes analysis of flowering time response to a wide range of natural and manipulated environments at levels ranging from DNA sequence variation to continental ecotype distributions. This NSF-funded Frontiers in Biological Research (FIBR) project – headed by Johanna Schmitt at Brown University – is a collaborative effort of four labs in the US as well as *Arabidopsis* laboratories at five research institutions in Europe. Part of this study entails establishing a set of five common gardens in Europe in Valencia, Spain; Oulu, Finland; Norwich, UK; Cologne, Germany; and Halle, Germany. At these sites large numbers of European *A. thaliana* accessions will be grown in multiple plantings synchronized with local populations in order to assess geographic and seasonal variation in selection on flowering time and other life history traits.

We are seeking research assistants who would be interested in living at one of the five European field sites and assisting with plant care and measurement. Applicants should have a bachelors degree in biology or a related science. Prior independent research

experience (particularly with plants) is necessary, as research assistants may be largely independent for prolonged periods of time. Although the primary duties involve plant care and measurement, successful applicants will have the opportunity to design and conduct independent research projects with the host laboratories based on the shared interests of the applicant and the host lab. These research assistantships involve a strong training component and were conceived as being analogous to Fulbright fellowships. Successful applicants will be awarded an NSF-fellow position. In addition to a fellowship stipend of \$25,000/yr plus health insurance, a portion of living expenses in Europe, approximately equal to monthly rent, would be provided by a cost-of-living stipend.

At the moment our greatest need is for September 2006-2007 in Halle, Germany where we have a collaboration with Matthias Hoffmann of the Martin-Luther-Universität Halle-Wittenberg (<http://www2.biologie.uni-halle.de/bot/boga/hoffmann/-hoffmann.html>). There will also be the opportunity to visit the other European field sites as part of the research team. German language skills would be helpful for this position.

Additional short-term and year long research assistantships may be available at the other European sites next summer. This is an excellent opportunity for graduating seniors interested in a research career to obtain further experience before applying to graduate school.

Further information about the project can be found at: <http://www.egad.ksu.edu/about.html>. To apply, please send a resume and contact information of three references to Johanna Schmitt (Johanna_Schmitt@brown.edu), Amity Wilczek (Amity_Wilczek@brown.edu) and Martha Cooper (Martha_Cooper@brown.edu). If you would like to meet with Johanna Schmitt to discuss the position at Evolution 2006 in Stony Brook or the Arabidopsis conference in Madison, please contact us as soon as possible.

Johanna Schmitt Stephen T. Olney Professor of Natural History Professor of Biology and Environmental Studies

Department of Ecology and Evolutionary Biology Box G-W Brown University Providence, RI 02912

phone: 401-863-3435 fax: 401-863-2166 <http://www.brown.edu/Departments/EEB/schmitt/-index.htm>

GuelphU BarcodeImagingSpecialist

Job: Biological Imaging Specialist position at the Canadian Centre for DNA Barcoding Location: Canadian Centre for DNA Barcoding, Biodiversity Institute of Ontario, University of Guelph, Guelph, Ontario, Canada. Background: The Canadian Centre for DNA Barcoding invites applications for a technician position in biological imaging to work in close association with lab managers, postdoctoral researchers and curatorial staff conducting research in species discovery and identification of insects, fish, birds using DNA barcodes. The Biodiversity Institute of Ontario (BIO) includes a Digital Media and Analysis Unit (DMAU) which will support numerous aspects of BIOs varied research program. Notably, the DMAU are be charged with creating digital records (including high-resolution images and video) of specimens as well as providing digital media and outreach materials to advance the understanding of biodiversity among researchers, students, and the public. The DMAU will also include advanced Global Information System (GIS) capabilities for use in ecological and other biodiversity research. www.biodiversity.uoguelph.ca Responsibilities: *Imaging technology: Preparation of specimens for biological imaging, limited curatorial responsibilities Experience in Biological and / or related imaging techniques required. *Computer work: Image analysis using a variety of software packages Qualifications: The appointment will be made at a level appropriate to the qualifications, experience and caliber of the successful candidate. The post requires a responsible person with a high degree of commitment, enthusiasm and attention to detail, excellent communication, managerial, organizational and technical skills. The post-holder will be required to lead and keep abreast of new developments in imaging technologies. Closing Date: Open until filled. Preferred starting date August 1, 2006. Contact: Send cover letter, résumé, to Dr Alex Smith, Biodiversity Institute of Ontario, Integrative Biology, University of Guelph, Guelph Ontario, N2G 1W1 or e-mail materials to salex@uoguelph.ca

– M. Alex Smith PhD Biodiversity Institute of Ontario Canadian Centre for DNA Barcoding Department of Integrative Biology University of Guelph Guelph ON N1G 2W1 (519) 824-4120 office ext. 56393 lab ext. 52709 www.barcodinglife.org salex@uoguelph.ca

IndianaU FishBehavEvol

The Martins Lab is searching for a full-time research associate/technician to join our zebrafish behavioral genetics team. The position involves spending about half-time on lab management (supervision of assistants, ordering supplies, management of the animal facility, etc) and half-time on research (behavioral data collection, data analysis and writing). We seek an individual with at least a Bachelor's degree in Biology or related field, and would also welcome an associate at the postdoctoral level. Some experience in behavioral data collection and fish husbandry is strongly desired, although training will be provided. We are searching for someone cheerful and cooperative, independent and experienced. Salary will be commensurate with education and experience, and the position includes full benefits. Submit letter of interest, resume and contact information for 3 references via email to Jeremy Bennett, using 'Martins Research Associate' as the subject line. Start date is August 1, with some negotiation possible; applications accepted until position filled. For further inquiries about the position, please contact Emilia Martins (emartins at indiana.edu) directly. Indiana University is an equal opportunity affirmative action employer.

Emilia P. Martins Department of Biology Indiana University Bloomington IN 47405

ph: (812)856-5840 FAX: (812) 855-6705
emartins@indiana.edu www.indiana.edu/~martinsl

IndianaUBloomington ResAssociate Sunflower

Research Associate – Rieseberg Lab

Department of Biology, Indiana University, Bloomington

The Rieseberg Laboratory in Biology has a 1-year opening for a full time Research Associate starting in early June 2006. The Rieseberg Lab conducts research in plant evolutionary genetics using the annual sunflower as a study system. The position will involve 1/2 time dedicated to lab management and 1/2 to re-

search. General lab care is a priority on a daily basis. Lab management responsibilities include ordering supplies, maintaining equipment, supervising work-study students, and overseeing lab organization/functioning. Research responsibilities involve assisting graduate students and/or post-docs with molecular bench work such as DNA and RNA extractions, PCR, (genotyping and sequencing), and data scoring/analysis. Some minor greenhouse work may also be required. Initial projects will be closely supervised, with increased independence possible as experience and expertise are accumulated.

We seek an individual with a Bachelor's or Master's degree in Biology or related field. Some laboratory experience is strongly desired, although training will be provided. Attention to detail and an ability to work with others on a daily basis are both necessary. Salary will be approximately \$26,000, with some adjustment possible according to education and experience. Full benefits. Submit letter of interest, resume and contact information for 3 references via email to Jeremy Bennett (jebennet at indiana.edu), using 'Rieseberg Research Associate' as the subject line. Start date is June 1st (with some negotiation possible); applications accepted until position filled. Direct inquires about the nature of the position to Briana Gross (brgross at indiana.edu) and Ben Blackman (bkblackm at indiana.edu).

bkblackm@indiana.edu bkblackm@indiana.edu

InstZoolLondon ResTech

Institute of Zoology Zoological Society of London

Research Technician in Molecular Ecology and Evolution

Starting salary GBP17,636 (including London Weighting)

Applications are invited for the post of Research Technician on a NERC-funded project to investigate the role of olfactory and gustatory receptor genes in sexual isolation among *Drosophila* species.

Experience in molecular biology techniques, especially with analysis of gene expression using real time quantitative PCR, would be advantageous. The post will be for 24 months and is available from 1 August 2006. The project is a collaboration with the laboratories of Prof. Mike Ritchie (St Andrews) and Prof. Roger Butlin (Sheffield) and will involve working in close liaison with colleagues in those laboratories. Please contact

Dr. Bill Jordan (bill.jordan@ioz.ac.uk) for further details and informal enquiries.

Applications should include a cover letter (including a statement of suitability for the post), a CV and the names and full contact details of three referees. Applications should be forwarded to HR Dept., ZSL, Regent's Park, London NW1 4RY or email hr@zsl.org

Closing date: 6th July 2006.

Read about our work on <http://www.zsl.org> REGISTERED CHARITY NO. 208728

Dr W C Jordan Institute of Zoology Zoological Society of London Regent's Park London NW1 4RY Tel.: 020 7449 6631 Fax.: 020 7586 2870 Email: bill.jordan@ioz.ac.uk or w.jordan@ucl.ac.uk Home page: <http://www.zoo.cam.ac.uk/ioz/people/jordanb.htm> w.jordan@ucl.ac.uk w.jordan@ucl.ac.uk

KansasStateU EvolGenomics

Visiting Scholar Program in Ecological Genomics: Sabbatical Opportunities at Kansas State University

Ecological Genomics: Genes in Ecology and Ecology in Genes

The Ecological Genomics Visiting Scholar Program provides sabbatical opportunities at Kansas State University for permanent faculty researchers interested in Ecological Genomics. Our multi-disciplinary Institute seeks to understand responses of organisms to their natural environment by combining functional genomic and ecological approaches. Applicants should contact the PI of a potential host laboratory at Kansas State University (<http://www.k-state.edu/ecogen/resgroup.html>) to explore space availability and overlap in research interests. The start-date and duration of appointments are flexible. Visiting scholars will have access to excellent university resources including Konza Prairie Biological Station LTER site (<http://climate.konza.ksu.edu/>), Division of Biology infrastructure, and gene analysis facilities such as the KSU Gene Expression Facility (<http://www.k-state.edu/gene-exp/> <<http://www.k-state.edu/gene-exp/>>).

Visiting Scholars will receive a generous stipend and a substantial monetary supplement to support research endeavors. Recipients are expected to present a research seminar of their work. Application instructions and information about the Ecological Genomics Program at Kansas State University can be found at:

<http://www.k-state.edu/ecogen/>. Review of applications will begin July 1, 2006, and will continue quarterly until program resources are committed. The Visiting Scholar Program is sponsored by a Kansas State University Targeted Excellence Award in Ecological Genomics.

Eligibility: Requires permanent faculty position in an academic institution. Applicants from national and international laboratories are also encouraged to apply. Please note that this opportunity is not intended for post doctoral studies.

THE APPLICATION PROCEDURE: Full applications consist of a description of proposed research*, general outline of budget, C.V., and a letter of support from the host PI at KSU. A cover letter also should be included indicating a proposed start date. Applications should be e-mailed as a PDF to dmerrill@ksu.edu or mailed to:

Ecological Genomics Visiting Scholar Program Kansas State University Division of Biology, 231 Ackert Hall Manhattan KS 66506-4901

*Descriptions of proposed research are not to exceed 5 numbered pages, single-spaced, 11 point font or larger (not more than 16 characters/inch) with one inch margins. Proposals must be fully referenced (references are not included in the five page limit). Sections of the proposal should include Specific Aims, Background and Significance, Preliminary data (if any), and Research Plan. An abstract of 200 words or less should appear on page one.

For more information on these opportunities, email us at ecogen@ksu.edu or call (785) 532-3482.

KSU is an Equal Opportunity/Affirmative Action employer, and actively seeks diversity among its employees.

Plan now to attend the 4th Annual Symposium

Genes in Ecology, Ecology in Genes

November 3-5, 2006, in Kansas City.

Visit <<http://www.k-state.edu/ecogen/symp2006.html>> <http://www.k-state.edu/ecogen/symp2006.html> for more details.

Ecological Genomics Institute Kansas State University, Division of Biology 231 Ackert Hall, Manhattan, KS 66506-4901 (785) 532-3482, www.ksu.edu/ecogen

dmerrill@ksu.edu

KewGardens e-Taxonomy

The Royal Botanic Gardens, Kew invites applications for the following position (closing date - 30 June 2006):

EDIT e-Taxonomy Co-ordinator Fixed term contract to February 2011

Working with a team of plant diversity specialists, you will be involved in work package 6 of the EU-funded EDIT (European Distributed Institute of Taxonomy) consortium. Work package 6 (Title: Unifying Revisionary Taxonomy) aims to bring together fragmented taxonomic and biodiversity resources for delivery via a web portal and to encourage integration of international taxonomic effort.

Your main duties will include researching, assembling and delivering the digital content for a web portal, focusing on palms and other monocot plant families, liaising closely with the portal designer at the Natural History Museum, London. Content for the web portal will include nomenclature, taxonomic descriptions, images, identification guides, geographical, ecological and conservation data. You will also liaise with a wide range of stakeholders and participate in discussions on data, portal requirements and taxonomic issues.

With a degree in Biology or related discipline, you will have experience of biodiversity data resources and training in a biodiversity-oriented discipline. You will ideally have a PhD in a Biological discipline, or equivalent work experience, and will be familiar with flowering plant systematics, information management and databases. You will have excellent communication and organisational skills and the ability to deal with challenging and complex issues. Self-motivation is also essential as the role demands autonomy and close attention to data quality.

Salary is £21,308 per annum (pay award pending) 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 { HYPERLINK "<http://www.kew.org>" } www.kew.org (click on the link at the bottom of the homepage). Alternatively, please contact the

HR Department, RBG Kew, on 020 8332 5184/5150 (24 hour answerphone). Please quote Ref EDIT1. Closing

date: 30 June 2006.

William J. Baker Herbarium Royal Botanic Gardens, Kew Richmond, Surrey, TW9 3AE, UK Tel: 020 8332 5224, Fax: 020 8332 5278

W.Baker@rbgkew.org.uk

Montpellier PopBiol

Population biology researcher, UMR BGPI (Biologie et Génétique des Interactions Plantes-Parasites, <http://umr-bgpi.cirad.fr/>), CIRAD, Montpellier, France. Detailed announcement in english available at: http://www.cirad.fr/en/empl_formation/poste/-page.php?id=108

Chercheur en biologie des populations, UMR BGPI (Biologie et Génétique des Interactions Plantes-Parasites, <http://umr-bgpi.cirad.fr/>), CIRAD, Montpellier, France. Appel à candidature détaillé en français disponible à: http://www.cirad.fr/fr/empl_formation/poste/page.php?id=106

–

Merci de noter mes nouvelles coordonnées Please note my new adress, phone and fax numbers

Jean Carlier

UMR BGPI, CIRAD TA 41 / K, Campus International de Baillarguet 34398 Montpellier Cedex 5

Tél: 33 (0) 4 99 62 48 09, Fax: 33 (0) 4 99 62 48 12
e-mail: jean.carlier@cirad.fr

Bâtiment K, bureau 120

Jean Carlier <jean.carlier@cirad.fr>

NHM London ResLeader

THE NATURAL HISTORY MUSEUM

RESEARCH LEADERS

Salary £26,652 - £55,000 per annum (or more for exceptional candidates)

The Natural History Museum (NHM) wishes to appoint a number of Research Leaders to grasp a unique

opportunity to make a significant contribution to the future scientific research effort of this world-class institution. The NHM explores the diversity of the natural world and the processes that generate that diversity. Systematics and other collections-based investigations are at the heart of our research. We seek research leaders who can contribute to advances in our core science areas, collections development and pursuit of emerging areas, particularly our priority Research Foci (<http://www.nhm.ac.uk/research-curation/science-directorate/science-policies-strategy/assets/-researchframework.pdf>) which stress interdisciplinary research. We are particularly interested in receiving applications from researchers in the following areas:

* Systematic Biology * Biodiversity, including * Response to Global Environmental Change * Population Genetics * Eukaryotic Microbial Biodiversity * Molecular Phylogeny, Co-phylogeny and Co-evolution * Evolution and Development

Appointments will be made to any of the four Life Sciences departments (Botany, Entomology, Palaeontology, Zoology) as appropriate. We are willing to appoint at any band on our research scale, subject to negotiation and forward planning of research income. We are happy to consider appointing a team of scientists working on a common theme. You will need to demonstrate a record of scientific publications in international journals, achievement in gaining external research funding, and scientific leadership.

Further details are available on request (fca@nhm.ac.uk). You are strongly recommended to make informal contact before application to one of the following Heads of Department:

Botany: Dr Johannes Vogel. Tel. +44 (0)20 7942 5282, Email j.vogel@nhm.ac.uk
 Entomology: Dr Martin Hall. Tel. +44 (0)20 7942 5715, Email mhall@nhm.ac.uk
 Palaeontology: Prof. Norman MacLeod, Tel. +44 (0)20 7942 5204, Email n.macleod@nhm.ac.uk
 Zoology: Prof. Phil Rainbow. Tel. +44 (0)20 7942 5275, Email p.rainbow@nhm.ac.uk

To apply, please send your CV, together with a covering letter, and the names and addresses of three referees to Frances Allen, Science Directorate, The Natural History Museum, Cromwell Road, London SW7 5BD; Email fca@nhm.ac.uk. Please indicate if you would prefer any of your referees not to be contacted prior to interview.

Closing date: 20th June 2006.

Please quote reference: NHM/RL/FA

Tony Maggio <t.maggio@nhm.ac.uk>

NHN-Leiden Cryptogamist

A vacancy for a cryptogamist at the National Herbarium of the Netherlands is now open for applicants: <http://www.vacatures.leidenuniv.nl/-index.php3?m=1&c14> Please make this known to all you think that should know it.

The National Herbarium of the Netherlands (NHN)

The National Herbarium of the Netherlands (NHN) is an inter-university institute of the Universities of Leiden, Utrecht, and Wageningen with a collection of over 5.5 million specimens of phanerogams and cryptogams from all over the world, and a plant biodiversity research program including floristics, taxonomy, phylogeny, biogeography, and molecular evolution. For the Research group Phanerogams and Cryptogams of the Netherlands and Europe (PCNE, NHN-Leiden University branch), we invite applications for the position of a SYSTEMATIC CRYPTOGRAMIST (tenure track) Vacancy number: 6-128

The candidate should have a PhD degree and subsequent experience in the alpha-taxonomy of one of the cryptogamic groups (algae, bryophytes, or fungi) including experience in field research, an excellent publication record, an extensive international network, and knowledge of herbarium curation. The candidate should have experience in phylogenetic analyses and integrating molecular data into traditional systematics. The establishment of an active research program and pursuit of external funding is part of the job requirements. A strong commitment to the teaching of undergraduate and graduate students is mandatory. The ability to speak Dutch or the willingness to learn Dutch is required.

Tenure track within the Faculty of Mathematics and Natural Sciences means appointment for a period of maximum 6 years. Within these 6 years there will be an evaluation moment no later than after 3 years. After the first period of three years, a further three year contract may lead to the decision if a permanent staff position is offered. Salary in the first three years ranging from EURO 2708,- / 3554- gross per month depending on experience and an adapted salary within the further three year contract.

Further information about this position can be obtained from Dr. M. Noordeloos (e-mail:

Noordeloos@nhn.leidenuniv.nl) or Dr. S.G.A. Draisma (e-mail:

Draisma@nhn.leidenuniv.nl). For general information on the Leiden branch of the NHN visit our website at <http://www.nationaalherbarium.nl/> Applications, including motivation and specific research goals/targets, a CV, and the names and contact information of three references, should be sent before June 30 to: Mw. M. van Schoonhoven, Dienst Personeel & Organisatie Faculteit der Wiskunde en Natuurwetenschappen Postbus 95022300 RA Leiden, The Netherlands Alternatively to: m.vanschoonhoven@science.leidenuniv.nl and type the vacancy number in the subject line.

Draisma@nhn.leidenuniv.nl

NYBotanicalGarden CuratorialAssist

JOB OPENING at The New York Botanical Garden Herbarium

Curatorial Assistant-Brazilian specimen catalogue

The New York Botanical Garden Herbarium has an immediate opening for someone interested in participating in all aspects of creating an on-line catalogue of its extensive collection of plant specimens from the interior upland of Brazil. The catalogue will provide a preliminary checklist of the region's flora and will facilitate studies of its diversity and conservation.

Required qualifications and experience include: entering information from labels of Brazilian plant specimens into computer database; taking digital images of specimens; curating, selecting, and filing specimens according to taxonomic and geographic criteria; and other collections-related tasks as needed. Ideal candidate will have minimum of a B.S. or B.A. in plant biology; taxonomy coursework; familiarity with scientific plant names and other biological information and South American geography; capacity for organized, detail-oriented, accurate, efficient work; experience with databases and herbarium methods; working knowledge of Portuguese or Spanish; ability to reach specimens in cabinets 8 ft. high and at ground level. Salary is commensurate with experience, excellent benefits including 4 wks vacation. This is a grant funded position for three years.

Please send resume and cover letter to: HR Representative- CA, The New York Botanical Garden

200th St. & Kazimiroff Blvd. Bronx, NY 10458-5126. Fax (718) 220-6504. Email: hr2@nybg.org. EOE/M/F/D/V.

jkallunki@nybg.org

NYBotanicalGarden ProjectAssist

JOB OPENING at The New York Botanical Garden Herbarium

Project Assistant-Brazilian specimen catalogue

The New York Botanical Garden Herbarium has an immediate opening for someone interested in participating in all aspects of creating an on-line catalogue of its extensive collection of plant specimens from the interior upland of Brazil. The catalogue will provide a preliminary checklist of the region's flora and will facilitate studies of its diversity and conservation. Duties will include: entering information from labels of Brazilian plant specimens into computer database; taking digital images of specimens; curating, selecting, and filing specimens according to taxonomic and geographic criteria; and other collections-related tasks as needed.

Required qualifications and experience include: Minimum of a B.S. or B.A. in plant biology; taxonomy coursework; familiarity with scientific plant names and other biological information and South American geography; capacity for organized, detail-oriented, accurate, efficient work; experience with databases and herbarium methods; working knowledge of Portuguese or Spanish preferred; ability to reach specimens in cabinets 8 ft. high and at ground level. Salary is commensurate with experience, excellent benefits including 4 wks vacation. This is a grant funded position for three years.

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jkallunki@nybg.org

PennStateU ResTech

Greetings, would like to post this if possible. Thank you very much. Raul

Population Genetics in the lab of Bruce McPherson at Penn State University Park, PA

We are hiring a RESEARCH TECHNOLOGIST for OUR lab in the Department of Entomology. Position is available this summer (July start preferred); initial appointment for one year (and likely can be extended to three years) with pay determined by experience level.

RESEARCH SUMMARY: Our lab is currently focused on development of molecular assays for the genus *Anastrepha*. Experiments concentrate on sequencing-based data for determining relationships between and within species. Lab web page <http://www.ento.psu.edu/~mcpheronlab/>) has more information on research.

REQUIRED EXPERIENCE: A Bachelor's degree in entomology/biology or a closely related field is a plus and some experience in basic laboratory molecular techniques are required. Additional qualifications desired: experience with database management, Microsoft products, and experience supervising others.

RESPONSIBILITIES: Isolation and molecular analysis of DNA using PCR and other techniques; Supervision of undergraduates; Data analysis of results from molecular sequencing; Ordering and laboratory maintenance.

APPLICATION: Please submit a CV or resume, contact information for two references, and a cover letter summarizing your qualifications and interest in the position via email to Raul Ruiz at: rur132@psu.edu. Applications will be evaluated as they arrive. Raul A. Ruiz USDA APHIS CPHST The Pennsylvania State University 501 ASI Building University Park, PA 16802 814-865-3345 Lab 814-863-2871 Office 814-865-3048 Fax ...wjediagday

rur132@psu.edu rur132@psu.edu

QueenMaryLondon EvolInfection

SENIOR LECTURER in INFECTION Applications are invited for this post, which would suit a candidate interested in applying an evolutionary perspective to research in infection and immunity. This will be a full time, indefinite non-clinical appointment (£ 41k-46k) The appointee will join the Centre for Infectious Disease in the innovative new ICMS labs (<http://www.icms.qmul.ac.uk/index.html>)

The successful applicant will develop an independent research programme complementary to current research on HIV, Herpesviruses, Mycobacterial disease, Oral pathogens, antimicrobial resistance and Immunology of mucosal pathogens.

The appointee will also play a key role in new undergraduate course development in Infection and Immunity for the School of Biological Sciences (<http://www.sbcs.qmul.ac.uk/>) and the Medical School.

Informal enquiries can be made to Professor Judy Breuer, Tel: +44 20 7377 7141 email: j.breuer@qmul.ac.uk

A formal advert and administrative details are posted here. <http://www.qmul.ac.uk/~ugbt112/infection.pdf>

Richard Nichols Professor of Genetics http://www.sbcs.qmul.ac.uk/people_r.a.nichols@qmul.ac.uk
r.a.nichols@qmul.ac.uk

SanDiegoZoo ComparativePrimateGenet

Job: Comparative Primate Genetics at CRES/San Diego Zoo

Conservation and Research for Endangered Species (CRES).

The Zoological Society of San Diego has a short-term technical position available to undertake comparative molecular genetic studies of primates. Supported by a National Science Foundation award to establish the Integrated non-human Primate Biomaterials and Information Resource, the person filling this position assist with the establishment of a resource for high quality DNA samples of known provenance by undertaking molecular genetic characterization of primate samples, especially cell cultures,. For further information and to submit an application, please see the job posting at www.sandiegozoo.org . The position will be filled as soon as possible.

Oliver Ryder oryder@sandiegozoo.org

Oliver A. Ryder, Ph.D. Kleberg Genetics Chair Conservation and Research for Endangered Species Zoological Society of San Diego Arnold and Mabel beckman Center for Conservation Research 15600 San Pasqual Valley Road Escondido, CA 92027 ph: 760 291-5452 fax: 760 291-5451 oryder@sandiegozoo.org
<http://cres.sandiegozoo.org> Adjunct Professor Di-

vision of Biological Sciences Department of Ecology Behavior and Evolution University of California, San Diego oryder@ucsd.edu <http://biology.ucsd.edu/faculty/ryder.html> Oliver Ryder <oryder@ucsd.edu>

StonyBrook evolgenetics

A Research Scientist position is available in evolutionary genetics of *Drosophila* and other model and non-model organisms in the Dept. of Ecology and Evolution at Stony Brook University.

Under the supervision of the Dept. Chair, the Research Scientist will design and perform research and coordinate collaborative projects in evolutionary genetics and genomics in the *Drosophila* system and allied models. Molecular analyses to be conducted include DNA, RNA, and protein extraction, PCR, Quantitative RT-PCR, molecular cloning, comparative genomics, molecular genetic marker development, and compilation of datasets for quantitative trait locus analysis. Coordination of collaborative projects at the organism and molecular levels in various non-model organisms will also be a responsibility of this position.

Qualifications: Ph.D. in biological field plus four years of experience in molecular evolutionary genetics and/or genomics. Experience in PCR, RT-PCR, linkage mapping, molecular cloning, functional molecular genetics, and comparative genomics. Experience with *Drosophila* is preferred.

Interested candidates should send c.v. to:

Chair, Dept. of Ecology and Evolution c/o Donna Di-Giovanni 650 Life Sciences Bldg. Stony Brook University Stony Brook, NY 11794-5245

Anticipated start date: 8/1/06 Deadline for receipt of applications: 6/25/06

John True URL <http://life.bio.sunysb.edu/ee/truelab/> jrtrue@life.bio.sunysb.edu office 631-632-8506 Dept. of Ecology and Evolution lab 631-632-8588 650 Life Sciences Bldg. fax 631-632-7626 Stony Brook University Stony Brook, NY 11794-5245

John True <jrtrue@life.bio.sunysb.edu>

UBerne PopEcol

PhD-POSITION IN POPULATION ECOLOGY

Dept. Conservation Biology, Institute of Zoology, University of Berne, Switzerland.

The position is funded by the Swiss National Science Foundation. The general aim of the study is to advance integrated population models in order to model the dynamics of local populations. Integrated population models are of growing interest as they make simultaneous use of different kinds of data allowing the estimation of otherwise inaccessible demographic parameters. The population models shall be developed such that they are suited to analyse population dynamics of a typical short-lived passerine bird (pied flycatcher *Ficedula hypoleuca*) and of a long-lived species with delayed recruitment (white stork *Ciconia ciconia*). From both species long time data series are available. The ideal candidate is a very motivated graduate student with strong skills in quantitative data analysis and a deep understanding in mathematics. Ideally the candidate has knowledge in Bayesian statistics. The candidate does not need to have a biological education, applications of graduated mathematicians or statisticians are welcome. The study does not contain field work.

The successful candidates will join an active research group consisting currently of 5 advanced research staff, 3 PhD-students and a varying number of guest scientists and masters students (www.conservation.unibe.ch). Besides the Conservation Biology group, the ecologically oriented Zoological Institute of the University of Bern consists of research groups on Aquatic Ecology (Ole Seehausen), Behavioural Ecology (Michael Taborski), Evolutionary Ecology (Heinz Richner), Population Genetics (Laurent Excoffier) and Synecology (Wolfgang Nentwig). Salaries will follow the schemes of the Swiss National Science Foundation.

Closing date: Open until filled, but all application materials, including a letter of motivation, CV and, possibly, list of publications should be received by July 1, 2006 to ensure full consideration. The positions will start at the earliest possible date. Please send all application material via postal or e-mail. For inquiries please contact michael.schaub@nat.unibe.ch.

Michael Schaub Zoological Institute - Conservation Bi-

ology University of Bern Baltzerstrasse 6 3012 Bern Switzerland

michael.schaub@nat.unibe.ch

Dr. Michael Schaub Schweizerische Vogelwarte CH-6204 Sempach Switzerland e-mail: michael.schaub@vogelwarte.ch Tel.: ++41 (0)41 462 97 66 Fax: ++41 (0)41 462 97 10 www.vogelwarte.ch &

Zoological Institute Div. Conservation Biology University of Bern Baltzerstrasse 6 CH-3012 Bern Switzerland e-Mail: michael.schaub@nat.unibe.ch Tel.: ++41 (0)31 631 31 63 Fax: ++41 (0)31 631 45 35 www.conservation.unibe.ch michael.schaub@vogelwarte.ch

UCSanDiego Tech

Conservation and Research for Endangered Species (CRES).

The Zoological Society of San Diego has a short-term technical position available to undertake comparative molecular genetic studies of primates. Supported by a National Science Foundation award to establish the Integrated non-human Primate Biomaterials and Information Resource, the person filling this position assist with the establishment of a resource for high quality DNA samples of known provenance by undertaking molecular genetic characterization of primate samples, especially cell cultures. For further information see the job posting at <http://www.sandiegozoo.org/CF/jobs/-JobResults.cfm> The position will be filled as soon as possible.

oryder@ucsd.edu

UCCambridge ResAssist

Department of Zoology University of Cambridge

RESEARCH ASSISTANT

£20,235 - £22,774 per annum.

Applications are invited for a Research Assistant position on a NERC-funded project to investigate the evolutionary genetics of primate colour vision. The position is based in the Evolutionary Genetics Group of the Department of Zoology, University of Cambridge (Laboratory of Nick Mundy: <http://www.zoo.cam.ac.uk/-zoostaff/egg/Index.htm>). The research is laboratory based and involves DNA sequencing of opsin genes. The successful candidate must have a Bachelor's degree, or equivalent, and an enthusiastic, academic interest in zoology, genetics and evolution. Experience in basic molecular biology techniques (PCR, gel electrophoreses, DNA sequencing) is advantageous but not required. The position is available for up to nine months. The starting date of the position is flexible, but the project must commence by September 2006.

For general enquiries please contact Dr. Brenda Bradley by email: bjb37@cam.ac.uk.

Applicants should send their C.V. together with a completed PD18 form (available at <http://www.admin.cam.ac.uk/offices/personnel/forms/-pd18/>) to the Departmental Administrator either via email: ag318@hermes.cam.ac.uk or by post to The Department of Zoology, University of Cambridge, Cambridge CB2 3EJ, UK.

The application deadline is 15 July 2006 or until the position is filled.

bjb37@cam.ac.uk bjb37@cam.ac.uk

UConnecticut Bioinformatics

The University of Connecticut is looking for a bioinformatician to work in a bioinformatics services facility. The main task will be to interact with biologists (mainly from the departments of Ecology and Evolutionary Biology, Molecular and Cell Biology, and Pharmacy) and help them to use computational approaches to solve their problems. The advertisement is at <http://www.biotech.uconn.edu/bf/bioinfrm.pdf>.

I would very much appreciate, if you could bring the advertisement to the attention of suitable candidates.

j.p.gogarten@uconn.edu j.p.gogarten@uconn.edu

UConnecticut MicrobialEvol

The Department of Molecular and Cell Biology at the University of Connecticut invites applications for two tenure-track positions at the ASSISTANT or ASSOCIATE PROFESSOR levels in the areas of 1) Functional Genomics of Complex Communities, 2) Molecular Evolution of Microbial Systems or 3) Genetics of Microbe/Host Interactions. We seek investigators using genome-wide approaches to investigate: gene expression and functions of microbes in complex environments, the evolution of metabolic pathways or regulatory networks, the roles of horizontal gene transfer in evolution, the effects of host associations on the evolution of bacteria and their host, or the coordination of microbe physiology with that of the host. Successful applicants are expected to establish a productive research program, teach undergraduate microbiology and contribute to graduate courses.

Start date: Fall 2007 (!). Applicants must have postdoctoral experience and an outstanding research record. UConn boasts strong research in microbial symbiosis, evolution, genomics, and ecology (<http://microbiology.uconn.edu>). The University of Connecticut, rated first among public universities in New England, is located in northeastern Connecticut with easy access to Boston and New York City.

Submit a CV, a concise statement of research and teaching interests, and three letters of recommendation to: Microbiology Search Committee Chair, Department of Molecular and Cell Biology U-3125, University of Connecticut, Storrs, CT 06269. Review of applications will begin June 21, 2006 and continue until the positions are filled. The Department's web page is <http://mcb.uconn.edu>. We encourage applications from underrepresented groups including minorities, women, and people with disabilities.

[http://www.mcb.uconn.edu/information/Job Ad for Micropositions.pdf](http://www.mcb.uconn.edu/information/Job%20Ad%20for%20Micropositions.pdf)

gogarten@gmail.com

UEdinburgh TempTeaching EvolBiol

Two posts in the Institutes of Evolutionary Biology & Immunology and Infection Research (Ashworth Labs), School of Biology, University of Edinburgh

Two posts are available for 9-10 months, to cover sabbatical absences of Nick Barton and Andrew Read. These will provide undergraduate and M.Sc. teaching

at senior undergraduate and Masters level. Teaching loads are not onerous and the positions would especially suit anyone interested in developing research grant or fellowship applications to work in these Institutes in subsequent years.

A Ph.D. in evolutionary biology, parasitology or a related area is required. Ability to teach quantitative methods in a biological context to final year students is essential for one of the posts. The posts can start on August 1st, or shortly thereafter to give time for preparation before term starts in mid-September. Salary will be at a rate of around £25,400 per annum or more, depending on experience. There may be a possibility of extending one of these posts for a further four years for a person who can cover parasitology/evolution/biometrics.

A variety of teaching is involved: requirements are flexible, depending on the candidates' experience. Teaching materials are already prepared. Courses include Honours teaching in basic statistics, parasitology, ecology and evolutionary biology for Zoology and Evolutionary Biology final year students; earlier year teaching in marine biology, ecology and evolution; evolutionary genetics for the M.Sc. in Quantitative Genetics and Genome Analysis (<http://www.qgen.com>); and teaching the foundations of evolutionary biology in the M.Sc. Evolution of Language and Cognition (<http://www.ling.ed.ac.uk/~simon/teaching/foundevol/>). Assistance in running the new Honours Programme in Evolutionary Biology will also be required.

CLOSING DATE 16th JUNE

To apply and for further details, see www.jobs.ed.ac.uk (vacancy numbers 3005939 and 3005934). Informal queries to Andrew Read (A.Read@ed.ac.uk) or Nick Barton (n.barton@ed.ac.uk)

n.barton@ed.ac.uk n.barton@ed.ac.uk

UExeter EcolConservation

Hi All

Please see note below on positions becoming available with us very soon. Apologies if cross-posting means you receive multiple copies.

With kind regards

Brendan

Dr. Brendan J. Godley Centre for Ecology &

Conservation School of Biosciences University of Exeter Homepage <<http://www.uec.ac.uk/biology/index.shtml>>. <<http://www.seaturtle.org/mtrg/>> Editor-in-Chief, Endangered Species Research <<http://www.int-res.com/journals/esr/>>

Multiple Appointments in Ecology and Conservation University of Exeter, Cornwall Campus (UK)

The School of Biosciences, University of Exeter is seeking to recruit up to four new staff for the second phase of growth on its Cornwall Campus.

<<http://www.uec.ac.uk/biology/index.shtml>>.

These posts will build on the existing strengths on the Cornwall Campus, which currently consists of 13 academic staff. Posts are available at all levels up to chair.

Chair / Reader in Ecology or Conservation Biology

We are seeking to recruit someone who will provide leadership in the area of ecology and/or conservation biology following the retirement of Professor Bryant. We would be particularly interested in appointing someone with strengths in field ecology or conservation but encourage all interested parties to apply.

Lectureships in Ecology and Conservation Biology

We have between two and four lectureships available in the field of ecology and conservation biology. We are looking to build on our existing strengths and buoyant undergraduate and postgraduate degrees programmes in ecology and conservation. We would be particularly interested in recruiting vertebrate and plant ecologists, in population and community ecology and conservation biology and genetics.

Timing

Posts are available from September 2006

.

Further information:

Interested applicants are encouraged to approach Prof. M.R. Evans (m.r.evans@ex.ac.uk) or Prof. N.J. Talbot (n.j.talbot@ex.ac.uk).

Further particulars:

Positions in Ecology and Conservation Biology

The School of Biosciences on the University of Exeter's Cornwall Campus has now been established for two years and currently consists of 13 academic staff (4 professors, 3 readers, 2 senior lecturers and 4 lecturers). This represents the end of the first phase of development, we are now seeking to recruit for the second phase and are planning for the third phase which will see the expansion of this group to approximately

30 academic staff. The staff on the Cornwall Campus all work within the Centre for Ecology and Conservation and future growth will be broadly within this area of biology. We have buoyant undergraduate and postgraduate degrees in ecology and conservation (currently recruiting 50 at undergraduate and 30 at postgraduate level). The group has a combined research income of about £1.5M and a research postgraduate population of 25.

Chair / Reader in Ecology and / or Conservation Biology

Following the retirement of Professor Bryant, we are seeking to recruit someone to provide leadership in ecology and / or conservation biology and to inform the development of the group as we move into future.

We would be interested in considering anyone whose research programme fell within the general areas of ecology or conservation biology. However, we would be particularly interested in recruiting someone with interests and expertise in field ecology. We would also benefit from recruiting someone whose work would utilise molecular or conservation genetics. The successful applicant will have a track record of obtaining external funding from a variety of sources, both governmental and non-governmental as appropriate for their research programme. He/she should have supervised research postgraduate students. Importantly the successful applicant will have a series of publications in high profile journals sufficient to be considered an international figure in the field by his/her peers.

We would expect any recruit at this level to have a teaching load (at both undergraduate and postgraduate level) commensurate with the maintenance of their research programme and to participate in the leadership, management and administration of the school across both campuses.

The successful applicant will be in a position to influence the appointment of the more junior positions. It may also be worth any applicants considering that between 2008 and 2012 the school of biosciences has plans to expand to 30-35 academic staff within ecology, evolution and conservation. These plans are externally funded as part of the development of the Combined Universities of Cornwall (of which the University of Exeter is a major partner) that is a crucial part of

— / —

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

UExeter EvoBiol

We are seeking to recruit up to four new staff for the second phase of growth of the Centre for Ecology and Conservation, University of Exeter, Cornwall Campus. These posts will build on the existing strengths in the Centre, which currently consists of 13 academic staff housed in a new building in a spectacular location in Cornwall outside of Falmouth. Posts are available at all levels up to chair. Quality of research is more important than specific area.

In general, we are looking to recruit:

Chair / Reader in Ecology or Conservation Biology. We are seeking to recruit someone who will provide leadership in the area of ecology and/or conservation biology following the retirement of Professor Bryant. We would be particularly interested in appointing someone with strengths in field ecology or conservation but encourage all interested parties to apply.

Lectureships in Ecology and Conservation Biology. We have between two and four lectureships (assistant professorships) available in the field of ecology and conservation biology. We are looking to build on our existing strengths and buoyant undergraduate and postgraduate degrees programmes in ecology and conservation. We would be particularly interested in recruiting vertebrate and plant ecologists, in population and community ecology and conservation biology and genetics.

Posts are available from September 2006.

Interested applicants should contact Prof. Matthew R. Evans (M.R.Evans@exeter.ac.uk) or Prof. Allen J. Moore (A.J.Moore@exeter.ac.uk).

Allen J. Moore Professor of Evolutionary Genetics Centre for Ecology & Conservation School of Biosciences University of Exeter Cornwall Campus Penryn TR10 9EZ UK

Telephone: +44 (0)1326 371 883 Fax: +44 (0)1326 253 638

E-mail: A.J.Moore@exeter.ac.uk

<http://www.uec.ac.uk/biology/research/staff-research-interests/allen-moore.shtml>

A.J.Moore@exeter.ac.uk A.J.Moore@exeter.ac.uk

UGlasgow Biostatistics

UNIVERSITY of GLASGOW

FACULTY OF INFORMATION AND MATHEMATICAL SCIENCES

ROBERTSON CENTRE FOR BIOSTATISTICS

Senior Research Fellow/Reader 12226/DPF/A3 £33,646 - £43,850 per annum

Research Fellow 12225/DPF/A3 £20,044 - £30,002 per annum

Biostatistician 12051/DPF/A3 £20,044 - £30,002 per annum

Applicants for these posts in Biostatistics may have interests in any area of Biostatistics, including Statistical Genetics, Clinical Trials and Statistical Epidemiology. The successful candidates will be expected to have excellent records of academic achievement and a commitment to enhancing the strong research profile of the Centre. Applicants for the post of Senior Research Fellow/Reader will be expected to attract and secure research funding and build a research group in their area of expertise.

Informal enquiries may be directed to Professor Ian Ford (tel 0141-330-4744; email ian@stats.gla.ac.uk). Information on the Centre and the linked Department of Statistics is available on the Web at www.rcb.gla.ac.uk and www.rcb.gla.ac.uk For an application pack please see our website at www.gla.ac.uk. Applications should be submitted to Ms Liz Anderson, Assistant Director, Robertson Centre for Biostatistics, Boyd Orr building, University of Glasgow, Glasgow G12 8QQ quoting the appropriate reference number. Applications should be received by 30 June 2006.

– Catherine Young Advertising Co-ordinator Tel. 0141 330 3379 Fac. 0141 330 3905

Catherine Young <c.young@admin.gla.ac.uk>

UGuelph LabTech Barcodes

Lab Technician Positions(s) at the Canadian Centre for

DNA Barcoding Location: Canadian Centre for DNA Barcoding, Biodiversity Institute of Ontario, University of Guelph, Guelph, Ontario, Canada.

Responsibilities: The Canadian Centre for DNA Barcoding invites applications for technicians to work in close association with lab managers and postdoctoral researchers conducting research in species discovery and identification in tropical insects using DNA barcodes. Research in our lab utilizes high-volume DNA isolation protocols optimized for use with robotic liquid handling systems. Barcode sequencing is performed using two ABI 3730 sequencers. DNA extraction, amplification and sequencing will generally be performed by a technician working independently, while sequence editing and analysis will be in closer collaboration with the supervising postdoctoral researcher. Applicants should be well-rounded individuals with a molecular biology and genetics background and strong time management skills.

*Molecular biology: Preparation of DNA extractions, PCR, DNA sequencing, and DNA sequence analysis. Occasional use of robotics may be required, but training can be provided.

*Computer work: Data analysis using a variety of software packages. Utilize molecular biology software (e.g. primer design, sequence alignment, database searches, etc.), and analysis of data Barcode of Life Datasystems (BOLD) software.

Qualifications: B.Sc. in molecular biology or related field. Coursework and/or experience in genetics.

Closing Date: Open until filled. Preferred starting date August 1, 2006.

Contact: Send cover letter, résumé, to Dr Alex Smith, Biodiversity Institute of Ontario, Integrative Biology, University of Guelph, Guelph Ontario, N2G 1W1 or e-mail materials to salex@uoguelph.ca

– M. Alex Smith PhD Biodiversity Institute of Ontario Department of Integrative Biology University of Guelph Guelph ON N1G 2W1 (519) 824-4120 office ext. 56393 lab ext. 52709 www.barcodinglife.org salex@uoguelph.ca

UHawaii EvolBiology

Assistant Professor of Biology: Position No. 86432T, University of Hawaii at Hilo, College of Arts & Sciences,

temporary, nine-month appointment to begin approximately August 2006 and end July 31, 2007; pending position clearance and funding; possibility of reappointment.

Duties: Teach undergraduate lecture and laboratory courses in cell and molecular biology, cell biology, biochemistry, and introductory (non majors) biology.

Minimum Qualifications: Ph.D. from an accredited college or university in a biological science discipline appropriate to the position, demonstrated expertise in cell and molecular biology.

Desirable Qualifications: Teaching experience at the college or university level and an active research program in biological sciences.

Salary: Competitive.

To Apply: Submit curriculum vitae, letter of application, transcript(s) showing degrees and course work appropriate to the position (copies are acceptable), and the names and e-mail addresses of three recent references to: Dr. Susan Jarvi at <<mailto:jarvi@hawaii.edu>> jarvi@hawaii.edu (preferred) or to Biology Department, University of Hawaii at Hilo, 200 W. Kāwili St., Hilo, Hawaii.

Inquires: Dr. Susan Jarvi, ph. 808-974-7358, fax 808-974-7693, email jarvi@hawaii.edu.

Deadline: First review of applications will begin 1 July 2006 and continue until the position is filled.

The University of Hawaii is an EEO/AA Employer D/M/V/W.

Sue Jarvi Associate Professor Chair, Biology University of Hawaii 200 West Kawili Street Hilo, HI 96720 808 974-7358 FAX 808 974-7693 jarvi@hawaii.edu

jarvi@hawaii.edu

ULausanne EvolZool

Professorship in Zoology

The Faculty of Biology and Medicine of the University of Lausanne invites applications for a position of assistant (tenure-track), associate or full professor starting in March 2007 or earlier. All areas of zoology will be considered provided that the candidate has a strong interest in organismic biology.

The position will be in the Department of Ecology and

Evolution which has a long track record of excellence in research. A generous start-up package and state-of-the-art research infrastructure will be available within an environment which favours collaborations.

The successful candidate is expected to develop an internationally recognized research program funded by external sources. Teaching duties include an undergraduate class of zoology. The appointee will supervise PhD students and participate to other training activities of the department. For further information, contact Laurent Keller.

Applications, including a curriculum vitae, a brief statement of research program and the names of three referees should be sent before July 15th, 2006 to Patrice Mangin, Dean of the Faculty of Biology and Medicine, University of Lausanne, Rue du Bugnon 21, CH-1005 Lausanne, Switzerland.

Applications from women are encouraged.

Laurent Keller Department of Ecology and Evolution Biophore University of Lausanne 1015 Lausanne Switzerland

<http://www.unil.ch/dee/page6763.html>
Laurent.Keller@unil.ch Laurent.Keller@unil.ch

Lau-

ULausanne PlantEvolEcol

Professorship in Plant Ecology

The University of Lausanne invites applications for an associate professorship starting in March 2007 or earlier. All areas of plant ecology will be considered.

The position will be in the Department of Ecology and Evolution, Faculty of Biology and Medicine with possible joint appointment with the Faculty of Geosciences and Environment, depending on the candidate's profile. A generous start-up package and state-of-the-art research infrastructure will be available within an environment which favors collaborations.

The successful candidate is expected to develop an internationally recognized research program funded by external sources. Teaching duties include an undergraduate class of plant ecology and field courses. The appointee will supervise PhD students and participate to other training activities of the Department. For further information, contact Nicolas Perrin

Applications, including a curriculum vitae, a brief statement of research program and the names of three

referees should be sent before August 31st, 2006 to Patrice Mangin, Dean of the Faculty of Biology and Medicine, University of Lausanne, Rue du Bugnon 21, CH-1005 Lausanne, Switzerland.

Applications from women are encouraged.

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>

ULaval EvolGenomics

The Department of Biology of Université Laval invites applications for a tenure-track faculty appointment in evolutionary genomics and bioinformatics at the rank of assistant professor. The person appointed in this position will form part of the Canada research chair in genomics and conservation of aquatic resources awarded to Louis Bernatchez (<<http://www.bio.ulaval.ca/louis.bernatchez/>><http://www.bio.ulaval.ca/louis.bernatchez/>). The overall objective of the chair is to generate knowledge that will stimulate the long term economic viability and social value of aquatic resource exploitation. The research program will also contribute to the understanding of evolutionary processes that are modulating genetic diversity structuring and organismal adaptation to environmental changes. Applicants should have a Ph.D. in biological sciences and relevant expertise in evolutionary genomics and bioinformatics; postdoctoral experience would be desirable. The appointee is expected to speak French within a year, to teach undergraduate and graduate courses in biology and bioinformatics, to supervise graduate students, to develop an independent grant-funded research program, and to participate in the research activities of the chair. Université Laval has an affirmative action policy committed to reducing gender imbalance; qualified women are strongly encouraged to apply. Closing date: October 31, 2006. The position could be filled as soon as January 1, 2007, but no later than May 1, 2007. Eligible candidates should submit a letter describing their qualifications and motivation for the position, a CV, and a copy of pertinent papers to the Chair of the Department of Biology, Gilles Houle, Département de biologie, Université Laval, Québec, QC G1K 7P4. FAX : 418-656-2043

<mailto:gilles.houle@bio.ulaval.ca>gilles.houle@bio.ulaval.ca
 Two letters of reference should also be sent directly to the Department.

Le Département de biologie de l'Université Laval sollicite des candidatures pour un poste de professeur (professeure) régulier, au rang d'adjoint, en génomique évolutive et bioinformatique dans le cadre de la chaire de recherche du Canada en génomique et conservation des ressources aquatiques (titulaire : Louis Bernatchez, (<<http://www.bio.ulaval.ca/louis.bernatchez/>-><http://www.bio.ulaval.ca/louis.bernatchez/>)).

L'objectif premier de cette Chaire est de générer des connaissances qui stimuleront la viabilité économique à long terme et la valeur sociale de l'exploitation des ressources aquatiques. Ce programme de recherche contribuera de plus à la compréhension des processus évolutifs qui modulent la structuration de la diversité génétique et l'adaptation des organismes face aux changements environnementaux. Formation et compétence requises : doctorat dans une des spécialisations pertinentes des sciences biologiques; expérience postdoctorale souhaitable; expertise en génomique évolutive et bioinformatique. Le (la) candidat(e) devrait pouvoir parler couramment le français dans un délai d'un an, enseigner en biologie et en bioinformatique aux trois cycles, posséder un excellent dossier de publications et de recherche, recruter des étudiants aux deuxième et troisième cycles, obtenir des subventions de recherche dans son domaine d'expertise et participer aux activités de la chaire. L'Université Laval a une politique d'équité en matière d'emploi et les femmes sont fortement encouragées à poser leur candidature. Date de clôture : 31 octobre 2006. Le poste pourrait être comblé dès le 1 janvier 2007 ou, au plus tard, le 1 mai 2007. Les personnes intéressées doivent faire parvenir un dossier de candidature à Gilles Houle, Département de biologie, Université Laval, Québec, QC G1K 7P4. Télécopieur : 418-656-2043 <mailto:gilles.houle@bio.ulaval.ca>gilles.houle@bio.ulaval.ca
 Ce dossier doit comprendre une lettre d'intention, un curriculum vitae détaillé et une copie des publications les plus pertinents. Deux lettres de référence doivent également parvenir directement au département.

Louis.Bernatchez@bio.ulaval.ca

UManchester ResTech

A research technician position is available for nine months to assist with studies of the genetic architec-

ture of complex traits. The technician will work in team of evolutionary geneticists to study the genetic basis of shape variation in animals and its implications for our understanding of evolution processes. Work will involve three dimensional digital imaging and measuring of complex morphological structures. There will also be opportunities to contribute to other ongoing research projects in evolutionary quantitative genetics.

This position is funded as part of a collaboration between Jason Wolf, Chris Klingenberg (both at The University of Manchester) and Jim Cheverud (Washington University, St Louis). The technician will work in Manchester, but will have opportunities to interact with all three investigators as Dr. Cheverud will be in Manchester for most of the tenure of the position.

The closing date for applications is 30 June 2006 and the projected start date is August 1st 2006, but the latter date is open to negotiation. For further details of the position see:

<http://www.newscientistjobs.com/-viewjob.action?job.id=NS20062556080&index=3>

For further details about the nature of the work that the technician will do and of the research project please contact Jason Wolf (jason@evolutionarygenetics.org) or Chris Klingenberg (cpk@manchester.ac.uk).

Individuals looking for longer term employment opportunities should inquire about forthcoming open technician positions.

jason@evolutionarygenetics.org

UOxford EvolZool

UNIVERSITY OF OXFORD

University Lecturership in Zoology
 in association with Magdalen College

Applications are invited for the above University Lecturership, tenable from 1 October 2006 or as soon as possible thereafter. The Lecturership is associated with a Tutorial Fellowship at Magdalen College. The combined University and College salary will be on a scale up to £47,078 per annum (under review), and additional substantial College allowances (including a pensionable housing allowance) are available.

The University and the College are seeking candidates with a proven record of teaching and research in zoology, and a track record of attracting research funding.

The Lecturership will be established at the interface of at least two of the Department's research groupings: behaviour, development, disease, ecology, entomology, evolution, and ornithology.

The appointee will be required to engage in research, which will contribute to the Department's research reputation; to teach, supervise and examine undergraduate and graduate students; and to contribute to administration in the College and Department.

Further particulars are available from Professor Paul H. Harvey, FRS, Head, Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS, email paul.harvey@zoo.ox.ac.uk, to whom applications should be sent for receipt not later than 7 July 2006. Please quote reference number MPS/5/4.

Interviews will be held on a date to be determined.

The University of Oxford and Magdalen College are Equal Opportunities Employers.

paul.harvey@zoo.ox.ac.uk

UOxford EvolZoology

UNIVERSITY OF OXFORD

University Lecturership in Zoology

in association with Magdalen College

Applications are invited for the above University Lecturership, tenable from 1 October 2006 or as soon as possible thereafter. The Lecturership is associated with a Tutorial Fellowship at Magdalen College. The combined University and College salary will be on a scale up to £47,078 per annum (under review), and additional substantial College allowances (including a pensionable housing allowance) are available.

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The appointee will be required to engage in research, which will contribute to the Department's research reputation; to teach, supervise and examine undergraduate and graduate students; and to contribute to administration in the College and Department.

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Interviews will be held on a date to be determined.

The University of Oxford and Magdalen College are Equal Opportunities Employers.

paul harvey <paul.harvey@zoo.ox.ac.uk>

UOxford HumanEvol

UNIVERSITY OF OXFORD

Department of Zoology

ACADEMIC FELLOWSHIP SCHEME Human Evolution

Applications are invited for this 5-year fellowship, which will lead to a permanent Faculty position in the Department of Zoology and an associated Tutorial Fellowship at St Hugh's College on the successful completion of a probationary period.

The Academic Fellowship Scheme is a national initiative funded by the Research Councils to provide a structured path into an academic career for contract research staff and other suitably qualified individuals. Applicants may have guaranteed research funding from a source other than the Academic Fellowship for at least part of the five-year fellowship period; the scheme is open to researchers supported on any type of grant funding and to holders of current fellowship awards. However, departmental funds are available to help support returners or other researchers without current research support. The Academic Fellow will:

- have a research interest in Biological Anthropology, with a preference for human evolution.

- take up their appointment by 30 September 2006.

- be paid on the research support scales during the fellowship period according to experience and stage of academic career. A College stipend and housing allowance will also be available as the appointee takes on the role of a Tutorial Fellow from the second year of the appointment.

The University will especially welcome applications from women and ethnic minorities.

Further particulars for the post(s) together with details of the Academic Fellowship Scheme are available on the university website at <http://www.admin.ox.ac.uk/-fp/> or from the Head of the Department of Zoology: paul.harvey@zoo.ox.ac.uk.

paul.harvey@zoo.ox.ac.uk

UOxford MalariaStatistician

The University of Oxford

Wellcome Trust Centre for Human Genetics

STATISTICIAN ACADEMIC-RELATED RE-
SEARCH STAFF GRADE IA: £20,044 - £30,002

Applications are invited for the post of Statistician within the Malaria Genomic Epidemiology Network (MalariaGEN: www.malariagen.net) funded through the Grand Challenges in Global Health initiative and coordinated from Oxford. Our goal is to contribute to the development of an effective malaria vaccine by discovering natural mechanisms of disease resistance, through state-of-the art analysis of genome variation combined with large-scale epidemiological studies in malaria-endemic regions.

The postholder will provide statistical support for these large-scale studies involving MalariaGEN partners in 20 countries, working closely with epidemiological, laboratory, and informatic teams based at Oxford University and the Wellcome Trust Sanger Institute. Working together with the Principal Investigator, the Senior Statistician and international experts in statistical genetics and population genetics they will contribute to the design and cost-effectiveness of large-scale genotyping experiments, including whole genome association studies costing in excess of £1 million. There will be opportunities for the postholder to contribute to the development of statistical applications to tackle practical roadblocks in the genetic analysis of malaria, such as population stratification and epistatic interactions. They will interact particularly closely with an enthusiastic group of informaticians and software engineers, and will help to provide training in statistical genetics and computational methods for MalariaGEN Fellows in 14 malariaendemic countries.

A background in statistical genetics is highly desirable but training could be provided in this area for a candidate with a very strong mathematical, computational or analytical background.

A detailed job description quoting reference H5-06-022-DK is available from the Personnel Administrator (tel: 01865 287508, email: personnel@well.ox.ac.uk, web <http://www.well.ox.ac.uk/vacancies/index.shtml>).

Please send your letter of application with full curriculum vitae and the names and addresses of two referees quoting the above reference number to: The Personnel Administrator, The Wellcome Trust Centre for Human Genetics, Roosevelt Drive, Oxford OX3 7BN or by email to personnel@well.ox.ac.uk or fax to 01865 287516.

The closing date for applications is Friday, 07 July 2006.

o_ Jonathan Marchini c/ /'_ Department of Statistics, University of Oxford (+) \(+\) 1 South Parks Road, Oxford, OX1 3TG

tel : ++44 1865 271125 web : <http://www.stats.ox.ac.uk/~marchini/> marchini@stats.ox.ac.uk

UOxford QuantBiol

UNIVERSITY OF OXFORD ACADEMIC FELLOWSHIP SCHEME QUANTITATIVE BIOLOGY

Applications are invited for this 5-year fellowship, which will lead to a permanent Faculty position in the Department of Zoology and an associated Tutorial Fellowship at Brasenose College on the successful completion of a probationary period.

The Academic Fellowship Scheme is a national initiative funded by the Research Councils to provide a structured path into an academic career for contract research staff and other suitably qualified individuals. Applicants may have guaranteed research funding from a source other than the Academic Fellowship for at least part of the five-year fellowship period; the scheme is open to researchers supported on any type of grant funding and to holders of current fellowship awards. However, departmental funds are available to help support returners or other researchers without current research support. The Academic Fellow will: - have or be on the way to building a record of internationally excellent research in biology, through an outstanding record of research that encompasses a quantitative aspect of the subject. - take up the appointment on or after 1 October 2006. - be paid on

the research support scales during the fellowship period according to experience and stage of academic career. College stipends will also be available. The University will especially welcome applications from women and ethnic minorities meeting the selection criteria, who are under-represented among its academic staff (section 38 of the Sex Discrimination Act 1975 and section 48 of the Race Relations Act 1976 apply). Further particulars for the post(s) together with details of the Academic Fellowship Scheme are available on the university website at <http://www.admin.ox.ac.uk/-fp/> or from the Head of the Department of Zoology: paul.harvey@zoo.ox.ac.uk (please quote reference number AT 06036) or from www.zoo.ox.ac.uk/-Current_Vacancies/ The closing date for applications is 4 August 2006.

-

paul.harvey@zoo.ox.ac.uk

UWales EnvGenomics

The University of Wales, Bangor seeks applications from candidates with a proven world-class record of research in environmental genomics capable of exploiting recently acquired state-of-the-art genomic and post-genomic equipment to investigate organism function within the environment. You will have a strong track record of research funding and academic leadership, commensurate with playing a leading role in the Welsh Centre for Integrative Research in the Rural Environment, and also linking with the collaborative Centre for Catchment and Coastal Research.

The successful candidate will lead research into the utilisation of existing and new genomic knowledge and technology in order to advance evolutionary and ecological theory, and understanding of ecosystem structure and function. Achieving this will be facilitated by linkage with the strong research base in gene regulation, metabolite profiling and molecular ecology already present in the two partner universities in Bangor and Aberystwyth.

Informal Enquiries should be addressed to:

Prof Gary Carvalho (g.r.carvalho@bangor.ac.uk) Dr. Sue Assinder, Head of School (s.assinder@bangor.ac.uk)

chrisg@bangor.ac.uk chrisg@bangor.ac.uk

Other

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AFLP Software STRand

I am just getting started with developing AFLP markers from the forest fungi on which I work, and am hoping to get some help in using the software that's out there. Looks like the file format for 3730 data is different than that used for the 3700 and others. I'm awaiting a version of Genographer that has been modified to work with 3730 data. I've also downloaded and installed STRand, but can't make sense of it. Is there anyone out there who can give me some step by step guidance in the use of STRand for 3730 data? I contacted their support but haven't heard back. I've heard good things about GeneMarker, but it's pricey (\$5K!).

Thanks, Bob Marra Plant Pathology & Ecology
The Connecticut Agricultural Experiment Station 123
Huntington St New Haven CT 06511

Robert.Marra@po.state.ct.us

CellLysing DNAextraction

Dear evoldir members,

I am setting up a new lab, including DNA extraction, and need some advice. In the past I have used grinding in liquid N to lyse cells in plant tissue before using Qiagen kits, but am not entirely satisfied with the results or the process. I would like to move to something more mechanized and efficient. I know some folks use the Mixer Mill 300 (from Reusch or Qiagen), but others use the Fast Prep Instrument (from Qbiogene). Does anyone have any first hand knowledge – or even hearsay – about which is better or more cost effective? If so, or you just would like to tell me about your own experiences with either instrument, please email me at deborah.overath@tamucc.edu.

I will post a summary of any replies in case others are interested!

Thanks,

Deb Overath

R. Deborah Overath, Ph.D. Assistant Professor of Biology Department of Physical and Life Sciences (ST 312) 6300 Ocean Drive, Unit 5800 Texas A&M - Corpus Christi Corpus Christi, TX 78412

Phone: (361) 825-2467 Fax: (361) 825-2742 email: deborah.overath@tamucc.edu

Climate rooms

Hi colleagues, our institute will move to another building in a few years. Since energy expenditure is high and only expected to increase, we should take the opportunity to reduce the ecological footprint of our institute.

My question: do you know examples of heat storage systems, or other types of efficient energetic design for climate rooms? We could then ask engineers to apply them in our new site.

thanks for any advice or experiences, Tom Van Dooren
Institute of Biology Leiden, The Netherlands

vdooren@rulsfb.leidenuniv.nl

Coleoptera nuclearmarkers

Hi,

we are busy with phylogeographic studies of Scarabs (Coleoptera) and are struggling to get enough good loci in a microsatellite library (even using enrichment).

Does anyone have experience with microsatellites in beetles and would be prepared to share this (especially encountered problems or special tricks or idiosyncrasies)?

Is it possible that Coleoptera (just as Lepidoptera) do not have that many microsatellite loci?

Could you recommend any other nuclear marker for phylogeographic and conservation genetic studies in

beetles?

Many thanks in advance, and if need - I will summarize the responses.

Best regards,

Ute Kryger (PhD) Scarab Research Group Department of Zoology & Entomology University of Pretoria Pretoria 0002 - RSA Fax +27 12 362 5242 Phone +27 12 420 5343

Ute Kryger <ukryger@zoology.up.ac.za>

Diff between means

“I have calculated a large (88-specimen x 88-specimen) matrix of distance coefficients from comparisons of RAPD (Random Amplified Polymorphic DNA) genotypes (sets of DNA-fragment presences or absences). From this matrix, I obtained a smaller (11-site x 11-site) matrix of site-to-site distances by taking averages of values in the specimen-to-specimen matrix. For example, in comparing Site 1 to Site 2, I took the average of all Site-1-specimen to Site-2-specimen coefficients. Now, I wish to compare pairs of site-to-site distance coefficients and make statements about whether the differences between these values are significant. Has a method been developed for testing the significance of differences between means in this situation?”

Thank you,

Ron MacKay Department of Biology Mount Saint Vincent University Halifax, Nova Scotia B3H 2T8

902-457-6293 ron.mackay@msvu.ca

Ron MacKay <Ron.MacKay@msvu.ca>

EvoPsych answers

Dear Colleagues,

Below is a tabled version of the responses I received to the question of how evolutionary psychology is perceived. I sent this query to evoldir and to the primary list serve for social/personality psychologists (SPSP). The table shows the frequency of positive and negative comments received, as well as my attempt to categorize

the nature of those comments.

Thanks very much for your helpful responses. Please get in touch with me if you have any questions or concerns.

Best regards,

Bill

POSITIVE RESPONSES

Hypothesis Generation evoldir = 1 SPSP = 6

Framework evoldir = 6 SPSP = 31

No details/other evoldir = 4 SPSP = 3.5

NEGATIVE RESPONSES

Implications/ evoldir = 1.5 SPSP = .5 Political uses

Just so stories/ evoldir = 6.5 SPSP = 8 Not tested

Not X-culture/ evoldir = 1.5 SPSP = 4 Not socialization

Not X-species evoldir = 1.5 SPSP = 1

Not genetic/ evoldir = 3 SPSP = 1.5 Bio'ly naïve

No details/ evoldir = 2 SPSP = 1.5 Other

Numbers represent frequency counts of social/personality psychologists (SPSP) and evolutionary biologists (evoldir) who endorsed a particular category of positive or negative reactions to evolutionary psychology. Responses were placed in up to two categories if more than one issue was raised (a common occurrence), in which case the two most emphasized categories were each allotted .5 of a response. Thus, the total number of respondents in both lists who made positive or negative responses in a particular category can be inferred from the totals.

Bill von Hippel <w.vonhippel@unsw.edu.au>

EvolQuant CourseNotes

I've just posted roughly 350 pages of class notes for a short course in Evolutionary Quantitative Genetics that I just gave in Denmark. The content is very current, ranging from using molecular markers to detect selection, quantitative genetics of microarrays, and the geometric constraints in multivariate trait response.

The course URL is <http://nitro.biosci.arizona.edu/-workshops/Aarhus2006/notes.html> See the pdf table

of contents for a full breakdown. The list of lectures (each 3+ hours) are:

Basic Statistical Machinery Linear Algebra and Linear Models Basic Concepts in Mendelian, Population and Quantitative Genetics Resemblance Between Relatives Basic Designs for Estimation of Genetic Parameters Inbreeding and Crossbreeding Genetic Drift Tests for Molecular Signatures of Selection Short-term Selection Response Analysis of Short-term Selection Experiments Long-Term Response and Selection Limits Individual Fitness and Measures of Univariate Selection Genetic Correlations and Multivariate Selection Response Measuring Multivariate Selection Phenotypic Evolution Models Major Genes, Polygenes, and QTLs QTL Mapping Quantitative Analysis of Regulatory Variation

Cheers

Bruce Walsh University of Arizona

jbwalsh@u.arizona.edu

FIS calculations

At the request of many Evoldir members, I will summarize the responses to my original inquiry, which was:

>Does anyone know of a program that will give confidence intervals >from bootstrapping over loci for F-IS, separately for every >population? > >I would like to compare F-IS values among populations for >microsatellite data. Most programs calculate only one overall F-IS >value for the entire set of populations. > >It would be tedious to create a set of single population input >files, and then analyze them separately. Although I have not >explored it thoroughly, I know that even this option will not work >in some cases. (Some programs will not calculate any F statistics >at all for an input file that has only one population.)

I would add two additional notes: First, in case the original posting was not clear, the specific goal is to have confidence intervals for F-IS for each individual population. Without these, one cannot say with any statistical certainty whether one population has more or less inbreeding than another population.

Second, most software programs test the null hypothesis of no population structure by permuting individuals, genotypes or gene copies over populations. (Or some similar "exact test".) But 1) this method does not provide confidence intervals, and 2) strictly speaking,

I believe that permutation approaches do not test the same hypothesis as bootstrapping or jackknifing over loci (when multiple loci are available). I will leave a discussion of that distinction for someone to pick up in another thread....

Please email the group if there are any major corrections to the summary below.

Programs that will calculate population-specific CIs for F-IS: - - - - -
 - GDA (<http://hydrodictyon.eeb.uconn.edu/people/plewis/software.php>) Will bootstrap over loci to generate confidence intervals. To get population-specific F-IS values in each population, exclude all but one population in the Misc menu. Very intuitive interface and menu system.

GENETIX <http://www.genetix.univ-montp2.fr/genetix/genetix.htm> Will both bootstrap over loci and perform permutation analyses for F-IS values in each population. The software is in French, so get out your dictionary if necessary. In the FSTATS menu, TEST SUR FIS and choose the bootstrap or permutation option. You can choose all populations as well as all loci separately.

SPAGeDi <http://www.ulb.ac.be/sciences/ecoevol/spagedi.html> I am told that this program will perform the desired analyses, but I have not verified this. The manual mentions one-delete jackknife procedures for estimating confidence intervals, but does not mention bootstrapping,

Programs that will not calculate population-specific CIs for F-IS: - - - - - FSTAT
<http://www2.unil.ch/popgen/softwares/fstat.htm> TFPGA <http://www.marksgeneticssoftware.net/tfpga.htm>
 These two programs will calculate significance for overall F-statistics by bootstrapping over loci. However, they will not calculate locus-specific F-IS confidence intervals. They will not perform these calculations on a file with only one population.

GENEPOP ON THE WEB <http://wbiomed.curtin.edu.au/genepop/> Calculates overall and locus-specific F-IS values, but does not specifically test the significance of F-IS, or provide confidence intervals. (Options 1, 5, 6) Significance is assessed with permutation tests.

ARLEQUIN 3 <http://cmpg.unibe.ch/software/arlequin3/> Runs permutation tests for an overall F-IS. Does not calculate locus-specific F-IS values. Does not bootstrap over loci. Laurent Excoffier has told me that the next version (late June) will compute FIS for each population, and test it by permutation, but no bootstrap CI will be provided.

Andy Bohonak –

Andrew J. Bohonak Associate Professor

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

=====

Phone: 619-594-0414 Fax: 619-594-5676 Email:
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honak@sciences.sdsu.edu

FourLevel AMOVA

Dear EvolDir members,

I am working on a multi-species phylogeography and I am looking for a way to perform a hierarchical AMOVA with 4 levels : within population, among populations within species, among species and among geographical regions. Arlequin can handle three levels but not four. Does anyone know a mean (and a software) to do this ? thanks,

Coralie BELTRAME

UMR 5173 MNHN/CNRS "Conservation des espèces, restauration et suivi des populations" (CERSP) 55, rue Buffon 75 005 PARIS tel : (33) 01 40 79 34 53 fax : (33) 01 40 79 38 35

beltrame@mnhn.fr

Fst ConfidenceIntervlas answers

Thank you for all the answers. There is a listing of all the answers I received. Unfortunately, it seems that no software is able to compute automatically C.I. of pairwise FST. I checked all the softwares that are mentioned in those answers and I can confirm that no one fulfilling my requirements. I decided to use the solution (the hard and long one...) proposed in the first answer included in this message. With a good work technique it takes me about 4 hours (instead of 1-2 day) to calculated CI for 277 pairwise comparisons. Good luck and many thanks again!

Philippe.

Original message:

Does somebody know a software allowing the estimation of confidence intervals for pair-wise Fst using bootstraps over loci? It seems that both Arlequin 3.01 and Fstat are only able to estimate confidence intervals for the overall Fst.

Thank you.

===I asked the same question about 8 months ago and received a lot of software suggestions, including GENEPOP, MSA, SPAGEDI, POPDIST, GENETIX and the ones you've already mentioned. However, browsing through the software I did not find any of them fulfilling my requirements (Newer versions might include what you are looking for). After spending weeks trying out and searching for appropriate software, I found that creating FSTAT inputfiles for each pair of populations and obtaining 95% CI for the overall Fst was the best (only?) solution. Know its a very tedious way around the problem, but with <100 pairs, good copy/paste skills and music on the ipod it should be possible to do in a day or two...

===I encountered the same problem in a study of ours. I decided to use "Resampling Stats" to calculate a bootstrapped "average pairwise Fst) across all our AFLP-loci. Maybe this is not the most elegant way how to do it, but it is at least one way to do it!

===I'm not aware of any software that can perform that task. I've recently had the same problem and ended up analysing 66 datapools seperately (in FSTAT) to get the C.I.'s on pairwise Fst's. Just a couple a weeks ago there was quite a similar question here on Evoldir concerning C.I.'s on Fis values on subpopulation-level. It seems to me that there is a big need for a piece of software to calculate C.I.'s on all levels. RSTCALC will calculate all the desired C.I.'s and tests, but only on Rst values. Guess that wasn't much help, but if you get some usefull replies, please post the answers.

===I believe TFPGA (free software) will accomplish what you're looking for. Here is the URL: <http://www.marksgeneticssoftware.net/tfpga.htm> TFPGA provides "Theta-P" values, but these are equivalent to Fst.

===You can do this in GDA (Genetic Data Analysis - Paul Lewis - free download from Paul's Web site). You'll have to select on pair of populations at the time, although (easily done within the program, ie you don't have to change the input file). Have you considered using permutation to test for the significance of your pairwise Fst values? This can be easily done in Fstat

or Genetix.

===I have used GDA (<http://hydrodictyon.eeb.uconn.edu/people/plewis/software.php>) for some of these types of calculations. In a single dataset with multiple populations, you can 'Exclude' (using the 'Misc.' menu) all populations but two, then calculate an FST and bootstrap over loci (options within the F-stats menu) to get a confidence interval. In order to change parameters of the bootstrap, go to F-stats -> Options -> Options for bootstrap. Unfortunately, you would have to do this for each pair of populations, but it seems to work well. Good luck!

===The program GDA (Genetic Data Analysis; Lewis and Zaykin 1999) will bootstrap over loci to give confidence intervals for pairwise Fst (theta). You have a be a little tricky to get the estimate though. Once you input your data into GDA, it will give you the option of excluding populations from each analysis. You have to exclude all populations but the two that for which you are interested in getting a pairwise estimate, and then estimate Fst and bootstrap over loci for the confidence interval. It won't give confidence intervals for the estimates in the pairwise theta matrix it estimates. It takes a bit longer this way, but I don't know of other programs that will give confidence intervals for pairwise estimates. GDA can be found at : <http://hydrodictyon.eeb.uconn.edu/people/plewis/software.php> philippe.girard@umontreal.ca philippe.girard@umontreal.ca

Fst confidence interval

Does somebody know a software allowing the estimation of confidence intervals for pair-wise Fst using bootstraps over loci? It seems that both Arlequin 3.01 and Fstat are only able to estimate confidence intervals for the overall Fst.

Thank you.

Philippe Girard. philippe.girard@umontreal.ca

Genemapper Microsatellites

Dear all,

I am trying to analyse 2 microsatellites with fluorescent primers, one labelled with 6-Fam and the other with Ned. I can see strong, clear bands on agarosa gels from PCR products at 53C and 56C respectively. However, when I analyse my samples on Genemapper I do not get any signal at all or, in a few cases, I see many peaks on a wider range than what I read from the agarosa gel. Other primers analysed on the same run with the same label provide clear peaks, so I assume settings on the machine are ok. Has any of you encountered similar problems? Thank you very much,

Isabel Calderon PhD student University of Barcelona

ISABEL CALDERON MORENO <calderon@ub.edu>

HRAS sequence

I would be grateful if anyone could direct me to information about the complete sequence of p21HRAS in Homo sapiens, complete with Intron/Exon annotation, source and references. To the best of my knowledge it should be a few thousand bp long. I have not been able to locate such a sequence. Most of what I could find were sequences of the mRNA transcript. I would also be grateful if anyone could tell me the reason for there being only the truncated/abbreviated (usually just ORF) sequences of HRAS without Exon/Intron indicated.

Thank you,

Uri Moran MSc. student

moranuri@post.tau.ac.il

LabExercises answers

Dear colleagues,

A few years ago I posted a message here asking if anyone knew of introductory biology laboratory write-ups that integrated inquiry-driven phylogenetic analyses and classical surveys of the major taxa. Several people asked me to post any that I found but I did not discover any at that time. Recently, however, some colleagues and I finished initial development of exercises along these lines, with CCLI funding. These

continue to be a work in progress but in case they would be of value to others I have posted them to the following website: <http://facstaff.uww.edu/mckinnoj/-UWWCCLIWriteups.html> Please feel free to download and use or modify any of the exercises that might be of interest. Please do let me know if you decide to use any, in whole or in part.

Cheers, Jeff

Jeffrey S. McKinnon, Coordinator, UW-W Undergraduate Research Program, Prof., Dept. of Biological Sciences, University of Wisconsin-Whitewater, 800 West Main Street, Whitewater, WI 53190, U.S.A. (w): 262-472-6200; (h): 262-472-8813; Fax: 262-472-5633 e-mail: mckinnoj@uww.edu <http://facstaff.uww.edu/mckinnoj/mckinnon.html> Jeffrey McKinnon <mckinnoj@uww.edu>

MissouriBotGarden Proceedings

“Species reconsidered: consequences for biodiversity and evolution” was the title of the 50th Annual Systematics Symposium of the Missouri Botanical Garden held in October, 2003. The proceedings have just been published in the Annals of the Missouri Botanical Garden, Vol. 93(1), May 2006. The volume includes papers by: Mary Winsor, David Wake, Jonathan Losos et al., Loren Rieseberg, Ann Sakai et al., Bruce Baldwin and Peter and Rosemary Grant.

Titles, abstracts, and author contact information are available at: <http://apt.allenpress.com/aptonline/?request=get-toc&issn=0026-6493&volume=-093&issue=01>

jlosos@oeb.harvard.edu

– PLEASE NOTE MY NEW EMAIL ADDRESS!!!

Jonathan B. Losos Department of Organismic and Evolutionary Biology 26 Oxford St. Harvard University Cambridge, MA 02138 617-495-9835 617-496-8308 (fax) <http://www.biology.wustl.edu/~lososlab/-losos.html> Jonathan Losos <jlosos@oeb.harvard.edu>

Multivariate SSRs

Dear EvolDir members: I have genotypes data of >50 microsatellite loci for ~400 samples of three *Helianthus* species, one is a homoploid hybrid species, and the other two are parental. I want to plot the individuals based on their genotypes, in order to test the relationships between the species. I am not interested in the phylogeny, just in the relative distances between individuals in multi-dimensional scale (k=no. of loci). The goal is to examine the relative position (in k dimensions) of the hybrid species relative to its parents. The problem with microsatellite data is that it is di-allelic data, i.e., for each character (=locus) I have two states for each individual, which could be identical (homozygote) or different (heterozygote), and are not independent. I assume (for now) that each locus is independent of the other loci (non-realistic, but it is corrected in a different analysis). Does anyone aware of a method to - and better: software - that does things like that? Free-ware are favorable, of course. Thanks in advance for answers Yuval

– Yuval Sapir, PhD

Dept of Biology Indiana University Bloomington, IN 47405 USA http://www.bio.indiana.edu/~rieseberglab/yuval_sapir.html ysapir@indiana.edu

PopExpansion examples

Hi,

I’m interested in doing a comparative analysis on rates of evolution in populations which have undergone an expansion and those that have remained stable. Basically, I’m looking for examples of populations which had a small long-term effective population size and then expanded. For example, island species which colonized the mainland. I also need sequence from a closely related species which has not expanded and an outgroup.

thanks,

Jane Charlesworth Sussex University

J.charlesworth@sussex.ac.uk

Publishing evolution

Dear Evolutionary Biologists

The Society for the Study of Evolution is reviewing the mode of publication of its highly-regarded international evolutionary biology journal *EVOLUTION*.

The Society has a commitment to intellectual and human diversity - one reflection of this is its office of non-North American Vice President. In that role, I would like to ask for your opinions on some issues regarding publication of evolutionary biology.

Please take a minute to answer the following questions. Please answer irrespective of your opinion - a random sample of opinions would be the best. Answers will be kept confidential, unless you specify otherwise.

Q1. If you have to pay page charges to publish in a good journal (typically in the order of USD60 per page), how much of a disincentive relative to other factors is this to submit to that journal?

Q2. Have you ever decided to not submit to a particular journal on the basis that you would incur page charges, and if so, how often (eg rarely, usually etc)?

Q3. Have you ever requested a waiver of page charges from any journal? Was it granted?

Q4. Are you aware that the Society for the Study of Evolution has low-cost membership fees, and that one of the benefits of membership is an allowance of 12 fee-free pages per year if your work is published in *EVOLUTION*?

Q5. Are you a member of the Society for the Study of Evolution, and if not, why not?

Q6. Have you published in *EVOLUTION*? How often?

Q7. What is the country/region from which your research funding comes?

Q8. Do your national funding bodies mostly allow application for publication charges?

Q9. Do you have any other comments on the subject of publication of evolutionary biology?

thank you for your time.

Paul Sunnucks

- Dr Paul Sunnucks Senior Lecturer in Zoology School of Biological Sciences Monash University, Melbourne Clayton Campus 3800 Victoria Australia ph + 61 3 9905 9593 fax + 61 3 9905 5613

email paul.sunnucks@sci.monash.edu.au

webpage: <http://www.biolsci.monash.edu.au/~staff/sunnucks.html> Paul Sunnucks
<Paul.Sunnucks@sci.monash.edu.au>

Pyla fusca samples

Dear all,

I am trying to get hold of samples of the mouth species *Pyla fusca* from its entire range in Eurasia and North America (from Alaska to Newfoundland and south to New Jersey, New Mexico, and California)

I would be very grateful to anyone who could provide a good-quality sample (ideally preserved in ethanol and not dried or formaldehyde-fixed).

Cheers Paul

- Paul Bloor, PhD student School of Biological & Earth Sciences Liverpool John Moores University Byrom St., Liverpool L3 3AF

Address until January 2007:

Departamento de Ecología Evolutiva Museo Nacional de Ciencias Naturales Calle José Gutiérrez Abascal, 2 28006 Madrid Spain

pbbloor@gmail.com

Roommate Evolution2006

At the last minute I have been invited to attend the 2006 Evolution meeting at SUNY-Stony Brook. However, on-campus housing is now closed, and off-campus housing for 2-4 nights is expensive and will probably involve renting a car. I can do this, but I would prefer to save my (nonprofit) company some money, and also avoid commuting, by sharing some on-campus housing.

I would be happy to pay half of the room cost, bring a sleeping bag and pad and camp out on the floor. I have found housing with friends for the first 2 nights (the 24th and 25th), but am still seeking it for the nights of the 26th and/or 27th.

(I work for the non-profit National Center for Science Education, and we spent much of last year working on the Kitzmiller v. Dover case where "intelligent design" was ruled to be unconstitutional. There will be a day-long session on this case on Monday, June 26, which is why I was invited. So I might be a not-entirely boring

guy to have hang around.)

Email me at matzkeATncseweb.org if you see a possibility for some arrangement. Perhaps a grad student out there wants to save a few bucks. Thanks!

Nick

PT blogpost with meeting details: http://www.pandasthumb.org/archives/2006/06/sse_2006_sessio.html PT blogpost with recent photo showing my sunny personality: http://www.pandasthumb.org/archives/2006/06/nick_in_new_mex.html Nicholas J. Matzke Public Information Project Director National Center for Science Education, Inc. 420 40th Street, Suite 2 Oakland, CA 94609-2509 Phone: (510) 601-7203 x307 Fax: (510) 601-7204 Toll-free: 1-800-290-6006 matzke@ncseweb.org <http://www.ncseweb.org> NCSE's work is supported by its members. Join today! <http://www.ncseweb.org/membership.asp> Nick Matzke <matzke@ncseweb.org>

SSR multivariate analysis answers

Thank you for all the people that responded to my inquiry. Down there are the answers. Of all the answers, I choose GenA1Ex6, (thanks to Peter Smouse) and already tried it. It is a module for Excel, fit to both Mac and PC, easy and intuitive to use. Based on my three-days experience, I can recommend it for such analyses, and perhaps for many more. Yuval

Here is the original question:

>Dear EvolDir members: >I have genotypes data of >50 microsatellite loci for ~400 samples of three Helianthus species, one is a homoploid hybrid species, and the other two are parental. I want to plot the individuals based on their genotypes, in order to test the relationships between the species. I am not interested in the phylogeny, just in the relative distances between individuals in multi-dimensional scale (k=no. of loci). The goal is to examine the relative position (in k dimensions) of the hybrid species relative to its parents. The problem with microsatellite data is that it is di-allelic data, i.e., for each character (=locus) I have two states for each individual, which could be identical (homozygote) or different (heterozygote), and are not independent. I assume (for now) that each locus is independent of the other loci (non-realistic, but it is corrected in a different analysis).

>Does anyone aware of a method to - and better: software - that does things like that? Freewares are favorable, of course. > ANSWERS: *****

Data modifications advices -

You could calculate a genetic distance called DPS, the proportion of alleles shared between individuals. This is an individual-based genetic distance suitable for codominant markers. The computer program MSA (Microsatellite Analyzer) by Dieringer & Schlotterer can do this. The software was published in Molecular Ecology Notes. After you got the individual-based distance matrix you could resolve this with one of many multivariate techniques. E.g. you could use MSD (multidimensional scaling) or PCA (principal component analysis). Both methods can be carried out with general stats software packages, e.g. SPSS or JMP. ——— (Rodney Dyer:)

I have software on my server (Multivariate Genotypes) at: <http://dyerlab.bio.vcu.edu/wiki/index.php/-Software>

that takes diploid multilocus data and turns it into multivariately normal data. You can look at the 2GenerV paper (pdf #10 on my publications page) to get an overview of how this works, or I would be happy to discuss it with you directly if you like. ———

Look at this page:

http://dyerlab.bio.vcu.edu/wiki/index.php/-Software#Multivariate_Genotypes there you'll have your data ready for PCA, CDA and related

—————
you may use the PCO, like a PCA but on genetic distances, GenAlex software performs this kind of method, but also the package ecodist of R software. ———

Freeware -

(Peter Smouse:) Dear Registered User of GenA1Ex We are pleased to advise that the official release of GenA1Ex 6 is now available: <http://www.anu.edu.au/BoZo/GenA1Ex/> <<http://www.anu.edu.au/BoZo/GenA1Ex/>> This version includes all of the features listed in Peakall and Smouse (2006) : Peakall, R., Smouse, P.E., 2006. GENALEX 6: genetic analysis in Excel. Population genetic software for teaching and research. Molecular Ecology Notes 6, 288-295. <http://www.blackwell-synergy.com/doi/abs/10.1111/j.1471-8286.2005.01155.x> <<http://www.blackwell-synergy.com/doi/abs/10.1111/j.1471-8286.2005.01155.x>> Molecular Ecology Notes <http://www.blackwell-synergy.com/loi/men> <<http://www.blackwell-synergy.com/loi/men>> Please note

that the t he current program and documentation files supersede all previous versions. Therefore, it is strongly recommended that you update your program and documentation. Further information about updating GenAlEx is provided in the 'Read me' file when you download the new documentation. We thank the many users of our beta releases of GenAlEx 6 for their positive and supportive feedback and bug reports. Enjoy! Rod Peakall and Peter Smouse April 7, 2006

——— Theres a program called GenAlEx which is a Microsoft Excel add-in which will create PCO plots for both dominant and codominant data. I'm not sure of the exact details (like the non-independence you mentioned) but you could look into it. Its free at:

— / —

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>

Science information

Dear Brian: could you post this question to the list:

1. Where can one find a phylogenetic tree for the production of estrogens?
2. Where can one find information on the phylogenesis of biological functions?

thanks,

barrai.

—

Italo Barrai, Emeritus of Genetics in the Department of Biology, University of Ferrara, 46 Via Borsari, 44100 Ferrara Italy Voice: 0532/291731 Hcopy: 0532/249761

Italo Barrai <v09@unife.it>

Seeds book

Hi everybody,

This one might be interesting for some of you. A new popular scientific book has just been published on

seeds. Being literally the only book of its kind on the subject, the scholarly written but highly readable account (judged so in an independent review) is a great educational tool and additional read for university students and everybody interested in plant structure and evolution.

Prepared by artist Rob Kessler and Wolfgang Stuppy, Kew's seed morphologist, "Seeds - Time Capsules of Life" is a book woven around the Millennium Seed Bank Project. It presents a natural history of seeds illustrated with some of the most spectacular examples of seeds and fruits found in nature. The story begins with the evolution of seeds and their structure and discusses their dispersal through space and time, the latter finally leading over to the Millennium Seed Bank Project which is featured in a separate chapter. Using seeds collected in the UK and many of the MSB Partner Countries, the highlight of the book are images taken with a scanning electron microscope (SEM) that have subsequently been artistically enhanced by Rob Kessler. For the first time ever, Seeds Time Capsules of Life reveals the minute and breathtaking detail of seeds to the public eye and presents their natural history before a scientifically sound background. The book has recently been reviewed in the June issue of the BBC Wildlife Magazine and is now available from the publisher's website, (www.papadakis.net), amazon (<http://www.amazon.co.uk/gp/product/1901092666/-026-9855724-4062031?v=glance&n&6239>) and other book dealers. An American edition will be published by Firefly in autumn.

Seeds - Time Capsules of Life by Rob Kessler & Wolfgang Stuppy Papadakis Publisher in collaboration with the Royal Botanic Gardens, Kew, 264pp, £35.- ISBN 1901092666 (hb)

roasty_@hotmail.com roasty_@hotmail.com

Snail Recapture label

We are investigating freshwater snail movements in the wetland in Northern Indiana (USA) and we want to support our genetic data with a re-capture study. We have used a water-proof paint "permapaque" (Opaque pigment marker, manufactured by Sakura) to mark the snails in the pond, however the paint goes off from the snail shells after a couple of weeks. We are now thinking of using tags glued onto the snail shells however, we have not found suitable one. We will be grateful if

anyone could advise us on any kind of labels (tags and water-proof glue, paint, etc.) which would not be toxic, will be water-proof, likely to last for at least several months (ideally throughout the whole season of about 5 months) and possible to use for marking freshwater snails of sizes around 5 to 10 mm.

Thanks in advance,

Monika

Monika Zavodna Department of Biological Sciences
Lilly Hall of Life Sciences Purdue University 915 W.
State Street West Lafayette, IN 47907 U.S.A.

phone: +1 765 494 9103 email: mza-
<mailto:mzavodna@purdue.edu> vodna@purdue.edu
mzavodna@purdue.edu mzavodna@purdue.edu

Software IDC

IDC, a simple new Linux/UNIX and Windows/DOS program for the calculation of independent contrasts, is now available at:

http://iguana.wustl.edu/~liam/programs/idc/-idc_manual.html IDC calculates independent contrasts for a fully bifurcating phylogeny with branch lengths and an arbitrary number of quantitative characters. It outputs the contrasts and the correlation and VCV matrices of the contrasts.

IDC can also simultaneously process an arbitrary number of trees and/or data sets which might be useful for obtaining estimates of error due to phylogeny misestimation and sampling error in the estimation of trait means.

IDC is available with a detailed manual written in .html and available from the link listed above and for download.

Please report any bugs, however the source code for this program is sufficiently simple that users may also be able to fix bugs themselves.

Thanks for trying out this software. I hope that it is as easy to use as is intended.

Liam Revell Washington University, Department of Biology web: <http://iguana.wustl.edu/~liam/> email: ljrevell@artsci.wustl.edu

ljrevell@artsci.wustl.edu ljrevell@artsci.wustl.edu

Software Structurama 1.0

Structurama 1.0

We are pleased to announce Structurama 1.0, a program for inferring population structure from allelic information sampled from some number of individuals. The program implements two models for population structure:

1. We consider the number of populations to be fixed to some number. This is the same model described by Pritchard et al. (2000) and implemented in the program structure.
2. We allow the number of populations to be a random variable with a Dirichlet process prior (Pella and Masuda, 2006). Here, the number of populations can be inferred.

The assignment of individuals is inferred in a Bayesian framework. Markov chain Monte Carlo is used to approximate the posterior probability of assigning an individual to a population. The program summarizes the results of the Bayesian MCMC analysis by using the 'mean' partition of individuals to populations. The mean partition is the partition of individuals to populations that minimizes the squared distance to the partitions sampled by the MCMC algorithm. (We use a distance on partitions first described by Gusfield.)

The program can be downloaded for free (free as in "free beer") from:

<http://www.structurama.org> Please e-mail us your comments or suggestions for new features.

Sincerely,

John Huelsenbeck Edna Huelsenbeck Peter Andolfatto
John Huelsenbeck Section of Ecology, Behavior and Evolution Division of Biological Sciences 9500 Gilman Drive University of California, San Diego La Jolla, CA 92093-0116, U.S.A.

E-mail: johnh@biomail.ucsd.edu Telephone: (858) 822-6764 FAX: (858) 534-7108 WWW: <http://brahms.ucsd.edu> John Huelsenbeck <johnh@biomail.ucsd.edu>

Sturgeon sex markers CDNA/AFLP

Dear colleges

I am going to do CDNA/AFLP to finding sex markers in Sturgeon (Acipenser). I would appreciate to recieving some information about its protocole and introduce some people who working in this regard. If is there any body who work about CDNA?AFLP, Please help me. Thank you for your cooperation.

best regards Mahtab Yarmohammadi

mahtab yarmohammadi
<mahtab_yarmohammadi@yahoo.com>

Subsampling question

Dear Colleagues,

A question:

I am comparing diversity between an adult population (nR) and a population of offspring made up of half-sib arrays (n5 (25 arrays of five individuals each)). To control for sample size effects, I want to subsample 25 random adults and one random individual from each of the 25 arrays. I want to perform 100 iterations and compare the means. My markers are dominant.

Has anyone done something similar and do you know of an efficient way to perform the subsampling and analysis? I have been unable to find an efficient way to take random subsamples from my dataset in any of the common programs (e.g. Popgene).

(Note: I am not using rarefaction in this instance, since it does not account for the relatedness of the half-sibs.)

Many thanks for any suggestions.

Thor Hanson University of Idaho, USA CATIE, Costa Rica

thor@rockisland.com

Text question

Quick question to the list here regarding an introductory text for non-bio majors that we are in the process of adopting.

The text in question is published by McGraw Hill and is entitled "Essential of Biology" by Sylvia S. Mader. The text does not contain reference to the Miller/Urey abiogenesis stuff and has a reference to the Institute for Creation Research (with such luminaries as Duane Gish and Ken Cummings).

Is it odd for a Bio 101 text to have references, even oblique ones, to an organization such as the ICR that has the moto, "We believe God has raised up ICR to spearhead Biblical Christianity's defense against the godless and compromising dogma of evolutionary humanism. Only by showing the scientific bankruptcy of evolution, while exalting Christ and the Bible, will Christians be successful in 'the pulling down of strongholds; casting down imaginations, and every high thing that exalteth itself against the knowledge of God, and bringing into captivity every thought to the obedience of Christ.'â?

Feel free to reply off list as this is a bit tangential to the main focus of this mailing list. If others are interested in the responses, let me know and I'll post them on my server.

Thanks,

– Rodney J. Dyer, PhD

Department of Biology Virginia Commonwealth University Richmond, Virginia 23284 <http://-dyerlab.bio.vcu.edu> rjdyer@vcu.edu

Unsuccessful Selection Expts

I am looking for references to artificial selection experiments (in genetically variable populations) that failed, i.e. there was no response to selection. I know of only two: one that I published some years ago on selection for directional asymmetry in eye size, and Maynard Smith and Sondhi's paper on selection for direc-

tion asymmetry in bristle number. If you know of any others, please email me at j-coyne@uchicago.edu.

Thanks!

Jerry Coyne <j-coyne@uchicago.edu>

Unsuccessful Selection Expts 2

Thanks to all who sent me references to papers on failures of response to artificial selection. I've compiled a list of these and will send it to anyone who is interested.

I would like to ask one more (but related) question: besides the work of Ziljstra, Brakefield, and their colleagues on development time in butterflies, does anyone know of experiments that selected for sexual dimorphism in a trait, that is for a trait whose expression was selected to differ in a consistent way between males and females?

Please email me at j-coyne@uchicago.edu if you know of any, or want a copy of the "failed selection experiment" list.

Thanks, Jerry Coyne

Jerry Coyne <j-coyne@uchicago.edu>

WithinPop Duplications

I am writing to ask some advice about existing empirical data on within-population gene duplication events. I am not talking about whole genome duplication. We have been studying a number of genes in arbusular mycorrhizal fungi. All the fungal isolates originate from one population. Recently, we have found that for many of the genes we looked at (18S, 5.8S, several ATPases, a gene encoding a binding that has a heat shock function) there is considerable within-population variation in copy number of these genes - we have shown this with real-time PCR and, for some genes, with southern hybridization.

Some people have commented to me that our findings simply weren't interesting because within-population variation in gene copy number was already well known in many other organisms, particularly in plants. However, in my literature searches I didn't come up with

much about within-population differences in gene copy number except for some recent papers about among-individual copy number in the human genome. In this last case, it seems the publications discussed the finding of among individual differences in gene copy number as something interesting and relatively unexpected.

So my question is whether it's true that this is already well known and well documented in other organisms?

Secondly, it seems that the frequency and commonness of among-individual and within-population gene duplication in organisms could be quite important. I have read quite a few papers recently discussing among-species differences in gene copy number for a wide variety of different taxa. It seems that the assumption in the analysis is that the copy number is constant for a given species. I wondered whether for those studies the researchers know that there is little variation in copy number in the species that they are talking about. If the within-species variation in gene duplication would be as large as the variation seen among species compared then this could limit or alter the interpretation of such studies.

We would be grateful for any comments about this.

Regards, Ian Sanders

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

Tel (direct): +41 21 692 4261 Tel (Secretary): +41 21 692 4260 Fax: +41 21 692 4265 Email: ian.sanders@unil.ch

http://www.unil.ch/dee/page7238_en.html

Ian.Sanders@unil.ch Ian.Sanders@unil.ch

p21HRAS answers

Dear lady/sir

I would be grateful if you could answer the following questions regarding the HRAS Homo sapiens Exon/Intron gene sequence found on web page:

http://www.ncbi.nlm.nih.gov/entrez/-batchseq.cgi?dopt=graph&extrafeatP4&out=-on&list_uidsQ493057&_fromG2130&_sfromG2130&_toG4729&_slenP00off 1. At the above address the gene is located on chromosome 11 approximately between nts 472,150-475,570. According to Ensembl This gene can be found on Chromosome 11 at location 522,243-

525,550. (From web page: http://www.ensembl.org/Homo_sapiens/geneseqview?db=core&gene=ENSG00000174775&flank5_display=0&flank3_display=0&exon_display=1&core&exon_ori=all&snp_display=off&line_numbering=sequence&submit=Update) Can you explain this discrepancy?

2. Is there a text version (that can be copy/pasted) of this same sequence (with Exons/Introns indicated)?

3. Is there a reference to this sequence (with Exons/Introns indicated) in any other web site (such as ncbi)?

Thank you

Uri Moran MSc. Student Tel Aviv University

First reply:

Dear Uri, 1) The difference between two databases is because each group has its own assembly.

2) You may search in Gene database and see this gene's record.

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genome&cmd=Retrieve&doptfull_report&list_uids265 In a Full report page you may chose "Gene Table" from the "Display" option pull down menu to see the text.

3) Links in the right side of the full report will show you where you may obtain more information about this record.

Regards, Simin

Second reply:

My guess is that that sequence you are looking for has derived from EST (Expressed Sequence Tags), and translated to complementary DNA (cDNA). This is the case with many genes in vast amount of species that retrieved from mRNA. The RNA has gone splicing before the reverse-transcription, and only the coding regions are in the gene-bank. , Yuval

Third reply:

Dear Uri!

Unfortunately I am not able to present the sequence to you, but I am sure you can find what you need. If you blast your mRNA with the human EST-library and the Human WGS-library and align the results, you should be able to find the sequence you need. I did that with several genes in sticklebacks.

Cheers,

Sascha

Fourth reply (complete correspondence):

Hi Uri,

I poked around the NCBI site some more, and I never was able to really see a gene sequence annotated with the display. I can see a line drawing of the sequence, but not the actual sequence. If I am missing something, please let me know.

I was able to download the gene sequence, unannotated, plus the sequences of the mRNAs (alternative splicing). So I aligned them (see attached file).

You can view this with JalView, BioEdit or any other multiple sequence alignment editor.

All of the introns begin with GT and end with AG, which is the rule for most eukaryotic genes.

Brian

On 6/5/06 9:25 AM, "moranuri@post.tau.ac.il" <moranuri@post.tau.ac.il> wrote:

> Dear Brian > > Thank you very much for your reply. > > In case you are interested, see correspondence with NCBI help desk below. > > Regards, > Uri

+ This Mail Was Scanned By Mail-seCure System at the Tel-Aviv University CC. — End forwarded message — Correspondence with Brian T. Foley

Hi,

Note that in both cases, the Ras oncogene is on the other strand (you will need the reverse compliment of the GenBank entry), And no genes are annotated on either of these chromosome 11 sequences. I found Exon 1, so now you need to blast exon 2 against chromosome 11.

Let me know if you need help.

Brian

BLAST of RAS exon 1:

>gi|29650323|gb|AC137894.5| Download subject sequence spanning the HSP Homo sapiens chromosome 11, clone RP13-46H24, complete sequence Length5000

Score = 119 bits (60), Expect = 2e-25 Identities = 60/60 (100%), Gaps = 0/60 (0%) Strand=Plus/Minus

```
Query 1 GGCAGGAGACCCTGTAGGAGGACCC-
CGGGCCGCAGGCCCTGAGGAGCGATGACG-
GAATA 60 |||
Sbjct 156059 GGCAGGAGACCCTGTAGGAG-
GACCCCGGGCCGCAGGCCCTGAGGAGCGAT-
GACGGAATA 156000
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PostDocs

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ArizonaStateU LandscapeGenet

Postdoctoral and Graduate Student Positions Spatial Analysis and Landscape Genetics/Ecology Arizona State University (Tempe)

NSF funded postdoctoral and graduate student research assistant positions are available in spatial analysis and landscape genetics or ecology. The successful candidates will aid in the development and testing of new methods and software (PASSaGE v2 - <http://www.passagesoftware.net>) for analyzing biological data in a spatial context. My laboratorys research generally covers a broad array of topics within computational evolutionary biology and bioinformatics, and is associated with the Center for Evolutionary Functional Genomics at the Biodesign Institute (<http://www.biodesign.org/centers/efg>) and the School of Life Sciences. Further information on the lab can be found at <http://www.public.asu.edu/~mrosenb> . Postdoctoral Fellow: Experience in spatial analysis, biological statistics, or data analysis is preferred, but no programming skills are required. Ideally, the successful candidate will become involved in ongoing projects in the lab (generally computational evolutionary biology and bioinformatics), but will also be encouraged to pursue independent research on topics related to the overall lab mission and their own background and interests. The position is available immediately, but there is flexibility in the start date. For more information contact Michael Rosenberg at msr@asu.edu. To apply, send a CV, description of research interests, and names of 2 references to the above email address.

Graduate Research Assistants: Prospective Ph.D. students should have general interests in evolution, computational biology, and/or bioinformatics. Admission will be administered through the graduate programs in

the School of Life Sciences (<http://sols.asu.edu/grad/igels/index.php>); applications for Fall 2007 are being accepted through December 15. A Masters degree is not required. If interested, please contact Michael Rosenberg at msr@asu.edu for more information.

Michael S. Rosenberg, Ph.D. Assistant Professor Center for Evolutionary Functional Genomics / The Biodesign Institute School of Life Sciences / Arizona State University msr@asu.edu <http://www.public.asu.edu/~mrosenb> msr@asu.edu msr@asu.edu

Brigham Young University EvolBiol

Postdoctoral & Graduate Student Positions in Evolutionary Biology at Brigham Young University

Two postdoctoral positions in systematics/evolutionary biology are available in the Department of Integrative Biology at Brigham Young University in Provo, Utah, USA (<http://inbio.byu.edu>). For both positions, the ideal candidate would be an investigator interested in using this experience to further develop her/his own independent research program - there should be sufficient time for the successful candidate to complete dissertation manuscripts, mentor undergraduate students, and pursue side projects.

1). Assembling the Tree of Life: "The Deep Scaly Project: Resolving Higher Level Squamate Phylogeny Using Genomic and Morphological Approaches" - An NSF-funded postdoctoral position is available in the Jack Sites' lab for molecular work on phylogenetic reconstruction of deep relationships of squamate reptiles. Support is available for up to two years pending satisfactory performance in the first year, with a starting salary of \$32k, plus benefits. The preferred start date will be 1 January 2007, with some flexibility, and the primary focus will be to generate a large molecular data set from multiple nuclear loci for a limited number of taxa. The project includes Co-PIs and collaborators from San Diego State Univ. (T. Reeder), SUNY at Stony Brook (J. Wiens), the Field Museum of Natural History (M. Kearney and O. Rieppel), Univ. of Texas - Austin (J. Maisano), and Yale Univ. (J. Gauthier), and will involve integration of molecular with fossil and morphological data from the same taxa. Applicants should have strong molecular skills in modern DNA, PCR, and sequencing technology, competence in development/optimization of primers for new genes for large-scale sequencing, and be thoroughly familiar with

conceptual issues and methods of phylogenetic inference. If interested, contact: Jack.Sites@byu.edu on or before 30 June 2006 to be considered. Please send a CV and statements of career goals and research interests.

2). Species-level Plant Systematics. An NSF funded postdoc position to work with Leigh Johnson on phylogenetic reconstruction and evolutionary inference within the phlox family in a research environment emphasizing low-copy nuclear genes, character evolution, qualitative and quantitative analysis of morphology, and integration of diverse data sets. Support is available for up to 18 months, pending satisfactory performance in the first year, with a starting salary of 30K plus benefits. Starting date between 1 September 2006 and 1 January 2007 preferred. An enthusiastic, self-motivated candidate with moderate to advanced molecular biology skills, desire/ willingness to learn new techniques, and thorough familiarity with conceptual issues and methods of phylogenetic inference is sought. Primary responsibilities will include completion of nuclear gene data sets, data analysis, and help with coding morphological data and the preparation of manuscripts. Candidates with an interest in phylogeographic studies and capable of field work in Patagonia will be given highest priority, with the potential to transition the research focus in this direction and extend the post-doc beyond 18 months (via a separate NSF funded opportunity). Interested candidates should contact: leigh.johnson@byu.edu on or before 15 July 2006; applications will be considered until the position is filled. Please send a CV, a statement of career goals and interests, and contact information for 3 references.

3. Graduate student positions in phylogeography, systematics, and evolutionary ecology. Positions funded in part by NSF to pursue graduate work at both the Masters and Ph.D. levels with an emphasis on phylogeography in Patagonian systems are available with Jerry Johnson (Fishes), Keith Crandall (Crustaceans), or Leigh Johnson (Plants). This opportunity is part of a collaborative research study (<http://patagonia.byu.edu>) that includes colleagues from Chile, Argentina, and Canada. Students with some fluency in Spanish, or a willingness to learn as part of their graduate study, are preferred. Applications for graduate study beginning Fall semester 2007 are due by 31 January 2007. Interested students are encouraged to contact investigators much earlier, by 1 September 2006 or soon thereafter, to begin dialogue regarding opportunities and the graduate program at Brigham Young University.

The evolutionary biology group at Brigham Young University has substantial depth in molecular systematics,

evolutionary ecology, population genetics, phylogenetics, coevolution, computational biology, and molecular evolution and includes, in addition to the above, Byron Adams, David McClellan, Duke Rogers, and Michael

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Brussels MOLARCH

Five positions are available for the Collaborative Research EUROCORES Program “Molecular archives of climatic history: exploring patterns of genomic differentiation in endemic species radiations of ancient lakes (MOLARCH)”. This Collaborative Research Project intends to combine phylogenetic and paleoclimate data to compare patterns of evolutionary diversification in endemic species assemblages with climate-driven lake level-fluctuations in the two most ancient freshwater lakes on the globe.

One postdoctoral research fellowship (3 years) in phylogenetic and ecological comparisons of invertebrate and vertebrate species assemblages from Lakes Tanganyika and Baikal (partim: molluscs, ostracods of both lakes, sculpins from lake Baikal, cichlids from Lake Tanganyika). Candidates must have a PhD and postgraduate or postdoctoral experience in phylogenetics. Experience of freshwater ecology is desirable, as is experience in the organisation of fieldtrips and relevant management skills. Candidates are expected to co-organize and participate in sampling trips to both lakes and to contribute to training programmes in related fields.

Expected start date July-September 2006.

Letter of interest, full C.V. and names of three referees to:

Dr Erik Verheyen, Vertebrate department, Royal Belgian Institute of Natural Sciences, Vautierstaat 29, 1000 Brussels, Belgium, (erik.verheyen@naturalsciences.be <<mailto:erik.verheyen@naturalsciences.be>><<mailto:erik.verheyen@naturalsciences.be>>

Within the same project similar positions are open at (i) the Department of Zoology, School of Natural Sciences, Trinity College, Dublin, Ireland, (ii) the Zoological Museum , POB 17 00014, University of Helsinki, Finland, (iii) the Institut des Sciences de l'Évolution

(CNRS - UMR 5554), Université Montpellier II (case postale 064), Place Eugène Bataillon, 34095 Montpellier cedex 05, France, and (iv) the Department of Zoology, Karl-Franzens-University of Graz, Universitätsplatz 2, A-8010 Graz, Austria.

Dr Isa Schön Royal Belgian Institute of Natural Sciences Freshwater Biology Vautierstraat 29 B - 1000 Brussels Belgium Tel.: + 32 2 62 74 312 Fax : + 32 2 62 74 113

Behind every gifted mother is a rather talented toddler.
isa.schoen@naturalsciences.be

HarvardU SymbioticBacteriaPopGenet

Postdoctoral Fellowship

Hydrothermal Vent Bacterial Biogeography

Harvard University Department of Organismic and Evolutionary Biology

Contact: Colleen Cavanaugh: (617) 495-2177 or cavanaugh@fas.harvard.edu, or John Wakeley: (617) 495-1564, wakeley@fas.harvard.edu

Additional details about the position: An NSF funded position is available for a postdoctoral fellow to study the population genetics and biogeography of symbiotic bacteria at deep-sea hydrothermal vents. Our research team is investigating the evolution of invertebrate-bacteria symbioses in the marine environment from genetic and genomic perspectives. The current postdoctoral opening is for someone to address the population genetics and historical biogeography of chemoautotrophic and methanotrophic endosymbionts hosted by bathymodioline mussels at deep-sea hydrothermal vents through genetic sequencing, in situ hybridization, and population genetic and phylogenetic analyses. We seek an applicant who will be available to join us on a research cruise out of Fiji to the Lau Backarc Basin in September 2006. Candidates with experience in microbial biology, molecular biology, population genetics, and phylogenetics are strongly encouraged to apply.

Harvard University is an Equal Opportunity Employer and encourages applications from Minority Group Members and Women

John R Wakeley <wakeley@fas.harvard.edu>

INRA Avignon QuantPopGenet

Two years post-doc position offered at INRA (Mediterranean Forest Research Unit, Avignon, France): Development of demo-genetic models for quantitative traits under selection.

see http://www.international.inra.fr/join_us/positions/post_doctoral_positions/post_doctoral_research_positions (Project #11) Specific conditions and detailed selection procedure are described on this web site: submission deadline for completed application package is 31st July 2006 Candidates with strong experience in quantitative genetics and population biology should first contact François Lefevre (lefevre@avignon.inra.fr), sending full CV and references.

Objectives: Demo-genetic models, which integrate demographic and genetic processes and their interactions, are used for a simulation approach of the evolution of forest tree populations in disequilibrium. Two complementary modelling platforms of this kind are currently developed in France: for spatially explicit individual-based models (CAPSIS, Dreyfus et al., 2005, <http://coligny.free.fr/>) and for metapopulation (METAPOP, Le Corre & Kremer, 2003). These models have been used to follow the trajectory of neutral genetic diversity and start to be used to follow the evolution of known QTLs under selection. However, for most adaptive traits, we expect that we will never have an exhaustive knowledge of all QTLs involved. In such a situation, given some integrated information on the genetic determinism of a trait of interest (e.g. genetic variances, heritability, ...), a classical approach consists in simulating an adequate distribution of QTLs and follow these QTLs. However, this approach still relies on strong assumptions that can affect the predictions of the demo-genetic models (Barton & Keightley, 2002; Porter & Johnson, 2002; Naciri-Graven & Goudet, 2003). The post-doc will investigate the impact of the modelling strategy for quantitative traits on the simulations produced by the demo-genetic models. In particular, the impact of a non-linear relationship between genotype and phenotype will be investigated. In a first phase of the project, different non-linear models will be compared to simple additivity and compared among each other for their predictions on the evolution of phenotypic diversity in various demographic and genetic sce-

narios. In a second phase of the project, modelling tools for the relationship between genotype and phenotype will be implemented on the CAPSIS platform and simulation studies will be conducted on demo-genetic modules that relate to two experimental situations currently under study in our lab: the micro-evolution of an exotic species (cedar) that was introduced 150 years ago and naturalised in 3 generations, the dynamics of recolonising tree species (beech and fir) along an altitudinal cline. In both cases, selection processes will be added to the other demo-genetic processes that are already included in the models: dispersal, growth, competition, mortality. Predictions in terms of spatial and inter-generational patterns of adaptive diversity will be compared to experimental data. Sensitivity analysis will also be conducted. This research will contribute to define criteria and indicators for monitoring the trajectory of adaptive diversity.

This project is related to the European Network of Excellence EVOLTREE (www.evoltree.org).

Barton NH, Keightley D (2002). Understanding quantitative genetic variation. *Nature Review Genetics* 3, 11-21. Dreyfus P, Pichot C, De Coligny F et al (2005). Couplage de modeles de flux de genes et de modeles de dynamique forestiere. *Les Actes du BRG* 5, 231-250. Le Corre V, Kremer A (2003) Genetic variability at neutral markers, quantitative trait loci and trait in a subdivided population under selection. *Genetics* 164, 1205-1219. Naciri-Graven Y, Goudet J (2003) The additive genetic variance after bottlenecks is affected by the number of loci involved in epistatic interactions. *Evolution* 57, 706-716. Porter AH, Johnson NA (2002) Speciation despite gene flow when developmental pathways evolve. *Evolution* 56, 2103-2111.

– *!*!* ATTENTION : nouvelles coordonnees *!*!*
 Francois Lefevre INRA, URFM - Unite de Recherches Forestieres Mediterraneennes (UR629) Domaine Saint Paul, Site Agroparc 84914 Avignon Cedex 9 tel: +33.4.32.72.29.01 (29.00) fax: +33.4.32.72.29.02

Francois Lefevre <lefevre@avignon.inra.fr>

IndianaU PopGenet

POSTDOC IN THE POPULATION GENETICS OF GENE EXPRESSION

An NIH-funded postdoctoral position is available in the lab of Matthew Hahn in the Department of Bi-

ology at Indiana University. The work examines the genetic and evolutionary basis of variation in transcriptional regulation in *D. melanogaster* via large-scale re-sequencing and gene expression assays, in collaboration with Dr. Sergey Nuzhdin at UC Davis. The postdoctoral candidate will also be encouraged to carry out independent computational or empirical work in the lab, especially projects that leverage the 12 sequenced *Drosophila* genomes to inform the proposed research.

There is a wide variety of research going on in the lab in addition to the current project, including studies of nucleotide, gene family, and gene expression variation within and between species. For a summary of work in the lab, please see: <http://www.bio.indiana.edu/facultyresearch/faculty/Hahn.html>

The candidate must have a Ph.D., preferably in population genetics, statistical genetics, computational biology, or phylogenetics. Programming skills aren't required, but the candidate must be willing to learn. Salary is \$40-\$45K (plus benefits) commensurate with experience. The anticipated start date for this position is September 1, 2006.

Indiana University has a large and active group in evolutionary genetics, and considerable resources are offered by IU's Center for Genomics and Bioinformatics. Bloomington is situated in scenic, hilly southern Indiana, near several parks and wilderness areas. The cultural environment provided by the University is exceptionally rich in art, music, and theater.

To apply, please send a CV and two references to Jeremy Bennet at jebennet@indiana.edu. Review of applications will start immediately and will continue until the position is filled.

Indiana University is an Equal Opportunity / Affirmative Action Employer.

Matthew Hahn <mwh@indiana.edu>

IowaStateU EvolGenomeOrganization

Postdoc: Evolutionary Theory of Genome Organization

A postdoctoral position is available immediately in the Proulx lab at Iowa State University (<http://www.eob.iastate.edu/>) to investigate the evolution of genome structure using mathematical, computational and bioinformatic tools. Our current research focus

includes the evolution of robustness in genetic networks (http://www.proulxresearch.org/papers_robust.htm), evolutionary theory for the evolution of network structure (http://www.proulxresearch.org/papers_TREE.htm), and the evolution of gene families (http://www.proulxresearch.org/papers_AllelicDivergence.htm). The postdoc will have broad opportunities to conduct research in any area related to the evolution of genome structure.

Candidates with a strong background in mathematics and computer science who are interested in applying these tools to biological problems are encouraged to apply. The position is immediately available.

To apply, send an email to postdoc@proulxresearch.org containing a letter of interest and CV. Include the names of three potential references on your CV. Applications will be reviewed until the position is filled.

Stephen Proulx Assistant Professor Ecology, Evolution & Organismal Biology 253 Bessey Hall Ames, IA 50011-1020 (515)294-0272 proulx@iastate.edu

www.proulxresearch.org Stephen Proulx
<proulx@iastate.edu>

MaxPlanckInstLeipzig MolAnthro

A postdoctoral position in molecular anthropology is available in the group of Prof. Dr. Mark Stoneking at the Department of Evolutionary Genetics, Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany. The position involves collecting and analyzing data to address various questions concerning human population history and the role of recent selection on the human genome. See our website (http://www.eva.mpg.de/genetics/files/-team_stoneking.html) for further details concerning ongoing projects. Applicants should have a Ph.D. in a relevant field and experience in collecting and analyzing molecular genetic data. The position is available from August 1, 2006, for an initial period of one year, renewable for up to five years. Send inquiries and application materials (CV, list of publications, and names of three references) to Mark Stoneking (stoneking@eva.mpg.de).

Dr. Mark Stoneking Max Planck Institute for Evolutionary Anthropology Deutscher Platz 6 D-04103 Leipzig Germany Phone: +49-341-3550-502 FAX: +49-341-3550-555 Secretary: +49-341-3550-504 e-

mail: stoneking@eva.mpg.de <http://www.eva.mpg.de/genetics/> stoneking@eva.mpg.de

McMasterU ConcordiaU PopGenomics GenomeEvol

Postdoctoral Fellowships: Population Genomics and Genome Evolution.

A number of postdoctoral positions are available in the laboratories of Dr. Donal Hickey Concordia University (Montreal) and Dr. Brian Golding McMaster University (Hamilton Ontario). These positions are supported by funds from Genome Canada, the Canada Research Chairs program and the Research Networks program of NSERC.

The focus of our research is on the patterns and processes of DNA sequence evolution within and between populations. We are especially interested in the effects of mutational bias, population structure and recombination rate on the distribution of sequence diversity within and between species. We are also interested in the comparison of molecular sequence evolution between organelle and nuclear genomes. In addition to the theoretical research, these projects will also involve computer-assisted analyses of DNA Barcode data (see http://barcoding.si.edu/index_detail.htm) and human HapMap data (see <http://www.hapmap.org/>).

Candidates must have completed a Ph.D. in the field of molecular evolution, theoretical population genetics, or a related discipline. Experience in statistical analysis and/or bioinformatics and computer programming is required.

Send a complete CV, a description of your research interests, and the names of at least two referees via email to either Brian Golding <Golding@McMaster.CA> or Donal Hickey <dhipkey@alcor.concordia.ca>. Include a subject header that clearly states "Application for Postdoctoral Fellowship".

Netherlands biparental care

Post-doc position:

Bi-parental care: the same game by different rules?

Netherlands Institute of Ecology, Heteren, The Netherlands

A post-doc position is available at the Department of Animal Population Biology of the Netherlands Institute of Ecology to work on the behavioural rules used by parents of each sex to provision offspring when there is bi-parental care. The work carried out by the post-doc will comprise two main components: Field experiments on the provisioning behaviour of birds, and mathematical modeling of negotiation models' under bi-parental care.

The post-doc position is part of a double project' funded by the NWO (Netherlands Research Organisation) Evolution & Behaviour' programme, aimed at promoting evolutionary approaches in research on human behaviour, granted to Dr Judith Semon Dubas (Developmental Psychology, Utrecht University) and Dr Kate Lessells (Animal Population Biology, Netherlands Institute of Ecology, Heteren). The other sub-project, on bi-parental care in humans, will be carried out by a Ph.D. student based at the University of Utrecht. The post-doc is expected to collaborate actively within the double project.

Requirements: The candidate should have completed a PhD in Behavioural or Evolutionary Ecology. They should have relevant experience in either field or laboratory experiments or in mathematical modeling, and interest in developing their abilities in the other of these two areas. The candidate should be willing to work flexible hours as required by fieldwork. A driver's license would be an advantage.

Appointment and conditions: The appointment will be for 3 years starting no later than August 20th 2006. Depending on training and experience, the maximum gross monthly salary is 3472. The post-doc will be based at the Netherlands Institute of Ecology, Centre for Terrestrial Ecology at Heteren, The Netherlands.

Information:

A more detailed description of the project may be downloaded from: <http://www.nioo.knaw.nl/-ppages/klessells/downloads/1/Postdoc.doc> Information about the Netherlands Institute of Ecology, the Centre for Terrestrial Ecology, and the Department of Animal Population Biology can be found at <http://www.nioo.knaw.nl/indexENG.htm> For additional information please contact Dr Kate Lessells (k.lessells@nioo.knaw.nl)

Application:

Applications, quoting the reference CTE-APB-06116

and including a detailed CV and the names of three scientific referees, should be sent to Prof. Dr J.A. van Veen, Centre Director, Centre for Terrestrial Ecology, NIOO-KNAW, PO box 40, 6666 ZG Heteren, The Netherlands, or preferably by e-mail to h.vanveen@nioo.knaw.nl. There is no fixed closing date, but applications received after 15th July 2006 may not be considered.

K.Lessells@nioo.knaw.nl

NorthCarolinaStateU SpeciationGenetics

Applications are invited for a postdoctoral research associate with Dr. Trudy F. C. Mackay in the Department of Genetics at North Carolina State University. The overall goal of this collaborative NIH-funded project between Dr. Mackay and Dr. Jerry Coyne, University of Chicago, is to determine the molecular genetic basis of pre- and post-zygotic reproductive isolation between two pairs of *Drosophila* species, *D. mauritiana*/*D. simulans*, and *D. santomea*/*D. yakuba*. The project will entail high resolution mapping of quantitative trait loci affecting pigmentation, hybrid sterility, mating discrimination and interspecific mating-song differences; and analysis of experimental evolution of hybrid swarms in laboratory populations.

Candidates will be required to have a PhD in Genetics, Statistics, Genomics or related field. The ideal candidate will be creative, have excellent molecular biology and statistical skills, a background in population and/or quantitative genetics, and experience working with *Drosophila*. The salary is in accordance with NIH guidelines. Review of applications will begin immediately, and continue until the position is filled. Please contact trudy_mackay@ncsu.edu for further information.

To apply, please submit applications, including a CV and the names and contact information of three references at our website at <http://jobs.ncsu.edu> and use the position number 01-09-0604 to locate this posting.

Women and members of other underrepresented groups are especially encouraged to apply. AA/EOE. In addition, NC State University welcomes all persons without regard to sexual orientation. ADA: call 919-515-3148.

Dr. Trudy F. C. Mackay WNR Distinguished Professor of Genetics Department of Genetics, Box 7614

North Carolina State University Raleigh, NC 27695-7614 Tel: 919-515-5810 Fax: 919-515-3355 Email: trudy_mackay@ncsu.edu

NorthDakotaStateU EvoBiol

The Department of Biological Sciences at North Dakota State University is sponsoring 2 postdoctoral positions to develop excellent teacher-scholars. Applications from highly qualified candidates for 2 two-year appointments in cellular/developmental/evolutionary biology are invited for positions beginning fall, 2006. The positions are 50% research and 50% teaching. Candidates will conduct original research in collaboration with a sponsoring faculty mentor within the department (see <http://biology.ndsu.nodak.edu/> for information on possible mentors.). Positions include research and travel allowances. Under the mentorship of a faculty sponsor, postdoctoral fellows will teach two courses per year in the following areas: cell biology, developmental biology, and evolution. These positions have some potential for conversion to a tenure-track appointment.

Candidates must have 1) a Ph.D. degree from an accredited institution in an appropriate discipline; 2) demonstrated research experience in cell/developmental/evolutionary biology; 3) evidence of peer-reviewed publication; 4) evidence of interest and ability in teaching at the undergraduate and graduate levels; 5) strong oral, written, and interpersonal communication skills, including demonstrated ability to work/collaborate with others. Preference will be given to candidates with teaching experience at the university level.

Applicants should submit 1) a letter of application detailing their suitability for a position and how it will advance their career; 2) a curriculum vitae; 3) a one-page research prospectus; 4) a sample course syllabus; 5) contact information (including telephone numbers and e-mail addresses) for three professional references to: Dr. Will Bleier, Chair Postdoctoral Search Committee, Department of Biological Sciences, North Dakota State University, P.O. Box 5517, Fargo, ND 58105-5517.

Review of applications will begin June 30 and continue until the positions are filled.

Wendy L. Reed Assistant Professor Department of Biological Sciences North Dakota State University Stevens Hall 218 Fargo, ND 58105

Office Ph. 701-231-5921 Lab Ph. 701-231-5902 FAX.
701-231-7149 wendy.reed@ndsu.edu

Wendy Reed <Wendy.Reed@ndsu.edu>

NottinghamU EvoDevo

Postdoctoral Research Fellow Evolution & Development School of Biology, Institute of Genetics Applications are invited for the above post, funded by the BBSRC, in the laboratory of Dr M Loose to study genetic regulatory networks (GRNs) underlying the development of vertebrate lens. The successful candidate will initially construct GRNs for lens development in the frog, *Xenopus laevis* and the ascidian, *Ciona intestinalis* using a combination of bioinformatics approaches including transcription factor binding site analysis. The aim is to identify and dissect the conserved components of the underlying GRNs and link the underlying network architecture with network function (see Loose and Patient 2004, *Dev Biol* 271:467-78 or Swiers et al, 2006 *Dev Biol* in press).

The project involves close collaboration with Dr Seb Shimeld (University of Oxford), who will be carrying out functional analysis of lens development in *Ciona intestinalis*, and with Christine Slingsby (Birkbeck College, London) and Nicolette Lubsen (Radboud University, Nijmegen). As a result of these collaborations, it will be possible to test predictions made from the GRN analysis in both *Ciona* and *Xenopus*.

Candidates must hold a PhD and ideally have an interest in development and gene regulation. Experience with relevant bioinformatics techniques such as transcription factor binding site analysis and GRN tools such as mFinder, NetBuilder and BioTapestry will be useful. Basic HTML skills will be an advantage (although training will be available).

Salary will be within the range £23,457 - £28,850 per annum, depending on qualifications and experience (salary can progress to £33,445 per annum, subject to performance). This post is available immediately and will be offered on a fixed-term contract for a period of up to three years, depending on qualifications and experience.

Informal enquiries may be addressed to Dr M Loose, Email: Matt.Loose@Nottingham.ac.uk.

Candidates should send a detailed CV and covering letter explaining their interest in the post, together with

the names and addresses of two referees, to Dr M Loose, Institute of Genetics, School of Biology, The University of Nottingham, Medical School, Queen's Medical Centre, Nottingham, NG7 2UH. Please quote ref. MED/22.

Closing date: 7 July 2006.

Matthew Loose <Matt.Loose@nottingham.ac.uk>

ParisVI PopBiol

Postdoc in population biology in Paris, France

Postdoc grants will be delivered by Paris VI Jussieu University to its laboratories, for foreign (not French) phd being less than 35 years old. The grants will be given for 1 year studies on topics selected by a scientific commission of the University.

Our lab UMR Paris VI-CNRS-MNHN 5173, Conservation des espèces, Restauration et Suivi des populations, Muséum National d'Histoire Naturelle, Paris, France (director : Denis COUVET) would like to present an application to this grant. For that purpose, we need an excellent candidate interested by our topic:

*Assessment of created populations of *Arenaria grandiflora* /L./, /a species on the brink of extinction in the Parisian region (**France**); *

The successful restoration of plants species in the wild depends on the knowledge of their habitat requirements and on the consideration of genetic, demographic and ecological traits that increase vulnerability to stochastic extinction processes. The experiment we performed on an endangered caryophyllaceae in the Parisian region (*Arenaria grandiflora*/ L.) is presented as an example of experimental restoration plan. In a case where inbreeding depression was suspected in the remnant populations, we created, in 1999, in the Fontainebleau forest near Paris, six replicates of a new population composed of plants from two different origins: Fontainebleau (the local population) and Chinon (200 km apart). Since the transplantation in the Fontainebleau forest, individuals have reproduced. We follow annually the dynamics of the populations.

The aim of this postdoctoral study is (1) to analyse the demographic data and (2) to use microsatellites to determine the origin of the plantlets born in the created populations (Fontainebleau, Chinon or both). In other words, we would like to assess if the plants from both origins have the same fitness. On a fundamental plan,

this study will give insights on local adaptation phenomena. It will also highlight the possible advantage to mix populations in the restoration plans.

We thus are looking for a Ph.D in population biology. Preference will be given to candidates with a background in population genetics and dynamics and have experience in molecular biology (microsatellites). Knowledge of the French language is not required.

We will select the best applicant among the candidates that achieve to apply before June the 20th. Please supply by email (machon@mnhn.fr) (1) a statement of interest, (2) a curriculum vitae, and (3) letters of recommendation.

If our file is selected by the University, the position will start late 2006.

For more information regarding the position, contact Pr Nathalie MACHON machon@mnhn.fr <mailto:machon@mnhn.fr>.

Nathalie MACHON <machon@mnhn.fr>

QueenMaryLondon 2 PathogenEvol

Queen Mary's School of Biological and Chemical Sciences

*London** School** of Hygiene and Tropical Medicine - Pathogen Molecular Biology Unit*

*_Two _**_Postdoctoral Research Fellows_*

Salary starting at £25,272 per annum, depending on experience

**Applications are invited for two postdoctoral research fellow positions, working within the School of Biological and Chemical Sciences (QMUL) and the Pathogen Molecular Biology Unit (LSHTM). The joint project will focus on analysing the role played by the unusual mitochondria of a human intestinal parasite, *Blastocystis hominis*, using molecular and cell biological techniques. *Blastocystis* is an anaerobic stramenopile (Silberman, Sogin, Leipe and Clark, Nature 380: 398) and contains mitochondrial remnants that appear to be distinct from those found in other anaerobic eukaryotes (see van der Giezen and Tovar, EMBO Reports 6: 525-530).

Essential requirements for both of these posts are a PhD in a relevant subject and previous experience in molecular biology and/or cell biological research. A

demonstrated ability to communicate well, work within a team, and maintain good laboratory records is also essential. Previous experience of working with organelles, especially mitochondria, and of cultivating microbial parasites would be advantageous.

Both full-time posts are available immediately, and are funded by the *Wellcome Trust* for a period of three years. One position will be based at each institution.

*Candidates wishing to apply for the post at QMUL should visit <http://www.sbcs.qmul.ac.uk/> <<http://www.sbcs.qmul.ac.uk/>> for all the relevant information and a BLUE application form, **or alternatively, please visit the Human Resources website on: <http://www.hr.qmul.ac.uk/vacancies/>. **Completed application forms together with a copy of your C.V quoting reference no. 06200/FS should be returned to Mrs Denise Griffiths, School of Biological & Chemical Sciences, Queen Mary, University of London, London, E1 4NS, (email: sbcs@qmul.ac.uk <mailto:sbcs@qmul.ac.uk>), by the closing date of 17th July 2006. *

*Candidates wishing to apply for the post at LSHTM should visit <http://www.lshtm.ac.uk/jobs/> **for further information and details on how to apply. Completed applications quoting reference no. GC10 should be sent to the Personnel Office, London School of Hygiene & Tropical Medicine Keppel Street, London WC1E 7HT (e-mail: personnel@lshtm.ac.uk <mailto:personnel@lshtm.ac.uk>) **by the closing date of 17th July 2006**.*

- Dr. Mark van der Giezen Lecturer in Microbiology School of Biological and Chemical Sciences Queen Mary, University of London Mile End Road, London E1 4NS, UK tel.: +44 207 8823057/fax: +44 208 9830973 e-mail: m.vandergiezen@qmul.ac.uk <http://www.vandergiezen.org> Mark van der Giezen <m.vandergiezen@qmul.ac.uk>

RutgersU ShellfishGenet

Postdoctoral Positions In Shellfish Genetics

Two postdoctoral associate positions are available at the Haskin Shellfish Research Laboratory, Rutgers University. The positions are supported by grants from NOAA Sea Grant and NSF. Research will have two focuses: 1) the identification and mapping of disease-resistance genes and quantitative trait loci in the eastern oyster; and 2) population genetics with a focus on

the role of reproduction and diseases in the differentiation of oysters. Applicants should have a Ph.D. and background in genetics and molecular biology. Prior experience in genotyping, cloning and sequencing is preferred. The appointments start on September 1, 2006 or soon after, and are for one year with possible renewal. Search will continue until the positions are filled. Interested individuals should submit a CV, a brief statement of interest, and three letters of recommendation to: Dr. Ximing Guo, Haskin Shellfish Research Laboratory, Institute of Marine and Coastal Sciences, Rutgers University, 6959 Miller Avenue, Port Norris, NJ 08349. Phone: (856) 785-0074 x4324; Fax: (856) 785-1544; Email: xguo@hsrl.rutgers.edu. Web: <http://www.hsrl.rutgers.edu>. Ximing Guo, Associate Professor Haskin Shellfish Research Laboratory Institute of Marine and Coastal Sciences Rutgers, the State University of New Jersey 6959 Miller Avenue, Port Norris, NJ 08349 Ph: 856-785-0074 x4324 FAX: 856-785-1544 Email: xguo@hsrl.rutgers.edu

Ximing Guo <xguo@hsrl.rutgers.edu>

Stockholm CanineEvol

Postdoc:

Population genetic studies of the origin and early history of the dog

A 2-year Postdoc position is available in the research group of "Evolutionary biology and forensics" at the Department of Biotechnology, Royal Institute of Technology, Stockholm, Sweden (www.biotech.kth.se/genetech/info/savolainen.html).

We are a small research group (Assistant professor Peter Savolainen and two PhD-students) performing world-leading research about the origin and early history of the domestic dog. We have in earlier studies of mtDNA shown that the dog probably has a single origin from wolf somewhere in East Asia (Savolainen et al, 2002, *Science*: 298,1610-1613), and that the Australian dingo originates from this population of East Asian domestic dogs (Savolainen et al, 2004, *Proc Natl Acad Sci U S A*: 101,12387-12390).

Our studies are based on a unique sample collection from more than 2,000 dogs representing all major populations worldwide. This collection is, to our knowledge, the most comprehensive for any domestic animal, most other collections consisting mostly of European breeds.

This puts us in a very good position for our further studies.

The over all aim for our work is to describe in detail the first origin and early history of the domestic dog. First we want to study in more detail the exact geographic origin and time for the origin of dogs, the number of founder animals (wolves), and the extent of subsequent interbreeding between dog and wolf. In the next step we will describe the spread around the world (routes and time points) from East Asia to Europe, America, Africa and Island Southeast Asia/Australia, and the first steps in the development of morphological variation leading to today's types and breeds of dog. Thus, the rather bold goal is to describe more or less everything about the genetic origin and history of the dog, leaving few fundamental questions unanswered.

Our earlier studies have been based on sequencing of the mtDNA control region, but we are now analysing also entire mtDNA genomes as well as Y-chromosome sequence and microsatellites. Since we have very powerful large-scale systems for DNA analysis, but have been understaffed for the population genetic analyses, we have at the moment a large amount of genetic data just waiting to be analysed. This is therefore a good chance for a Postdoc with a good knowledge in population genetics to rapidly generate a number of papers.

We are looking for a Postdoc with a good knowledge and experience in population genetics, phylogenetics and statistics, to help us analyse our large data set. Some practical lab skills would be preferable, but the important thing is a good knowledge in population genetic and phylogenetic methods and ability in manuscript writing. The applicant should, at the start of appointment, have obtained a PhD-degree not more than five years earlier.

The Postdoc would receive a stipend (tax free) of 17,000-19,000 Swedish crowns per month (exact sum not fixed at this point), equivalent to 1,800-2,000 euros per month.

There is no exact deadline for applications, the position is supposed to be started during the autumn 2006.

If interested in applying for this position, send an email to Peter Savolainen (savo@biotech.kth.se), containing a letter describing your previous research experience (including a description of your skills in for example population genetics, phylogenetics, statistics, computer programming and molecular genetics lab work), a CV and publication list.

– Peter Savolainen, Ph.D. Assistant Professor Molecular Biotechnology Albanova University Center KTH-Royal Institute of Technology SE-106 91 Stockholm

Sweden

Email: savo@biotech.kth.se Tel: int+46-8-5537 8335 Fax: int+46-8-5537 8481 Homepage www.biotech.kth.se/molbio/info/savolainen.html
savo@biotech.kth.se savo@biotech.kth.se

Switzerland LandscapeGenet

The Swiss Federal Research Institute WSL and its 500 staff members are committed to contribute to a landscape of high quality and to the protection of humans from natural hazards. In the department Ecological Genetics, we initiate a landscape genomics project on adaptive variation in an alpine plant species. For this one-year project, starting this summer, we are offering the position of a

PostDoc in landscape genomics

You will carry out an environmental association analysis in the model species *Arabis alpina* to identify and characterize molecular markers exhibiting habitat-specific allele frequencies. In close collaboration with the University of Grenoble (P. Taberlet, S. Manel), you will elaborate the study design, organize and carry out field collections, and perform the marker assessment (AFLPs) in the lab. Data analysis and publication will conclude the study.

Your qualifications: PhD in biology or environmental sciences, good practical skills in molecular lab work, strong background in the analysis of population genetic data, experience in field work (rugged, alpine terrain), flexibility and commitment.

A small, motivated team with a well-equipped molecular laboratory and an excellent logistic support are waiting for you.

Interested? Please send your complete, written application, including photo, using reference number 445 to Mrs. Monika Huber, Swiss Federal Research Institute WSL, Human Resources, Zuercherstrasse 111, CH-8903 Birmensdorf, Switzerland. Further information can be obtained from Dr. Felix Gugerli (Tel: +41-(0)44-739 25 90) or Dr. Rolf Holderegger (Tel: +41-(0)44-739 25 27).

Dr. Rolf Holderegger, Deputy Section Head, Section of Ecological Genetics, WSL Swiss Federal Research Institute, Zürcherstrasse 111, CH-8903 Birmensdorf, Switzerland; Tel. +41 44 739 25 27; Fax. +41 44 739 22 15; e-mail: rolf.holderegger@wsl.ch; www.wsl.ch/

staff/rolf.holderegger/

Rolf Holderegger <rolf.holderegger@wsl.ch>

UAdelaide AncientDNA

Two post-doctoral positions available at the new Australian Centre for Ancient DNA (ACAD) at the University of Adelaide, Australia. (<http://www.ees.adelaide.edu.au/research/acad/>)

Using ancient DNA to examine the environmental impacts of climate change and humans over the past 50,000 years

An ARC-funded position is available to study ancient DNA sequence data from Southern Hemisphere populations of megafaunal species to examine the genetic impact and role of climate change and human colonisation in Late Pleistocene and Holocene extinctions. The 3-year project will involve rigorous ancient DNA laboratory techniques in the internationally leading facilities at ACAD, fieldwork in South America, South Africa, New Zealand and Australia, collaborations with museums, archaeologists and local cavers, and complex bioinformatic computational analyses. A PhD student is associated with the project, and co-supervision will be part of the role. The project supervisors are Prof. Alan Cooper (University of Adelaide) and Prof. Tim Flannery (South Australia Museum). A PhD or equivalent experience in a relevant discipline (ancient DNA, palaeoecology, population genetics, or archaeology) is required, along with excellent written and oral communication skills with the ability to liaise, collaborate and interact with a wide range of international scientific researchers. Excellent laboratory analytical skills in molecular biology or biochemistry would be an advantage. Salary: (Level A) Australian \$53,509 - \$57,438 per annum (Level B) \$60,464 - \$71,802 per annum plus an employer superannuation contribution of 17% applies. Further information, including the selection criteria may be obtained from Mrs Gail Edwards email: gail.edwards@adelaide.edu.au. Applications, addressing the selection criteria, quoting the reference number 11085, and including residency status, names, addresses and/or email details of three referees, should be forwarded in duplicate to Maria Lekis, School of Earth and Environmental Sciences, The University of Adelaide, South Australia 5005, or email: maria.lekis@adelaide.edu.au by 23 June 2006.

Ancient DNA studies of human evolu-

tion and migration National Geographic Society 'GENOGRAPHIC PROJECT' (<https://www3.nationalgeographic.com/genographic/atlas.html>)

A postdoctoral position is about to become available on this largescale project to map the timing, location and nature of human dispersals around the world. This preliminary notification is to seek interested applicants. The 5 year Genographic project involves a number of leading international centres, and ACAD will contribute ancient DNA typing of mitochondrial and Y chromosome loci from ancient human (and hominid) specimens from around the world. The complex laboratory studies will be supported by newly developed molecular methods and dedicated sequencing resources at ACAD, and significant analytical resources through the Genographic Project and partners. A large fieldwork component will be involved, along with extensive collaborations with museums, archaeologists and other members of the Genographic Project. An experienced postdoc is required to perform the fieldwork, complex laboratory analyses, provide regular communication between the parties and organize data management and analysis. Relevant skills would include a PhD in ancient DNA, archaeology, anthropology or molecular genetics and experience in areas such as SNP multiplex typing and advanced laboratory methods. The salary and conditions are to be confirmed, but an experienced and highly capable postdoc is sought. Interested parties are invited to contact Prof. Alan Cooper alan.cooper@adelaide.edu.au for further information. It is hoped that details of the full application will be announced in late July. –

Prof. Alan Cooper, Federation Fellow

Darling Blg (DP 418), Rm 209b University of Adelaide North Terrace Campus South Australia 5005 Australia

Email: alan.cooper@adelaide.edu.au Ph: 61-8 -8303-5950/3952 Fax: 61-8-8303 4364

<http://www.ees.adelaide.edu.au/research/acad/>
CRICOS Provider Number 00123M

alan.cooper@adelaide.edu.au

UArizona Bioinformatics

Postdoc position: theoretical population genetics and bioinformatics of evolvability

Evolutionary capacitor mechanisms such as alternative

splicing and the heat shock protein Hsp90 store variation in a latent form and reveal it later. Capacitors appear to be common, and could have a significant impact in facilitating evolution. The project is to develop theoretical population genetic models of evolutionary capacitance in finite populations, and to test predictions of the models in the case of the yeast prion [PSI+] using a bioinformatic / comparative genomic approach. A variety of concepts in evolutionary biology will be explored and made rigorous, including evolvability, preadaptation and genetic assimilation.

The postdoc will work with PI Joanna Masel (<http://eebweb.arizona.edu/Faculty/bios/masel.html>) at the University of Arizona in Tucson. NIH funding is secured, and the position is renewable over multiple years. Preferred start date is Aug 1 2006. Ph.D. with strong quantitative background and computational and/or modeling experience is required. Prefer experience in some of: bioinformatics, comparative genomics, evolutionary theory, computational methods based on linear algebra, other algorithm experience, finite Markov chains, PERL, MySQL, other computational or mathematical biology. Apply at www.uacareertrack.com/applicants/Central?quickFind=183751 or contact Joanna Masel at masel@u.arizona.edu for more information.

masel@U.Arizona.EDU masel@U.Arizona.EDU

UBritishColumbia MolecularEvol

Postdoctoral: molecular and genomic evolution

A postdoctoral position is available at the University of British Columbia in the lab of Keith Adams to study molecular evolution and evolutionary genomics in plants. Research in the lab currently focuses on polyploidy, gene duplication, and hybridization and their effects on gene expression and gene evolution. For more details see: http://www.landfood.ubc.ca/research/faculty_webpages/adams.htm Research for the position would pertain to the above topics or related areas in the evolution of genes and gene expression. The research likely will involve a combination of dry and wet lab work. Candidates with a strong background in comparative genomics, bioinformatics, or molecular evolution are preferred. The position is available as early as July and there is some flexibility in start date.

For more information contact Keith Adams at keitha@interchange.ubc.ca To apply send a CV, a descrip-

tion of your research interests, and names of 3 references to the above email address.

keitha@interchange.ubc.ca

UCLA ConservationGenet

POSTDOC: plant molecular ecol-
ogy/population/conservation genetics at UCLA

A postdoctoral position is available in Fall 2006 to study/model contemporary seed dispersal in the laboratory of Victoria Sork, University of California, Los Angeles. The post-doc position, which is part of an NSF-collaborative project between Sork and Peter Smouse (Rutgers), will involve a combination of field work, laboratory work, and statistical modeling to develop new approaches to the study of gene movement through seeds, using valley oak as its model system. The nature of the exact project will depend on the expertise and interests of the candidate. In addition, this person can establish a related project addresses complementary questions. Candidates must have strong molecular and/or statistical modeling skills, and background in population genetics.

Please email a statement of interest in the position highlighting your areas of expertise and research interests, with names and electronic addresses of three references to vlsork@ucla.edu. Please attach a CV, and 2-3 publications or manuscripts (Word or pdf format). Applications are accepted starting May 31 and reviewed upon receipt until the position is filled. Ideal starting date is September 2006.

UCLA University is an equal opportunity employer.

Victoria Sork Professor and Chair, Dept of Ecol & Evol
Biology Professor, Institute of the Environment

phone: 310-825-7755 Fax: 310-206-0484

Victoria Sork <vlsork@ucla.edu>

UChicago PopGenet

A postdoctoral position in statistical/computational population genetics is available in the group led by Jonathan Pritchard at the University of Chicago.

Current research in the lab focuses on aspects of human genetic variation and evolution including (i) methods for identifying targets of natural selection, (ii) population genetics of structural variation, (iii) methods for identifying the genes that contribute to complex traits, and (iv) history and structure of human populations. We are interested both in the development of statistical methods as well as in data analysis. The successful applicant will work on a project relating to one of these general areas, according to his/her interests.

Further information about our research can be found at <http://pritch.bsd.uchicago.edu>. Our group enjoys close interactions with a very strong community of groups in population/statistical genetics, genomics, and complex traits at the University of Chicago.

We seek applicants who are highly motivated and creative, with strong computational skills. Applications should include a CV, statement of research experience and interests, and contact information for three referees. Inquiries and applications should be directed to J. Pritchard (pritch at uchicago dot edu) and cc-ed to Linda Davis (ldavis at bsd.uchicago dot edu).

Jonathan Pritchard Department of Human
Genetics The University of Chicago <http://pritch.bsd.uchicago.edu> Jonathan Pritchard
<pritch@uchicago.edu>

UEdinburgh EvolGenomics

Postdoctoral Position in Evolutionary Genomics

An opportunity is available to work with Peter Keightley (University of Edinburgh) and Adam Eyre-Walker (University of Sussex) on the evolution of gene regulatory elements in mammals.

The great organismal complexity of mammals is believed to be determined to a large extent by the complexity of gene regulation. The elements that control the timing and specificity of gene expression are for the most part located in noncoding DNA, and are typically less well conserved than coding sequences. However, the understanding of the nature of the sequences that control gene expression is incomplete, and, in particular, the mode and strength of natural selection that operates on sequence variation is largely unresolved. The aim of this project is quantify the level of natural selection acting upon gene regulatory elements. To this end we aim to (i) more accurately quantify the differences in

constraint in gene regulatory elements in hominids and murids and (ii) collect polymorphism data from wild mice with a view to using population genetic methods to quantify the level of natural selection. The sequencing component of the project will be undertaken by a research assistant, so the principle responsibility of the post-doc will be the analysis of the polymorphism data and the quantification of constraint. The post will be held at the University of Edinburgh. Applicant should have a PhD, a record of published research in an area relating to evolutionary genomics, and strong analytical and computing skills.

Informal enquiries can be addressed to Peter Keightley - keightley_evolg2006@spambob.net . Information about work carried out in our lab is available on the website: <http://homepages.ed.ac.uk/eang33/> The start date is negotiable.

Applications should include a cover letter outlining research interest and motivations and a C.V. with the names of 3 referees, and should be made via the University of Edinburgh online job application website <http://www.jobs.ed.ac.uk/> .

azzggsdf444233@yahoo.co.uk

UEdinburgh HostParasiteCoevol

Job: Post-Doc on Host-Parasite Coevolution in Edinburgh, UK

Funding body: Wellcome Trust Duration: 36 months, starting Sept 1/2006 (flexible) Hours: Full-time Supervisor: Dr Tom Little Informal enquiries: tom.little@ed.ac.uk

This is a Wellcome Trust funded post on host-parasite co-evolution. The project is focused on a model system where the host species is the crustacean *Daphnia*. To gain insight into evolutionary dynamics and the genetic basis of disease resistance in this invertebrate, the project may involve a variety of approaches depending on the skills and interests of the applicant. These may include: 1) field sampling and experimental infections or other whole organism studies of infection phenotypes and genetic variation for resistance; 2) molecular work (For example, QTL and microarray analysis) to uncover key components of the immune system. Molecular work has recently been enabled by the completion of the *Daphnia* genome sequence. The project will be based in Tom Little's laboratory in the Institute of Evolution-

ary Biology at the University of Edinburgh (<http://www.biology.ed.ac.uk/research/institutes/evolution/>) but there will be ample opportunity to interact with the international *Daphnia* genomics consortium (<http://daphnia.cgb.indiana.edu/>).

Person specification:

You should have a strong interest in evolutionary biology and/or host-parasite interactions. A PhD is required, and a proven ability to publish scientific papers is preferred.

Starting Date Sept 1/2006 (flexible)

Apply at <http://www.jobs.ed.ac.uk>. Reference: 3006013

Salary

The role is grade AR1A and attracts an annual salary of £20,044 to £30,002 for full-time hours.

Tom Little, Wellcome Trust Senior Research Fellow Institute of Evolutionary Biology School of Biological Sciences, University of Edinburgh Edinburgh EH9 3JT, UK

tom.little@ed.ac.uk tel: 0131 650 7781 fax: 0131 650 6564

<http://www.biology.ed.ac.uk/research/institutes/evolution/> <http://www.biology.ed.ac.uk/research/institutes/evolution/homepage.php?id=tlittle> <http://daphnia.cgb.indiana.edu/> Tom Little <tlittle1@staffmail.ed.ac.uk>

UFlorida Polyploids

POSTDOCTORAL POSITION IN POLYPLOID RESEARCH

We seek a highly motivated and enthusiastic individual to pursue studies on the evolutionary consequences of polyploidy in *Tragopogon*. *Tragopogon* has been a model system for multiple origins of polyploidy in modern times and is now being used as a model group in which to study the earliest stages of genome evolution in polyploids. Our lab has recently resynthesized F1 hybrids and polyploids between all three diploid species that occur in the United States (*T. dubius*, *T. pratensis*, and *T. porrifolius*). The successful applicant will be responsible for maintaining these lines in the greenhouse, conducting molecular genetic work (PCR, RT-PCR, Southern, cloning, sequencing, etc.) in the lab-

oratory, and supervising undergraduate students. Applicants with experience in molecular genetics and with growing plants in the greenhouse are desirable. Funds are currently available for two years of support [with the possibility of extending the position to a third year]. Starting date is flexible, but before 15 August 2006 is preferred.

Applicants should send a CV and names of three references via email to Doug Soltis (dsoltis@botany.ufl.edu), Department of Botany, University of Florida, Gainesville, FL 32605.

Doug Soltis <dsoltis@botany.ufl.edu>

UHawaii 2 EvoGenet

Post-Doctoral positions in Evolutionary and Ecological Genetics

The University of Hawaii is recruiting two Post-Doctoral positions in Evolutionary and Ecological Genetics to begin immediately and conclude on May 14, 2009. One Post-Doc will be based at the Hilo campus (Island of Hawai'i) and the other at the Manoa campus (Island of O'ahu) of the University of Hawai'i. The successful candidates will work as a team in the Ecological and Evolutionary Genetics (EEG) focal area within the University's current EPSCoR grant "Collaborative Research for Ecology, Evolution and Cyberinfrastructure". The EEG focal area has two main research objectives; 1) The study of biogeography and phylogenetics of marine, aquatic, and terrestrial biota to better understand the origin, dispersal, and diversification of Hawaiian taxa, and 2) Evolutionary and ecological functional genetics.

The islands of Hawai'i serve as an optimal location to study the processes of colonization and radiation. Understanding population structure, the genetics of adaptation and environmental effects on gene expression will be at the core of this research. The extreme climatic diversity found across the islands and especially the Island of Hawai'i, where one can find virtually every climate type, provides ample opportunity to study these important evolutionary processes. Examples of the projects presently ongoing in this focal area include:

* Ecological genomics of the model tree species, *Metrosideros polymorpha*/ * Adaptation of Hawaiian crickets to lava flow and cave habitats from a maritime species. * Biodiversity assessment of marine, freshwa-

ter and terrestrial macroalgae in the Hawaiian islands * The effects of behavior and extreme climatic diversity on population structure, local adaptation, and speciation in Hawaiian Picture-winged *Drosophila*. * Population structure of amphidromous gobies in the context of complex near and offshore currents, and significant upslope weather events.

Creative people who think in terms of interdisciplinary approaches to answering complex questions and who have a track record of productive collaborations are encouraged to apply.

Minimum qualifications: Ph.D. from an accredited university. Excellent communication skills. Research experience using a variety of molecular techniques to answer ecological and evolutionary questions.

***Desirable Qualification*s**: Previous experience in gene expression studies, the use of Beckman CEQ 8000, microarray spotters and scanners, and real-time PCR. Active interest in research questions relevant to the Pacific Islands especially Hawai'i.

Contact Information

Please send CV, and contact information of three references, in addition to a cover letter with a statement of research interests to either Cam Muir (cmuir@hawaii.edu <mailto:cmuir@hawaii.edu>) on the Island of Hawai'i, or Jo-Ann Leong (joannleo@hawaii.edu <<http://us.f383.mail.yahoo.com/ym/Compose?&To=joannleo@hawaii.edu>>) on the Island of O'ahu. Review of applications will begin August 1, 2006 and will continue until the positions are filled). Please send application package electronically as a single file with the file name format of:

yournameEEGpostdocapplication.doc (or *.pdf).

Cam <cmuir@big.uhh.hawaii.edu>

UKonstanz MolEvol

Two Postdoc positions in molecular evolutionary biology are available in the lab of Axel Meyer in the Department of Biology at the University of Konstanz, in Germany. The evolutionary biology group is an international group of students and postdocs that consists of about 20 people from 10 different countries. The language in the lab is English.

We are looking for energetic postdocs who are inter-

ested in speciation, molecular evolution, bioinformatics/genomics and/or evolutionary developmental biology. The specific research projects involve research on the patterns of relationships and population genetics of cichlid fishes as well as the discovery and functional characterization of genes underlying the diversification of cichlids in Africa and in Nicaragua.

The great lakes in East Africa house some of the worlds most diverse freshwater ecosystems. Lakes Victoria, Malawi and Tanganyika are particularly well-known for their adaptive radiations of hundreds of endemic species of cichlid fishes. We are interested in understanding speciation, phylogeography, molecular evolution and molecular phylogenetics of these cichlid fish assemblages. We also want to identify and characterize the function of genes that are involved in the phenotypic diversification and presumably speciation of cichlid fishes. Several molecular biological, “devo-evo” and genomic approaches, including candidate gene approaches, DNA-chip technology, characterization of ESTs, in situ hybridization in cichlids and transgenics in zebrafish are used to address these questions. We are also interested in evolutionary genomic questions and the evolution of novel gene functions after gene and genome duplications.

Some recent publications of the lab include: Verheyen et al. (2003). The origin of the superflock of cichlid fishes from Lake Victoria, East Africa. *Science* 300: 325-329. Salzburger et al. (2005). Out of Tanganyika: Genesis, explosive speciation, key-innovations and phylogeography of the haplochromine cichlid fishes. *BMC Evolutionary Biology* 5: 17. Barluenga et al. (2006). Sympatric speciation in Nicaraguan crater lake cichlid fish. *Nature* 439: 719-23 Braasch et al. (2006). Asymmetric evolution in two fish-specifically duplicated receptor tyrosine kinase paralogs involved in teleost coloration. *Molecular Biology and Evolution* 23:1192-1202.

Funding is available for at least 2 years. Postdoc salaries (BATII/a pay scale) are approximately 45 to 50,000 Euros annually, (depending on marital status, age, etc.) before deductions for taxes, health insurance and retirement contributions.

The positions are open immediately. The review and invitation of applicants will begin at the end of June 2006 and will continue until these positions are filled. To apply, please email a curriculum vitae, including a list of publications, a statement of research interests, and the names and email addresses of two references to axel.meyer@uni-konstanz.de.

Prof. Axel Meyer, Ph.D. Department of Biology Konstanz University 78457 Konstanz, Germany Email:

axel.meyer@uni-konstanz.de

For more information visit <http://www.evolutionsbiologie.uni-konstanz.de/-index.php?section=10>

Axel Meyer <axel.meyer@uni-konstanz.de>

ULausanne TreeFrogs

We are looking for a Post doc and/or a PhD student to join an on-going project on sex-specific markers in European tree frogs (*Hyla arborea*). In particular we aim at 1) characterizing the evolution and phylogeny of a sex-linked gene common to several Hylid species (Berset-Brändli et al *Mol.Biol.Evol.*23:1104-1106) and 2) investigate the population genetics of other sex-specific markers. Competences and techniques likely to be useful include DNA extraction, PCR, sequencing, genome walking, phylogenetic and selection analyses, population-genetic statistics. Working place: Department of Ecology and Evolution, University of Lausanne http://www.unil.ch/dee/page5090_en.html Outline of research programs and list of publications of our group: http://www.unil.ch/dee/page9071_fr.html Further information and applications: 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>

UOregon MolEvol

A postdoctoral position in molecular evolution is available at the University of Oregon in the laboratory of Joe Thornton (UO Center for Ecology and Evolutionary Biology). Candidates emphasizing either computational or laboratory approaches are encouraged to apply.

RESEARCH: We study the mechanisms and dynamics by which genes evolve new functions; we also develop and evaluate phylogenetic techniques for this purpose. Current projects include: 1) Using phylogenetic and biochemical reconstruction of ancestral gene sequences,

molecular functional assays, and structural analysis to test hypotheses about the evolution of function in the nuclear hormone receptor gene family; 2) Using computational techniques to characterize the accuracy of ancestral sequence inference and develop improved algorithms and software; 3) Developing new phylogenetic methods to diagnose horizontal gene transfer and improve phylogenetic accuracy when the evolutionary process is heterogeneous. Time for research on other relevant projects initiated by the postdoc is expected.

For more information, please consult the lab website (www.uoregon.edu/~joet) or our recent publications in *Science* 312:87 (2006), *Cell* 120:343 (2005), *Nature* 431:980 (2004), *Trends in Genetics* 21:310 (2005), *Nature Reviews Genetics* 5:366 (2004), *Science* 301:1714 (2003), *PNAS* 98:5671 (2001).

ENVIRONMENT: The University of Oregon provides a very attractive environment for evolutionary research. Our program in Evolution, Development, and Genomics unites an intellectually diverse, highly collaborative group of evolutionary, molecular and computational biologists. State-of-the-art facilities for molecular and computational analysis are provided. Computational biologists have the opportunity to be co-advised by Prof. John Conery. Eugene is a very pleasant small city with a high quality of life, a progressive culture, and great opportunities for outdoor recreation.

QUALIFICATIONS: Ph.D. in biology or computer science. Candidates should have a strong research background in one or more of the following: laboratory molecular biology, phylogenetic and evolutionary analysis, and/or software development.

START DATE: Flexible, between 1 September 2006 and 1 January 2007. The position is fully funded for up to three years, contingent on performance.

CONTACT: Please contact Joe Thornton (joet@uoregon.edu, 541-346-0328) to inquire about this position. Applicants should submit a CV, research statement, and the names and contact information for three references.

To assure full consideration, applications must be received by 31 July 2006, but position will remain open until filled.

The University of Oregon is an Equal Opportunity/Affirmative Action Institution committed to cultural diversity and compliance with the Americans with Disabilities Act. Women and minorities encouraged to apply. We invite applications from qualified candidates who share our commitment to diversity.

Joe Thornton, Ph.D Assistant Professor Center

for Ecology and Evolutionary Biology University of Oregon #5289 Eugene, OR 97403 541-346-0328 (phone); 541-346-2364 (fax) joet@uoregon.edu webpage: www.uoregon.edu/~joet

UOxford StatGenet

Statistical Methods for the Analysis of Genome-Wide Association Studies (3 years)

Academic-related Research Staff Grade 1A: Salary: £ 20044 to £ 30002 (bar) p.a. (subject to review from 1 August 2006 as part of the implementation of the National Framework Agreement for staff in higher education)

A 3-year fixed-term research position, funded by the US National Institute of General Medical Sciences (NIGMS), is available to work jointly with the research groups of Professor Peter Donnelly and Dr Jonathan Marchini, on statistical issues in modern genetic studies. The start date for the post is negotiable but would ideally be as soon as possible. Well-qualified successful applicants are likely to be appointed at or near the top of the salary scale given above.

The post relates to the development, study, and application of novel statistical methods for genome-wide association studies for human diseases. The research will involve a collaboration with 10 other research groups funded as part of a consortium called ENDGAME (Enhancing Data analysis for Genome-wide Association MEthods). In addition, the Donnelly and Marchini groups are closely involved in the Wellcome Trust Case Control Consortium, (chaired by Donnelly) which is currently generating data for genome-wide association studies for 2,000 cases and 3,000 controls for each of eight common diseases. This post thus combines the opportunity to work in leading analytical research groups at the cutting edge of major empirical studies.

Candidates should have a strong background in modern statistics and its application. An existing background in the application of statistics to genetics would be an advantage, but candidates wishing to move into the genetics field are also welcome to apply. Good computational skills are essential and candidates should be able to program in a low level language such as C or C++. Candidates should have, or expect soon to have, a doctorate. The Department of Statistics in Oxford is one of the largest and strongest in the UK, and a world leader in statistical genetics.

Informal enquiries should be directed to donnelly@stats.ox.ac.uk and/or marchini@stats.ox.ac.uk. Further particulars will be available from <http://www.stats.ox.ac.uk>, or the address below.

Applications should comprise a curriculum vitae and a list of publications together with the names, addresses, telephone, fax and e-mail details of three referees.

Applications (7 copies, one copy for candidates outside the UK) should be submitted to Personnel Administration, Department of Statistics, 1 South Parks Road, Oxford, OX1 3TG. Applications faxed to +44 1865 272595 or e-mailed to jobs@stats.ox.ac.uk are acceptable as long as they are followed by hard copy. Please always quote reference number: AM-06-005.

The closing date for applications is Friday, 9 June 2006 – o... Jonathan Marchini c/ /' - Department of Statistics, University of Oxford (+) \ (+) 1 South Parks Road, Oxford, OX1 3TG

tel : ++44 1865 271125 web : <http://www.stats.ox.ac.uk/~marchini/>
marchini@stats.ox.ac.uk

UParis11 MolEvolGenet

Position Title: Postdoc, Molecular Evolutionary Genetics

Position Location: U Paris 11 (Orsay) France

Position Description: A post doc position is available in the lab Ecologie, Systematique et Evolution in the University of Paris 11 (Orsay). The targeted starting date is September 1, 2006, but is flexible. Our lab works on a broad range of projects in evolutionary biology, e.g. host-parasite co-evolution, biological invasions, reproductive systems, genome evolution, using experiments as well as mathematical modelling.

The project aims at detecting and studying the evolution of genes involved in the specialization and the speciation of a model parasite, *Microbotryum violaceum*. *Microbotryum violaceum* is a sexually transmitted disease. This fungus constitutes a complex of sibling species, specialized on different Cayophyllaceae. This project aims at detecting genes that have rapidly evolved, and differently between close species, assuming that these genes will have important functions in speciation, specialisation, host-parasite co-evolution. EST libraries are under construction for 5 sibling species of

Microbotryum. Signatures of positive or diversifying selection will be investigated by comparing orthologs among these genomes, e.g. using the ratio of synonymous vs non synonymous mutations. These genes will then systematically be sequenced in the whole species complex, and their genealogies will be compared to those of conserved genes. The variability of these genes will also be analysed within populations and compared to neutral markers (microsatellites, SNP, ..).

For this position, a Ph.D. in evolutionary biology, molecular ecology, or related field is required. Preference will be given to candidates with a background in population genetic theory, statistical genetics, evolutionary bioinformatics, and have experience in molecular biology, including standard DNA techniques (PCR and sequencing). Ideally, the candidate will be involved in various on-going projects in the lab, but also, he or she would be encouraged to design and be responsible for independent research that involves the collection, analysis and publishing of data. Knowledge of the French language is not required.

For more information regarding the position contact Dr. Tatiana Giraud tatiana.giraud@ese.u-psud.fr. Please supply a statement of interest, curriculum vitae, and letters of recommendation.

Tatiana

Tatiana Giraud

Chargée de recherches Departement Genetique et Ecologie Evolutives Laboratoire Ecologie, Systématique et Evolution UMR 8079 CNRS-UPS-ENGREF Bâtiment 360 Université de Paris-Sud 91405 Orsay cedex France

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<http://www.ese.u-psud.fr/bases/upresa/pages/-giraud/index.html> <http://www.ese.u-psud.fr/> Tatiana Giraud <Tatiana.Giraud@ese.u-psud.fr>

UParisSud ProtistDiversity

A post-doctoral position to work in protist diversity, phylogeny and biogeography financed by the French Research Council (CNRS) is available for 1+1 years to work in the team "Microbial diversity and evolution" under the supervision of Purificación López-García and David Moreira.

PROJECT

The diversity of microbial eukaryotes inhabiting the deep ocean is still poorly known. Recent SSU rDNA molecular surveys have revealed the occurrence of divergent protist lineages in deep-sea plankton and, particularly, deep-sea hydrothermal sediments. However, these studies remain very fragmentary. We propose in this project the molecular characterisation of protist diversity in various deep-sea oceanic samples, including plankton and sediments. SSU rDNA will be used as a reference phylogenetic marker, but additional conserved genes will be considered. Comparative analyses will be done to correlate protist diversity with environmental features and with geographic data. In addition, the detection of divergent eukaryotic lineages will be applied, if possible, to resolve problematic regions of the global eukaryotic phylogeny. The latter is still not well established and the incorporation of environmental sequences may have a positive impact in tree reconstruction by increasing the taxonomic sampling.

For further reading about our research interests and having access to our publications, visit our webpage at <<http://www.esu.u-psud.fr/microbiologie/>><http://www.esu.u-psud.fr/microbiologie/> **JOB LOCATION**

Unité d'Ecologie, Systematique & Evolution, CNRS UMR 8079 Université Paris-Sud, bâtiment 360 91405 ORSAY Cedex, France Phone +33 1 69 15 76 08 <http://www.esu.u-psud.fr/microbiologie/> Our institute is located at the campus of Orsay, which is 25 km south from Paris (30 min by direct train) in a peaceful and pleasant green area. The university hosts a large variety of scientific institutes and entertains interactions with other institutions. For more detailed information, you can visit the university site at <http://www.u-psud.fr/> **QUALIFICATION & APPLICATION**

The candidate must have his/her PhD and can be of any nationality except French. He/she should be familiar with microbial eukaryotes, molecular biology techniques (PCR, cloning, etc) and phylogenetic analyses. Experience on classical microbial ecology and statistics will be also appreciated.

Starting date - the contract is available from October-November 2006. The contract will be signed for one year, renewable for a second year. The salary will be calculated by the French CNRS as a function of the candidate's experience (minimum of approximately 1600 net per month).

CONTACT

Inquiries accompanied of a curriculum vitae and the name of one/two referees should be addressed to: <<mailto:puri.lopez@ese.u-psud.fr>>puri.lopez@ese.u-

psud.fr

Purificación López-García

Unité d'Ecologie, Systématique & Evolution, CNRS UMR 8079 Université Paris-Sud, bât. 360 91405 Orsay Cedex, France

Phone +33 1 69 15 76 08 Fax +33 1 69 15 46 97 e-mail: puri.lopez@ese.u-psud.fr <http://www.esu.u-psud.fr/microbiologie/> puri.lopez@ese.u-psud.fr

Vienna MHC Evol

Title: MHC genetics - Vienna One Postdoc position in MHC genetics is available in the genetics lab of Franz Suchentrunk at the Research Institute of Wildlife Ecology, University of Veterinary Medicine Vienna, Austria, in co-operation with Helmut Schaschl (Konrad Lorenz Inst. for Ethology, Vienna).

The position is connected to a project on MHC genes and endoparasites in brown hares, *Lepus europaeus*, to understand the meaning and consequences of immunogenetic diversity for individual fitness in wild living mammals. In this project we use brown hares (*Lepus europaeus*) as a mammalian model to assess and analyse the consequences of sequence variation of two MHC class II genes (DRB, DQB) on parasite burden and other fitness parameters in natural populations. To understand the meaning of allelic MHC variability we investigate relationships between sequence variation at the studied loci and individual endoparasite load, various fitness parameters such as body condition and female reproductive success, as well as CD4+ T-cell counts. To account for possible environmental (e.g., population-specific parasite communities) or population genetic and phylogeographic influences on such relationships, we study populations in Austria and Belgium.

The successful applicant will be responsible for establishing and characterizing MHC genes in brown hares, as well as for supervising a lab technician in the routine lab work. Furthermore, she/he will be responsible for analysing the data (population genetic, evolutionary and phylogenetic analyses) and writing manuscripts. In this context practical experiences in genetics are essential (PCR, cloning, sequencing, microsatellite analysis, SSCP, basic bioinformatic tools, desirable skills: real-time PCR, TGGE). Most desirably, the candidate should have a strong immunogenetic and/or population

genetic background. Project language will be English. Funding is available for 3 years. Postdoc salaries (FWF-Austrian Science Funds- pay scale) are before tax and NI are 2.878,60 Euro, 14 times per year. Depending on marital status and children this salary translates into a net monthly salary of ca. 1750 Euro (14 x per year, with reduced tax rate for the 13th and 14th salary). The successful applicant is supposed to start earliest on 1st of October 2006. The application deadline is 31 July 2006, and the review, evaluation, and invitation process will start thereafter. Applicants should send their CV, including a list of publications and oral presentations, as well as the names/(e-mail-)addresses of two references to: franz.suchentrunk@vu-wien.ac.at

Franz Suchentrunk Research Institute of Wildlife Ecology University of Veterinary Medicine, Vienna Savoyenstr.1, A-1160 Vienna, Austria phone: ++43 1 4890915-130 fax: ++43 1 4890915-333

Franz.Suchentrunk@vu-wien.ac.at

Vienna IIASA Speciation Dynamics

IIASA's Evolution and Ecology Program investigates how evolutionary dynamics shape ecological populations and communities. We seek a

Postdoctoral Research Scholar

to develop and analyze innovative numerical models of biological speciation. In these models, individuals are situated on two-dimensional landscapes and are subject to multi-locus genetics and local ecological interactions. More detailed information about this approach is available through the following reprints:

+ Doebeli M & Dieckmann U (2003). Speciation along environmental gradients. *Nature* 421: 259-264 <http://www.iiasa.ac.at/~dieckman/reprints/DoebeliDieckmann2003.pdf> + Dieckmann U & Doebeli M (1999). On the origin of species by sympatric speciation. *Nature* 400: 354-357 <http://www.iiasa.ac.at/~dieckman/reprints/DieckmannDoebeli1999.pdf> + Doebeli M & Dieckmann U (2004). Adaptive dynamics of speciation: Spatial structure. In: *Adaptive Speciation*, eds. Dieckmann U, Metz JAJ, Doebeli M & Tautz D, pp. 140-167. Cambridge University Press <http://www.iiasa.ac.at/~dieckman/reprints/DoebeliDieckmann2004.pdf> Candidates will have a PhD in theoretical biology, physics, applied mathematics, or computer science. Previous experience

with individual-based models will be an asset, and good programming skills in a compiled language like C will be important.

This position is for one year and can be extended for two additional years. The annual salary of EUR 27,000 to 30,000 will be exempt from all income taxation in Austria (should other Austrian income exist, it will be taxed according to the principle of income aggregation). Additional benefits apply, including a relocation allowance.

IIASA is located in the summer palace of Austria's former royal family, ca.15 km south of Vienna. More information about the International Institute for Applied Systems Analysis (IIASA) is available at

http://www.iiasa.ac.at/docs/IIASA_Info.html More information about IIASA's Evolution and Ecology Program (EEP) is available at

<http://www.iiasa.ac.at/Research/EEP/> To apply, please email the following documents to EEP's Program Leader Ulf Dieckmann at dieckmann@iiasa.ac.at: CV with full list of publications, statement of research interests, relevant reprints or preprints, and one or more letters of recommendation. Informal inquiries prior to application can be made at the same email address. This position will remain open until filled. Review of applications will commence July 15, 2006.

This position has been advertised in "Die Zeit" on June 14, 2006 and in "The New Scientist" on June 24, 2006.

Ulf Dieckmann Phone +43 2236 807 386 Program Leader +43 2236 807 275 (secretary) Evolution and Ecology Program +43 2236 807 231 (secretary) International Institute Fax +43 2236 71313 for Applied Systems Analysis Email dieckmann@iiasa.ac.at A-2361 Laxenburg Web www.iiasa.ac.at/Research/EEP Austria www.iiasa.ac.at/~dieckman dieckman@iiasa.ac.at

Virginia Commonwealth University PopGenet

POSTDOC: Population Genetics

An postdoctoral position is now available in the laboratory of Dr. Rodney Dyer, Virginia Commonwealth University, Richmond Virginia. This 2-year position will focus on the spatial distribution of genetic variation within sets of Sonoran desert plants and their obligate insects as a component of the NSF Grant entitled, "The Evolution of Genetic Structure in Species-Specific

Plant-Insect Relationships: The Relative Importance of Biogeographical and Coevolutionary Processes” with CO-PI John Nason (Iowa State University).

The successful applicant for this position will be expected to be fluent in use of genetic markers (microsats/afp/issr) and have a desire to engage in field work in the Sonoran desert. Applicants with programming and/or statistical modeling experience are encouraged to apply. Additional projects established by the candidate will also be encouraged. The Dyer laboratory has the capacity for high throughput DNA extraction and genotyping as well as its own computational cluster. Additional resources available at VCU include the Center for the Study of Biological Complexity (<http://www.vcu.edu/csbc/>), the Center for Environmental Studies (<http://www.vcu.edu/cesweb/>), and

the Rice Center for Environmental Education (<http://www.vcu.edu/rice/>). VCU is a Category-1 research institution and an equal opportunity employer.

If interested in applying for this position, send a CV, research statement, a few representative publications/manuscripts, and the names (and email addresses) of three professional references to rjdyer@vcu.edu. Applications are accepted starting immediately and will be accepted until this position is filled. The ideal start date for this position is Fall 2006, although some flexibility is available.

– Rodney J. Dyer, PhD

Department of Biology Virginia Commonwealth University Richmond, Virginia 23284 <http://dyerlab.bio.vcu.edu> rjdyer@vcu.edu rjdyer@vcu.edu

WorkshopsCourses

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Honolulu ConservationGenet Jan7-20

The American Genetic Association in conjunction with the National Cancer Institute, The Laboratory of Genomic Diversity, Frederick, Maryland, NOAHS-Smithsonian Institution and The Hawaii Institute of Marine Biology is presenting a 12-day intensive course in Conservation Genetics beginning January 7th thru January 20th, 2007 at The Hawaii Institute of Marine Biology, Coconut Island, Honolulu, Oahu Hawaii.

The course will be directed by Dr. Stephen J. O’Brien and taught by renowned scientists in methods, interpretation, and applications of molecular genetic analyses for conservation of endangered species. Local host,

Dr. Brian Bowen, Assistant Researcher, Hawaii Institute of Marine Biology and his colleagues will also co-teach this course.

Applicants should be conservation-minded scientists (advanced graduate students, post-docs, teachers, and researchers with advanced degrees) of any nationality from academia, government, NGOs, or industry who are studying the genetics of endangered species and who will apply the knowledge gained from this course to the conservation of such species.

Interested individuals can contact us at congen@ncifcrf.gov or visit the website for course details at: <http://home.ncifcrf.gov/ccr/lgd/congen2007/-index.asp> roca@ncifcrf.gov roca@ncifcrf.gov

Lisbon MathBiolMed Sep11-15

Second Summer School on “Mathematics in Biology and Medicine” Instituto Gulbenkian de Ciência, Lisbon, Portugal

September 11-15, 2006

URL: <http://eao.igc.gulbenkian.pt/mbm2006/-index.html> We welcome students, post-docs and researchers interested in learning and discussing theoretical approaches to population dynamics and genetics, ecology, epidemiology, immunology, developmental biology and neurobiology.

Lecturers Ricardo Azevedo, University of Houston, USA. Carlos Brody, Cold Spring Harbor, USA. Dan Coombs, University of British Columbia, Canada. Troy Day, Queens University, Canada. Simon Levin, Princeton University, USA . Gil McVean, University of Oxford, UK.

Organizing Committee Jorge Carneiro, Francisco Dionisio, Gabriela Gomes, Isabel Gordo-IGC

Information and Contacts Applicants should send a short CV and a letter of motivation until the 31st of July to gmartins@igc.gulbenkian.pt (Greta Martins) <http://eao.igc.gulbenkian.pt/mbm2006/-index.html> Contact for scientific information: igordo@igc.gulbenkian.pt
igordo@igc.gulbenkian.pt

UBologna EukaryoteEvol Sep17-22 deadline

DEADLINE FOR APPLICATIONS - 30 JUNE 2006
SUMMER SCHOOL “GENOME EVOLUTION IN EUKARYOTES (GEE)” , 17-22 September 2006

Dear EvolDir Members,

We are please to announce the first Summer School “Genome Evolution in Eukaryotes (GEE)” organized by the University of Bologna, and to be held in the University Residential Centre of Bertinoro (Ravenna - Italy) from 17th to 22nd of September 2006.

You will find all infos about the Course at the GEE website (www.gee.unibo.it)

Please note that the application deadline is the 30th of June 2006. So you have only a few days left!

Best wishes,

Dr. Marco Passamonti GEE Summer School Secretariat

Marco Passamonti Dipartimento di Biologia Evoluzionistica Sperimentale via Selmi 3 I-40126 Bologna (Italy) tel. +39/0512094162 fax +39/0512094286 mpassa@alma.unibo.it

mpassa@alma.unibo.it

Marco Passamonti Dipartimento di Biologia Evoluzionistica Sperimentale via Selmi 3 I-40126 Bologna (Italy) tel. +39/0512094162 fax +39/0512094286 mpassa@alma.unibo.it

mpassa@alma.unibo.it

ULisbon Bioinformatics

BIOINFORMATICS

INTERNATIONAL CALL FOR APPLICATIONS

2006/2007 Edition

The Faculty of Sciences of the University of Lisbon (FCUL), Portugal, is pleased to announce the fifth edition of PGBIOINF, the FCUL post-graduate Programme in Bioinformatics (2006-2007) and the FCUL Master course in Bioinformatics according to the new European rules.

The courses consists of 30 weeks of intensive courses, steered under the responsibility of the FCUL and with the participation of the researchers of the Instituto Gulbenkian de Ciência (IGC), a service of the Fundação Calouste Gulbenkian where some of the courses will take place. It will train up to 20 specialists in Bioinformatics. By complementing PGBIOINF with a dissertation work, students can obtain a MSc or a PhD in Bioinformatics at FCUL. Students of Biological or Informatics profile can both apply. All courses are in English.

For information about the course and details on applications and deadlines consult the programme website (<http://bioinformatics.fc.ul.pt> <<http://-bioinformatics.fc.ul.pt/>>).

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Instructions

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

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

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

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

Afterward

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