
E v o l D i r

June 2, 2008

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

Forward

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

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

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



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Conferences

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Adelaide AustralAsiaGeneticsSoc Jul7-10 DeadlineExtended

GSA2008 Abstract Submissions
 Reply-To: Jack da Silva
 <jack.dasilva@adelaide.edu.au> Resent-Message-Id:
 <200805020042.m420gsqg014117@Gorash7.UTS.McMaster.CA>
 Resent-Date: Thu, 01 May 2008 20:42:54 -0400

GSA2008 Genetics Society of AustralAsia Annual Meeting Adelaide, 7-10 July 2008 <http://www.adelaide.edu.au/gsa2008/> The deadline (May 1) for abstract submissions has passed. However, we have a few slots remaining and will accept additional abstracts on a first come, first served basis.

Please note that student registration includes a banquet ticket.

Jack da Silva <jack.dasilva@adelaide.edu.au>

Einsiedeln Switzerland PhDStudents EMPSEB14 Sep8-13 DeadlineExtended

The registration deadline for the 14th European Meeting for PhD Students in Evolutionary Biology in Einsiedeln, Switzerland is pushed back until the 15th of May 2008.

Please consult: www.empseb.unibe.ch Best regards,

Francisca Segers

Francisca Segers <francisca.segers@esh.unibe.ch>

EMBL Heidelberg YeastEvolutionaryGenomics Oct1-5

EMBO Workshop on Evolutionary and Environmental Genomics of Yeasts

EMBL Heidelberg, Germany, 1-5 October 2008

The workshop will bring together scientists who use the yeast model and work in different areas - cell biology, molecular genetics, systems biology genomics and population genetics - in order to show and to explore further how integrated research programs using yeast as a model could be as successful in ecology and evolution as they have been in cellular and molecular biology.

The webpage is now open for registration. Session will include talks from invited speakers and short talks selected from submitted abstracts: http://www-db.embl.de/jss/EmblGroupsOrg/conf_92 Invited Speakers:

Geraldine Butler, University College Dublin, Ireland
 Duccio Cavalieri, University of Florence, Italy
 Ronald W. Davis, Stanford University, USA
 Daniela Delneri, Manchester University, United Kingdom
 Bernard Dujon, Institut Pasteur, France
 Maitreya Dunham, Princeton University, USA
 Justin Fay, Washington University in St. Louis, USA
 Duncan Greig, UCL, USA
 Michael Hood, Amherst University, USA
 Wen Hsiung Li, University of Chicago, USA
 Ryszard Korona, Jagiellonian University, Poland
 Vassiliki Koupoufanou, Imperial College at Silwood Park, United Kingdom
 Jun-Yi Leu, Institute of Molecular Biology, Taiwan
 Rong Li, Stowers Institute, USA
 Ed Louis, Nottingham, United Kingdom
 John McCusker, Duke University, USA
 Andrew W. Murray, Harvard University, USA
 Stephen Olivier, Manchester University, United Kingdom
 Sarah P. Otto, University of British Columbia, Canada
 Peter Philippsen, University of Basel, Switzerland
 Tzachi Pilpel, Weizmann Institute of Science, Israel
 Jure Piskur, Lund University, Sweden
 Paul D. Sniegowski, University of Chicago, USA
 Claus O. Wilke, University of Texas at Austin, USA
 Gael Yvert, Ecole Normale Supérieure de Lyon, France
 Clifford W. Zeyl, McGill University, USA

Dr. Michael Knop EMBL Cell Biology and Biophysics Meyerhofstr. 1 D-69117 Heidelberg Germany

phone: 0049-6221-387631 (office) 0049-6221-387127 (lab) 0049-6221-387337 (lab again) fax: 0049-6221-387512 (fax) knop@embl.de <http://www.embl-heidelberg.de/ExternalInfo/knop/> http://www-db.embl.de/jss/EmblGroupsHD/g_153.html Michael Knop <knop@embl.de>

Halifax Evolutionary Protistology Jul21-26 deadlines2

PROTIST2008 is this year's combined meeting of ISEP (the International Society for Evolutionary Protistology) and ISOP. It will be held July 21-26 in Halifax, Canada.

*The deadline for Early registration rates is MAY 15th. Register now! *The deadline for Abstract submissions has been extended to MAY 20th. *It is strongly recommended that you book your accommodation by MAY 20th.

Visit <https://protist2008.dal.ca/> today for on-line registration and other details.

Looking forward to seeing you all there! Alastair Simpson Sina Adl

Alastair.Simpson@Dal.Ca

IrvineCA MEEGID IX Oct30-Nov1 2

October 30 - November 1, 2008 9th International Congress on Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID IX)

Principal Organizers: Michel Tibayrenc (Institut de Recherche pour le Développement, France) Francisco J. Ayala (Ecology and Evolutionary Biology, University of California, Irvine)

Location: UC Irvine Student Center, University of California, Irvine A major event in genetics and the evolution of infectious diseases. Topics include: genetics, genomics, proteomics, population biology, mathematical modeling, and bioinformatics. Papers can report on the host, the pathogen (viruses, parasitic protozoa, helminths, fungal organisms, and prions), or the vector for vector-borne diseases. Papers considering co-evolution phenomena are particularly encouraged. All infectious models can be considered, including those of veterinary or agronomical relevance. Special emphasis will be given to health problems of particular interest to Mediterranean and tropical countries: AIDS,

malaria, tuberculosis, sleeping sickness, leishmaniasis, ebola, bird flu, chikungunya, cattle and crop pathogens.

Abstract submission deadline: July 30, 2008

Keynote Speakers: Francisco J. Ayala, University of California, Irvine (Evolution of Malaria; Darwin's Revolution) Robin Bush, University of California, Irvine (Influenza Evolution) Koussay Dellagi, Centre for Research and Surveillance of Emerging Diseases in the Indian Ocean, Tunisia (Chikungunya Epidemics) Appolinaire Djikeng, J. Craig Venter Institute, Rockville, Maryland (Viral Genomics) Henry Harpending, University of Utah, Salt Lake City (Infectious Diseases and Human Evolution) Annie Rimoin, University of California, Los Angeles (Implementing Active Surveillance of Human Monkeypox in the Democratic Republic of Congo) Michel Tibayrenc, Institut de Recherche pour le Développement, France (Integrated Evolutionary Epidemiology: Where are We Now?) Nathan Wolfe, University of California, Los Angeles (Viral Forecasting)

Register at <http://www.th.ird.fr//site.meegid/-menu.htm> Denise Chilcote for F.J. Ayala and M. Tibayrenc

"Francisco J. Ayala" <fjayala@uci.edu>

Henry Harpending (University of Salt Lake City): Infectious Diseases and Human Evolution

Tovi Lehmann (NIAID, NIH). Vector population genetics and genomics.

Martine Peeters (IRD Montpellier, France). HIV molecular evolution. 'Anne Rimoin (UC Los Angeles) : implementing active surveillance of human monkeypox in the democratic republic of Congo.

Michel Tibayrenc (IRD, Bangkok, Thailand): Integrated evolutionary epidemiology: where are we now?

Nathan Wolfe (UC Los Angeles): Viral forecasting

Best regards,

Michel Tibayrenc, MD, PhD Editor -in-chief Infection, Genetics and Evolution (Elsevier) <http://www.elsevier.com/locate/meegid> See impact factor at: <http://www.th.ird.fr/downloads/edito.pdf> IRD representative in Thailand IRD Representative Office French Embassy 29, South Sathorn Road, Bangkok 10120, Thailand Tel : + (66 2) 627 2190 Fax : + (66 2) 627 2194 Cel: + (66 81) 82 64 056 E-mail : Michel.Tibayrenc@ird.fr Website : <http://www.th.ird.fr> Michel.Tibayrenc@ird.fr

IrvineCA MEEGID IX Oct30-Nov1 Registration 2

29/04/08

Dear Colleagues,

registration online for the MEEGID IX congress is now available. Go to the website of the congress: <http://www.th.ird.fr/site.meegid/menu.htm> and click on "registration".

Updated list of keynote speakers include:

Francisco J. Ayala (Dept Ecology and Evolution, UC Irvine, California): (i) Evolution of malaria; (ii) Darwin's Revolution

Robin Bush (Dept Ecology and Evolution, UC Irvine, California): Evolution of bird flu.

Koussay Dellagi (Centre for Research and Surveillance of Emerging Diseases in the Indian Ocean). Chikungunya epidemics.

Appolinaire Djikeng (J. Craig Venter Institute, Rockville, Maryland, USA) Viral genomics.

Jerusalem ZoonoticDiseaseEvolution May27-28

Dear Friends,

Attached you may find the final program of the workshop "Human-animal interactions in the circum Mediterranean area: interdisciplinary approach - archaeology, ecology and evolution- of zoonotic diseases" which will take place 27th-28th May 2008, Jerusalem, Israel.

We will appreciate it if you can spread the information to your colleagues who may be interested in this topic.

Hope to see you all

Gila and Anne

Gila Kahila Bar-Gal, Ph.D Koret School of Veterinary Medicine Hebrew University of Jerusalem P.O.Box 12, Rehovot, 76100, Israel

Tel: (972)-8-9489888,

Fax: (972)-8-9467940 email: bargal@agri.huji.ac.il

Kahila Bar-Gal Gila <bargal@agri.huji.ac.il>

Marseilles 12th Evolutionary Biol Sep24-26

Dear All,

We are pleased to inform you that the 12th Evolutionary Biology Meeting at Marseilles will take place on 24th 25th 26th September 2008.

We are also pleased to inform you that the video of the oral presentations of the 11th Evolutionary Biology Meeting at Marseilles are available at: http://sites.univ-provence.fr/webtv/?liste=biology_meeting_2007 For more information, do not hesitate to go on: <http://sites.univ-provence.fr/evol-cgr> Best wishes,

Axelle Pontarotti

Egee@univ-provence.fr

Marseilles 12th Evolutionary Biol Sep24-26 abstracts

Dear All,

We are pleased to inform you that the first accepted abstracts of the 12th Evolutionary Biology Meeting at Marseilles are now available on our website: <http://sites.univ-provence.fr/evol-cgr> Best wishes,

Axelle Pontarotti

Universite EGEE <Egee@univ-provence.fr>

Porto Portugal 11th GABBA Jun13

Dear all, We are sending you the divulgation poster of the 11th GABBA (Graduate Program in Areas of Basic and Applied Biology) Annual Symposium, which this year will take place on June 13th at Porto, Portugal. The main subject will be 'Homeostasis: The struggle

for equilibrium?'. We have gathered world-wide recognized scientists in their fields to discuss different aspects of this fascinating topic.

See in attachment all the details. You can also find this information at gabba.up.pt. Please spread the word! Hope to see you all there,

Best regards, The students of the 11th Edition of the GABBA Program

patricy@hotmail.com

Raleigh North Carolina Genomics Jun4-7

There is still time to register for the AGA Symposium, Genetics and Genomics of Behavior, June 4-7, Raleigh, NC.

The Sheraton Hotel in downtown Raleigh is offering a special accommodation rate for Symposium participants, but you must reserve by MAY 4th. Register by calling 1-800-325-3535.

This year's AGA conference will explore current status and future trends in the genetic architecture of behavior, neurogenetic mechanisms of behavior, and evolution of behavior. In addition to a stellar group of invited speakers, there will be an opportunity for platform presentations from participants who submit abstracts.

Competitive scholarships for travel and registration will be available for students and postdoctoral fellows.

Details and registration at www.agasymposium2008.org agajoh@oregonstate.edu

Raleigh North Carolina Genomics Jun4-7 registration

Genetics and Genomics of Behavior, June 4-7, Raleigh, NC.

LAST CALL FOR REGISTRATION!

General meeting registration is still open. Registration costs are low and space remains available for poster

presenters and attendees (but space is increasingly limited).

Details and registration at
www.agasympoium2008.org agaajoh@oregonstate.edu
agaajoh@oregonstate.edu

Rennes France PopulationGenetics Aug25-28

Bonjour,

Nous avons le plaisir de vous annoncer la tenue du prochain « Petit Pois Dérivé » à Rennes à Agrocampus, du 25 au 28 août 2008.

Vous pouvez trouver toutes les informations utiles sur le site du colloque : <https://colloque.inra.fr/ppd2008> la date limite pour les inscriptions et les propositions de résumé est fixée à 15 juin 2008 *

cordialement

l'équipe organisatrice

Dear Colleagues,

We are extremely pleased to make the announcement of the 30th meeting "Le Petit Pois Dérivé" (annual meeting organized by the French Populations Genetics and Biology Group), to be held at Rennes (Western France), August 24-28 2008. This meeting aims to bring together researchers interested in evolutionary biology.

The closing date for registration is June 15th 2008. *Register now!* The deadline for Abstract submissions is June 15th. It is strongly recommended that you book your accomodation as soon as possible.

Visit <https://colloque.inra.fr/ppd2008> for on-line registration and other details.

We very much look forward to welcoming you to Rennes this August.

Isabelle Baumgarten <Isabelle.Baumgarten@agrocampus-rennes.fr>

StAndrews ComparativeGenomics Jun13 final poster call

Comparative Genomics - final call for posters

We are inviting submissions of abstracts for posters at the Scottish Bioinformatics Forum Comparative Genomics meeting in St. Andrews, Scotland, 13th June 2008.

Submission deadline: 29th May Maximum abstract length 200 words. Please send your abstract to cjanssen@sbforum.org

Full details and conference program: http://www.sbforum.org/events.php?e_idA Comparative genomics is a new field of increasing power. Within a decade, we have moved from having a handful of sequenced species to thousands, and numbers will continue to increase. This presents enormous opportunities to make discoveries of biological and medical interest, but also requires new approaches. The bottleneck is shifting from the time taken to sequence genomes, to the time taken to decide how to analyse them. However, exciting and novel results are already emerging. Internationally renowned invited speakers and a poster session will present cutting-edge developments in this fast-moving and exciting field.

– Daniel Barker <http://bio.st-andrews.ac.uk/staff/db60.htm> The University of St Andrews is a charity registered in Scotland : No SC013532

Daniel Barker <db60@st-andrews.ac.uk>

UCaliforniaIrvine WEB2008 May25

Final Reminder:

Western Evolutionary Biologists Meeting – Irvine, CA May 25

The Network for Experimental Research on Evolution (NERE) invites evolutionists to attend the 2nd annual Western Evolutionary Biologists Conference on May 25, 2008.

Registration is free, but mandatory. ***Final Registra-

tion deadline is May 15.

For more information and registration visit the web-2008 website at: <http://www.lifesci.ucsb.edu/web-2008/> NERE will cover transportation to the meeting for NERE members. We encourage graduate students and postdocs to attend. Evolutionists in the University of California System should contact their local Associate Director (see website for more information) to arrange transportation.

At the meeting, NERE will present the 2008 WEBY Award (Western Evolutionary Biologist of the Year), The 2007 WEBY winner was Al Bennett.

The 2008 WEBY Address will be given by Kevin Padian of UC-Berkeley. Congratulations to Kevin!

About NERE: See also: <http://nere.bio.uci.edu/> NERE, the Network for Experimental Research on Evolution, is a University of California Multicampus Research Program funded and administered through the UC Office of the President and its constituent UC campuses. NERE (pronounced "near") supports collaboration, communication, and graduate education concerned with research on biological evolution. NERE serves as a conduit for interactions between evolutionists within the University of California system and between University of California scientists and the global scientific community.

Titles of presentations: Experimental manipulation of the rock-paper-scissors game

Genetic and molecular mechanisms underlying F2 hybrid breakdown between allopatric populations

When Rock And Scissors Beat Paper: The Role of Alternative Mating Strategies in Speciation

Female choice for correlated male traits increases offspring survival: 'good genes' is good genetic integration.

Searching for Orthologous Sequences and Measuring Selection Between Two Closely Related Species of Rockfish (Sebastes)

A test of kin selection: Kin effects on dispersal and social aggregation in juvenile Desert Night Lizards (*Xantusia vigilis*)

Fixation of deleterious mutations via epistasis is important in adaptive sweeps.

Evolutionary history explains biodiversity effects on plant productivity

Morphological and thermal properties of mammalian insulation: implications for the evolutionary transition to an aquatic lifestyle

A new molecular analysis of the evolutionary age of Lacertid lizards (Squamata)

Effects of Habitat Fragmentation on Genetic Variability in Insular Populations of Caribbean Rock Iguanas

The evolutionary origins of phototransduction in animals

The role of recombination in creating and suppressing antibiotic resistance

Experimental Evolution of Numerical Discrimination in *Drosophila melanogaster*: Preliminary Results

Interactions between the direct and indirect effects of predators determine life history evolution in a Trinidadian killifish

Testing an assumption of a model for the evolution of maternal provisioning (placentas)

The evolution of cheating in wild *Bradyrhizobium*

– Todd Oakley Associate Professor Ecology Evolution and Marine Biology University of California-Santa Barbara Santa Barbara, CA 93106

ph 805-893-4715 <http://www.lifesci.ucsb.edu/eemb/labs/oakley> – Todd Oakley Associate Professor Ecology Evolution and Marine Biology University of California-Santa Barbara Santa Barbara, CA 93106

ph 805-893-4715 <http://www.lifesci.ucsb.edu/eemb/labs/oakley> oakley@lifesci.ucsb.edu oakley@lifesci.ucsb.edu

UEdinburgh GenomicsQuestions Jun4

Asking Questions with Genomics

Institute of Evolutionary Biology, University of Edinburgh

4th June, Ashworth Laboratories, King's Buildings

We are delighted to be hosting a one-day workshop exploring how new genomic technologies can be used to ask questions in biology. The aim is to bring together researchers from a broad range of biological disciplines to share expertise and experiences of using genomic and post-genomic technologies to bring fresh insights to fundamental biological processes.

The workshop has been generously sponsored by Roche, Illumina and the University of Edinburgh.

The workshop will include UK and international invited speakers. Planned topics include:

Brain and Behaviour, Community Genomics, Development, Genome Evolution, Host-Parasite Coevolution, Quantitative Genomics, Sexual Selection, and Speciation.

Confirmed speakers:

Casey Bergman (Manchester) Tracey Chapman (UEA) Chris Haley (Edinburgh) Andrew Hudson (Edinburgh) Brian Lazzaro (Cornell) Simone Meddle (Edinburgh) Darren Obbard (Edinburgh) Richard Preziosi (Manchester)

The workshop will take place at the Institute of Evolutionary Biology, Ashworth Laboratories, Kings Buildings, Edinburgh. For further details please visit the website <http://www.biology.ed.ac.uk/-genomeworkshop/Home.html> or email Dave Shuker (david.shuker@ed.ac.uk).

The workshop is open to all and there is no registration fee. Morning coffee, a sandwich lunch, and afternoon tea will be provided. To help with catering, the organisers would be grateful if those wishing to come could register by sending an email to genomics2008@ed.ac.uk.

Many thanks, the Organising team,

David Shuker, Mark Blaxter, Frank Jiggins and Tom Little.

— Bart Pannebakker Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Road Edinburgh EH9 3JT Scotland UK e-mail: Bart.Pannebakker@ed.ac.uk

*** NEW TELEPHONE NUMBER: +44 131 353 4140 ***

fax: +44 131 650 6564

web: <http://westgroup.biology.ed.ac.uk/BartP/-BartP.html> – The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

Bart.Pannebakker@ed.ac.uk

Bart.Pannebakker@ed.ac.uk

UIowa Evolution of Sex Jun16-19 Registration

LAST CALL FOR REGISTRATION!

1. General meeting registration is still open. Registration costs are low and space remains available for poster presenters and attendees (but space is increasingly limited). Please register as soon as possible at:

<http://cgg.biology.uiowa.edu/sexrec/regform2.php>

2. Information on Venue, Travel and Accommodation is available at:

<http://cgg.biology.uiowa.edu/sexrec/venue.php>

3. The final schedule of 45 talks is available at:

<http://cgg.biology.uiowa.edu/sexrec/-SexRecSchedule.pdf>

4. A list of confirmed attendees and their titles is available at:

<http://cgg.biology.uiowa.edu/sexrec/attendees.php>

----- General Announcement:

³EVOLUTION OF SEX & RECOMBINATION: IN THEORY AND IN PRACTICE²

June 16-19, 2008, at the University of Iowa, Iowa City, USA.

<http://cgg.biology.uiowa.edu/sexrec>

The Roy J. Carver Center for Comparative Genomics and the Department of Biology at the University of Iowa will host an international conference on the evolution of sex & recombination. This conference will immediately precede the 2008 Evolution meeting taking place in nearby Minneapolis, Minnesota (June 20-24).

Talks will be given by invited speakers at both the junior and senior level. Contributed talks and posters will be given by conference attendees at all levels of seniority.

Topics include: -Advantages of sexual reproduction - Experimental evolution of sex -Estimating recombination rates -Mating types & sex determination -Linkage, selection & population size -Sex chromosomes -Sex & pathogenesis -Sexual selection -Sexual conflict

Confirmed invited speakers: Anil Agrawal University of Toronto Philip Awadalla University of Montreal Doris Bachtrog University of California, San Diego Graham Bell McGill University Bill Birky University of Arizona Rhona Borts University of Leicester Bernardo Carvalho Universidade Federal do Rio de Janeiro Brian Charlesworth University of Edinburgh Nick Colegrave University of Edinburgh Tim Cooper University of Houston Ursula Goodenough Washington University-St. Louis Joe Heitman Duke University Michael Hood Amherst College Alex Kondrashov University of Michigan Curt Lively Indiana University Michael Lynch Indiana University David Mark Welch MBL, Woods Hole Stephanie Meirmans University of Bergen Andy Peters University of Wisconsin-Madison Steve Proulx Iowa State University Bill Rice University of Califor-

nia, Santa Barbara Isa Schön Royal Belgian Institute of N.S. Marcy Uyenoyama Duke University Jerry Wilkinson University of Maryland Cliff Zeyl Wake Forest University

An additional 19 contributed talks have also been selected from among faculty, post-doc and graduate student applicants.

A symposium issue to be published in Journal of Heredity is being planned and all presenters will have the opportunity to contribute a paper to the issue.

Enquiries are encouraged (including potential sponsors) and should be directed to the organizers: sexrec@uiowa.edu

On behalf of the organizing committee, thanks.

We hope to see you in Iowa City in June!

John Logsdon –

John M. Logsdon, Jr., Ph.D. Associate Professor Director, Roy J. Carver Center for Comparative Genomics University of Iowa Department of Biology 319 335 1082 office 310 Biology Building 319 335 1083 lab Iowa City, IA 52242-1324 319 335 1069 FAX

email <john-logsdon@uiowa.edu> web <<http://cgc.biology.uiowa.edu>> <<http://euplotes.biology.uiowa.edu>>

UIowa Evolution of Sex Jun16-19 Update

Final UPDATE:

1. General registration is still open. Space remains available for poster presenters and attendees, but it is limited. Please register as soon as possible at:

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John Logsdon –

John M. Logsdon, Jr., Ph.D. Associate Professor Director, Roy J. Carver Center for Comparative Genomics University of Iowa Department of Biology 319 335 1082 office 310 Biology Building 319 335 1083 lab Iowa City, IA 52242-1324 319 335 1069 FAX

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

UKonstanz Germany Communication Evolution Sep4-7

“Communication and cooperation - from genes to behaviour”. A symposium in honour of Hubert “Jim” Markl

International Conference at the University of Konstanz, Germany 04.-07. September 2008

This interdisciplinary symposium will bring together scientists from the fields of sociobiology and neuroethology to discuss new concepts and ideas. We hope that this meeting will facilitate communication between these biological subdisciplines and encourage integrative approaches. Plenary talks by leaders in their respective fields will cover animal communication and cooperation at levels ranging from genes, to individuals, societies, and populations. Discussions of relevant aspects of biophysics, neurobiology, physiology, genetics, ecology and ethology under the unifying concept of evolution promises to further the understanding of the “how” and the “why” behaviour.

We especially invite PhD students and Postdocs working in pertinent fields to apply for participation in the symposium. There are time slots reserved for oral contributions by younger scientists and we plan to have a poster session as well. There are no registration fees and we will attempt to reimburse travel and accommodation costs (see “Registration”).

This symposium is meant to celebrate the 70th birthday of Professor Dr. Dr. h.c. mult. Hubert Markl. Hubert “Jim” Markl played an internationally prominent role during the founding and establishing of the fields of both sociobiology and neuroethology.

For more information please visit <http://www.markl.phenon.de/>.

UPadua Italy Biological Nomenclature May29-30

Updating the Linnaean Heritage: Names as tools for talking about animals and plants

29th to 30th of May 2008 Two-day Meeting at University of Padua, Italy, Local organiser: Sandro Minelli FLS Organising Committee : Sandra Knapp, Tim Littlewood, Alessandro Minelli, Vaughan Southgate on behalf of The Linnean Society

Getting the names of things right is still essential if we are to interpret, understand and share our knowledge of biological diversity.

The 250th anniversary of the publication of Linnaeus’ 10th edition of *Systema Naturae*, the start of modern zoological nomenclature, will be recognised at this meeting, at which an international panel of renowned scientists will present current perspectives and challenging proposals about names for taxa and names for other important biological objects and concepts.

This is an important meeting for all working in systematics and taxonomy as well as museum curators, those involved in biodiversity assessment and wildlife conservationists worldwide. Historians of science may also find it helps in understanding the development of the present system of biological nomenclature and the ways in which that has evolved over time.

The different venues for the event, the Accademia Galileiana, the historical Botanical Garden and the Palazzo del Bò, Archivio Antico will link the meeting to Padova’s long standing academic tradition and provide a unique opportunity for delegates to move biological science forward in a historic setting (see http://en.wikipedia.org/wiki/Botanical_Garden_of_Padova, http://en.wikipedia.org/wiki/University_of_Padua). Spending a few days in May in Padua (Padova), one of

Italy's beautiful historic cities, a short distance from Venice, will be enriching not only scientifically, but aesthetically as well. Please join us.

For registration and more information follow the links from <http://www.linnean.org/fileadmin/events2/-events.php?detail=3D114> Dr Ellinor Michel

Executive Secretary International Commission on Zoological Nomenclature Natural History Museum, London SW7 5BD +44 (0)207-942-5653 (alternative number - 5516) iczn-em@nhm.ac.uk

www.iczn.org
e.michel@nhm.ac.uk

e.michel@nhm.ac.uk

UPlymouth InsectEvolution Sep3-5

The Annual Meeting of the Royal Entomological Society will take place at the University of Plymouth, UK, on September 3-5 2008.

Abstracts for both oral and poster presentations are invited. There will be general entomology sessions, but abstracts in the following areas are particularly welcome:

- * Marine and coastal entomology
- * sexual selection in insects
- * aquatic entomology
- * heamatophagus insects
- * Molecular entomology
- * insects and climate change

The deadline for abstracts is 31 May 2008.

For further information please see <http://www.royensoc.co.uk>. Specific enquiries can be made to Peter Smithers: p.smithers@plymouth.ac.uk <<mailto:p.smithers@plymouth.ac.uk>>

Some financial support is available from the RES for students wishing to attend the meeting. Please see the website for further details.

Dr Mairi Knight School of Biological Sciences University of Plymouth Drake Circus Plymouth Devon PL4 8AA UK

tel: +44 (0)1752 238 633 fax: +44 (0)1752 232 970
email: mairi.knight@plymouth.ac.uk

Mairi Knight <mairi.knight@plymouth.ac.uk>

UppsalaU SexualSelection Oct3 2

Dear all!

This is a reminder for all researchers (Ph.Ds, post-docs and senior) working with sexual selection - most welcome to a discussion workshop day aiming to develop sexual selection theory.

Friday the 3rd of October at the Evolutionary Biology Centre in Uppsala.

Aims: To develop and reflect over sexual selection processes, i.e. competition for matings, competition to be chosen as a mate, competition for breeding opportunities, sexual conflicts, dynamics in sexual selection etc., in animals, plants and theory. What processes are predominantly studied in which sex and why? How can we by discussing gender perspectives in sexual selection contribute to a more gender-neutral evolutionary biology theory.

The workshop is aimed for evolutionary biologists and funded by GenNa (see <http://www.genna.gender.uu.se/>).

Most welcome, the deadline for application is 1st of June. Send a mail!

Ingrid & Malin

Ingrid Ahnesjö & Malin Ah-King

Ingrid.Ahnesjo@ebc.uu.se & Malin.Ah-King@gender.uu.se

– Malin Ah-King Centrum för genusvetenskap Uppsala universitet Box 634, 751 26 Uppsala Thunbergsv 3 H Telefon: 018-471 22 77 Fax: 018-471 35 70 www.gender.uu.se/node133 E-mail: Malin.Ah-King@gender.uu.se

[Malin Ah-King <malin.ah-king@gender.uu.se>](mailto:Malin.Ah-King@gender.uu.se)

UStAndrews ComparativeGenomics June13

Comparative Genomics - call for poster abstracts

We are inviting submissions of abstracts for posters at

the Comparative Genomics meeting in St. Andrews, 13th June 2008.

Submission deadline: 29th May Maximum abstract length 200 words. Please send your abstract to [cjanssen \(at\) sbforum.org](mailto:cjanssen@sbforum.org)

Full details and conference program: http://www.sbforum.org/events.php?e_idA Comparative genomics is a new field of increasing power. Within a decade, we have moved from having a handful of sequenced species to thousands, and numbers will continue to increase. This presents enormous opportunities to make discoveries of biological and medical interest, but also requires new approaches. The bottleneck is shifting from the time taken to sequence genomes, to the time taken to decide how to analyse them. However, exciting and novel results are already emerging. Internationally renowned invited speakers and a poster session will present cutting-edge developments in this fast-moving and exciting field.

– Daniel Barker <http://bio.st-andrews.ac.uk/staff/db60.htm> The University of St Andrews is a charity registered in Scotland : No SC013532

db60@st-andrews.ac.uk db60@st-andrews.ac.uk

Vienna CatEvolution Aug24-27

9th International Feline Retrovirus Research Symposium - Vienna, August 24th - 27th 2008

Dear Colleague

On behalf of the organizing committee for the 9th International Feline Retrovirus Research Symposium to be held in Vienna, Austria, August 24-27, 2008, I am pleased to invite you and members of your group to submit abstracts of your latest work. The conference promises to be an innovative and exciting blend of retroviral research, advances in the cat as a model of infectious disease, cat genomics and viral and host evolution.

Felids and their associated retroviruses offer an unique opportunity to study evolution of both pathogenic and apathogenic viruses as well as endogenous retroviruses and the co-adaptation of their respective hosts. The scientific committee therefore also specifically encourages contributions from researchers interested in feline and viral evolution.

Submitted abstracts will be reviewed by the scientific committee and assigned to oral or poster presentations

(your preference would be helpful) and the best of these would receive partial or full financial support for attendance. A significant amount of the budget will be allocated for this, so we really would encourage abstract submission.

Please visit the conference website at <http://www.retrovirus.at> for additional information, submission of abstracts, and registration. Please note the deadline for abstracts is June 6, 2008 and an early registration discount deadline is at the same date. Please feel free to contact the local organizing committee (office@retrovirus.at) with any questions.

Best wishes,

Dieter Klein

Dr. Adolf Steinrigl Institute of Virology Department of Pathobiology University of Veterinary Medicine 1210 Vienna, Austria Tel.: +43 1 25077 2333 Fax.: +43 1 25077 2390 adolf.steinrigl@vu-wien.ac.at

Steinrigl Adolf Stefan <Adolf.Steinrigl@vu-wien.ac.at>

Villanova PA MendelSymposium Sep21-23

Mendel Symposium Featuring Sean B. Carroll, Dan Hartl, David Hillis, Evelyn Fox Keller, and Kenneth Miller Sunday, Sept. 21, to Tuesday, Sept. 23, 2008. Villanova University, Villanova, PA

Mendel in the 21st Century: The Scientific, Social, and Ethical Impact of Genetics in Our World This two-day interdisciplinary academic symposium, will be held on Villanova's campus from Sunday, Sept. 21, to Tuesday, Sept. 23, 2008. The University is hosting the symposium as part of its campus-wide celebration to commemorate the 80th anniversary of the awarding of the Mendel Medal. In addition, the College of Liberal Arts and Sciences at Villanova is a proud co-sponsor of the traveling exhibit, Planting the Seeds of Genetics: Gregory Mendel, which will be at the Academy of Natural Sciences in Philadelphia from May 28 to Sept. 24, 2008. As an Augustinian institution of higher education, Villanova is one of the custodians of the Mendel legacy. As an Augustinian priest trained in mathematics, physics, and biology, Mendel is an icon of interdisciplinarity. Accordingly, this symposium will include a series of engaging speakers in fields ranging from molecular genetics, genomics, biotechnology and evolutionary

biology to history and philosophy of science, psychology, ethics, medicine, and law. Speakers will discuss the impact of 21st century genetics in our society from the perspective of their respective disciplines.

Registration for the symposium is free.

Mendel in the 21st Century Symposium at Villanova: <http://www.villanova.edu/mendelsymposium/>
Mendel exhibit at the Philadelphia Academy of Natural Sciences: <http://www.anasp.org/press/->

featured_exhibits.php#mendel For questions, email Angela DiBenedetto, Department of Biology: angela.dibenedetto@villanova.edu or Todd Jackman, Department of Biology: todd.jackman@villanova.edu

Todd Jackman Associate Professor Villanova University Office: 610-519-5502 Lab: 610-519-5503 <http://todd.jackman.villanova.edu>
todd.jackman@villanova.edu

Todd Jackman <todd.jackman@villanova.edu>

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BlackHillsStateU IntegrativeGenomics

Black Hills State University - Masters of Science in Integrative Genomics

Four Masters Graduate Assistant (GA) positions are available for Fall 2008 (September) or January (2009) in Integrative Genomics (IG) Masters program at Black Hills State University, Spearfish, SD. The

GA positions are available to students interested in working with any member of the IG faculty (<http://www.bhsu.edu/Academics/TheColleges/-CollegeofArtsandSciences/DepartmentsandPrograms/Masters/Faculty/tabid/4950/Default.aspx> <<http://www.bhsu.edu/Academics/TheColleges/CollegeofArtsandSciences/DepartmentsandPrograms/Masters/Faculty/tabid/4950/Default.aspx>>).

Integrative Genomics is an interdisciplinary graduate program that combines genomics, ecology, evolution, and physiology to better understand the evolutionary forces that have shaped the mechanisms that are im-

portant to species interactions in the wild. The program is designed to provide those seeking a Masters degree the necessary skills and concepts to work cooperatively with others in a research area that takes a systems-wide approach and incorporates an organism's history and natural environment to understand organization and expression at the genomic level. Exposure to modern techniques and instrumentation in the laboratory and field prepares students for success in both academic and other biotechnology-related pursuits.

Integrative Genomics GAs receive an annual stipend of \$16,640 and additional funds for laboratory supplies and expenses.

For an overview of the IG program and application information please visit our website <http://www.bhsu.edu/Academics/TheColleges/-CollegeofArtsandSciences/DepartmentsandPrograms/Masters/tabid/2164/Default.aspx> <<http://www.bhsu.edu/Academics/-TheColleges/CollegeofArtsandSciences/DepartmentsandPrograms/Masters/tabid/2164/Default.aspx>> or contact

Garth M. Spellman, Ph.D. Assistant Professor CCBR/Westcore Black Hills State University 1200 University Street, Unit 9053 Spearfish, SD 57799-9053 ph: 605-642-6854 garthspellman@bhsu.edu <<mailto:garthspellman@bhsu.edu>> <http://www.bhsu.edu/artssciences/asfaculty/gspellman/-Welcome.html> < <http://www.bhsu.edu/artssciences/asfaculty/gspellman/Welcome.html> >

Founded in 1883, Black Hills State University is located in beautiful Spearfish, SD, the hub of the Northern Black Hills with a population of more than 10,000. Located on I-90, 10 minutes from the Wyoming border, Spearfish is only 46 miles from Rapid City, 65 miles from Mount Rushmore National Memorial and is an hour drive from Devils Tower and the Badlands of South Dakota. Spearfish Canyon < <http://www.spearfishcanyon.com/> > , one of the oldest and most scenic canyons in the west, is a local favorite for hiking, biking and sightseeing.

Garth M. Spellman, Ph.D. Research Faculty CCBR/Westcore Black Hills State University 1200 University Street, Unit 9053 Spearfish, SD 57799-9053 ph: 605-642-6854 fax: 605-642-6762

garthspellman@bhsu.edu <http://www.bhsu.edu/artssciences/asfaculty/gspellman/Welcome.html>

GarthSpellman@bhsu.edu

EAWAG Switzerland HostParasiteEvolution

Eawag is the Swiss Federal Institute for Aquatic Science and Technology, a Swiss-based and internationally operating aquatic research institute within the ETH domain.

The Department Aquatic Ecology (group of Bas Ibelings) seeks for

PhD student in the evolution of host-parasite interactions

The PhD student will participate in a collaborative research project GEDIHAP with several other PhD students and host-parasite researchers from the ETH Zürich, the Swiss Federal Institute for Forest Snow and Landscape Research, WSL, and Eawag to study the influence of environmental factors (natural and human induced) on host - parasite interactions. In the project the impact of 2 environmental stress factors (climate change and water pollution) on the population dynamics and co-evolution of the diatom *Asterionella formosa* and parasitic chytrid fungi is studied.

For this, from CCESS (Competence Center Environment and Sustainability of the ETH Domain) financed project, we are looking for a highly motivated candidate with an interest in evolutionary biology, population genetics and host-parasite interactions. The research is balanced mixture of field and lab based studies, experiments will be done under controlled conditions in the lab as well as under natural conditions in lakes. Hosts and parasites will be screened using molecular tools like microsatellites, which are available for both. Part of the work will be done in the Netherlands.

We offer a stimulating research environment in a lively and social institute in Kastanienbaum (near Luzern) and Dübendorf (near Zürich) in a department with several other evolutionary and ecological research groups with a focus on host parasite interactions. The PhD candidate will be actively involved in workshops and courses organized within the GEDIHAP framework. The position will be for a period of three years, and should start as soon as possible (August 2008 or soon thereafter). The ideal candidate has both experimental as well as molecular skills (PCR, sequencing, genotyping). A Diploma or Master degree or equivalent) in biology or related subject is necessary for admission.

The working language in the group is English.

Applications should include a letter of interest with a description of pertinent experience, curriculum vitae, a list of publications (if any), the names (with e-mail address) of two potential references, and copies of the certificates of academic qualifications.

Please submit your application by 1 June 2008 as one PDF file to Sandra Isenring, Eawag, Human Resources Department: recruiting@eawag.ch, indicating reference number 084401. For further information, consult <http://www.cces.ethz.ch/projects/feh/GEDIHAP> or contact Bas Ibelings (Tel + 41 41 349 2174), bas.ibelings@eawag.ch

“Ibelings, Bas” <Bas.Ibelings@eawag.ch>

Eawag UBern Fish PopGen

A PhD Student Position in Eawag and University of Bern

Influence of habitat fragmentation on brown trout populations

A three-year PhD position on population genetics and ecology of brown trout is available in the Department of Fish Ecology & Evolution at the Center of Ecology, Evolution & Biogeochemistry (CEEB) in Eawag, the Swiss federal institute of aquatic science and technology (<http://www.fishecology.ch/>).

The PhD project is part of a larger project, called ENHANCE. ENHANCE is a problem-oriented, interdisciplinary research project funded by the Competence Center for Environment & Sustainability (CCES) of the ETH Domain. ENHANCE tests and evaluates ecosystem connectivity with state-of-the art molecular genetic experiments and population dynamic analysis. The successful candidate is expected to develop a research project that uses molecular ecological techniques to evaluate the consequences of habitat fragmentation and de-fragmentation on multiple populations of brown trout (*Salmo trutta*). The student will enroll for a PhD course in Ecology & Evolution at the Institute of Zoology, University of Bern (<http://www.zoology.unibe.ch/>) and will collaborate with other research institutes participating in ENHANCE (ETH, WSL, EPFL), as well as with researchers at Eawag and the Institute of Zoology.

The successful candidate should have thorough training

either in population ecology or population/conservation genetics, and basic training in the other discipline. M.S. degree in one of these disciplines is essential. Preference will be given to candidates with experience in handling DNA markers (e.g., microsatellites) and molecular genetic analyses. Because the PhD-student is expected to collaborate with research groups in several disciplines, teamwork abilities and ability to collaborate across disciplines are also essential. We expect a highly motivated student with demonstrated writing skills, who can work independently. Languages: fluent English (required) and possibly German/French. The place of employment will be at CEEB in Kastanienbaum, near Lucerne in Switzerland. The center is located in front of Lake Lucerne and has good access to the city Lucerne. Our lab is fully equipped for molecular genetic and ecological studies.

This is a three-year position with a standard salary of Eawag for PhD students. Expected starting date is June 1st, 2008 or later, but not after October, 2008. For your application please send a CV, an abstract of your M.S. research, a short summary of your scientific interests and three names of references. Deadline of the application is May 15th, 2008. Send your application as hard copy to: Nadja Pepe, Eawag, Fish Ecology and Evolution, Seestrasse 79, CH-6047 Kastanienbaum, Switzerland Or electronically to: Dr. Armin Peter, armin.peter@eawag.ch

For additional information on the project: Armin Peter, Phone +41 41 349 21 36, e-mail: armin.peter@eawag.ch or Hitoshi Araki, hitoshi.araki@eawag.ch. For information on the Institute of Zoology and the University of Bern: Ole Seehausen, ole.seehausen@eawag.ch.

Hitoshi.Araki@eawag.ch Hitoshi.Araki@eawag.ch

HannoverU EvolutionaryBiology

New MSc-Program in Evolutionary Biology and Biomedical Sciences

The Graduate School for Biomedical Sciences Hannover at University of Veterinary Medicine Hannover Foundation (TiHo) offers a research-oriented Master of Science Program in Evolutionary Biology and Biomedical Sciences for German and foreign students.

This modular Master's program presents a unique combination of Evolutionary biology and veterinary medicine, with a flexible, modular curriculum that al-

allows you to tailor your study to match your particular interests.

The program is grouped into three specialist areas focusing on

- evolution, animal biodiversity and behaviour;
- cellular, developmental and systems neurobiology;
- infection biology.

During the first semester, all three areas will be covered. In the second semester, you will select courses of your choice from two of the three themes. The second year (semesters 3 + 4), your study will focus your studies on just one of these tracks.

Admission to the program requires a BSc degree in Biology, Biochemistry, Biomedicine or related subjects. We offer a fast-track route (without master thesis) to our PhD program for excellent students.

What you can expect

TiHo is unique among institutions for higher education in Germany in its possibility to provide interdisciplinary courses with subjects ranging from Veterinary Sciences (e.g., what makes an organism a pathogen?) to modern Evolutionary and Conservation Genetics (evolutionary definition of conservation units), Behavioural Biology of Primates (e.g., acoustic communication and the origin of language), and selected topics in Physiology, Cell Biology and Neurobiology.

The University of Veterinary Medicine Hannover is Germany's oldest independent establishment of veterinary education with

- research priorities in infectious diseases, neuroscience, clinical research, animal health and food safety;
- six clinics, 15 institutes, two interdisciplinary departments;
- affiliated institutes and field stations for epidemiology and animal ecology;
- an animal farm for teaching and research and the animal welfare centre;
- the WHO Collaborating Centre & Veterinary Public Health;
- the EU Reference Laboratory for Classical Swine Fever;
- international partnerships and cooperative agreements with more than 30 universities.

For further information please contact: www.tiho-hannover.de/studium/gs/index.htm or:

Dr. Beate Poettmann Phone +49-511-953-8091, Fax

+49-511-953-8053 Graduate School for Biomedical Sciences Hannover Stiftung Tierärztliche Hochschule Hannover Buenteweg 2 D-30559 Hannover Germany

Prof. Dr. Stefan Koenemann Institute for Animal Ecology and Cell Biology University of Veterinary Medicine Hannover Buenteweg 17d D-30559 Hannover Germany

Tel.: + 49 [0] 511 953-8881 Fax: + 49 [0] 511 953-8584 Email: stefan.koenemann@tiho-hannover.de <http://www.tiho-hannover.de/einrichtung/botanik/koenemann.htm> Stefan Koenemann <Stefan.Koenemann@tiho-hannover.de>

LaurentianU AmphibianEvolution

Evolutionary Ecology and Amphibian Emerging Infectious Diseases

I am seeking a highly motivated and independent person to fill an MSc. position in my lab. The research will be in the scope of Emergent Infectious Diseases in Amphibians (Ranavirus & Chytrid fungus). These two diseases are causing mass die-offs in amphibian populations but the evolution, ecology, dynamics and effects of the pathogens are still largely unknown. The student will work in the context of host-parasite co-evolution by combining field work and experiments depending on his/her interests. The candidate is encouraged to create and develop his/her own project in the mentioned area. Good aptitude for fieldwork, molecular ecology skills and especially population genetics basics are expected as well as good communication skills.

Starting date: Candidates are expected to commence their studies between June - September 2008.

Full funding of approximately \$15,000/year is guaranteed for 2 years through a combination of TAships and RAships. Additional scholarships will be available by competition.

How to apply: Interested students should contact me via email, including a cover letter describing background and interests (including specific interests in my lab), cv, transcripts (unofficial is fine).

– “It takes all the running you can do to keep in the same place.”

Dr. David Lesbarrères Associate Professor & Graduate Coordinator

Genetic & Ecology of Amphibians Research Group (GEARG) Department of Biology - Laurentian Univer-

sity

http://biology.laurentian.ca/Laurentian/Home/-Departments/Biology/Faculty_and_Staff/Professors/-lesbarreres/lesbarreres.htm 935 Ramsey Lake Road, Sudbury, Ontario P3E 2C6, Canada phone: 705-675-1151 ext. 2275 Fax: 705-675-4859

dlesbarreres@laurentian.ca

LincolnU FishBarcoding

PhD Position: Bio-protection Centre, Lincoln University, New Zealand.

Biosecurity, high-risk ornamental fish and molecular genetic detection

New Zealand is a world-leader in the design and implementation of biosecurity systems used to protect its unique indigenous fauna and flora. This includes the use of state-of-the-art technologies to detect and prevent the establishment of high-risk exotic species and their diseases.

A PhD scholarship is available to develop DNA barcoding as a rapid and reliable diagnostic method to identify targeted exotic ornamental (aquarium) fish. Ornamental fish come from many countries where their health status is unknown. Furthermore, the mixing of fish in wholesale warehouse tanks before export to New Zealand means shipments may contain species other than those legally permitted for import. These species are difficult to detect visually, but they represent a significant risk to New Zealand's pristine waterways, potentially competing with native species and introducing exotic pathogens. Laboratory procedures will principally concern the generation and analysis of fish DNA barcode sequences, and sequences of other genes as appropriate. These data will subsequently be used to investigate diagnostic platforms based on technologies such as micro- or macro-arrays, high resolution melt (HRM) analysis, or a novel nano-engineered molecular assay. Accordingly, the student will develop appropriate molecular genetic hypotheses that test the suitability of barcode gene targets, fish taxonomic and evolutionary relationships, and biotechnological limits.

This Ministry of Agriculture and Forestry, Biosecurity New Zealand (MAFBNZ) funded PhD scholarship will be taken up at Lincoln University, Christchurch, New Zealand. Principal supervisors will be Drs Karen Armstrong and Shelley Ball (Lincoln University, [\[www.lincoln.ac.nz/\]\(http://www.lincoln.ac.nz/\); Bio-Protection Centre\), with advisory input from Drs Suzanne Keeling and Colin Johnston \(MAFBNZ, <http://www.biosecurity.govt.nz/>; Investigation and Diagnostic Centre, Wallaceville\). This team combines internationally-recognised expertise in DNA-based species identification systems with experts in delivery of biosecurity systems. Training will therefore involve the transfer of valuable skills required in the rapidly growing field of sciences for biosecurity, and establish a sound pathway to further academic or relevant employment opportunities within New Zealand or abroad.](http://-</p>
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Applicants should have a keen interest in the development and application of molecular technologies and hold, or expect to hold, a high grade undergraduate or Masters-level degree (or equivalent) in relevant life sciences. The award covers a fulltime stipend, registration fees, and project costs for a three-year study.

Please e-mail your CV to Dr Karen Armstrong at armstron@lincoln.ac.nz. The closing date for applications for this studentship is 20/6/08.

National Centre for Advanced Bio-Protection Technologies PO Box 84 Lincoln University Canterbury NEW ZEALAND p + 64 3 325 3696 f + 64 3 325 3864

Dr. Shelley L. Ball Research Officer Molecular Diagnostics Laboratory National Centre for Advanced Bio-protection Technologies Box 84, Lincoln University Canterbury, New Zealand Phone: 64 (3) 325-2811 or 64 (3) 325-3696, extension 8411 if calling after hours, dial 325-3838, ext. 8411 FAX: +64 (3) 325-3844 (when dialing from overseas, dial 011 before the 64) E-mail:ball@lincoln.ac.nz <http://-/bioprotection.lincoln.ac.nz> Bio-Protection is a National Centre incorporating staff from Lincoln University, Massey University, AgResearch, Crop & Food Research and seven other collaborator institutes that conducts world class research and development to meet the biosecurity and pest management needs of New Zealand's primary industries and natural ecosystems

Shelley Ball <ball@lincoln.ac.nz>

Montreal EvolutionaryBiology and Engineering

Graduate Projects in Evolutionary Biology and Engineering

The laboratory of animal form and function (Biolog-

ical Sciences) and the laboratory of the Canada Research Chair on analysis, characterization and optimization of complex flows (École Polytechnique) offer multi-disciplinary research projects on the investigation of interactions of animals in a fluid environment in an evolutionary context.

The structure and shape of organisms are optimally adapted for life in moving fluids. We use direct experimentation and computational modeling to understand how organisms function at different sizes, shapes and flows. Biologically inspired design of engineering systems is receiving a great deal of attention from the mechanical engineering research communities and additionally the field of biological fluid mechanics is benefiting from tools developed by the engineering community. We use videomicroscopy, particle visualisation, electron microscopy, experimental developmental biology, micromanipulation, numerical, analytical and theoretical models of fluid dynamics.

During the graduate project(s) the candidate(s) will work on live animals and computer models of i) animals >1mm in size, ii) jellyfish swimming, and/or iii) filter feeding in chordates to better understand the origin of morphological novelties and the evolution of clades with disparate taxa. Additionally, these systems have utility in the design of heart valves, micro sized robots and miniature pump systems, respectively.

The University of Montreal is among the top 100 universities worldwide and the École Polytechnique is one of the three biggest engineering schools in Canada.

We are looking for students with the following assets (but not required): - Canadian citizen or permanent resident - Grade average of A- (3.7) or better for the last two years of university studies or grade average of B+ for the B.Sc. - B.Sc. in biology, physics, or mechanical engineering - Interest in animal functional biology, fluid mechanics, engineering design - Experience in Computational Fluid Dynamics and microscopy

Chris Cameron Sciences biologiques Université de Montréal C.P. 6128, Succ. Centre-ville Montreal, QC, Canada H3C 3J7 phone: (514) 343-2198 c.cameron@umontreal.ca

Dominique Pelletier, Canada Research Chair École Polytechnique Université de Montréal 2500, chemin de Polytechnique Montréal, Qc H3T 1J4 (514) 340 4711 Dominique.Pelletier@polymtl.ca

Chris Cameron <c.cameron@bms.bc.ca>

MPI EvolBio LifeCycleEvolution

There is an opening for a motivated PhD student at the Max Planck Institute for Evolutionary Biology (formerly MPI for Limnology) to work on a project titled "The evolution of complex parasite life cycles".

Many parasites have complex life cycles that involve switching between several host species. An increase in life cycle complexity entails clear costs (e.g. parasites must be transmitted between separate hosts as opposed to simply reproducing in the current host and they are likely faced with physiologically and immunologically divergent host environments). Given these costs, the evolution and maintenance of life cycle complexity is paradoxical. Current theory suggests that parasites may avoid mortality due to predation and/or be able to reach a larger size at maturity when incorporating hosts at higher trophic levels, while parasites that add hosts at a lower trophic level may facilitate transmission to the final host and thereby reduce mortality rates. The PhD project would address questions of importance in life cycle evolution using a life history approach and the tapeworm *Schistocephalus solidus* as a model system. This parasite has 3 hosts in its life cycle; a copepod, a stickleback, and a piscivorous bird. A major advantage of this system is that the bird final host can be replaced by an in vitro system, permitting the entire life cycle to be conveniently kept in the laboratory. Particular questions of interest include: What advantages come with adding the bird host into the life cycle of *Schistocephalus*? Why doesn't *Schistocephalus* grow in birds? How does the parasite invest in switching between hosts and how is growth divided between hosts? Is parasite investment into growth and/or transmission-related traits flexible and context-dependent?

This project is being conducted in collaboration with Geoff Parker and Jimmy Chubb (University of Liverpool). They are producing mathematical models about life history evolution in complex life cycle parasites. We intend to test their predictions and collect empirical data for further refinement of their models.

The position is for 3 years and is research-oriented; there are very few teaching duties. A Diplom, Master's degree or equivalent postgraduate degree is required. Students with an interest in life history evolution and host-parasite interactions are especially encouraged to apply. Research experience with small animals is con-

sidered an asset. The MPI for Evolutionary Biology is located in the city of Ploen in Northern Germany and has excellent research facilities. The position will remain open until filled.

Interested students should send their CV to Prof. Manfred Milinski and Daniel Benesh:

Prof. Manfred Milinski Executive Director Max-Planck-Institute for Evolutionary Biology Department of Evolutionary Ecology August-Thienemann-Strasse 2 D-24306 Ploen, Germany email: milinski@evolbio.mpg.de

Daniel Benesh Max-Planck-Institute for Evolutionary Biology Department of Evolutionary Ecology email: benesh@mpil-ploen.mpg.de <http://www.mpil-ploen.mpg.de/> benesh@mpil-ploen.mpg.de

NHM London FernApomixisEvolution

PhD studentship at the Natural History Museum and Imperial College London

Evolution of Apomixis in Ferns

Supervisors: Harald Schneider (Natural History Museum, London) & Vincent Savolainen (Imperial College).

3 Year studentship to carry out a PhD on the evolution of apomictic ferns using molecular and bioinformatics approaches. This is a unique opportunity to carry out a PhD supervised by two leading scientists at two of the UK's most prestigious research institutes. The studentship will cover University tuition fees, a maintenance stipend or bursary and research funding (travel costs, laboratory costs). The research program will involve state of the art molecular laboratories and bioinformatics, fieldwork in tropical countries, and access to arguably the best fern collections in the world.

Starting date: October 2008.

Applications are welcome from candidates who have, or expect to obtain, a minimum of an Upper-second class degree and/or a Masters-level degree in a relevant subject such as molecular biology, bioinformatics and/or molecular systematics.

Candidates should be UK or EU citizens

For more information and to apply for this studentship please send a CV and details of two academic referees

to: Dr. habil. Harald Schneider Department of Botany Natural History Museum London SW7 5BD, UK. email: h.schneider@nhm.ac.uk

Closing date: Friday 20th June 2008

<<Savolainen and Schneider studentship (2).pdf>>

Harald Schneider Research Leader Department of Botany Natural History Museum London Cromwell Road SW7 5BD, UK +44 (0)20 7942 6058 h.schneider@nhm.ac.uk

Harald Schneider <h.schneider@nhm.ac.uk>

NHM Paris DispersalHeritability

A 3 year PhD position is available in our laboratory (UMR 7179, Natural History Museum, Paris) to work on heritability of dispersal behaviors (see attached file for a detailed description of the project). The work will be supervised by Pr Michel Baguette and Dr HÃ©lÃ©ne FrÃ©ville. The candidate will also benefit from the expertise of many other researchers involved the project.

The starting date of the position is October 1st, 2008. The position is open to all nationalities, providing that the candidate has a Masters degree. Knowledge of the French language is not a requirement. The salary is approximately 1650 /month.

Interested candidates should send a detailed CV, a letter of interest, a list of publications (if any) and the contact details of 2 references to Michel Baguette (baguette@mnhn.fr) or HÃ©lÃ©ne FrÃ©ville (freville@mnhn.fr). The deadline for application is June 12th, 2008. An interview of pre-selected applicants will be organised in Paris (or by phone) around June 18th.

For further information (informal enquiries are encouraged), please email us.

Please share this PhD studentship advertisement with any interested parties.

Michel Baguette & HÃ©lÃ©ne FrÃ©ville

Virginie Stevens <stevens@mnhn.fr>

ParisFrance BioinformaticsEvolution

Dear Evoldir

A 3-year PhD studentship is available at Université Pierre et Marie Curie (Paris, France) to study lateral gene transfers and genomic evolution, mostly through bioinformatics approaches. The project will be supervised by Dr Philippe LOPEZ (bioinformatics, phylogenomics) and Dr Eric BAPTESTE (evolutionary biology, philosophy of sciences), within UMR 7138 'Systematique, Adaptation, Evolution'.

This project will involve bioinformatic analyses, genomic and metagenomic studies, phylogenetics and of course lots of fun discoveries (see below for a short summary). A full description of the proposal can be found at

http://pbg-05.snv.jussieu.fr/phd/-phd_lopez_bapteste.pdf The position is open to EU citizens. The ideal applicant should have an MSc in Evolutionary Biology or Mathematics or Bioinformatics, and should show a great interest in evolution. The position will start anytime from October to December 2008. Requests for further information and applications (a CV, cover letter and names of 2 academic referees) should be made to Philippe LOPEZ (philippe.lopez@upmc.fr) or Eric BAPTESTE (eric.bapteste@snv.jussieu.fr). The deadline for applications is June 1st, 2008.

Université Pierre et Marie Curie is located in the historical center of Paris, by the Seine river and in front of the Jardin des Plantes, and is the largest french university (ranked 1st in France, 6th in Europe and 39th worldwide). Scientific environments is stimulating, since the host unit has strong connections with a wide variety of biologists: deep sea oceanographers, transposons specialists, experts from Museum National d'Histoire Naturelle and so on.

Thank you for your attention, we're looking forward to hearing from you,

Philippe Lopez Eric Bapteste

Short summary of the proposal:

Over the last years, our views of the evolution of microbial genomes changed radically. It is now admitted that these genomes are affected by evolutionary processes conjugating both vertical inheritance and lateral gene transfer, via phages, plasmids and integrons. Genomes recombine, become larger or smaller by gene losses and gains, according to rules that still largely remain to be determined. This PhD aims at studying the evolution of microbial genomes fluidity via genomics and metagenomics approaches to understand how the genetic material flows within Life's three domains. This

ambitious project relies first on the unprecedented accumulation of molecular data from organisms in pure culture (the genomic data) and from the sequencing of whole microbial communities in their environment (the metagenomic data). Second, it exploits the latest developments in bioinformatics : phylogenetic methods of tree and network reconstruction, and possibly in silico modeling of microbial genomes evolution. This PhD addresses three major questions: - Does the nature of the mobile genetic material change over time and across lineages? - How does the environment influence genomic fluidity? - Are in situ and in silico data supporting similar conclusions?

philippe.lopez@upmc.fr

Paris Memory Evolutionary Biol

PhD Genetic and environmental variation of memory
CNRS Gif Sur Yvette, France

A 3 year PhD position is available in the Laboratory of Evolution, Genomes, and Speciation (LEGS, CNRS) in Gif sur Yvette (France) to work on the evolutionary biology of memory. The starting date of the position is programmed for September 1st 2008. In *Drosophila*, 4 different memory phases have been described (short-term, middle-term, anesthesia-resistant and long-term). Using selection experiments, population comparisons and conditioning assays, we are addressing issues such as: Genetic and environmental variations of learning and memory among *drosophila* species and populations, fitness benefits and costs of the different memory phases, effect of ecologically-relevant stress on the memory phases. The successful candidate should be highly motivated and will develop his/her own project in this area. Candidates should have a master degree in Evolutionary Biology, Animal Behavior or Neuroscience. Some experience with *Drosophila* behavior, genetics or molecular methods would be helpful but are not required. The application is open to all nationalities and is funded by the European Research Council (the salary is around 1700 Euro/Month taxes included). No pre-existing knowledge of French is required to work in the lab, although some knowledge makes living in France easier. Gif sur Yvette is located 40 min from downtown Paris. To apply, send your CV, a letter describing your research interests and some ideas for a project to Frederic.mery@legs.cnrs-gif.fr. Arrange for one or two letters of recommendation to be sent to the same

address.

The review of applications will begin on June 15, 2008.

Frederic Mery Laboratoire Evolution, Genomes et Speciation CNRS - Bat 13 Avenue de la Terrasse F-91198 Gif sur Yvette Cedex France

E-mail: Frederic.Mery@legs.cnrs-gif.fr Phone (Office): (33) 1 69 82 37 32 Phone (Lab): (33) 1 69 82 38 63 Fax: (33) 1 69 82 37 36

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Frederic Mery Laboratoire Evolution, Genomes et Speciation CNRS - Bat 13 Avenue de la Terrasse F-91198 Gif sur Yvette Cedex France

E-mail: Frederic.Mery@legs.cnrs-gif.fr Phone (Office): (33) 1 69 82 37 32 Phone (Lab): (33) 1 69 82 38 63 Fax: (33) 1 69 82 37 36

Web: <http://www.legs.cnrs-gif.fr/-perso.php?id=106&lang=fr> Frederic Mery <Frederic.Mery@legs.cnrs-gif.fr>

Senckenberg GlobalChangeGenetics

Senckenberg.GlobalChangeGenetics

Graduate position:

A PhD position is available in global change biology/population genetics at the Department of Limnology & Conservation, Senckenberg Research Institute and Natural History Museum, Germany.

Current models suggest that global warming will lead to massive species extinctions in the near future. It is expected that certain traits increase susceptibility towards changing climate, including reduced dispersal, low genetic diversity, small population size, isolation and low tolerance towards temperature changes. In Europe, several cold-adapted species of plants and animals persist as isolated glacial relicts in high altitudes. Many of these species combine several, if not all of the above-listed factors and may thus be among the first species to become extinct if global temperature shows further increase. The PhD candidate will develop and apply genetic markers (e.g., microsatellites, AFLP, sequence data) to investigate genetic population structure in cold-adapted, montane species in central European mountain ranges. In particular, research will focus on patterns of gene flow and isolation among populations, inbreeding levels within isolated relict populations, and

to identify conservation units. Besides the molecular part, field work and controlled laboratory experiments on temperature and general stress tolerance will be conducted. The study is not focused on a certain taxonomic group; research will thus likely comprise both plant and animal species. We are looking for a highly motivated student with a strong interest in biodiversity, conservation and population genetics. The candidate is expected to have some experience in the laboratory, ideally with the application of microsatellite markers and/or DNA sequencing. Knowledge of German language is no precondition, but we expect the willingness to learn some German during the stay. A valid international drivers licence is required for field sampling. The Senckenberg Research Institute and Natural History Museum (head quarter in Frankfurt am Main) is among the largest natural history museums in Europe and has a longstanding tradition in high quality biodiversity research. The Department of Limnology & Conservation is located at the research station Gelnhausen. The station has all facilities required for this research (fully equipped molecular lab, laboratories for sample sorting and microscopical analysis, field equipment). Gelnhausen is a quaint town in close proximity to Frankfurt am Main. The city has a picturesque historic Old Town with several historic sites from the medieval times and is surrounded by beautiful mountain ranges. Frankfurt am Main, an international city with a rich and diverse cultural life and unique international transport connections, can be reached within 30 minutes by car or train. In order to apply, please send an application sheet, CV, publication list and contact data of two references per email to:

Dr. Carsten Nowak Senckenberg Research Institute & Natural History Museum Research station Gelnhausen, Dep. Limnology & Conservation Email: cnowak@senckenberg.de www.senckenberg.de Applications will be considered until the position is filled.

Senckenberg wishes to increase the share of women in areas where they are underrepresented, and strongly encourages women to apply. Senckenberg has an affirmative action policy for the disabled and especially encourages them to apply.

cnowak@senckenberg.de cnowak@senckenberg.de

Spain TropicalBiodiversity

ANNOUNCEMENT of Master's Degree Program in

“Biodiversity in Tropical Areas and its conservation” (MBATC)

The Master’s Degree Program in “Biodiversity in Tropical Areas and its conservation” is a one-year MSc program (75 ECTS) offered jointly by the International University Menendez Pelayo (UIMP, Ministry of Science, Spain), the Spanish National Research Council (CSIC, Ministry of Science, Spain), and the Universidad Central del Ecuador (UCE, Ecuador). The program is fully funded by the CSIC, with a strong emphasis on fellowships for Latinamerican students; the title is an official European MSc degree conceded by the UIMP; and the program will be taught in Ecuador, with an emphasis on practical studies in natural reserves.

The program is international, with a minimum of 15 and a maximum of 30 students, most of them funded by the program.

ROUTE TO PHD DEGREE.- Excellent graduates from the MBATC program have the possibility to continue their PhD studies in CSIC Departments (Real Jardín Botánico, Museo Nacional de Ciencias Naturales, etc.) through separate application calls opened each year. They can also apply to other programs in the Spanish science system (Universidad Complutense de Madrid, etc.), or to any European or American university, as this MSc title is an official European degree.

WHAT DO I NEED TO BE ABLE TO APPLY TO MBATC?.- You are eligible to apply to the program if you hold a Bachelor’s degree in any suitable field, especially on biosciences: biology, forestry, or agriculture, but also in geography, for example. You must need to be proficient in Spanish language.

FINANCIAL SUPPORT.- The CSIC offers 5 full scholarships (6300 euros/student) and 5 for registration fees (1300 euros/student). The program finances 10 additional full scholarships for Latin American applicants.

HOW TO APPLY?.- The application period for studies starting in September 2008 begins 19 May 2008 and closes 10 July 2008. You can find all the information and detailed instructions on how to apply at

<http://www.rjb.csic.es/fichacurso.php?id=265> If you have any questions regarding the program, please contact Director Jesus Munoz at <jmunoz@rjb.csic.es>

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Jesús Muñoz e-mail: jmunoz@rjb.csic.es Real Jardín Botánico (CSIC) Plaza de Murillo 2 tlf. +34 91 420 3017 E-28014 Madrid fax. +34 91 420 0157 ESPAÑA (Spain)

http://www.rjb.csic.es/fichapersonal.php?id_investigador

<http://kraken.unex.es/kraken/> KRAKEN research group (environmental modelling, data processing & analysis) <http://www.synthesys.info/index.htm> (SYNTHESYS: EU funds short visits to our institution)

Jesús Muñoz <jmunoz@rjb.csic.es>

UBergen FishEvolutionaryBioeconomics

PhD in the interface between evolutionary fisheries ecology & bioeconomics!

This PhD position is available in research group “Evolutionary Fisheries Ecology” (EvoFish) at the Department of Biology, University of Bergen, Norway. The position is for 3 years, with the start preferably not later than in September, 2008.

For more information on the research group EvoFish and the new position, see <http://bio.uib.no/-evofish/>, or for the full jobb ad, go directly to <http://www.jobbnorge.no/visstilling2.aspx?stillid=-3D48112&lang=3DEN> mikko.heino@imr.no

UBern BehaviouralEvolution

TWO PhD-POSITIONS in BEHAVIOURAL EVOLUTION are available at the Department of Behavioural Evolution of the Zoological Institute, University of Bern, Switzerland.

(1) One study will focus on the sharing of tasks, commodity trading and reciprocity in a cooperatively breeding cichlid where helpers pay to stay in a safe territory. Behaviour, group composition, threat and resource availability will be experimentally manipulated. In addition, long-term fitness effects of differences in the propensity to stay and help or to disperse will be measured in the field. (2) The second project investigates the proximate and ultimate mechanisms of co-existence of flexible and fixed alternative reproductive tactics within a species. The model system is a snail-brooding cichlid where bourgeois males are exploited by two types of parasitic males. This study will involve experimental manipulation of tactic frequencies and fe-

male behaviour, measurement of reproductive fitness and sperm competition, and perhaps some modelling.

Applicants should have a master's degree (or Diplom) in Biology and research experience in animal behaviour, a firm, theoretical background in behavioural and evolutionary evolution, and a strong commitment to basic science. Practical skills in the work with fish, both under water and in the lab will be very helpful. The successful candidates will be collaborating with the other members of the group, which will include approximately 4 advanced research staff, 6 PhD- students and a varying number of master and bachelor students. Besides research, PhD students are expected to assist in undergraduate teaching and supervision, with a training load not exceeding 10 percent of working time. Salaries will follow the scheme of the province of Bern and the Swiss National Research Foundation (approx. 34,000.- to 40,000.- CHF/year).

Closing date: Open until filled, but all application materials, including CV, a summary of research experience, copies of any published or in-press papers if applicable, and 2 letters of recommendation, should be received by May 30, 2008 to assure full consideration. The position will start at the earliest possible date and will be for three years. Candidates should indicate in a cover letter when they could take up the position.

Please send material to the secretary's office, c/o Marlis Gerteis, Dept. Behavioural Evolution, University of Bern, Baltzerstr. 6, CH-3012 Bern, Switzerland; or as an e-mail attachment to marlis.gerteis@esh.unibe.ch. For further information please see <http://zoology.unibe.ch/behav/> or contact Michael.Taborsky@esh.unibe.ch

Michael Taborsky <michael.taborsky@esh.unibe.ch>

UCC Ireland Arabidopsis Natural Variation

UCC Ireland Arabidopsis Natural Variation

PhD Fellowship (Arabidopsis natural variation)

University College Cork, Ireland

Our lab is seeking applications for a PhD fellowship to conduct research on genetics of reproduction in polyploid plants. The successful applicant will work within a small team investigating both sexual and asexual reproduction (apomixis). Applicants should ideally have

a First Class Honours Degree or MSc in an appropriate discipline. In particular, we seek applicants who have previously gained research experience in Arabidopsis genetics, particularly on topics such as genetics, association/QTL mapping, DIC/fluorescence microscopy, in situ hybridisation, cytogenetics or chromatin analysis in Arabidopsis thaliana. The PhD Fellowship is funded for three years and collaborators include Dr Magnus Nordborg (Uni of Southern California), Dr Tom Juenger (Uni of Texas) and Dr Tim Sharbel (IPK Gatersleben). Prospective applicants should send an e-mail before 16 June 2008 outlining your research interest and motivations, including: (a) your C.V. (please list any publications and experimental skills) & (b) contact details and e-mail addresses for 3 referees to:

Dr. Charles Spillane, Genetics & Biotechnology Lab, Biochemistry Dept & Biosciences Institute, University College Cork, Cork, Ireland.

E-mail: c.spillane@ucc.ie

Spillane Lab : www.ucc.ie/spillane Collaborator websites:

Juenger lab: <https://webspaces.utexas.edu/tjuenger/> <
<https://webspaces.utexas.edu/tjuenger/>>

Nordborg lab: <http://walnut.usc.edu/> <
<http://walnut.usc.edu/>>

Sharbel lab: http://www.ipk-gatersleben.de/Internet/Forschung/CytogenetikGenomanalyse/Apomixis <
http://www.ipk-gatersleben.de/Internet/Forschung/CytogenetikGenomanalyse/Apomixis>

"Spillane, Charles" <C.Spillane@ucc.ie>

UIdaho Phage Adaptive Evolution

Math Modeling_Spatial Structure_Virus Adaptation

A PhD Research Assistantship (RA) is available to work with Professor Steve Krone at the University of Idaho. The RA will work on the mathematical modeling component of a study of adaptive evolution of bacteriophages growing in spatially structured environments and subject to fluctuating environmental conditions. This is an opportunity to be part of a highly interdisciplinary research project that combines experimental evolution and mathematical modeling. The RA will interact with mathematical modelers in other projects and with Krone's phage lab, which is one of three in

the UI Department of Biological Sciences; the other two (Brown and Wichman) phage labs are in close proximity and help to provide a collaborative and stimulating environment.

This project (Spatial Structure and Adaptive Evolution of Viruses) is one of four supported by the renewal of our \$9.7 million NIH Center of Biomedical Research Excellence (COBRE) grant. The RA will be part of our IBEST group at UI (<http://www.ibest.uidaho.edu/-ibest/index.html>), a dynamic and interdisciplinary research group with excellent resources, and will have the option of working on a Ph.D. in either Mathematics or Bioinformatics and Computational Biology.

Qualifications: Student should be highly motivated, have a strong mathematical background and ability to code in C++. Knowledge of Unix and data structures would be helpful. Although no prior background in biology is necessary, the student should have a serious desire to learn about microbial population biology. Mathematically inclined biology students will also be considered.

The stipend pays US\$20,000 per year and tuition, fees, and health insurance are covered. In addition, funds are available to attend conferences.

HOW TO APPLY: For preliminary screening, email a statement of background and interests, TOEFL scores (for foreign applicants), GRE scores (if you have them), and a copy of transcripts of academic courses taken. Starting date is flexible.

Contact: Steve Krone (krone@uidaho.edu) to apply and for further information.

Web site: Steve Krone (<http://www.webpages.uidaho.edu/~krone/>)

Dr. Steve Krone Professor Department of Mathematics University of Idaho Moscow ID 83844-1103, USA
Phone: 1-208-885-6317 Fax: 1-208-885-5843

krone@uidaho.edu krone@uidaho.edu

ULausanne 3 BehaviouralEvolution

Three PhD-positions in BEHAVIOURAL EVOLUTION are available at the Department of Ecology and Evolution, University of Lausanne, Switzerland.

(1) One study is on parent-offspring conflict by focussing on nestling begging behaviour and sib-sib communication (i.e. so-called sibling negotiation). This

project will be based on recent unpublished results suggesting that nestlings produce nest-specific vocal signals to indicate their level of need. The project will also deal with several original issues including the role of individual recognition and punishment on sib-sib communication as well as the evolution of proto-language. This study will be carried out in wild barn owls. One or two PhD-positions depending on the applicants.

(2) The second project investigates the proximate and ultimate mechanisms of the adaptive function of melanin-based colour traits. Although the expression of melanic pigments is often non-condition- dependent, darker wild vertebrates are more aggressive, sexually active and resistant to stress than lighter individuals. We recently identified a candidate gene that could account for covariation between the degree of melanin-based coloration and other physiological and behavioural traits. The aim of PhD-projects would be to (i) determine whether variation in the products of the candidate gene is due to a polymorphism at that gene, differential gene expression or post-translational modification of the gene product, (ii) assess the adaptive function of variants of this candidate gene, and (iii) identify the adaptive function of melanin- based coloration by analysing long-term datasets and by performing experimental studies with wild animals. This study will be carried out in wild barn owls and tawny owls. One or two PhD-positions depending on the applicants.

Applicants should have a master's degree (or Diplom) in biology and research experience in evolutionary biology with a strong theoretical background as well as a good experimental approach. For the project on the candidate gene applicants should have a good expertise in molecular biology and lab work. Practical skills in the work with birds (raptors) is helpful but not compulsory. The successful candidates will be collaborating with the other members of the group, which will include approximately 4 advanced research staff (3 post-docs and a professor), 5 PhD-students and a varying number of master students. We are located in the Department of Ecology and Evolution at the University of Lausanne (Switzerland) situated on the shores of Lake Geneva. The Department provides a pleasant and exciting research environment and a strong PhD program (21 group leaders, 41 post-docs and 45 PhD-students working on many different fields).

Besides research, PhD students are expected to assist in undergraduate teaching and supervision, with a training load not exceeding 10 percent of working time.

Closing date: Open until filled, but all application materials, including CV, a short summary of research ex-

perience, copies of any published or in-press papers if applicable, a letter of motivation and name of two reference persons by email to Alexandre Roulin, Biophore, Dept of Ecology and Evolution, University of Lausanne, Switzerland. Email: Alexandre.Roulin@unil.ch tel: +41 21 692 41 89 More details on the group at <http://www.unil.ch/dee/page7006.html> Alexandre Roulin Department of Ecology & Evolution Biophore University of Lausanne CH-1015 Lausanne Switzerland

Desk 3202 Tel: 0041 21 692 41 89 Private: 0041 21 691 43 29 Mobile: 0041 79 686 08 64 Fax: 0041 21 692 41 65 Email: Alexandre.Roulin@unil.ch Website: <http://www.unil.ch/dee/page7006.html> To: Alexandre.Roulin@unil.ch

U**Lausanne ComparativeGeneExpr**

A PhD position is open for a collaborative project between the labs of Prof. Marc Robinson-Rechavi (Evolutionary Bioinformatics) and Prof. Sven Bergmann (Computational Biology). The project concerns the comparative modular analysis of gene expression in vertebrate development. The student will work with, and improve, computational methods of microarray analysis from the Bergmann lab, and ontology alignment methods from the Robinson-Rechavi lab, and apply them to publicly available data.

The project will shed light on the fundamentally modular nature of the regulation of development in animals, and its evolution. Methodological advances of general use are also expected.

We are looking for an autonomous and ambitious student, with a strong mathematical background (physicists, computer scientists, engineers), and knowledge of biology. Previous experience with evolutionary and/ or developmental biology is a plus but not a requirement. Willingness to work with real (and often noisy and complex) biological data is necessary. Fluency in English is a requirement.

Please send a CV and contact information of two references to marc.robinson-rechavi@unil.ch

Websites for additional information: <http://serverdgm.unil.ch/bergmann/> <http://www.unil.ch/dee/page22707.html> <http://bgee.unil.ch/> --- Marc Robinson-Rechavi Department of Ecology and Evolution Biophore 3219, University of Lausanne, 1015 Lausanne, Switzerland tel: +41 21 692 4220 fax: +41

21 692 4165 <http://www.unil.ch/dee/page22707.html> Swiss Institute of Bioinformatics http://www.isb-sib.ch/groups/Evolutionary_Bioinformatics.htm La liberte ne s'use que quand on ne s'en sert pas

Marc Robinson-Rechavi <Marc.Robinson-Rechavi@unil.ch>

U**Lausanne ParasitismEvolution**

PhD studentships in Lausanne, Switzerland

Evolution & Parasitism

We are seeking two motivated students with an interest in parasite ecology and evolution to join our group working on avian malaria.

Candidate should have interest in intensive field work and have a good background in molecular biology and its use in evolutionary and ecological biology.

She/he must have a Masters degree (MSc) in order to qualify for our PhD program.

One aspect of the project (student 1) will be to experimentally test the effects of the Plasmodium parasite on its host, the great tit *Parus major*, as well as the immune response of the host. The competition between different strains of the parasite will also be studied using qPCR to follow the course of primary infection.

The other part of the project (student 2) will deal with the vector of the Plasmodium, a mosquito species. Host choice experiments, as well as the effects of the parasite on life history traits of the vector will be experimentally studied. This part will be partly conducted in the museum of zoology in Lausanne in collaboration with Dr Olivier Glaizot.

Both students will have to collaborate intensively.

We are located in the Department of Ecology and Evolution at the University of Lausanne (Switzerland). The Dept. of Ecology and Evolution in Lausanne is situated on the shores of Lake Geneva and provides a pleasant & exciting research environment and a strong PhD program.

The studentships are for a period of 3 years. Starting date ideally by late spring, early summer 2008 but this date can be extended for exceptional candidates. Closing date for application is 19 Mai 2008. To apply, applicants should send a CV, a letter of motivation and name of two reference persons by EMAIL to Philippe Christe,

Dept of Ecology and Evolution, University of Lausanne, Switzerland. Email: philippe.christe@unil.ch

More details on the group at: <http://www.unil.ch/dee/page6999.html> Philippe.Christe@unil.ch

ULeuven SticklebackEvolutionaryBiol

4 YEAR PhD POSITION IN EVOLUTIONARY BIOLOGY

Catholic University of Leuven, Leuven (B)

A 4 year PhD position for an evolutionary biologist is vacant at the Laboratory of Animal Diversity and Systematics (Catholic University of Leuven) in the research group of Prof. Filip Volckaert to perform a study entitled: "Strong selection pressures and micro-evolutionary responses in the three-spined stickleback".

Project description: The project investigates the conceptual and methodological integration of ecology and evolutionary biology. The successful candidate will study the evolutionary response of the three-spined stickleback to strong selection pressures (predation and parasitism) in an ecological context. Patterns of phenotypic variation will be explored in natural populations and phenotypic adaptation tested experimentally. The rapid evolutionary response at the genomic level will subsequently be studied under natural and experimental conditions. The stickleback is a prime model for evolutionary research with access to an impressive molecular toolbox, enabling the understanding of the link between phenotypic and genomic responses to environmental and anthropogenic factors. Evolution in sticklebacks has been studied in our team over the past five years (Raeymaekers et al. 2005 and 2007, Molecular Ecology; Raeymaekers et al. 2008, Evolutionary Applications). The project starts on 1 October 2008 and is supervised by prof. Filip Volckaert and dr. Joost Raeymaekers.

The research team: The Fish Genetics Team has a strong expertise in phenotypic, neutral and adaptive evolution, including field monitoring, experimental design, medium-throughput genotyping, the analysis of genetic, genomic, and phenotypic data with up-to-date statistical approaches, and modeling for heuristic and operational analyses. Topics addressed include phylogeny, barcoding, phylogeography, the study of hybridisation, population genetics, local adaptation

and rapid evolution (natural and fisheries induced), enhanced selection in aquaculture (aquaculture genomics), bioinformatics, co-evolution between host and parasite, spatio-temporal dynamics of nursery grounds and the sustainable management of aquatic habitats. Our team comprises 6 PhD students, 4 postdocs, 2 technicians and a team leader. The historic KULeuven, founded in 1425, has a very stimulating research environment. The modern city of Leuven with its medieval roots offers a high quality of life.

Candidate profile: Strong motivation, background in evolutionary biology, interest or experience in field based experimental research, open to international contacts with other research groups, is strongly recommended. Research will be carried out in collaboration with a multidisciplinary team of ecologists, parasitologists, evolutionary biologists and population geneticists. Importantly, this position is only vacant for prospective students fluent in the Dutch language.

Financing: The successful candidates fellowship (approximately 1600 / month netto) is funded by a national project of excellence granted by the KULeuven (GOA). The candidate is expected to apply for a national IWT fellowship by September 2008.

Application deadline: Please send a letter of motivation, C.V., and two letters of reference to Filip Volckaert by June 15 2008. For more information contact joost.raeymaekers@bio.kuleuven.be or filip.volckaert@bio.kuleuven.be.

Address:

Dr. Filip Volckaert Laboratory of Animal Diversity and Systematics Catholic University of Leuven Ch. Deberiotstraat 32 B-3000 Leuven Belgium Phone: +32 16 32 45 75 E-mail: filip.volckaert@bio.kuleuven.be URL: <http://bio.kuleuven.be/dev> Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

UMontpellier BacteriaPhageCoevolution

PhD "Experimental coevolution between bacteria and phage in stressful environments"

Institute of Genetics and Evolution, University of Montpellier, France

A 3 year PhD position is available in our laboratory to work on coevolutionary dynamics in spatially and

environmentally heterogeneous systems.

How do organisms adapt to stressful conditions and what are the implications of spatial heterogeneity in stress for tightly-coupled interactions with other species? The thesis will address these basic questions and a suite of more detailed unknowns through experimental investigations of microbial host-parasite associations involving *Pseudomonas fluorescens* and its lytic bacteriophage. The exciting prospect of this research is demonstrating how limits to adaptation in bacterial hosts and their coevolving parasites create pattern in diversity, life-history tradeoffs, and generative mechanisms of diversity such as mutation rates.

The starting date of the position is October 1st, 2008, is open to all nationalities, and knowledge of the French language is not a requirement. The salary is approximately 1750 euros/month.

The successful candidate will have a Masters degree with training in evolutionary biology, and preferably have experience in microbiology or experimental evolution. Interested candidates should send a letter of motivation, CV, and the contact details of two references to Dr. Michael Hochberg (mhochber@univ-montp2.fr) no later than the 20th of May. Contacts for additional information on the project are welcome.

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This thesis will be conducted in the Ecology and Evolution of Communities group, which currently has 3 permanent researchers (M Hochberg, O Kaltz & N Mouquet), 1 technician, 3 postdocs and 1 PhD student. Our team has expertise in both theoretical and empirical approaches to understanding evolutionary pattern. We are financed by an Agence National de la Recherche grant, and this will cover all laboratory costs and several trips to conferences and to collaborators' laboratories.

Recent publications by our research team include:

Buckling A., Wei Y., Massey R.C., Brockhurst M.A. & Hochberg M.E. 2006. Antagonistic coevolution with parasites increases the cost of host deleterious mutations. *Proceedings of the Royal Society of London B* 273: 45-9.

Brockhurst M.A., Hochberg M.E., Bell T. & Buckling A. 2006. Character displacement promotes cooperation in bacterial biofilms. *Current Biology* 16:2030-2034

Brockhurst M.A., Buckling A., Poullain V. & Hochberg M.E. 2007. The impact of migration from parasite-free patches on antagonistic host-parasite coevolution. *Evolution* 61: 1238-1243

Poullain V., Gandon S., Brockhurst M.A., Buckling A.

& Hochberg M.E. 2008. The evolution of specificity in evolving and coevolving antagonistic interactions between a bacteria and its phage. *Evolution* 62: 1-11

Venail P., MacLean R.C., Bouvier T., Brockhurst M.A., Hochberg M.E. & Mouquet N. 2008. Diversity and productivity peak at intermediate dispersal rate in evolving metacommunities. *Nature* 452:210-214

Urban M.C., Leibold M.A., Amarasekare P., De Meester L. Gomulkiewicz R., Hochberg M.E., Klausmeier C.A., Loeuille N., de Mazancourt C., Norberg J., Pantel J.H., Strauss S.Y., Vellend M., Wade M.J. 2008. The evolutionary ecology of metacommunities. *Trends in Ecology and Evolution* (in press)

Michael Hochberg <mkhochb@yahoo.com>

UppsalaU EvolutionAnimalMatingSystems

PhD-position in Animal Ecology at the department of Ecology & Evolution, EBC, Uppsala:

Multimodal sexual signaling and the evolution of animal mating systems under environmental perturbation

A 4-year PhD position is available on a project investigating the evolution of signaling under various environmental regimes, and how signaling constraints may affect sexual selection and mating systems in pipefishes.

The project aims to characterize the genetic mating systems and the intensity of sexual selection in experimental populations of pipefish under various environmental treatments. A second goal of the project is to explore the effects of various sensory modalities such as visual, olfactory and auditory cues. The study organisms are the deep-snouted pipefish (*Syngnathus typhle*), the straight-nose pipefish (*Nerophis ophidion*) and the snake pipefish (*Entelurus aequoreus*). These three marine species are sex-role reversed, i.e., females compete more intensively for mating opportunities for males. Females likely rely on multiple cues to communicate with males and to compete with other females in order to increase their mating success.

An explosive growth of filamentous algae following eutrophication in our waters increases water turbidity and reduces visibility. Consequently, sexual selection on visual signals (such as pipefish ornaments and courtship behaviour) may be impaired, and females may be forced to use other signals such as chemical or auditory ones.

The project aims to investigate such alternative signals. Moreover, we and others have noted a sudden dramatic increase in population density of the snake pipefish *Entelurus aequoreus*, presumably due to a general rise in water temperatures. This makes it important to test predictions about population density and the intensity of sexual selection to assess unexpected consequences from climate change. This part of the project has specific relevance for biodiversity research.

The long-term goal of the project is to understand how ecological factors and environmental perturbation may shape mating systems and alter sexual selection and to understand the relative contributions of signaling modalities to the sexual selection process. The project will consist of field work at Kristineberg Marine Research Station, Fiskebäckskil, along with molecular analysis in Trondheim, Norway and College Station, Texas, and data analysis in the Uppsala department. The Department of Ecology and Evolution/Animal Ecology has an active and successful graduate student program. The close links with other departments within the Evolutionary Biology Centre offers excellent possibilities for interdisciplinary research in evolutionary biology. The PhD project is part of a Science Research Council project on mating systems and sexual selection in sex-role reversed pipefish, in collaboration with Norwegian and US researchers.

The successful candidate should have a degree (240 Swedish academic credits worth of courses with at least 60 academic credits) at the advanced level or the equivalent (for instance if acquired abroad) in biology. The project is suitable for someone with a strong interest in sexual selection and sexual signaling and the link between these processes and mating systems. We consider previous experience in laboratory experiments, statistical analysis of such data, field work and particularly experience in such work on fishes as an advantage. We place emphasis on personal suitability. We expect candidates to work in a group as well as independently and have good organizational skills. Applicants are obliged to participate in an organized PhD training program. Strong English communicative skills are a must. Salary follows the guidelines from Uppsala University (rising from approximately 15000-22000 SEK/month in 4 years).

How to apply: Please e-mail a statement of interest and research goals (one page max), CV, publication list, a transcript of academic courses taken and a letter of recommendation sent by a referee to anders.berglund@ebc.uu.se. Also, give names and e-mail addresses of two additional references. The application deadline is the 30 June 2008, and the project can start earliest (preferred, but negotiable) at September 1st,

2008. Informal enquiries to anders.berglund@ebc.uu.se are welcome.

Prof. Anders Berglund Animal Ecology/Department of Ecology and Evolution, Evolutionary Biology Centre, Uppsala University Norbyvägen 18D 752 36 Uppsala, Sweden e-mail: anders.berglund@ebc.uu.se tel: 46(0)184712643, mobile: 46 (0)701679030, fax: 46(0)184716484 <http://www.iee.uu.se/-zooekol/default.php?type=3Dpersonalpage&id=-3D66&lang=en> anders.berglund@ebc.uu.se anders.berglund@ebc.uu.se

UStAndrews SystemsBiology

Dear EvolDir Members,

Please share the below PhD studentship advertisement with any interested parties. Thank you, Anne Smith

A PhD student position is available in the laboratory of V Anne Smith at the University of St Andrews. Please visit <http://biology.st-andrews.ac.uk/-vannesmithlab/> for more information on the lab, and feel free to contact me at anne.smith@st-andrews.ac.uk with questions.

A pdf of the below PhD advertisement is downloadable from: <http://biology.st-andrews.ac.uk/-vannesmithlab/SULSA2008.pdf> SULSA Prize PhD Studentship in Systems Biology

Gene and protein networks related to breast cancer

Systems biology is a growing area, combining modelling and computational analysis with biological experimentation. It enables us to understand biological processes on a broad-scale like never before: for example, instead of analysing a gene or its protein in isolation, we now analyse entire networks. Such systems level understanding impacts research in multiple areas, including cancer biology.

In this studentship, you will examine gene and protein regulatory networks related to breast cancer. You will both build computational models and perform biological experiments. The project will lever two systems biology methods-dynamical systems modelling (DSM) of large cellular networks and Bayesian network (BN) inference of network structure-to produce data-driven models of gene and protein regulation networks relevant to breast cancer. DSM handles well the sparsity of data; however, networks are manually described

and uniqueness is difficult to verify. BNs complement this by recovering network structure de novo from data and predicting several alternative structures; however, they have high data demands. You will use these two complementary methods to suggest structures consistent with the data and to identify the key experiments required to discriminate between alternative solutions.

You will be based at St Andrews University and jointly supervised by Dr V Anne Smith (St Andrews), Prof John W Crawford (Abertay), and Prof David J Harrison (Edinburgh). Dr Smith will provide expertise on BNs; Prof Crawford and Prof Harrison will provide expertise on DSM and biological experimentation respectively. As a SULSA Student, you will also have the opportunity to engage in the SULSA (Scottish Universities Life Science Alliance) community across Scotland, including meetings with other SULSA Students. For more details, please contact anne.smith@st-andrews.ac.uk and/or visit: <http://biology.st-andrews.ac.uk/vannesmithlab/> Funding by SULSA plus St Andrews Biology: stipend and fees covered to EU level

– Dr V Anne Smith School of Biology Sir Harold Mitchell Building University of St Andrews St Andrews, Fife KY16 9TH United Kingdom +44 (0)1334-463368 anne.smith@st-andrews.ac.uk biology.st-andrews.ac.uk/vannesmithlab/

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UTuebingen EvolutionaryGenetics

PhD position in evolutionary genetics

Topic: Genetic architecture of natural variation in pathogen defence

The PhD project is concerned with a comprehensive genetic analysis of the natural variation in resistance against pathogens. It aims at obtaining fundamental knowledge as to the evolution of host defences in nature. The project relies on a unique model system, consisting of the nematode *Caenorhabditis elegans* as a host and various bacteria as pathogens. The results are expected to have an impact on three biological research themes that are of particular current interest: the animal innate immune system, behavioural defences, and the evolution of the genetic architecture of complex

traits.

The project is supervised by Dr. Hinrich Schulenburg (currently University Tübingen, Germany, but moving to Kiel University, Germany, in autumn 2008) and Dr. Jan Kammenga (Wageningen University, The Netherlands). It is funded by the German Science Foundation (SCHU 1415/6-1). The project will be based at the new Department for Animal Evolutionary Ecology at Kiel University, Germany, while some important experiments will be performed in Wageningen. Both labs are active in various fields of evolutionary ecology and provide an international and interactive atmosphere.

Requirements for the position: High motivation, excellent background in either evolutionary genetics or immunology, knowledge of basic molecular techniques (PCR, fragment analysis), handling of complex experimental set-up, statistics, teamwork, ideally some experience with *C. elegans* or bacteria, fluency in English.

Please email me your application as a single merged pdf-file including CV, a one-page summary of research interests, and two references from senior scientists. Deadline for applications: 9 June 2008. Start of position: Aug/Sept 2008. Women are especially encouraged to apply. Severely handicapped people will be preferentially considered in case of equivalent qualifications. For further details + questions + your application, send an email to hinrich.schulenburg@uni-tuebingen.de.

Dr. Hinrich Schulenburg

Department of Animal Evolutionary Ecology Zoological Institute University of Tuebingen Auf der Morgenstelle 28 72076 Tuebingen Germany Tel.: +49-7071-2975342 Fax: +49-7071-295634 Email: hinrich.schulenburg@uni-tuebingen.de

Hinrich Schulenburg <hinrich.schulenburg@uni-tuebingen.de>

UTurku LemmingPopulationBiology

PhD student position (alternatively Post Doc) and Masters student position available at Section of Ecology, Department of Biology, University of Turku; application deadline 30.5.2008.

TITLE: LEMMING IMPACT ON THE TUNDRA; INSTRUCTOR: LAURI OKSANEN

There has been a major lemming outbreak on the mainland tundra of northernmost Norway, especially at

higher altitudes. As shown by the graphs below, small rodent dynamics have been entirely different above and below the 500 m contour. The lemmings have now crashed but for a plant evolutionist, the fun has just begun. Last year, we made tens of rodent exclosures in different habitats, from a productive birch forest on a south facing mountain slope to unproductive heaths and snow-beds at higher altitudes. The composition of the vegetation was studied in exclosures and on open plots, using the point frequency method. Similar vegetation studies were also made on islands of IeÄjÄvri. Four islands (within red circles in the attached satellite image) have lemming exclosures but are otherwise accessible and have had gray-sided voles since 1991. Four islands have been kept lemming free. We can thus study the impacts of lemmings making comparisons both between and within islands. The islands also allow us to study processes, which require larger spatial scale, e.g. impacts of lemmings on nutrient cycling and sexual reproduction of plants.

To exploit this unique situation, I want to hire two plant evolutionist. Candidates from master's level (pro gradu, examensarbete, hovudfag) to post doc level are considered. Funding is, however, guaranteed for this year only; applications for 2009-11 are pending. The Finnish masters & PhD student's stipendium is 1313 per month (tax free); the post doc stipendium is 1700. Besides basic evolution training, the successful applicant should have mental readiness to work in harsh conditions. Previous experience of tundra/mountain nature is an advantage. A detailed project description is found on my homepage (<http://users.utu.fi/-lauoks/2008-suunnitelma>). My homepage also contains information concerning the sites. The successful candidate is expected to start working in the project from 10.07.2008

applications with CV and list of publications should be mailed to: lauoks@utu.fi by 30.5. 2008. Decision will be announced within a week

Lauri Oksanen, Professor in Plant Ecology Section of Ecology, Department of Biology University of Turku FI-20014 Turku, Finland

phone: +358-2-333 55 57

Lauri Oksanen <lauoks@utu.fi>

UWesternAustralia
MolecularDataGIS

PhD Positions: Genes, GIS, Biodiversity & Evolution

UWA: School of Plant Biology and Centre for Legumes in Mediterranean Agriculture, Faculty of Natural and Agricultural Sciences.

Murdoch University: State Agriculture Biotechnology Centre and Centre for Comparative Genomics.

These projects integrate statistical, ecogeographic, and genetic expertise at an exciting time when biology is increasingly realising the power of ecology and statistics to make sense of it. The projects centre on genetics for management of biodiversity.

Project 1: The use of GIS and molecular data for the ultimate benefit of farmers and conservation. We have used Geography Information Systems and molecular markers to maximise diversity within plant germplasm collections. The PhD would further develop this methodology (core collection concept) and apply it to a large existing collection of one of the most important pasture plants in Australia (subterranean clover).

Project 2: Detection of genomic regions under selection. We are using Geography Information Systems and molecular markers to identify genomic regions adapting to environmental change. The PhD will develop these methods in subterranean clover and red clover in collaboration with Kazusa DNA Research Institute in Japan. Visits to Japan would be likely.

Project 3: Genetic monitoring of disease resistance in clover. This program will use existing and new microsatellite DNA to compare red and subterranean clovers, and develop QTL maps. The project provides the opportunity for fieldwork at various locations in WA.

Project 4: Genetics of flowering time in clover. At UWA and Murdoch University we are interested in the genetics of flowering time. The PhD student will use data obtained from our two mapping populations of subterranean clover in existing or novel programs to map the flowering time QTLs. There would be fieldwork too.

Requirments: BSc (Hons1), Masters, or equivalent, in biostatistics, molecular biology, population genetics, or molecular ecology. Solid research and communication skills, citizen or permanent resident of Australia, however, scholarships are available to non-Australians depending upon their education and research record.

Application: Australian and non-Australian applicants must apply through the University of Western Australia or Murdoch University websites for relevant scholarships. See <http://www.scholarships.uwa.edu.au/home/postgrad> for UWA and <http://wwwcomm.murdoch.edu.au/>

handbook/study/scholarships.html for Murdoch scholarships. Before preparing an application, applicants should send CV, academic record, and details of two academic referees by email to Dr Megan Ryan (megryan@cyllene.uwa.edu.au), Dr Kioumars Ghamkhar (kioumars@cyllene.uwa.edu.au), or Professor Rudi Appels (rappels@ccg.murdoch.edu.au). For further information phone: +61-8-6488-7120.

Dr Kioumars Ghamkhar ARC Research Fellow (Plant Genomics, Diversity, and Evolution) Centre for Legumes in Mediterranean Agriculture (CLIMA) Faculty of Natural and Agricultural Sciences University of Western Australia 35 Stirling Highway Crawley 6009

Voice: +61 8 6488 7120 Fax: +61 8 6488 1140 Email: kioumars@cyllene.uwa.edu.au
kioumars@clima.uwa.edu

Kioumars Ghamkhar <kioumars@cyllene.uwa.edu.au>

UZurich Computational Evolutionary Genomics

PhD thesis in computational evolutionary genomics

A three-year Ph.D. studentship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. The Wagner lab at the University of Zurich studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Ongoing projects range from laboratory evolution experiments in yeast to human population genomics. A sample of our research can be found at <http://www.bioc.uzh.ch/wagner/>.** Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and /or fundamental organizational principles of life.

The successful candidate will have a strong background in bioinformatics and computational biology. Fluency in a major scripting language such as perl, and experience in software development is a must. Also necessary is a strong background in biology. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further

We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and can work independently. The working language in the laboratory is English. German skills, although helpful, are not essential.

Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch <mailto:jobs_aw@bioc.uzh.ch>: CV including publication list (if available), a scanned academic transcript (list of grades in university courses), a statement of research interests not exceeding two pages, and three references. Please include the word COMP in the subject line. Applications will be considered until the position has been filled.

Christiane Gujan Administrative Assistant of Prof. A. Cafilisch and Prof. A. Wagner Zurich University Institute of Biochemistry Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Tel. 0041 (0)44 635 55 49 Fax 0041 (0)44 635 68 62

Christiane Gujan <gujan@bioc.uzh.ch>

UZurich Drought Adaptation

Master project

* *

Drought adaptation in a Cape species rich genus

* *

The Cape flora is a biodiversity hotspot, with more than 10000 plant species in 90000 km². The massive speciation that generated this huge diversity was probably associated with a change in the climate from a wet, all-year rainfall system to summer droughts.

//

/Phyllica /(Rhamnaceae), one of the typical fynbos elements, is with ca. 150 species is one of the fastest radiating clades in the Cape flora. The genus has very distinctive leaves, these vary from broad in species found in wetter environments, to hard, narrow and revolute in species more associated with drought. The leaves may reflect a set of drought adaptations.

We will use GIS (geographic information system) to model the drought to which each species is associated. We will also investigate the structure and function of the leaves to locate specific drought adaptations. We will use these to test the hypothesis that the leaves are

indeed drought adapted, and that they determine the niches which the species can occupy.

We will do extensive fieldwork in the Cape region during the southern spring of 2008 (September to December). Ecological data on the growth form, leaves insertion and pubescence (leaves and stem) will be recorded, together with habitat data. The work will be based at the University of Cape Town.

Master project under the supervision of Prof. Peter Linder, in collaboration with Serge Haemmerli, PhD student

If you are interested please contact Serge Haemmerli:

044 634 23 89

serge.haemmerli@systbot.uzh.ch

<mailto:serge.haemmerli@systbot.uzh.ch>

Or come to my office O27A at the Institute for Systematic Botany,

Zollikerstrasse 107, 8008 Z¹rich

– Serge Haemmerli PhD student Institute for Systematic Botany University of Z¹rich Zollikerstrasse 107 CH-8008 Z¹rich Switzerland Ph: +41 (0)44 634 8416 serge.haemmerli@sysbot.uzh.ch <http://www.systbot.unizh.ch/institut/personen/-person.php?l=d&idc> Serge Haemmerli <serge.haemmerli@systbot.uzh.ch>

UZurich ExperimentalEvolution

PhD thesis in experimental evolution

A three-year Ph.D. studentship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. The Wagner lab at the University of Zurich studies biological evolution on all levels of organization, from genes, genomes, and genetic networks

to whole organisms. Ongoing projects range from laboratory evolution experiments in yeast to human population genomics. A sample of our research can be found at <http://www.bioc.uzh.ch/wagner/>.** Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and /or fundamental organizational principles of life.

A successful candidate will have substantial research experience with microbiological and molecular biological techniques, acquired in research projects with an evolutionary orientation. Experience in performing microarray experiments will be a plus. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further

We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and can work independently. The working language in the laboratory is English. German skills, although helpful, are not essential.

Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch <mailto:jobs_aw@bioc.uzh.ch>: CV including publication list (if available), a scanned academic transcript (list of grades in university courses), a statement of research interests not exceeding two pages, and three references. Please include the word EXPEVOL in the subject line. Applications will be considered until the position has been filled.

–

Christiane Gujan Administrative Assistant of Prof. A. Cafilisch and Prof. A. Wagner Zurich University Institute of Biochemistry Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Tel. 0041 (0)44 635 55 49 Fax 0041 (0)44 635 68 62

Christiane Gujan <gujan@bioc.uzh.ch>

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Columbia SC LabTech

A full-time lab tech (Research Specialist I) position is available in a freshwater ecological genetics lab in Columbia, SC. Primary duties include maintenance of plankton cultures (mainly *Daphnia*), work with live organisms, general genetics techniques and lab management. Minimum Qualifications: Bachelor's degree in a related field, or high school diploma and four (4) years related research experience. The successful candidate must have a driver's license and driving record that qualifies him/her to drive university vehicles and be able to lift 20 kg. The successful candidate will be detail-oriented and have excellent organizational and time-management skills, good communication skills, the ability to work independently as well as part of a team, and an understanding of scientific operations and record-keeping. Preference will be given to candidates with the following characteristics: prior experience working in a live-animal, aquatics or genetics lab, working knowledge of freshwater biology, working knowledge of basic genetics techniques, problem-solving skills, ability to supervise undergraduate assistants, and the initiative to become a resource for other members of the lab.

The position includes health insurance, leave and retirement benefits. The minimum starting salary is \$24,635.

To apply, go to <http://uscjobs.sc.edu> and search for Requisition #000419.

Current research activities in the lab can be found at <http://www.biol.sc.edu/faculty/~dudycha>. Inquiries, cover letters, resumes and reference contact informa-

tion should be sent via email to Dr. Jeff Dudycha at dudycha@biol.sc.edu. Individuals graduating this year must send this information to ensure that their applications receive consideration.

dudycha@biol.sc.edu dudycha@biol.sc.edu

DukeU LabManager YeastEvolutionaryGenetics

Laboratory Technician Yeast Evolutionary Genetics/Genomics Duke University

Description

The Magwene lab (Department of Biology, Duke University) seeks applicants for a full time laboratory technician/laboratory manager position. The successful applicant will have a strong background in molecular and/or microbiology, good troubleshooting and organizational skills, and the ability to work independently.

BA/BS required. Salary commensurate with experience.

Contact

To apply for this position please email a cover letter, CV/resume and the names and contact information for three references to: paul.magwene@duke.edu

For more information see: <http://biology.duke.edu/-magwene/lab/> Paul Magwene Assistant Professor Department of Biology Duke University pmmagic@gmail.com

EmoryU ResTech ComparativeGenomics

POSITION AVAILABLE:

Lead Research Specialist Department of Human Genetics Emory University Atlanta, GA

The Thomas and Young Laboratories (see http://www.genetics.emory.edu/labs/thomas/thomas_lab_index.php and <http://www.research.yerkes.emory.edu/Young/index.htm>)

whose research programs are focused in the fields of comparative genetics and genomics are seeking a 'lead research specialist'. Primary experimental responsibilities will include development of genotyping assays, subsequent genotyping via PCR, DNA sequencing, genomic library hybridizations and bacterial artificial chromosome (BAC) fingerprinting. In addition to these specific projects, this position will also include performing other general molecular/cellular biology techniques such as DNA/RNA extractions and RT-PCR, as well as the use of a suite of computer programs to be used in the development of a vole genetic map and comparative physical maps. Minimum qualifications include a bachelor's degree in a related field and two years of research experience, or equivalent combination of experience, education, and training. Applicants are expected to be responsible and dedicated individuals with strong organizational skills, the ability to work independently and with others, and have significant experience working in a research laboratory setting. Demonstrated experience with large-scale genotyping projects or with screening genomic libraries is preferred, but not required.

If interested, submit letter of interest, CV and contact information for three references via email to Dr. James Thomas (jthomas@genetics.emory.edu). For more details please visit: https://sjobs.brassring.com/1033/-ASP/TG/cim_home.asp?partnerid=25066&siteid=5043 and refer to job requisition ID: 5529BR.

James W. Thomas, PhD Assistant Professor Department of Human Genetics Emory University School of Medicine 615 Michael St., Suite 301 Atlanta, GA 30322 Tel (404)727-9751 Fax (404)727-3949 email:jthomas@genetics.emory.edu

lamcgraw@gmail.com

ImperialCollegeLondon WildlifeEpidemiology

Short Research Project in Wildlife Epidemiology

Casual summer research assistant to investigate the epidemiology of Louping Ill Based at Imperial College London and the University of Aberdeen, United Kingdom Temporal and Spatial Dynamics of a Vector-borne Wildlife Disease System

Duration: 4 months (on a casual basis) Start date: August / September 2008 (flexible) Salary: £1851 per month (approx.)

We are seeking a temporary graduate or higher level researcher with good quantitative skills to join a 4 month project starting May 2008 to investigate the epidemiology of Louping Ill (LI), a tick-borne wildlife disease affecting northern areas of the United Kingdom. The LI system involves a variety of hosts, including red grouse, mountain hares, sheep and red deer, and is of economic importance to sheep and grouse moor management. This project aims to develop models of the temporal and spatial dynamics of LI transmission between tick vectors and the hosts of the disease, exploring the impact of seasonality and host density on LI epidemiology. The project would be suitable as the placement project for an appropriate Masters course.

The research assistant will have an interest in ecology and epidemiology along with programming skills (for example in C++, Mathematica or Matlab) and ability to analyse differential equations. The researcher will be based primarily at the Centre for Population Biology, Silwood Park Campus, Imperial College London, and will have opportunities to visit the University of Aberdeen.

Applications (including CV and cover letter) or enquiries should be sent to Dr Penelope Hancock (p.hancock@imperial.ac.uk) or Dr Steve Palmer (s.palmer@abdn.ac.uk).

Websites: <http://www3.imperial.ac.uk/cpb>
<http://www.aces.ac.uk/projects/> <http://www3.imperial.ac.uk/people/p.hancock> <http://www.abdn.ac.uk/biologicalsci/staff/details.php?id=3Ds.palmer&fit>

Closing date: 13th June 2008

p.hancock@imperial.ac.uk p.hancock@imperial.ac.uk

**LouisianaStateU
EvolutionaryGenetics**

*RESEARCH ASSOCIATE 2 Department of Biological Sciences

Required Qualifications: (RA2) Bachelor's degree or equivalent in Biology or related field. Additional Qualifications Desired: (RA2) Experience gathering genetic data, particularly DNA sequences and/or microsatellites; additional familiarity with and/or interest in evolutionary genetics and comparative phylogeography. Responsibilities: (RA2) conducts comparative phylogeographic research in a plant-insect community, including molecular lab work and some fieldwork. An offer of employment is contingent on a satisfactory pre-employment background check. Application deadline is May 16, 2008 or until a candidate is selected. Send statement of interest, CV (including e-mail address), and contact information for two professional references to:

Dr. Bryan Carstens Department of Biological Sciences
Louisiana State University Ref: #012809 Baton Rouge,
LA 70803

Phone: (225) 578-0960 E-mail: carstens@lsu.edu

LSU IS AN EQUAL OPPORTUNITY/EQUAL ACCESS EMPLOYER

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fax (225) 578-2597

carstens@lsu.edu carstens@lsu.edu

**NatlU Ireland
ComputationalBiologySupport**

Hi folks,

There is a position of computational biology support person in my group. You will be required to manage a linux cluster of some hundreds of processors and also to interact with people interested in computational biology issues, mainly in the area of molecular evolution.

The position is of three-year duration, with the possibility of further extension. The remuneration package is worth approximately 51,000 Euro (79,500 USD; 40,600 GBP) per annum.

My group is at the National University of Ireland Maynooth. This is a small university approximately 25 Km west of Dublin city

More information can be found at: <http://-bioinf.nuim.ie/> Best,

James

— Dr. James O. McInerney, Bioinformatics Laboratory, Department of Biology, National University of Ireland, Maynooth, Co. Kildare, Ireland. P: +353 1 708 3860 F: +353 1 708 3845 E: james.o.mcinerney@nuim.ie — Website — <http://bioinf.nuim.ie/>

James McInerney <james.o.mcinerney@nuim.ie>

**NEON Boulder CO
EvolutionaryBiol**

PHD in Animal Ecology/Infectious Disease

The National Ecological Observatory Network (NEON, Inc.), a nonprofit science corporation dedicated to understanding how changes in climate, land use and invasive species impact ecology, has an immediate opening for a staff scientist in Boulder, Colorado. We are looking for individuals who are problem solvers who can successfully apply experience, judgment, and creativity to both short- and long-term challenges.

Responsibilities:

- Develop and oversee sampling designs to track abundance, diversity, and population dynamics of insects, small mammals, and birds - Develop and oversee sampling designs to monitor the presence of animal-borne diseases - Develop QA/QC protocols for field sampling and data processing - Develop the scientific rationale for scientific measurements and methods

Minimum Qualifications in Education/Experience:

- PhD in ecology, evolution, or related field - 5 years research experience in animal and/or disease ecology, specifically related to insects, small mammals, or birds
- Extensive field experience - Experience working in a collaborative scientific enterprise

Specialized Skills:

- Scientific writing and review - Proficiency in analyses that correlate biological data with abiotic variables and ability to perform such analyses within a geospatial framework - Experience in of knowledge of a start-up environments is beneficial, - Ability to work independently, but as part of an active Science team - Strong communication and interpersonal skills - Undertake responsibilities beyond those associated with individual research projects

Physical Requirements:

- The candidate may be exposed to conditions in the field, and therefore must be able to traverse uneven ground such as dirt banks, stream beds, and shallow ponds carrying equipment and materials up to 40 lbs.

Compensation and Benefits:

- Salary negotiable. Some travel will be required and salary is commensurate with experience. This is a full-time, salaried position. Benefits include health care, paid vacation, and retirement plan.**

TO APPLY:

Please send your resumes and inquiries to Careers@NeonInc.org or call 561-542-6343 and ask for Scott.

THIS COMPANY is an Equal Opportunity Employer. Women, Minorities, Veterans and Disabled Persons are encouraged to apply. Send cover letter, resume, salary history, and salary requirements to Careers@NeonInc.org

- Rebecca Hufft Kao, PhD Staff Scientist National Ecological Observatory Network (NEON) 3223 Arapahoe Avenue, Ste. 210 Boulder, CO 80303 720-746-4841 bkao@neoninc.org www.neoninc.org bkao@neoninc.org

NHM London BioinformaticsTech

Bioinformatics Technician Natural History Museum London, UK Department of Entomology 6 Month Temporary Position £22,167 plus benefits Closing Date: 16th June 2008

The Natural History Museum is one of the world's leading museums, internationally recognised for its dual role as a centre of excellence in scientific research and as a leading exponent in the presentation of natural history to the general public through exhibitions, public programmes and the web.

The post holder will improve the bioinformatics infrastructure and support molecular systematics research staff and PhD students. A Masters degree (MSc/MRes) in Bioinformatics or comparable qualification is required. Familiarity with standard software used in DNA sequencing and phylogenetics, ability to script in Perl/Python, and good knowledge of the Linux operating system are expected.

This post is available for six months initially, to start as early as possible.

Please email Prof. Alfried Vogler (A.Vogler@nhm.ac.uk) at the Natural History Museum for informal enquiries.

For further information, including a full job description, and to apply online please visit the Natural History Museum website at www.nhm.ac.uk/jobs
A.Vogler@nhm.ac.uk A.Vogler@nhm.ac.uk

Queensland StatisticalGenetics

QIMR reference number: 49/08 Closing date for receipt of applications: 5:00pm Friday 23 May 2008 .

The Queensland Institute of Medical Research is one of the largest medical research institutes in the southern hemisphere, with programs in areas such as cellular and molecular sciences, epidemiology and population health, human genetics, cancer biology, biotechnology, infectious diseases and vaccine development.

Applications are invited for a Research Officer to join

the Queensland Statistical Genetics Laboratory at the Queensland Institute of Medical Research. The position will develop and implement methods for the analysis of high-throughput genetic and genomic data in large samples. Applicants are required to have a PhD in quantitative, population, statistical or human genetics, or a related field. Postdoctoral experience in the analysis of genetic data and/or experience with computer intensive statistical method (e.g. MCMC) are highly desirable. The successful applicant will have (co)authored papers in journals with a good impact factor.

Salary range is \$60,412 to \$64,848 per annum commensurate with qualifications and experience. Attractive salary packaging and superannuation options also apply. This is a full-time appointment until December 2010 with the possibility of review subject to funding availability.

Further Information including a position description and selection criteria is available from www.qimr.edu.au/employ or Professor Peter Visscher on (07) 3362 0166 or Peter.Visccher@qimr.edu.au <mailto:Peter.Visccher@qimr.edu.au>

Applications should address the selection criteria and include a curriculum vitae, proof of qualifications and the names and contact details of three professional referees.

Please quote reference number 49/08 and send applications to: vacancies@qimr.edu.au <mailto:vacancies@qimr.edu.au> or:

The Human Resources Officer The Queensland Institute of Medical Research PO Royal Brisbane Hospital QLD 4029

E-mail: vacancies@qimr.edu.au <mailto:vacancies@qimr.edu.au>

Peter M. Visscher Queensland Statistical Genetics Queensland Institute of Medical Research 300 Herston Road Herston, Queensland 4006, Australia tel. +61 7 3362 0166 fax. +61 7 3362 0101 <http://genepi.qimr.edu.au> < <http://genepi.qimr.edu.au/> > peter.visscher@qimr.edu.au

Peter.Visscher@qimr.edu.au

RBG Edinburgh PlantBiodiversity

Plant Biodiversity Scientist; Royal Botanic Garden Edinburgh, UK

Salary £22,032 to £28,540

The Royal Botanic Garden Edinburgh is seeking applications for a permanent Plant Biodiversity Scientist. The post holder will be expected to develop a research programme that contributes towards understanding responses of plant biodiversity to environmental changes such as habitat loss and fragmentation, climate change, and land management.

The primary focus will be on vascular plants in European and Eurasian temperate systems, with the expectation that the post-holder's research will contribute towards biodiversity conservation in the UK. There will, however, be opportunities to develop projects involving study systems elsewhere and interactions with the broad range of international research projects at RBGE will be encouraged. The post would be particularly suited to an early career researcher who shows outstanding potential. You will have a strong publication record, be able to develop research projects independently, have the ability to collaborate with other scientists at RBGE and have good communication skills. Applicants should possess a PhD and preferably some post-doctoral experience. Details on the scientific remit and research of the Royal Botanic Garden Edinburgh can be found at www.rbge.org.uk/science/ . Informal enquiries about the post can be made to Dr Pete Hollingsworth (p.hollingsworth@rbge.org.uk). The post attracts generous holiday entitlement and Civil Service Pension benefits. The job description and person specification can either be obtained from Irene Morrice (telephone +44 (0) 131 248 2814 or email i.morrice@rbge.org.uk) or can be downloaded from <http://www.rbge.org.uk/-about-us/vacancies.=A0Applications> by CV, including a covering lettershould be received no later than Friday, 6 June 2008.

– The Royal Botanic Garden Edinburgh is a Charity registered in Scotland (No SC007983)

p.hollingsworth@rbge.org.uk

SanAntonio Texas MalariaResistanceEvolution

RESEARCH ASSISTANT: MALARIA PARASITE GENETICS

We are searching for an enthusiastic research assistant to work on drug resistance evolution in malaria par-

asites. We are using a number of approaches to locate genes underlying drug resistance in the parasite genome and to understand the processes by which parasites adapt to drug treatment. Our current focus is on genome-wide association methods for genetic mapping, and copy number variation. The successful candidate will be responsible for culturing malaria parasites in the laboratory, measuring drug resistance, and conducting molecular assays (sequencing, SNP genotyping, microsatellites).

Requirements: Bachelors or Master's degree in a biological science or related field. Experience with cell culture and/or molecular biology methodology essential. US based applicants only.

Job description and application details are posted at http://www.sfbr.org/pages/-employment_posting_detail.php?id=192 Tim JC Anderson Southwest Foundation for Biomedical Research PO Box 760549 San Antonio Tx 78245-0543

Tel: (210) 258 9596 Fax: (210) 670 3344 email: tanderso@sfbrgenetics.org

tanderso@sfbrgenetics.org

Seattle FishPopGeneticist

Research Geneticist / Statistician

The NOAA-Fisheries Northwest Fisheries Science Center in Seattle, WA, is currently seeking to fill a full-time position as either a Research Geneticist or a Mathematical Statistician at the GS-12 level. The position is initially for two years, with a potential extension to four years.

The Conservation Biology Division is seeking a broadly trained statistical modeler. The position will be expected collaborate with several programs within the division on a variety of topics and species, including both fish and marine mammals. Examples of potential projects include: developing models for analysis of molecular genetic data for stock discrimination and stock-of-origin assignment, analysis of local adaptation and natural selection inferred from molecular markers, estimation of reproductive success and selection gradients; assess and design sampling approaches to the collection of population abundance, productivity, and distribution data, with particular attention to spatial co-variation resulting from physical and biological habitat conditions; assisting with marine mammal stock as-

sessments and risk analysis. The incumbent will work in a broadly interdisciplinary environment with ecologists, toxicologists, geneticists and others. A very strong statistical background and the ability to collaborate with experimentalists on practical management issues are essential. See <http://www.nwfsc.noaa.gov/-research/divisions/cbd/index.cfm> for more information on the NWFSC's Conservation Biology Division.

Application for this position is on-line through USAJOBS (www.usajobs.opm.gov). Announcement Number: NMF-NWC-2008-0029. Open period: May 15, 2008 to June 16, 2008.

Mike.Ford@noaa.gov

Smithsonian LabTech EvolutionaryGenetics

Genetics Laboratory Technician Center for Conservation and Evolutionary Genetics Smithsonian Institution

We are recruiting a technician to participate in a variety of projects in conservation and evolutionary genetics. The position will involve PCR and DNA sequencing, analysis of microsatellites, and other molecular genetic methods as required. The position is available initially for one year and will begin in June 2008. Remuneration will be in the range of \$24-30,000, depending on experience. Minimum qualification is a bachelor's degree in biology or similar field, or an equivalent combination of education or experience. Demonstrated laboratory experience is required.

To apply, email (1) a brief letter of application detailing your experience in evolutionary and molecular genetics, (2) a current curriculum vitae or resume, and (3) names, addresses and phone numbers of at least three references to Dr. Robert Fleischer (fleischerr@si.edu). Deadline for applications is 23 May 2008. Please contact Dr. Fleischer if you have any questions concerning the position.

Center for Conservation and Evolutionary Genetics National Zoological Park National Museum of Natural History Smithsonian Institution PO BOX 37012 MRC 5503 Washington, DC 20013-7012 USA

"Fleischer, Robert" <fleischerr@si.edu>

UAlaska MuseumDirector

The quickfind link is:

www.uakjobs.com/applicants/Central?quickFindb936

The initial date for reviewing the applications is Monday, July 7.

The University of Alaska Fairbanks is searching for a Director of the University of Alaska Museum of the North. The Museum, an AAM-accredited museum of natural and cultural history, is a center for the collection and preservation of objects from and related to Alaska and for research and education pertaining to the North. The Museum is the only University natural history museum in Alaska, and it is unique in maintaining research collections in: Life Sciences (botany, entomology, ichthyology, mammalogy, and ornithology), Earth Sciences (geology and paleontology), Anthropology (archeology and ethnology), Fine Arts, History, and the Alaska Center for Documentary Film. There are over 2 million objects and specimens in the Museum, including collections from the circumpolar north and Pacific rim. The Museum also serves as the official state repository for scientific specimens collected on State, Native, and Federal lands.

The Museum's collections provide key information critical to questions of past and present biodiversity and include key indicators of local and global environmental and cultural change and sustainability. Through its collections-based research, teaching, and public learning programs, the museum shares its collections and knowledge with local, national, and international audiences of all ages and backgrounds. The Museum staff and collections comprise an integral part of instruction at the University. The collections support undergraduate and graduate courses and provide material for undergraduate projects, graduate theses, and professional research projects in many disciplines and for interdisciplinary studies. Objects in the collections are also used for traveling and in-house exhibitions. The permanent exhibit galleries and the changing exhibits are viewed by over 100,000 visitors annually. The Museum Store is a popular component of the Museum with visitors and the community. Museum public programs include the docent and volunteer programs and special lectures and events. The Museum enjoys widespread support from the community.

Knowledge, skills and abilities required for this posi-

tion. 1. An advanced degree in a discipline appropriate to the Museum and appropriate for tenure in a UAF academic department. 2. A substantial record of research, publication, and education in a field of natural and/or cultural history. 3. Experience in museum administration, with preference given to experience in a university-affiliated museum and familiarity with the development of research collections in multiple disciplines. 4. A track record of excellent management skills, with evidence of successful leadership in program building, personnel operations, fundraising, marketing, and public relations. Typical education or training required for this position (including licenses). An advanced degree in a discipline appropriate to the Museum and appropriate for tenure in a UAF academic department.

Job Duties 1 Record Duty: The Director of the University of Alaska Museum of the North will be responsible for its leadership and will have primary responsibility and authority for organizing, managing, and facilitating multidisciplinary research; fundraising; budget planning and management; and personnel and public relations. The Director is spokesperson and advocate for the Museum within and outside the University.

Length of time and type of experience required for this position. A substantial record of accomplishment in research, publication, and instruction in a field of natural and/or cultural history; experience in progressively responsible museum administration; and a track record of excellent management skills with evidence of effective leadership. Preferred knowledge, skills or abilities for this position. The successful candidate will show evidence of commitment to developing the Museum's stature and its prominent, independent role within the University of Alaska. Finalists will demonstrate an understanding and support of the Museum's tripartite mission of research, teaching, and public service and will show evidence of interest and capability to manage programs with strong interdisciplinary and international components.

Special Instructions to Applicants Applicants must attach a Curriculum Vitae, letter of interest in the position, vision statement and the names and contact information of five (5) references.

If you have difficulty applying to this position please contact UAF Human Resources at 907-474-7700 for assistance. Special Conditions of Employment Information Equal Opportunity/Affirmative Action: The University of Alaska is an equal employment opportunity/affirmative action employer

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>

UAlberta ResTech PopulationGenomics

Research Technician - Population Genomics

Department of Biological Sciences, University of Alberta

A position is available for a research technician in population genomics at the Department of Biological Sciences, University of Alberta. For full details and online application procedures, please view the University of Alberta careers website at <http://www.careers.ualberta.ca/>. This position is listed under Support Staff Positions / Technical (Science and Medicine).

Competition No. -

S10035256

Posting Date -

May 22, 2008

Closing Date -

June 6, 2008

Position Type -

Full Time - Grant Funded

Salary range -

\$3,007.55 to \$3,746.17 per month

Grade -

06

Hours -

35 per wk

This position offers a comprehensive benefits program. This position ends December 31, 2009.

Duties

* Identifies samples to be analysed from the laboratory database * Ensures accurate record keeping and sampling integrity for samples at all states of preparation and analysis * Prepares genomic DNA extractions from samples, and readies extracts for genotyping analysis * Performs microsatellite PCR and fragment detection

using standard equipment, software, and procedures * Provides assistance to project staff and visiting scientists in laboratory techniques * Carries out standard experiments mainly using molecular biology techniques * Conducts day-to-day laboratory preparation and maintenance tasks * Assists with periodic training on standard genetic techniques

Qualifications

* Laboratory Technology Diploma or Certificate required * Experience with genomic DNA extraction, PCR, and DNA capillary electrophoresis * Demonstrated ability to track a large number of samples through multi-step procedures required * Familiarity with fragment analysis software * Experience with aseptic technique * Experience with plants, insects or fungi an asset * Demonstrated ability with respect to organization, attentiveness to detail, and ability to work quickly and accurately * Demonstrated ability to carry out standard laboratory arithmetic * Strong oral and written communication skills * Computer proficiency using MS Office applications; experience with databases an asset

How to Apply

Apply Online

Please visit the University of Alberta careers website for online application procedures. Note: Online applications are accepted until midnight MST of the closing date.

Applications may be forwarded to:

Mail -

Matthew Bryman - Department of Biological Sciences
CW405 Biological Sciences Building University of Alberta
Edmonton, Alberta T6G 2E9

Fax -

(780) 492-9234

Email -

mbryman@ualberta.ca

Matt Bryman <mbryman@ualberta.ca>

UColorado ComparativeGenomics

Comparative Genomics Laboratory Technician Position
U. Colorado School of Medicine

The Consortium for Comparative Genomics at the University of Colorado School of Medicine has an opening for a master laboratory technician in its high-throughput genomics laboratory. This is a full-time position funded by the Consortium for Comparative Genomics and the UC Cancer Center. The successful candidate will be expected to perform major and minor facets of molecular biology laboratory work required for running and maintaining the Roche-454 FLX ultra-high throughput genome sequencer operated by the Consortium. The position is an excellent opportunity for interested persons to become heavily involved with diverse cutting-edge comparative genomics research (medical and otherwise). The position will be supervised by David Pollock and Todd Castoe, and the postdoc would also be joining the evolutionary genomics research group led by David Pollock (HYPERLINK "<http://www.evolutinoarygenomics.com>" www.evolutinoarygenomics.com).

The position would be located at the new UC-Health Sciences Center Anschutz Medical Campus in Aurora, Colorado, on the outskirts of Denver. (<http://www.uchsc.edu/>)

Specific Duties: The duties of the position holder will center around performing all technical laboratory aspects required to run diverse samples on a 454-FLX high-throughput automated genome sequencer housed in the School of Medicine. Specifically, the job involves assessing sample quality and quantity from users, communicating with users and other directors regarding sample diagnosis and project design, carrying out molecular biology laboratory work including PCR, oligo ligation, and other misc. steps within the 454-FLX sample preparation protocol, and maintaining an organized accounting of reagent use and costs. This position requires close interaction with various project directors as well as smooth integration with other laboratory work housed in the UC Cancer Center Core facility. There is also broad future potential, if desired, for the position to expand into intellectual design and implementation of experiments, and also into specific collaborative work with participating scientists.

Requirements: A master¹s degree in a relevant field or equivalent experience is preferred (e.g. bachelor¹s degree plus two or more years work experience). The candidate must be a highly motivated, self-organizing and independent worker with the ability to also collaborate in a team setting. Computer literacy is required, and additional computer experience with Unix, and/or programming experience is a plus. Any genomics, DNA sequencing, or statistical experience is also a strong plus, but not absolutely required. Deep understanding of molecular biology is preferred.

Salary: The salary range for this position is between \$35,000 and \$65,000 per annum, depending on qualifications.

To apply: Please forward a cover letter, CV/Resume and names of three references to Kathy R. Thomas, Administrative Coordinator, Computational BioScience Program, PO Box 6511, Mailstop 8303, Aurora, CO 80045-0511, or email to HYPERLINK "<mailto:Kathy.R.Thomas@uchsc.edu>" Kathy.R.Thomas@uchsc.edu

Review of applicants will begin immediately and continue until the position is filled. Multiple openings may be available.

The University of Colorado is committed to diversity and equality in education and employment.

Todd.Castoe@UCHSC.edu Todd.Castoe@UCHSC.edu

UGeorgia ResTech PlantEvolution

RESEARCH TECHNICIAN POSITION: PLANT EVOLUTIONARY ECOLOGY UNIVERSITY OF GEORGIA

A full-time research technician position is available starting immediately in the laboratory of Shu-Mei Chang in the Department of Plant Biology at the University of Georgia. The general research interests of lab are to understand how evolutionary and ecological factors may influence the mating systems in flowering plants. Current projects include conservation genetics of endangered species, evolution of separate sexes in flowering plants and functional analyses of male traits in hermaphroditic plants. Field and greenhouse experiments are a big component of these projects so it is crucial that the candidate can work outdoor and in the greenhouse in conditions that can be demanding, including working in hot GA summer weather.

Responsibilities also include bench work in the laboratory, such as DNA extraction, PCR, allozymes and microsatellite DNA genotyping, and measuring morphological and life history traits of plants. Candidates are expected to have some basic knowledge on laboratory techniques such as PCR and DNA extraction. Other duties include: overseeing day-to-day management of the laboratory including the purchasing of supplies and equipment; insuring proper operation and maintenance of laboratory equipment; entering and managing electronic data files; working with undergraduate research

assistants; maintaining greenhouse plants, and training of student workers. The position is ideal for a highly motivated person interested in gaining field and laboratory skills prior to starting graduate school or other work in the life sciences.

Requirements for the position are a bachelor's degree in biology, plant biology, ecology, evolution, or a related field as well as basic computer skills. The ideal candidate has a strong work ethic, positive attitude, excellent communication and organization skills, and the desire to acquire new field and laboratory research skills. Research experience in plants and an enthusiasm for field work will be advantageous.

To apply, please send a CV, a letter describing research background and interests and names and contact information of two references to: Shu-Mei Chang, chang@plantbio.uga.edu. Applications will be reviewed until position is filled. Salary is commensurate with experience and includes benefits.

chang@plantbio.uga.edu chang@plantbio.uga.edu

UHawaiiHilo EvolutionaryBiol

Assistant Professor of Biology: Position No. 86432T, University of Hawaii at Hilo, College of Arts & Sciences, temporary, nine-month appointment to begin approximately August 2008; pending position clearance and funding, with possibility of reappointments.

Duties: Teach undergraduate and graduate courses in conservation biology, evolution, ecology, biostatistics or introductory biology. Advise students, engage in scholarly activity, participate in University and community service.

Minimum Qualifications: Ph.D. from an accredited college or university in a biological science discipline appropriate to the position, demonstrated expertise in conservation biology, ecology and/or evolution. Desirable Qualifications: Teaching and research experience at the college or university level, familiarity with Hawaiian ecosystems and conservation issues. Salary: Competitive. To Apply: A complete application must include: cover letter explaining how the minimum and desirable qualifications are met, vitae, the names and addresses, email and telephone numbers of three (3) current professional references, transcript(s) showing degrees and course work appropriate to the position (copies are acceptable, however official transcripts will

be required prior to employment). All requested documents/information become the property of the University. Submit to: Dr. Elizabeth Stacy, Biology Department, College of Arts & Sciences, University of Hawaii at Hilo, 200 W. Kwili St., Hilo, HI 96720-4091 or to estacy@hawaii.edu (email applications preferred).

Inquires: Dr. Elizabeth Stacy, ph. 808-933-3153, email estacy@hawaii.edu Deadline: Continuous Recruitment. First review of applications will begin June 15, 2008 and continue until the position is filled. University of Hawaii at Hilo is an EEO/AA Employer D/M/V/W.

Elizabeth Stacy Assistant Professor Department of Biology University of Hawaii 200 West Kawili Street Hilo, Hawaii 96720 Phone: 808-933-3153 Fax: 808-974-7693 Email: estacy@hawaii.edu

estacy@hawaii.edu estacy@hawaii.edu

UIIdaho ResTech EvolutionaryGenomics

Scientific Aide / Laboratory Technician Genomics of Amphibian Declines University of Idaho

Amphibians around the world are being threatened by an emerging pathogen, the chytrid fungus *Batrachochytrium dendrobatidis* (Bd). A scientific aide / laboratory technician position is available in the Rosenblum lab, where functional and comparative genomics approaches are used to understand the mechanistic relationship between frogs and Bd. Specifically we are interested in understanding the impact of Bd on mountain-yellow-legged frogs, an endangered species in the Sierra Nevada Mountains.

The Scientific Aide will assist the principal investigator and laboratory personnel in performing molecular research in host-pathogen genomics, specifically using whole-genome sequencing and gene expression techniques to better understand the genetic basis of chytrid pathogenicity and frog susceptibility. In addition he/she will provide technical and administrative support for running the laboratory.

Minimum qualifications include a bachelor's degree in related field or equivalent combination of education and/or experience. Demonstrated laboratory experience is also necessary. Additional desirable qualifications include a master's degree and experience in molecular biology. Salary will be \$28,000 - \$32,000 DOE.

Details about the job responsibilities and the necessary qualifications can be found at www.hr.uidaho.edu (announcement # 17536094533). Applications consisting of a cover letter, CV, and three letters of recommendation must be submitted online at www.hr.uidaho.edu no later than June 2nd, 2008.

Please direct inquiries directly to Erica Rosenblum at rosenblum@uidaho.edu <http://www.webpages.uidaho.edu/~rosenblum/> Erica Bree Rosenblum <rosenblum@berkeley.edu>

UIowa ManagerComparativeGenomics

POSITION AVAILABLE:

Research Scientist (rank open) Manager, Roy J. Carver Center for Comparative Genomics

The University of Iowa, Department of Biology & Roy J. Carver Center for Comparative Genomics

The University of Iowa Department of Biology invites applications for an Assistant Research Scientist, Associate Research Scientist or a Research Scientist, who will manage all laboratory functions of the Roy J. Carver Center for Comparative Genomics (“CCG”; <http://cgg.biology.uiowa.edu/>) in addition to conducting externally-funded research. The ideal candidate will develop and implement new research methods and protocols to advance the mission of the CCG and Department of Biology, with a focus on comparative and functional genomic research. In collaboration with the CCG Director, the candidate will also manage the CCG budget and identify opportunities to secure long-term financial stability for the CCG. Additional responsibilities include maintaining and developing CCG resources, providing training and research assistance to CCG members in genomics methods, preparing seminars, and supervising CCG laboratory personnel. The candidate is expected to develop an active, externally-funded research program, independently, or in collaboration with CCG faculty. Significant laboratory space, resources and equipment are available to the Manager for conducting research. Salary and rank will be commensurate with experience and qualifications.

Education Required: A person in this classification has the academic knowledge of a discipline that is generally associated with a Doctoral degree or equivalent professional degree, i.e., Ph.D, M.D., D.D.S or D.V.M.

Experience Required: PLEASE NOTE: THE DEPARTMENT WILL HIRE ONE POSITION, ASSISTANT RESEARCH SCIENTIST, ASSOCIATE RESEARCH SCIENTIST, OR RESEARCH SCIENTIST.

Required Qualifications for all ranks: PhD degree (or equivalent) in biology or related field with experience in molecular genetics/genomics techniques. Excellent written and verbal communications skills. Demonstrated job-related experience with and/or commitment to diversity in the work/academic environment is required.

To be eligible for the Assistant Research Scientist position, candidate will have demonstrated the ability to plan and execute a research study through some progressively responsible independent research work, select research problems and analyze results obtained.

To be eligible for the Associate Research Scientist position, candidate must be able to perform research involving new theories and /or technologies and must have contributed to a number of peer-reviewed publications that have had a major impact on advancing the field or discipline.

To be eligible for the Research Scientist position, candidate must have a significant record of research productivity as evidenced by peer-reviewed publications. Must demonstrate the ability to manage all or part of a research project.

Experience Desirable: Desirable Qualifications for Assistant Research Scientist position: Ph.D. in genetics/molecular evolution/ population genetics/ statistical genetics/ bioinformatics. Experience in bioinformatics (including data analysis/software design/ programming/ implementation; UNIX system administration). Experience in DNA sequencing, real-time PCR, microarray methods and protocol development. Some experience in grant writing is desirable.

Desirable Qualifications for Associate Research Scientist position: Ph.D. in genetics/molecular evolution/ population genetics/ statistical genetics/ bioinformatics. Experience in bioinformatics (including data analysis/software design/ programming/ implementation; UNIX system administration). Experience in DNA sequencing, real-time PCR, microarray methods and protocol development. Prior experience in securing external grant funding is highly desirable. Prior supervisory experience is highly desired.

Desirable Qualifications for Research Scientist position: Ph.D. in genetics/molecular evolution/ population genetics/ statistical genetics/ bioinformatics. Experience in bioinformatics (including data analysis/software design/ programming/ implementation; UNIX system ad-

ministration). Experience in DNA sequencing, real-time PCR, microarray methods and protocol development. Experience with budget management is desired. Prior experience in successfully securing external grant funding is highly desired. Prior supervisory experience is highly desired.

To apply for this position requisition number 55436: Please go to Jobs@uiowa; <http://jobs.uiowa.edu/> Salary: commensurate with experience

The University of Iowa is an Affirmative Action/Equal Opportunity Employer. Women and minority candidates are encouraged to apply.

—

John M. Logsdon, Jr., Ph.D. Associate Professor Director, Roy J. Carver Center for Comparative Genomics University of Iowa

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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>

UMaryland Genomics bioinformatics

UNIVERSITY OF MARYLAND School of Medicine
INSTITUTE FOR GENOME SCIENCES

The newly created Institute for Genome Sciences (IGS) at the University of Maryland, School of Medicine seeks to fill several Faculty, Postdoctoral Fellow and Bioinformatics positions.

The Institute is led by Claire M. Fraser-Liggett, Ph.D., one of the world's preeminent genome scientists and previous Director and President of the Institute for Genomic Research (TIGR). The Institute for Genome Sciences houses an interdisciplinary, multi-departmental team of collaborative investigators with a broad spectrum research program related to the genomics of infectious disease agents, human microbial metagenomics, functional genomics, and bioinformatics. The impact of the IGS team on the field of genomics has been substantial, with more than 500 publications during the past 15 years that have been cited more than 30,000 times.

Within the Institute are two state-of-the-art resource centers: the Genomics Resource Center (GRC), a high-

throughput, state-of-the-art core laboratory supporting the scientific programs of IGS and external collaborators with multiple DNA sequencing, genotyping, and array platforms and the Informatics Resource Center (IRC) which provides genome assembly, annotation, and data analysis services.

IGS is recruiting additional faculty members to join its interdisciplinary scientific team. We are looking for highly collaborative investigators at all stages of their careers that have a track record in the application of large-scale approaches to the study of biological systems. We are looking to complement our existing expertise, and applicants with funded research programs in comparative genomics, statistical genomics, human genetic variation, and systems biology are encouraged to apply. There are many opportunities for collaborations with colleagues in IGS and across the School of Medicine in both basic and translational research in cardiovascular disease, cancer biology, and infectious disease and participation in graduate and medical education.

IGS is in a period of rapid expansion with many new research appointments anticipated in the next five years. To view detailed job descriptions for open IGS positions see our website at <http://www.igs.umaryland.edu> All faculty and postdoctoral applicants should submit curriculum vitae, statement of research interest and names of three references to IGS-jobs@som.umaryland.edu

Consideration of candidates will begin upon receipt of applications and will continue until the positions are filled. AA/EOE/ADA

www.hr.umaryland.edu carollee@wisc.edu carollee@wisc.edu

UMiami Tech AphidMolEvolution

Research Technician Biology Department, University of Miami, FL

A full-time research technician position is available in the Biology Department at the University of Miami, FL in the laboratory of Dr Alex Wilson (<http://www.bio.miami.edu/acwilson/home.htm>).

Primary research projects will focus on but are not limited to: the ecology, genetics and molecular evolution of aphids. Primary responsibilities comprise but are not limited to standard molecular biology activities, microarray analyses, sequence analyses, microsatellite

DNA fragment analysis, extraction of DNA and RNA from insects, primer design, PCR, gel electrophoresis, cloning of PCR amplicons, preparation of DNA sequencing reactions, molecular database searching, insect rearing and greenhouse tasks. Skills in some of these duties are required.

This position is available May 1, 2008 for one year, with continuation contingent on performance and available funds. Salary will be commensurate with experience and will include benefits.

Education: B.A. or B.S. degree and experience in molecular biology, evolution, genetics or a related field. Previous laboratory experience with molecular biology and/or genomics is preferred. Familiarity with computational skills; Mac OS, Windows and Linux/Unix is a plus. Experience with rearing insects and growing plants is preferred and familiarity with genetics is required. The successful candidate is expected to be highly motivated, to have excellent team and organizational skills.

A cover letter, curriculum vitae and the names and contact information, including email addresses and phone numbers, of at least three people who agreed to be referees are required to be considered for this position.

Review of applications will begin immediately and will continue until a suitable applicant is found. For more information email: Alex Wilson, acwilson@bio.miami.edu

–

Dr Alex Wilson

Assistant Professor

Department of Biology

University of Miami

1301 Memorial Drive

Coral Gables, Florida 33146-0421

USA

Phone: (305) 284 2003

Office: Cox Science Room 253

<http://www.bio.miami.edu/acwilson/home.htm> acwilson@bio.miami.edu acwilson@bio.miami.edu

“Research Experience for Undergraduate”

An NSF-funded Research Experience for Undergraduate (REU) position is open for field work in Panama and laboratory research at the Ann Arbor campus of the University of Michigan.

The position is for 8-10 weeks. Fieldwork will take place during June and July of 2008 and will be based out of the research facilities of the Smithsonian Tropical Research Institute on Barro Colorado Island in the Panama Canal. Responsibilities will entail assisting a doctoral student in collecting data on individual growth characteristics, microenvironment, and GPS coordinates for a large sample of rainforest trees from which leaves will be collected and returned to the University of Michigan for chemical analysis. Individual trees will be sampled in the 50-ha Forest Dynamics Plot on Barro Colorado Island, as well as several smaller forest plots extending from the Caribbean to the Pacific coasts of Panama.

During August, responsibilities will entail processing dried leaf samples for analysis of alkaloid defense compounds using HPLC (high-performance liquid chromatography) in the Molecular Ecology Laboratory at the University of Michigan. This can be considered an opportunity to conduct an independent undergraduate research project.

Please contact:

Brian Sedio PhD Student Dept. of Ecology and Evolutionary Biology University of Michigan bse-dio@umich.edu

Thank you for your help.

Chris Dick

Christopher W. Dick Ecology and Evolutionary Biology University of Michigan 830 North University Ave Ann Arbor, MI 48109-1048

Office phone 734-764-9408

<http://www.lsa.umich.edu/eeb/people/cwdick/-index.html> Christopher Dick <[cwick@umich.edu](mailto:cwdick@umich.edu)>

UNewBrunswick ProtistanDiversity

UMichigan SummerFieldWork

University of New Brunswick - Marine Protistan Diversity The Department of Biology, University of New Brunswick (Fredericton), seeks applicants for a tenure-track position at the Assistant-Associate Professor level

in Marine Protistan Diversity. The successful candidate will develop a strong research program examining genomic diversity from evolutionary and environment perspectives, emphasizing comparative genomics and protistan diversity at the species to genomics level in marine heterotrophic and/or phototrophic protists. Specific research areas include, but are not limited to: exploring species diversity through molecular biology; evolution of organelles and organismal attributes; genome structure and function; and diversity with regards to biochemical and cellular processes. The candidate will be expected to mentor undergraduate and graduate students, as well as postdoctoral fellows, and teach undergraduate and graduate courses appropriate to departmental need and the candidate's expertise. The successful candidate must have a track record in research that will be highly competitive in attracting external research funding and HQP. The position is associated with the Canadian Institute for Advanced Research (CIFAR) and its newly established Integrated Microbial Biodiversity (IMB) program. The successful applicant will join a network of international researchers as a Scholar in the CIFAR IMB Program (information on this program can be found at www.cifar.ca). The applicant will also contribute to the Marine Environmental Barcoding component of the international Barcode of Life, a project aimed at investigating protistan biodiversity in the ocean with molecular techniques. The successful candidate will join biology, comparative genomics, bioinformatics and biodiversity (CEMAR: www.unb.ca/cemar). Additional research strengths in the Department of Biology include aquatic ecology and fish biology, conservation biology, and evolutionary biology. Information about Biology at UNB is available at

www.unb.ca/fredericton/science/biology.

A PhD and relevant postdoctoral experience is required.

The closing date for applications is August 4, 2008. To apply, send a letter describing your research and teaching interests, a curriculum vitae with names, addresses, and e-mail contacts for three referees, representative publications, and a statement of teaching philosophy to:

Gary W. Saunders, Chair Department of Biology University of New Brunswick P. O. Box 4400 Fredericton, NB E3B 5A3

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. Applicants should indicate current citizenship status. This position is subject to budgetary approval.

Stephen Heard

sheard@unb.ca Professor and Associate Chair Dept. of Biology

506-452-6047 University of New Brunswick FAX 506-453-3583 Fredericton, NB E3B 6E1

Steve Heard <sheard@unb.ca>

UOttawa 2 EvolBiol

As advertised in Nature (May 6), we are seeking to fill two faculty positions in the Department of Biology at the University of Ottawa. Exceptional candidates with evolutionary interests are encouraged to apply. Note that applicants from more senior ranks will also be considered. Ability to teach in French is a requirement. Details are below.

The University of Ottawa, at the heart of Canada's capital, is one of our country's leading research universities. We are a cosmopolitan community of over 40,000 students, faculty and staff who live, work and study in both English and French. We are proud to be Canada's university.

The Department of Biology, University of Ottawa invites applications for following two tenure track positions:

Assistant Professor in developmental biology Assistant Professor in the areas of microbiology or neurobiology

Exceptional candidates in other areas of biology will also be considered.

Appointments will normally be at the Assistant Professor level, but applications from candidates at higher ranks may be considered. Successful candidates will join a vibrant, research-intensive Department (<http://www.biology.uottawa.ca/>) with strengths in bioinformatics, cellular/molecular biology, ecology, evolution and physiology. The Department is also home to interdisciplinary initiatives provided through the laboratory facilities of the Center for Advanced Research in Environmental Genomics (<http://www.careg.uottawa.ca>). Successful candidates will participate in undergraduate and graduate teaching programs in Biology, Biopharmaceutical Sciences and/or Environmental Sciences. Candidates must have a PhD and a proven research record in one of the above research areas and be able to teach in both English and French.

For a detailed description of this position, please visit our website at: <http://www.hr.uottawa.ca> Applicants should send a description of their proposed research and teaching interests, as well as a curriculum vitae, and the names of four referees before May 31, 2008 to: Search Committee, Department of Biology, University of Ottawa, 30 Marie Curie, Ottawa, Ontario, Canada K1N 6N5. Fax: 613 562 5486.

In accordance with Immigration Canada regulations, all qualified individuals are invited to apply; however, preference is given to both Canadian citizens and permanent residents. The University of Ottawa also has an employment-equity policy. We therefore strongly encourage women, Aboriginal people, members of visible minorities and persons with disabilities to apply.

Sise au cur de la capitale du Canada, l'Université d'Ottawa est l'une des principales universités à vocation de recherche du pays. Son effectif étudiant, son corps professoral et son personnel regroupent plus de 40 000 personnes qui vivent, travaillent et étudient en français et en anglais dans un milieu des plus cosmopolites. C'est avec fierté que nous nous affichons comme « l'Université canadienne ».

Le département de Biologie de l'Université d'Ottawa sollicite des candidatures pour les postes suivants :

Professeur(e) adjoint(e), biologie du développement
Professeur(e) adjoint(e), microbiologie ou neurobiologie (Postes menant à la permanence)

Les candidat(e)s exceptionnel(le)s dont la recherche porte sur d'autres domaines de la biologie seront aussi considéré(e)s. Les nominations seront normalement effectuées au rang de professeur adjoint; toutefois, les candidat(e)s de rang plus élevé peuvent être considéré(e)s. Vous vous joindrez à un département offrant un milieu dynamique de recherche (www.biologie.uottawa.ca) en bioinformatique, biologie cellulaire/moléculaire, écologie, évolution et physiologie. Le département est aussi le lieu d'initiatives multidisciplinaires rendues possibles grâce aux laboratoires du Centre de Recherche Avancée en Génomique Environnementale (www.crage.uottawa.ca). Vous participerez aux programmes d'enseignement de premier cycle et des cycles supérieurs en biologie, en sciences biopharmaceutiques et(ou) en sciences de l'environnement. Vous devez posséder un diplôme universitaire de troisième cycle, un programme de recherche important et indépendant dans un des domaines mentionnés ci-dessus et être capable d'enseigner en français comme en anglais.

Pour obtenir de plus amples renseignements sur

ces postes, veuillez consulter notre site Web au www.rh.uottawa.ca . Veuillez faire parvenir une description de vos intérêts en recherche et en enseignement, votre curriculum vitae et le nom de quatre personnes pouvant fournir une lettre de recommandation, avant le 31 mai 2008,

— / —

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>

UPuertoRico InvertebrateCollection ResearchTech

UPuertoRico.InvertebrateCollectionResearchTechnician
Scientific Research Technician à UPRM Invertebrate
Collection

A two-year full time position is available for a scientific research technician at the Department of Biology, University of Puerto Rico at Mayagüez (UPRM). The projected starting date is August to October, 2008. The position plays a key role in a NSF-funded project aimed at reorganizing and digitizing the UPRM invertebrate collection (> 80% insects; see <http://academic.uprm.edu/franz/>). The chosen candidate will closely interact with Biology and Marine Science faculty, as well as with graduate and undergraduate students to coordinate and perform curatorial activities such as specimen preservation and identification, specimen barcoding, georeferencing, databasing (using the Specify software package), and digital imaging. Prior experience with any of these tasks is advantageous, as is the ability to use biodiversity databases and web design applications. An undergraduate or advanced degree in invertebrate zoology is preferred. Good social skills are critical to help promote the collection at all levels. Knowledge of English and Spanish or a willingness to learn is desirable. The position is ideal for a highly motivated person interested in tropical invertebrate diversity and modern collection stewardship.

The salary is adjusted to the UPRM pay scale and includes a full benefits package covering social security, health insurance, and a holiday bonus.

To apply, please send a CV, names and contact information of two references, and letter of interest to Nico Franz, franz@uprm.edu <<mailto:franz@uprm.edu>>.

Applications will be reviewed immediately until the position is filled.

Nico Franz <franz@uprm.edu>

USFishWildlife ConservationGeneticist

Geneticist

This is a Term Position not to exceed 13 months, however, may be extended up to 4 years. The position is located in the Department of Interior, Fish and Wildlife Service, Warms Springs Regional Fisheries Center. The position works with a team of scientists, as a member of the Center's Applied Research program in Conservation Genetics. The position serves as coordinator of laboratory operations for the Genetics Laboratory, conducts molecular genetic analyses of fish populations, and uses DNA markers and automated DNA analyzers/sequencers to collect genotypic, gene frequency, and DNA sequence data on hatchery and wild populations of aquatic organisms.

SALARY RANGE: 38,162.00 - 54,942.00 USD per year

OPEN PERIOD: Monday, May 12, 2008 to Monday, May 26, 2008

For more information or to apply see <http://www.usajobs.gov/> and search for Job Announcement Number: R4-08-189668-MC or geneticist.

Greg_Moyer@fws.gov

USFishWildlife PopulationGeneticist

Regional Geneticist and Program Head of the Applied Research Program in Conservation Genetics, U.S. Fish and Wildlife Service, Abernathy Fish Technology Center, Longview, WA

The Abernathy Fish Technology Center (Center), Longview, WA, provides applied fishery research and development capabilities to the U.S. Fish and Wildlife Service (Service), Pacific Region/CNO (CA, ID, NV, OR, and WA). With an annual operating budget of approximately \$3+ million (base and soft monies) and a

current total staff of 28, the Centers applied research programs assist mitigation, restoration, and recovery efforts through the scientific development and evaluation of new methods, concepts, systems, and. The Center maintains Applied Research Programs in the fields of Ecological Physiology, Conservation Genetics, Nutrition, Hatchery Reform/Integrated Hatchery Management and Pathology.

The incumbent serves as the Regional Fish Geneticist and Head of the Pacific Region/CNOs Applied Research Program in Conservation Genetics at the Center. The incumbent is the Pacific Region/CNO, Fisheries Programs lead authority and subject matter expert on molecular, population fish genetics issues and provides technical expertise and recommendations to the Regional Directorate on international, national, and Region-wide fish conservation issues and policies. The incumbent serves as the primary liaison for the Service to: other Federal and State agencies; tribal governments; and non-governmental organizations on the application of molecular population genetics techniques used in the conservation and management of fishery resources. The incumbent supervises five or more professional and technical staff in the Applied Research Program in Fish Genetics (Program). The Program consists of: the development of program and Regional policies to fully protect and conserve genetic resources of wild/natural populations; the genetic characterization of hatchery and wild/natural stocks; the establishment of propagation guidelines to prevent loss of genetic variation and conserve genetic diversity in hatchery and wild/natural stocks; and the monitoring of change in the genetic resource and life history patterns of hatchery and wild/natural stocks.

Major duties include the following: -Develop, coordinate, design, and implement complex applied research investigations to advance knowledge about hatchery protocols, fish rearing methods, natural population structure, and the influence of modified propagation methods in order to conserve genetic resources of populations of fish.

-Genetically identify and characterize hatchery and wild/natural stocks.

-Plan and oversee broodstock selection procedures and genetic studies associated with implementing or improving hatchery management policies.

-Supervise technical and professional staff.

-Prepare a wide variety of written materials.

-Conduct interactions with other professionals in the field of molecular population genetics by reviewing articles and reports, attending professional meetings, and

responding to questions and challenges among subject matter experts and other professionals to maintain professional credentials.

Requirements: Ph.D. with work experience in molecular population genetics or related discipline. The incumbent must be highly motivated, outgoing, with demonstrated ability in successful coordination and teamwork, and supervision of technical and professional employees.

Salary: \$77,670 to \$100,976/year

Closing Date: May 30, 2008

Contact: Applications accepted only from U. S. citizens. Applications MUST be received online via the USAJOBS, the Federal Governments Official Jobs Site, <http://www.usajobs.opm.gov>, by the closing date. The Federal Government is an Equal Opportunity Employer. For general questions about the position please contact Judith Gordon, Center Director, at 360-425-6072, x350.

Judy Gordon Center Director U. S. Fish & Wildlife Service Abernathy Fish Technology Center 1440 Abernathy Creek Road Longview, WA 98632 (360)425-6072, ext. 350 voice (360)636-1855 FAX judith.gordon@fws.gov e-mail <http://www.fws.gov/aftc> Center Web Page

Judith.Gordon@fws.gov

UVienna PopulationBiology

The Faculty of Life Sciences of the University of Vienna announces the position of a

Full Professor of Population Biology and Biogeography of Plant

(full-time permanent position under private law). The University of Vienna intends to increase the number of women on its faculty, particularly in high-level positions, and therefore specifically invites applications by women. Among equally qualified applicants women will receive preferential consideration.

The candidate should have an excellent international track record in modern research in the area of plant population biology related to plant biogeography. The research should focus on processes and functional traits determining the formation of distribution limits from a local via a regional to a global scale including causes

and mechanisms of human-mediated shifts of distribution area, population size and density of plant species. Readiness for close co-operation with researchers of related departments - e.g., in the areas of animal population biology, community ecology, vegetation and landscape ecology, conservation biology, evolutionary biology - is expected.

Successful candidates will have the following qualifications:

- PhD and post-doctoral experience at a university or other research institution. (Austrian or equivalent international academic degree in the relevant field)
- Outstanding research and publication record, with an excellent reputation as an active member in the international academic community (Habilitation (venia docendi) or equivalent international qualification in the relevant field is desirable)
- Experience in designing, procuring and directing major research projects, and willingness and ability to assume the responsibility of team leadership
- Experience in university teaching, and willingness and ability to teach at all curricular levels, to supervise theses, and to further the work of junior academic colleagues

The University of Vienna expects the successful candidate to acquire, within three years, proficiency in German sufficient for teaching in Bachelor programmes and participation in committees

The University of Vienna offers

- Attractive terms and conditions of employment with a negotiable and performance-related salary, associated with a retirement fund - A "start-up package" for the initiation of research projects - An attractive and dynamic research location in a city with a high quality of life and in a country with excellent research funding provision - A grant for relocation to Vienna, where appropriate

Candidates should send an application containing at least the following documents:

- Academic curriculum vitae - Brief description of current research interests and research plans for the immediate future - List of publications together with a) specification of five key publications judged by the applicant to be particularly relevant to the advertised professorship together with an explanation of their relevance b) PDF versions of these five publications provided either as email attachments or through URLs of downloadable copies - List of talks given, including detailed information about invited plenaries at international conferences
- List of projects supported by third-party funds - Short

survey of previous academic teaching and list of supervised PhD theses

Applications in English should be submitted per e-mail (preferably as pdf attachments) to

Dorothea.Prenner@univie.ac.at no later than June 15th, 2008 with reference 20/6-2008.

gerald.schneeweiss@univie.ac.at

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Accelrys petition followup 3

Hi all -

I would like to offer my apology to Accelrys and its employees for suggesting that the company would not follow through on their commitment to supply non-locked, non-expiring license keys to all current GCG customers with "perpetual" licenses. As I mentioned in my last posting Accelrys is now involved in that process and I have received my new key. It was never my

intent to discredit Accelrys, nor its employees. I merely had not been informed that the process was underway. I am sorry that I miswrote and hope that any hard feelings can be overcome. Thank you.

Cheers - Steve Steven M. Thompson stevet@bio.fsu.edu
<http://bio.fsu.edu/~stevet/cv.html> FSU SCS / BioInfo
 4U

Florida State University School of Computational Science

1st floor DIRAC 150G Tallahassee, Florida 32306-4120
 850-644-4490

2538 Winnwood Circle Valdosta, Georgia 31601-7953

229-249-9751

stevet@bio.fsu.edu stevet@bio.fsu.edu

Antiviral defence genes

Dear all,

I am compiling a list of genes that are specifically important for the defence against viruses at any point of infection in any vertebrate (or even animal) system. I hope to get an exhaustive list of gene names, (proposed) function(s) and source DNA sequences.

If you could give me any hint, names, publications or whatever I would be very happy to get into contact with you.

Cheers, Robert

robert.kraus@wur.nl

Antiviral defence genes answers

Dear all,

some time ago I asked the community for info about genes that are important for animal, or more specifically, vertebrate immune defense vs. (RNA) viruses. First of all, there is a huge variety of "candidates" of genes and mechanisms but only few are studied in context of natural variation. Moreover there is no synthesizing work on that issue. For fields like evolutionary genetics, ecological immunity or host-pathogen biology it would be highly interesting, though, to sum up the current knowledge from some model systems, and use this info in non-model systems.

I personally think it is worth while writing a review on that issue and publishing it to the scientific community. If there is interest in this action by some of you who feel experienced in these issues please let me know (robert.kraus@wur.nl).

For now, here is a condensed list of suggestions that I got. All of these are suggested to be starting points. The actual screening of the literature may be some nice work of its own (see comment on the need for a proper review above...):

- RNAi <http://www.current-biology.com/content/-article/abstract?uid=3DPHIS09609822> 06012085
<http://download.cell.com/pdfs/0092-8674/-PHIS0092867407009774.pdf>

- The immune repertoire of the sea urchin

Dev Biol. 2006 Dec 1;300(1):349-65. Epub 2006 Sep 3. The immune gene repertoire encoded in the purple sea urchin genome. Hibino T, Loza-Coll M, Messier C, Majeske AJ, Cohen AH, Terwilliger DP, Buckley KM, Brockton V, Nair SV, Berney K, Fugmann SD, Anderson MK, Pancer Z, Cameron RA, Smith LC, Rast JP.

- APOBEC3: Langlois, M. A., and M. S. Neuberger. 2008. Human APOBEC3G can restrict retroviral infection in avian cells and acts independently of both UNG and SMUG1. Journal Of Virology 82:4660-4664.

- There are around 2000 immune related genes in the human genome which are prime candidates for your list. A search through Pubmed and Web of science should pull functional infection/expression, association and knock-out studies. Genome websites/databases will be yet another good resource. Although this is an exhaustive effort, there will still be many players left out because we simply do not know a majority of the genes that are involved in viral infection and progression. An interesting point is that, some genes (such as mitochondrial and other energy metabolism genes) which expected to have no anti viral properties show up as important players depending on the type of viral infection.

- Jeurissen, S. H. M., A. G. Boonstra-Blom, S. O. Al-Garib, L. Hartog, and G. Koch. 2000. Defence mechanisms against viral infection in poultry: A review. Veterinary Quarterly 22:204-208.

- MacDonald, M. R. W., S. M. Veniamin, X. Guo, J. Xia, D. A. Moon, and K. E. Magor. 2007. Genomics of antiviral defenses in the duck, a natural host of influenza and hepatitis B viruses. Cytogenetic And Genome Research 117:195-206.

robert.kraus@wur.nl

Chloroflexus samples

Dear Evoldir-ers,

I am looking for some Chloroflexus aurantiacus living cells. I just need some bacterial cells for DNA extraction. I would like to know if somebody are cultivating them and can send me samples. I thank you in advance.

Charlotte Noyer PhD student Integrin Advance Biosystems Marine resource centre

Barcaldine, Oban

Argyll, Scotland, PA37 1SE

Tel : +44 1631 720765

Fax: +44 1631 720590

charlottenoyer@yahoo.fr

Dry ice shipping

Dear colleagues,

I am intending to send RNA samples on dry ice from Europe (i.e. Germany), to the US and I am having trouble finding a carrier that accommodates such a shipment. I wonder if anybody could give some advice on how best to ship such material.

Thanks!

Tina

Bettina Harr PhD Max-Planck-Institut fuer Evolutionsbiologie Abteilung Evolutionsgenetik August-Thienemannstrasse 2 24306 Ploen (Germany) email: harr@evolbio.mpg.de

Tel: ++49 4522 763 287 [http://tina-10-1.genetik.uni-koeln.de/~ website/](http://tina-10-1.genetik.uni-koeln.de/~website/) Become Carbon neutral today Visit: www.savingspecies.org Bettina Harr <harr@evolbio.mpg.de>

Evolution2008 DormRoom

Hello,

I am an undergraduate student attending the Evolution 2008 conference in Minneapolis from June 20th - 24th. I have currently not booked a room to stay in, as the dorms are full. If anyone has booked a double room and is interested in splitting the dorm fee, please notify me at rebeccavanderhooft@gmail.com.

Thanks, Rebecca Vanderhooft

rebeccavanderhooft@gmail.com

Evolution Intro course

Dear All,

I am going to teach part of an introductory course on Evolution to first year biology students after the summer break, thus I am starting to gather ideas for discussion sessions. I thought it might be appealing for students to watch movies that either introduce or discuss evolutionary ideas, especially if they are tangibly relevant to their every day life or to society in general. I thought of showing them Flock of Dodos, for example, but, upon viewing it a second time, I realized that it would not be appropriate for a group of European (primarily Swiss) students, because it's too US-based.

Does anybody have other suggestions for movies about evolution (theory, biology, case studies, society, etc...) that might stir discussion for beginning undergraduates?

Than you very much for any input on this question.

Elena

Prof. Elena Conti, Ph.D. University of Zuerich, Institute for Systematic Botany Zollikerstrasse 107, 8008 Zuerich, SWITZERLAND Ph: 0041 44 634 8424 Fax: 0041 44 634 84 03 email: ContiElena@access.unizh.ch [http://www.systbot.unizh.ch/-institut/personen/person.php?l=d&id\\$](http://www.systbot.unizh.ch/-institut/personen/person.php?l=d&id$) <http://www.systbot.unizh.ch/mediterranean/index.htm> Elena Conti <ContiElena@access.unizh.ch>

Evolution lab practicals

Dear all

We are teaching a new introductory evolution course for first semester students. In addition to our regular lectures, we have a weekly practical slot of 3-4 hours. In this context we are looking for suggestions for practicals on ANY subtopic within the realm of EVOLUTION that we could perform with up to 100 students in ONE room, without hoardes of teaching assistants being available.

I would be grateful for ANY suggestions!

Thanks in advance and best,

Dr. Wolf Blanckenhorn Zoological Museum University of Zurich-Irchel 34 (building)-J (floor) -98 (office) Winterthurerstrasse 190 CH-8057 Zurich

Phone: +41 44 635.47.55 Fax: +41 44 635.47.80 E-mail: wolf.blanckenhorn@zm.uzh.ch
http://www.zm.uzh.ch/zmneu/forschung/-blanckenhorn_wolf.html <http://www.esf.org/-thermadapt> wolfman@zm.uzh.ch wolfman@zm.uzh.ch

Facebook evolution simulation

I've created a Facebook application that may interest many readers of EvoDir. It's called Evarium, and it places an animated simulation of evolution with sexual selection, sexual conflict, mutation, and genetic drift on your Facebook profile page. You can learn more about it at <http://evarium.com/>. If you're logged in as a Facebook user, you can also install Evarium from that page.

Facebook is used by tens of millions of high school and college students, so Evarium may be of particular interest to teachers of high school or college courses featuring evolution. However, Evarium isn't meant as a pedagogical tool comparable to, for example, EvoBeaker. It's best described as an educational toy, mostly fun but potentially instructive as well. At present, it's available on Facebook only, but if time allows, I'll bring it to MySpace and some other platforms.

Ralph Haygood rhaygood@duke.edu

Ralph Haygood <rhaygood@duke.edu>

Genemapper and Vista

Dear colleagues,

I'm seeking to install Genemapper (v 3.7) on my computer which is running the novel and frustrating Windows Vista operating system (Home Premium).

I'm failing at the first hurdle as the Genemapper installer tells me:

* You have to logon to the local machine to install

Genemapper software. * Genemapper software requires Service Pack 1 or higher on a Windows XP Operating Systems.

I'm running a new computer so hardware requirements are all met, I'm logged on to my "local machine".

Has anyone out there actually managed to install and run Genemapper under a Vista operating system? If so, could you please point me on the right path?

Regards,

Michael Whitehead

– Michael Whitehead PhD candidate School of Botany and Zoology Australian National University Canberra ACT 0200 Telephone: +61 (0)2 6125 4172 Facsimile: +61 (0)2 6125 5573 Email: michael.whitehead@anu.edu.au

michael.whitehead@anu.edu.au
 michael.whitehead@anu.edu.au

Haplotype Inference Answers

Thank you to all who suggested various programs for haplotype inference from sequence data. Here are some of the replies:

Please see our recent paper in Molecular Ecology: Haplotype reconstruction for scnp DNA: a consensus vote approach with extensive sequence data from populations of the migratory locust (*Locusta migratoria*) ZU-SHI HUANG, YA-JIE JI and DE-XING ZHANG Molecular Ecology, Vol. 17 Issue 8, pages 1930-1947 <http://www.blackwell-synergy.com/doi/abs/10.1111/j.1365-294X.2008.03730.x> We have also written a Perl script package to implement the consensus vote approach. The software can be downloaded from the following website: <http://www.ioz.ac.cn/department/-agripest/group/zhangdx/ZhangDX.E.htm> In addition, the software can also convert PHYLIP format input file to the input file formats of several popular haplotype reconstruction packages. ++

collapse: <http://darwin.uvigo.es/software/-collapse.html> ++

In Bioperl we have a module that reads Alignments and turns them into Population objects and these can be written out in PHASE. <http://bioperl.org/wiki/-HOWTO:PopGen> ++

Use Arlequin version 3 or higher by L. Excoffier. If

you have two samples that look like this: Specimen1 CTGGAGGTCAGAAGCG Specimen2 CTGGASGTCYGAAGCK Make a file that looks like this: [Profile] Title="sample" NbSamples=1 DataType=DNA LocusSeparator=NONE GenotypicData=1 GameticPhase=0 MissingData='?' [Data] [[Samples]] SampleName="all" SampleSize SampleData={ Specimen1 1 CTGGAGGTCAGAAGCG CTGGAGGTCAGAAGCG Specimen2 1 CTGGAGGTCTGAAGCG CTGGACGTCCGAAGCT } The top sequence has just one allele, and the bottom has two alleles resolved randomly. Then run through the ELB algorithm under "Haplotype interference". The output gives you the optimal solution and a distribution of solutions. ++

DnaSP will infer haplotypes from sequence data. ++

You could try SNAP Workbench from the Carbone lab. It does a lot of other things than converting sequences into haplotypes as well. For instance, it converts sequences to all kinds of formats. Here is the link <http://www.cals.ncsu.edu/plantpath/people/-faculty/carbone/workbench.html> ++

PGEToolbox can do this, as long as you have got Matlab ++ There is also the program HAPLOBLOCK, that I myself have not used, but students of mine have and said it was useful, perhaps this helps.

Jaime Elizabeth Blair, PhD Postdoctoral Fellow Department of Biology Amherst College jblair@amherst.edu Phone: (413) 542-8333 <http://www.amherst.edu/~jblair> <http://jaime.e.blair.googlepages.com> "Jaime E. Blair, PhD" <jblair@amherst.edu>

Interspecies competition

Dear Evoldir members,

I am teaching an ecology course for undergraduate students in Biology. I am trying to set up either a field or a lab experiment addressing the issue of inter-species competition. Approximately 120-160 students are attending this course each semester and therefore it is quite hard to set up an experiment for all these students. I am wondering if anyone of you could suggest something that is duable for such a big audience. Thank you in advance. All the suggestions will be posted to Evoldir.

Aris

–

ARIS PARMAKELIS, PhD. DEPARTMENT OF ECOLOGY AND TAXONOMY FACULTY OF BIOLOGY NATIONAL & KAPODISTRIAN UNIVERSITY OF ATHENS PANEPISTHMIOUPOLI ZOGRAFOU, GR-15784, ATHENS, GREECE Tel.: ++302107274736 aparmakel@biol.uoa.gr parmakel@nhmc.uoc.gr parmakel@edu.biology.uoc.gr <http://www.nhmc.uoc.gr/>

Aristeidis Parmakelis <aparmakel@biol.uoa.gr>

Interspecies competition answers

Dear EvolDir members,

A few days ago I posted a question in EvolDir regarding "Suggestions for inter-species competition experiment". Many of you replied and made very useful suggestions. I am posting these replies since I consider they will be of use to many of you. I would like to thank all those that replied, I think I now have a good idea of how to set up some experiments both in the field and in the lab. Thanks a lot.

Aris

—Compilation of responses—

Hello,

We are doing this kind of teaching here in Montpellier with around 100 students. We are using Chlamydomonas for that purpose. It grows fast, does not require sterile equipment and you can order many different strains from the web.

We have two sets of experiments, one where students measure the outcome of competition between a strain of Chlamydomonas and Klebsormidium sp. (another algae that we isolated from a soil sample) and a second set where they study competition between two strains of Chlamydomonas, the wild type one (CC125) and one that resists to an herbicide (strain CC2473 that resists to atrazine). The first experiment focus on interspecific competition while the second is designed to study natural selection.

The way we organize this is that, for each experiment, small groups of 4-5 students run a single replicate of each treatment. We then pool all results (using a web interface) and all students have to analyze the complete data set. The most interesting part of this is that most of the time some aspects of the experiment fail.

Students have to deal with that and must also cope with heterogeneity in data. I think these issues are really central in educating students to scientific thinking. And still, students seldom face these problems in the context of a class.

If you want more details on these experiments, feel free to ask! On the web-site from which you can order the strains (<http://www.chlamy.org>), you will also find some teaching kits, I think. I never used these, but it might prove useful in your case.

Sincerely,

Jean-Baptiste Ferdy Institut des Sciences de l'Évolution de Montpellier CNRS UMR 5554 Université de Montpellier 2 34 095 Montpellier cedex 05 tel. +33 (0)4 67 14 42 27 fax +33 (0)4 67 14 36 22

Dear Aris I took an undergraduate class of Ecology in Colombia where we play "Othello" to understand concepts of inter-species competition in Ecology. Do you know this game? It's a game based on strategy and you "compete" with your opponent for space in a table of 8x8 spaces. Here is a link in wikipedia where is explained the game. <http://en.wikipedia.org/wiki/Reversi> Good look in your class. Ivania

Hello, Our department has an undergraduate ecology lab that focuses on competitive exclusion, using spider species as the study organisms. Students measure web diameter, angle, distance from ground, and an approximation of strand density. They use chi-square and we encourage them to test between ecologically similar species (e.g. between two different orb weavers). I can email you a .pdf of the lab if you like. Good luck! Jen Hamel jahamel@mizzou.edu <mailto:jahamel@mizzou.edu> University of Missouri - Columbia Tel. 573-882-4189 www.biosci.missouri.edu/cocroft/Jennifer/-jennifer.htm

Hello, I teach an undergraduate ecology class, and use a great set of software called EcoBeaker (SimBiotic Software: <http://www.ecobeaker.com/>) to help teach a number of ecological concepts. The simulation software is very easy to use, the directions are clear, and the labs are visually appealing. There is often some control over the options if you want to play around, and students can output data and graphs for further analysis. They also provide full lab exercises, with good questions, to go along with each lab. I've had a very good experience with this program, and its compan-

ion, EvoBeaker. I realize this isn't a field or laboratory demonstration per se, but it may be appropriate for such a large class. Cheers, Maarten Vonhof Assistant Professor, Department of Biological Sciences and Environmental Studies Program Western Michigan University 1903 W. Michigan Avenue Kalamazoo, MI 49008-5410 Phone: (269) 387-5626, Fax: (269) 387-5609 E-mail: maarten.vonhof@wmich.edu

Hi Aris, I run an interspecific competition experiment in my Ecology lab using Tribolium flour beetles based on the classic experiments of Park. I have up to 100 students so the lab is suitable for large groups. Do you run the lab with all the students or divide them into groups? If you have the facilities to divide them into smaller groups, this experiment might work as it requires students to spend time at the microscope sorting out the

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>

LondonZoo 6 VolResearchAssist

Would you be interested in working on an exciting research project at London Zoo?

We are looking for up to 6 volunteers to assist on a project looking at coordination in human groups from the 20th July to 14th September.

This project uses RFID (radio frequency identification technology) to examine how language might promote coordination in human groups. Traditionally, research on the conflict between cooperation and competition has focussed on pairs acting for personal gain (e.g. prisoner's dilemma). However, our global ecological success depends largely on cooperation in groups. Within groups individuals act fundamentally selfishly but can pursue a common goal from which all members benefit, requiring coordination. The complexity of human coordination might stem from our ability to combine theory of mind with vocal communication. The experiment will be held at ZSL London Zoo and participants will be zoo visitors.

Volunteering would require your presence at London Zoo for a minimum of 3 days per week.

Please direct any enquiries to Claire Narraway (Claire.narraway@zsl.org) with a copy of your CV and we will set up a meeting with you where questions can be asked and the co-researchers will be present.

The Zoological Society of London is incorporated by Royal Charter Principal Office England. Company Number RC000749 Registered address: Regent's Park, London, England NW1 4RY Registered Charity in England and Wales no. 208728

Claire.Narraway@zsl.org

MatchTools MTNavigator

Dear all,

Does anybody know how can I get a copy of Match Tools and MT Navigator software? This ABI software allows for reference based mutation detection and allele identification. Unfortunately, it has been discontinued and substituted with the new, and very expensive, SeqScape. Other software suggestions are very welcome too.

Thank you,

Cristina

Cristina Pomilla, PhD

Sackler Institute for Comparative Genomics American Museum of Natural History Central Park West at 79th Street New York, NY 10024

Phone: (212) 3137602 Fax: (212) 7695277 Email: cpomilla@amnh.org; cristina.pomilla@nyu.edu
<http://genomics.amnh.org> <http://congen.amnh.org>
 cpomilla@amnh.org

Migrate problems

Dear colleagues,

I am actually trying to get estimations of migration rates (based on mitochondrial gene and nuclear microsatellite) between 6 species of fish using the program Migrate. But I am facing two problems:

(1) Based on a mitochondrial gene, I get clear signature

of introgression between two non reproductively isolated species while some species are completely isolated. In opposite, based on microsatellite data (13 loci) the gene flow between all the species appear to be the same (around 1 migrant per generation). Other methods like genetic distance calculations and assignment methods show significant genetic difference between species and the same signal of introgression between two species (same as based on mitochondrial DNA). The 13 microsatellites are highly polymorphic (10 to 30 alleles) and all species have alleles in common. I have about 50 samples per species. I do not understand the inconsistency between methods and results... Why migrate does not give any signal?

(2) Also, studies that uses migrate to infer migration rates always present standard deviation in the number of migrants between populations or species. In all my run, if i do not change the number of short and long chain as well as the number of recorded genealogies (i also run multiple chain at different temperatures), the values of numbers of migrants doe not change at all! As I increase the length of the run, the values remain stable. Is the commonly presented uncertainty related to difference between runs that use different parameters?

I am greatfull to all for any explanation,

Cheers,

Matt

Matthieu Leray <leray_matthieu@hotmail.com>

MorningGlories ModelStudySystems

Hello Evolutionary Biologists:

I am compiling a list of researchers who use morning glories as study organisms in their evolutionary investigations. If you involve morning glories in your work could you please contact me and I'll give you the details of what I'm doing with this. The first thousand respondents will get free morning glory seeds (that's a morning glory joke for you Drosophila people)!

Thanks in advance, Rick E. Miller Email: rick-miller@selu.edu

Department of Biological Sciences Southeastern Louisiana University Hammond, LA 70402 985 549-5556

<http://www2.selu.edu/Academics/Faculty/>

rickmiller/ rickmiller@selu.edu rickmiller@selu.edu regards

Thejaswi

– THEJASWI SHIVANAND PhD Student National Centre for Biological Sciences Tata Institute of Fundamental Research GKVK Campus, Bellary Road, Bangalore - 560 065 India

Thejaswi Shivanand <thejaswi@ncbs.res.in>

MouseDir ListServ

Dear Colleagues,

The newly established Max Planck Institute for Evolutionary Biology in Ploen, Germany recently held a two-day symposium for Evolutionary Biologists work with Wild Mice (*Mus musculus* ssp.).

One of the results of this meeting was the establishment of a ListServ specifically serving the mouse Evolutionary Biology community. The list is meant to facilitate communication among our community in matters concerning resources, information, future meetings, job opportunities, etc.

If you have interest in joining the ListServ please send a message to: imailsrv@evolbio.mpg.de and in the body (not subject!) type the following command: `subscribe mousedir <your name here>`

Thank you,

Rick Scavetta

– Rick J Scavetta Max-Planck-Institut fuer Evolutionsbiologie Abteilung Evolutionsgenetik August-Thienemannstrasse 2 24306 Ploen (Germany) Tel.: 04522 763 279 scavetta@evolbio.mpg.de

rscavett@uni-koeln.de

PAUP and OSXLeopard

As you know the Mac version of PAUP* currently requires either Mac OS 9, or Mac OS X with Classic installed. However many users have upgraded to new Mac OS X Leopard, that means they no longer have the graphic interface anymore. I have found a commercial software called Geneious that can support current version of PAUP*, which means you can run PAUP* within this commercial software with a nice graphic interface. Geneious itself is written by JAVA so it is cross platforms, any operating system can run it.

PAUP* users can download Geneious for free and Geneious offers a 2 weeks trails.

I believe this is helpful for some evolutionary biologists.

Cheers,

Chen Chen

chen chen <cche213@gmail.com>

Msvar update problems

Dear All

I have been trying to run the latest version of msvar (update 1.3) but the program consistently shows error messages when a single locus (`init_v_file` too short) or multiple loci are run. I have prepared all the files as per the instructions in the read me file. I haven't come across very many recent papers that have used the new version of the program. If someone has expertise in running the program, could you please let me know and I can send you some of my files for your comments. Thank you.

Peter Moens

It is with great personal sadness that I report the passing of Prof. Peter Moens.

Peter was a professor at York University in Toronto. Those who knew him can attest to his fire and vigor in all things scientific. In addition to becoming famous for his work on chromosome dynamics and synatonemal complexes he volunteered much of his time to the community and was the managing editor of GENOME (the Canadian journal for genetics research) for 25 years. He was a fellow of the Royal Society of Canada.

A memorial gathering will be held on Friday May 2nd,

2008 from 7-10 pm at the 3rd floor lounge of the Lumbers Building, York University, Toronto.

A good friend to genetics and evolutionary biology in Canada.

Brian

Brian Golding E-mail: Golding@McMaster.CA Department of Biology FAX: 905-522-6066 McMaster University Tel: 905-525-9140 ext 24829 1280 Main Street West Hamilton, Ontario, L8S 4K1

Phenoscape

Dear Colleague:

We have created a new 'Friends of Phenoscape' discussion and announcement list and would like to invite you to join at the following URL: <https://lists.sourceforge.net/lists/listinfo/phenoscape-discuss>. As you may be aware, the Phenoscape project (<http://phenoscape.org>) was funded by NSF-DBI and supported by the National Evolutionary Synthesis Center (NESCent, <http://nescent.org>) to develop the first informatics system to integrate evolutionary, anatomical, developmental, and genetics data. We are prototyping this approach with ostariophysan fish morphology in relation to zebrafish phenotypes, and in the past year we have made a number of technical and conceptual advances in using ontologies in the context of evolutionary biology. These include the development of a multispecies ontology (Teleost Anatomy), a taxonomy ontology (Teleost Taxonomy), a curatorial interface for curating characters (Phenote), evidence codes to reflect homology, and considerable discussion and syntheses of how to computationally relate these data. Phenoscape will serve the broad community of comparative evolutionary and developmental morphologists by providing web-based access to integrated information and will foster new discoveries at the interface between evolution and developmental genetics.

Our discussions to date have been within the NCBO community and our project group. The purpose of this mailing list is to open up our discussion of issues, because many are of general interest to comparative evolutionary and developmental biologists. Our goals, which include development of the most generalizable tools and approaches, require broad participation, and we would like to have you join us.

We would also like to use the opportunity to point

you to our project blog at <http://blog.phenoscape.org/>, where we will summarize topical discussions from this list along with other announcements. Instead of regularly checking the site for updates, you may also use your favorite newsreader or news aggregator (such as Safari, NetNewsWire, Google Reader, and many more) to belong to our news feed at <http://blog.phenoscape.org/feed/>, and your newsreader will automatically alert you to new posts.

We welcome your participation.

Paula Mabee, Monte Westerfield, and Todd Vision

& Phenoscape team: Hilmar Lapp, Jim Balhoff, Wasila Dahdul, Peter Midford, John Lundberg

Paula Mabee <pmabee@usd.edu>

PopulationGenetics data

Hello EvolDir readers:

I am conducting a meta-analysis of population genetic data (SSR, AFLP, RFLP, etc.) to test for correlations between variation within populations and environmental heterogeneity in the region surrounding each population. The hypothesis is based upon the following logic:

- Heterogeneous environments should favour local adaptation and divergence between populations
- Gene flow between populations should mix alleles
- Populations inhabiting heterogeneous environments should have higher levels of genetic variation due to the combined action of gene flow and heterogeneous selection

We found evidence for this pattern in a quantitative trait in lodgepole pine (Yeaman and Jarvis 2006) and suspect that it may also occur with molecular markers because of either direct selection or linkage to selected loci.

We are looking for any studies that have measured variation in molecular markers for at least 7 populations with the following characteristics:

- Terrestrial organism - 'wild' species (non-pest/non-agricultural)
- Not a recent colonization/invasion
- Individuals within each population sampled over a small range relative to the distance between populations (example: population radius of 1km, > 10 km separating populations).
- No fewer than 5 individuals sampled in any population; mean of >10 individuals per popula-

tion. - Geographical coordinates (Lat/Long or UTM) available for each population

If you are willing to share data from a study that fits these characteristics, please contact Sam Yeaman at 'yeaman@zoology.ubc.ca'. We are reviewing relevant literature but want to make sure we don't miss any useful datasets.

Thanks for reading, Sam Yeaman

Department of Zoology University of British Columbia
Vancouver BC V5T 2P8

Reference:

Yeaman, S. and Jarvis, A. 2006. Regional heterogeneity and gene flow maintain variance in a quantitative trait within populations of lodgepole pine. *Proceedings of the Royal Society, Series B.* 273:1587-1593.

yeaman@zoology.ubc.ca yeaman@zoology.ubc.ca

Population genetics simulation software

Hi, all,

Can anybody suggest a software package for individual based metapopulation genetics simulation of diploid organisms under different population sizes, migration rates, migration models and extinction-recolonisation rates. The program should be able to output genetic parameters at every generation (or every ten-hundred generations). Easypop does not seem to have an option of incorporating extinction-recolonisations.

Thanks Asta

Asta Audzijonyte Monterey Bay Aquarium Research Institute <http://www.mbari.org/staff/audzi-audzi@mbari.org>

audzi@mbari.org

PopulationGenetics Simulation software

Dear Asta and other evoldirians,

It seems that my first message did not get through quite

well on some computers. Here is a "cleaner" version:

We are developing a user-friendly simulation package, called ***ECOGENETICS*** with an individual-based module that allows defining all kinds of species and landscape geometries:

Landscape =====* Patch topology and connectivity * Patch size * Patch extinction rate * Effect of inter-patch environment on dispersal

Life-cycle =====* Birth * Survival * Reproduction * Dispersal * Aging * Death * Density-dependent behaviour * Sex-dependent behaviour * Gene-dependent behaviour * Random behaviour * Clonal, hermaphrodite (with selfing) or sexuate reproduction * Generation overlap

Genetics =====* Neutral genetics * Up to 8 loci, with up to 256 alleles * Autosomal, X, Y chromosomes and mitochondrial * KAM and stepwise mutation regime

Input =====* Graphic interface for the patch topology. * Inter-patch environment compatible with GIS Idrisi and Biomapper format * User-friendly interface for the definition of the life-cycle * Batch mode for sensitivity analyses * Batch mode for Approximate Bayesian Computation (ABC)

Output =====* Text files (for easy work with R) * Compatible with F-Stat and Pop-Gen * Various graphics for the preliminary simulations * Wright's statistics * Pedigree

You can download a poster presenting EcoGenetics (with a few screenshots): Small format (4.76 Mb): <http://www2.unil.ch/biomapper/ecogenetics/Hirzel-Ecogenetics-2008.pdf> Big format (7 Mb): <http://www2.unil.ch/biomapper/ecogenetics/Hirzel-Ecogenetics-2008-Poster.pdf> This program can not yet been downloaded. I am currently writing the help file so that it may be used by a wider audience. Please contact me (Alexandre.Hirzel@unil.ch) if you are interested by a collaboration.

Kind regards,

Alexandre

Alexandre.Hirzel@unil.ch

qPCR system suggestions

Dear All: I'm part of a small, but diverse, group of re-

searchers looking to purchase a qPCR system for gene expression analysis, SNP genotyping, etc. The group ranges from no to moderate experience with qPCR. We are considering Biorad, Stragene, Applied Biosystems and Eppendorf systems, but would appreciate any suggestions/comments from labs that have a system that they would - or would not - recommend. We are looking for a 96 well format system, in the \$30-50k range, that would be user-friendly for a group of 4-8 grad students. If there is any general interest in the opinions sent in, I can post them on this list.

Any suggestions are appreciated -

Thomas

Thomas Merritt, PhD Assistant Professor Department of Chemistry and Biochemistry Laurentian University 935 Ramsey Lake Road Sudbury, Ontario P3E 2C6 Canada e-mail: tmerritt@laurentian.ca phone:705-675-1151 ext. 2189

tmerritt@laurentian.ca tmerritt@laurentian.ca

Roommate Evolution 2008

Hello EvolDir,

I am a PhD student from Queen's University in Ontario. Myself, and one other PhD student from Queen's have booked a hotel room for the Evolution meeting in June. We are hoping to cut down on costs by recruiting one or maybe two extra roommates (the hotel will provide at least one cot, in addition to the two beds). Please see the details of the room below.

If you are interested in sharing the room with us, please contact me at 0jam3 (at) queensu.ca.

James Morris-Pocock PhD Candidate Queen's University Kingston, Ontario

Days Inn University of Minnesota 2407 University Avenue S.E. Minneapolis, Minnesota 612-623-9303

Dates: June 20, 21, 22, 23, 24

Cost: Approximately \$48/night, less if we get a 4th roommate also.

0jam3@queensu.ca 0jam3@queensu.ca

Roommate Evolution 2008 2

Hello EvolDir people,

I have just realized that I reserved a double room in Yudof Hall for the Evolution conference but only need one bed. I'd be happy to share the room with a fellow female evolutionary biologist who's still in need of a place to stay. We'd split the cost of the suite (\$96 / 2) and I have the place booked for Friday the 20th to Tuesday the 24th.

Please contact me if you're interested at lgc@rice.edu

Have a great day,

Lesley Campbell

Lesley Campbell <lgc1@rice.edu>

Shipping Reagents Overseas

Hi All,

We are trying to conduct PCR and sequencing overseas in the Philippines. Although every other vendor has been willing to ship to the Philippines, providing our normal pricing but with added shipping costs, ABI (hum Darth Vader's theme here) wants to charge us 2-3 times our normal prices, just for shipping things to the Philippines instead of our lab in Boston. We were quoted \$77,000 for a \$20,000 reagent order.

Seems to me a reasonable alternative is to bring the reagents over ourselves. We thought of hand carrying them, but the TSA (again, hum Darth Vader's theme here) can't assure us that they won't confiscate our reagents. We thought of dry shippers, but the temperature of the liquid nitrogen is too cold. We've thought of FedEx or other express mail, but the 5lb of dry ice that can be shipped on airliners will only last 48 hours, and they can't guarantee that the shipment will make it in less than 72.

For some reagents (e.g. taq), we can get things locally, although it is a bit more expensive. For things like bigdye, we are stuck.

I'm sure we aren't the first people to want to ship things

overseas and keep them cold. Does anyone out there have any ideas? I'm running out of ideas.

Thanks Paul

Dr. Paul H. Barber Boston University Boston University Marine Program 5 Cummington St. Boston, MA 02215 617-358-4589 office 617-358-4590 lab 617-353-6340 FAX pbarber@bu.edu <http://people.bu.edu/~pbarber/> Paul Barber <pbarber@bu.edu>

SISG 2008 roommate

Hi, A friend would like to find a Male roommate to share the room during Jun 15/16 ~ Jun 20 at the statistical genetics course in Seattle. If your dates overlap with his, please contact him directly at: zibokstate@gmail.com<miraceti@gmail.com>

Thanks.

lzhu34@gmail.com

Software DAMBE update

Dear All,

I have just uploaded a new version of DAMBE (5.0.15) at DAMBE's release site: <http://dambe.bio.uottawa.ca/dambe.asp> Major updates include:

1. A special Protein maximum likelihood method for phylogenetic analysis of highly diverged taxa. The implementation is similar to that of Rodriguez-Ezpeleta, N., H. Brinkmann, G. Burger, A. J. Roger, M. W. Gray, H. Philippe, and B. F. Lang. 2007. Toward resolving the eukaryotic tree: the phylogenetic positions of jakobids and cercozoans. *Curr Biol* 17:1420-1425. The amino acids are coded into four categories:

Small polar: S C T N D Large polar: Q E K R H Y W
Small nonpolar: P A G V Large nonpolar: I L M F

As one would expect, such a recoding will not go well with recently diverged taxa, but appears to work well with highly diverged taxa.

To access the function, read in a file with aligned amino acid sequences into DAMBE (or protein-coding

nucleotide sequences to be translated into amino acid sequences in DAMBE), and click the menu "Phylogenetics|Maximum likelihood|ProtML for highly diverged seqs". A dialog will be presented for you to set tree-searching options or set number of resamples for bootstrap or jackknife.

2. DNDML+: This new function combines the strength of tree-search in fastDNAML with the richness of substitution models in PAML's BASEML. A compromise is made to speed up the computation, i.e., the parameters and topology are not estimated simultaneously. The function first does a quick tree, then estimate the parameters using the tree, then use the fixed parameters to search tree,

To access the function, click the menu "Phylogenetics|Maximum likelihood|DNAML+". A dialog will ensue for you to choose substitution models and set tree-searching options.

3. The sequence editor is revised. The sequence alignment editor in previous versions was designed to edit sequences of unlimited length. However, switching sequence segments in and out the display window causes problems. This new version limits the sequence length to 32767 which should be alright in most cases.

4. I have added neXML (<http://www.nexml.org>) support. This function requires you to install Microsoft's MSXML6.msi which is linked next to the DAMBE installation page. You should install this first before installing DAMBE. If you do not install MSXML6.msi, you will receive an error during DAMBE installation which you may ignore. Everything should be as usual except that neXML support would be missing.

For saving sequences in neXML format, just click "File|Save/convert sequence format". In the ensuing dialog box, click the "Save as type" dropdown box. You will find many different sequence formats, such as MEGA, PHYLIP, PAUP, PAML, etc., with neXML being the last one.

For reading sequences in neXML format, just click "File|Open standard sequence file". In the next dialog box, click the "File of type" dropdown box. You will find many different sequence formats such as MEGA, PHYLIP, PAUP, PAML, etc., with neXML being the fourth from the bottom.

You can also read and save trees as well as non-sequence data in neXML formats.

Eventually I hope that I will only need to support the neXML format, although I know that stabilizing selection in favour of neXML format is still pretty weak.

neXML is still an evolving project and there are other

alternative XML specifications for phylogenetics. For the time being, neXML seems to make sense to me.

(There is no VISTA version yet as I have not yet installed VISTA on any of my computers. Heard that the Windows after VISTA would be meaner and leaner. Hope that it is true.)

Best Xuhua

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

Software In Co Fam

Dear Evoldir members,

Version 1.0 of the software In_Co_Fam is ready to be downloaded from the site

< <http://www.uvigo.es/webs/c03/webc03/XENETICA/XB2/Jesus/Fernandez.htm> > <http://www.uvigo.es/webs/c03/webc03/XENETICA/XB2/Jesus/Fernandez.htm> This software allows for the detection of erroneous assignments when dealing with pairwise estimations of coancestry from molecular information. In particular the software detect incongruous triplets of FS (not being reciprocally full-sibs) and incompatibilities with the Mendelian rules of allele transmission in full sibs families of more than two individuals. One practical application of the software, as well as deeper explanations on the kind of errors that can be incurred when inferring genealogical relationships from pairwise estimations of coancestry, can be found in Rodríguez-Ramilo et al. (2007) *Aquaculture* 273: 434 442.

Sincerely

Jesús Fernández Martín Departamento de Mejora Genética Animal 34-91 3471487 Instituto Nacional de Investigación y 34-91 3572293 (FAX) Tecnología Agraria y Alimentaria (INIA) jmj@inia.es Crta. A Coruña Km. 7,5 28040 Madrid (SPAIN) <http://www.uvigo.es/webs/c03/webc03/XENETICA/XB2/Jesus/Fernandez.htm>

Jesús Fernández <jmj@inia.es>

Software MIXED PROTEIN TREEFINDER

A new unpaid TREEFINDER version is online at:

www.treefinder.de TREEFINDER is a software to compute phylogenetic trees from molecular sequences.

New features are:

- mixed protein model: MIX - Dayhoff groups protein model: DG - improved model proposer

A mixed protein model MIX[B1,B2,...] is a linear combination of empirical base models B1,B2,... with weights that are optimized along with the tree. More precisely, their parameter vectors are combined. The MIX does interpolate between the base models, and also extrapolate when weights are negative. The MIX does often fit data much better than any of its base models alone. The user decides which and how many models to mix, the complexity depends on the number of models included. Given enough independent base models, the MIX allows to model any kind of linear dependency between the amino acid replacement parameters, and with 190 or 210 independent base models the MIX becomes equivalent to the 20-state GTR.

The MIX does also work with 20-state RNA models.

The model proposer proposes MIX'es if they are appropriate.

The model proposer does now display the scores and parameters of all models tested. User-defined candidate sets are possible.

Please note that I am still not being paid for my work and that I had no income for years. I wonder if somebody finds TREEFINDER worth offering me a compensation, a wage, a position, a perspective.

Gangolf Jobb

Gangolf Jobb <gangolf@treefinder.de>

Software msBayes update

Dear Evoldir-ers,

The updated msBayes (v20080515) is ready for download at <http://msbayes.sourceforge.net/> msBayes (pronounced em es bayeszz) allows complex and flexible comparative phylogeographic inference.

More specifically, you can test for simultaneous divergence or colonization across multiple co-distributed pairs of taxa (populations and/or species). It uses hierarchical approximate Bayesian computation (HABC) to estimate hyper-parameters given DNA sequence data. The HABC algorithm uses a finite sites version of ms, the classic coalescent simulator written by Dick Hudson.

The hierarchical model incorporates uncertainty into each set of taxon- pair demographic parameters (sub-parameters) while estimating hyper- parameters that characterize the congruence in divergence/colonization times across the co-distributed taxon-pairs.

Sub-parameters include:

post-divergence migration rates ancestral population sizes descendent population sizes population size change parameters recombination Divergence/colonization times

New features:

One can run a constrained analysis where the number of different divergence times (PSI) is fixed to any user-defined value. In this case, additional hyper-parameters are estimated. For example, after running an initial unconstrained analysis, one can subsequently run an analysis where the number of different divergence times (PSI) is fixed to the estimate from the initial unconstrained analysis. In this constrained, analysis, each of these PSI times are estimated as are the number of taxon-pairs that were split at each of these PSI times. One can use a greatly expanded set of summary statistics for the HABC acceptance/rejection algorithm. This includes four measures of Shannons allelic diversity Index as well as sub-population measurements of various pair-wise differences metrics and number of segregating sites metrics. Automatic calculation of Bayes factors that quantify posterior support for hyper-parameter values Can constrain any taxon-pair sub-parameters to any user-defined value Can convert estimates of mean divergence times into Earth years Allows at least a 10-fold higher number of Hyper-prior simulations (draws) Improved error checking such as identifying when local linear regression fails

Down the road: multi-locus msBayes

msBayes runs on Linux, Mac OS-X, and most POSIX systems. Although you need to use command line interface, it is fairly simple. msBayes is written in perl,

C, and R. msBayes is released under the GNU Public License.

Sincerely, Team msBayes

Mike Hickerson Wen Huang Eli Stahl Naoki Takebayashi

Mike Hickerson, Ph.D. Assistant Professor Biology Department Queens College, CUNY 65-30 Kissena Boulevard Flushing, NY 11367-1597 Tel: 718 997 3447 michael.hickerson@qc.cuny.edu http://-qcpages.qc.cuny.edu/Biology/fac_stf/hickerson.php Eli Stahl Assistant Professor Department of Biology University of Massachusetts, Dartmouth 285 Old Westport Rd. North Dartmouth, MA 02747 estahl@umassd.edu <http://molpopgen.org/elistahl/elistahl.html> Naoki Takebayashi

Assistant Professor

311 Irving I Bldg Institute of Arctic Biology and Department of Biology and Wildlife

University of Alaska, Fairbanks

Fairbanks, AK 99775, USA

Ph: (907) 474-1178

ffnt@uaf.edu

<http://www.faculty.uaf.edu/ffnt/> Mike Hickerson
<michael.hickerson@qc.cuny.edu>

Software quantiNEMO

Dear Evoldir members,

We would like to draw your attention to quantiNEMO, an individual-based, genetically explicit stochastic simulation program.

quantiNEMO was developed to investigate the effects of selection, mutation, recombination, and drift on quantitative traits with varying architectures in structured populations connected by migration and located in a heterogeneous habitat. QuantiNEMO is highly flexible at various levels: population, selection, trait(s) architecture, genetic map for QTL and/or markers, environment, demography, mating system, etc.

Executables for several platforms, user's manual, and source code are freely available under the GNU General Public License at <http://www2.unil.ch/popgen/-softwares/quantinemo> Program Note:

Neuenschwander, S., Hospital, F., Guillaume, F. and Goudet, J. (2008) quantiNEMO: an individual-based program to simulate quantitative traits with explicit genetic architecture in a dynamic metapopulation, *Bioinformatics*, btn219.

Best regards,

Samuel Neuenschwander, Frederic Hospital, Frederic Guillaume, Jerome Goudet

Samuel Neuenschwander
<Samuel.Neuenschwander@unil.ch>

SouthAfrica Volunteers SmallMammals

Volunteer needed as field assistants for the project:

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

>From September onwards

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

What kind of people are needed? Biology/zoology/veterinary students with a BSC/Vordiplom or equivalent are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o' clock), and stops its activity with dusk (19 o' clock). Work during nights might also be necessary. Work in the field will be done for 5-6 days a week. Applicants must be able to manage extreme temperatures (below 0 at night, sometimes over 40C during days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small group.

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

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their uni-

versity for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 750 (around 65 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 2000 or 170 Euro/month). Including extras, you should expect costs of about 250 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

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

When and how long: Currently we are looking for one volunteer to start middle of August, two volunteers to start beginning of September and two to start beginning of December. Volunteers are expected to stay at least 2 months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to carsten.schradin@zool.uzh.ch.

More information under www.stripedmouse.com Contact via e-mail: carsten.schradin@zool.uzh.ch

Dr. Carsten Schradin

Research Assistant, Zoological Institute, Department of Animal Behavior,

University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland.

Tel: +41 - (0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences,

University of the Witwatersrand, South Africa.

Dr. Carsten Schradin Research Associate, Zoological Institute, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel; +41 - (0)44 635 5486 Fax: +41 - (0)44 635 5490

(Tel. secretary: +41 - (0)44 635 5271)

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

Succulent Karoo Research Station, Goegap Nature Reserve, Private Bag X1, 8240 Springbok, South Africa.

visit <http://www.stripedmouse.com> Carsten Schradin
<carsten.schradin@zool.uzh.ch>

SSESB Diversity call for mentors

Approximately 20 undergraduates will be participating in the NSF- and NESCent-supported Undergraduate Diversity at SSE/SSB program. This program, which brings students to the annual Evolution meeting, has been running continuously since 2003.

An important component of the program is the mentoring that students receive from graduate students, post-docs and faculty. Several have already volunteered to serve as mentors this year (including some who volunteered in previous years), but we need about a half dozen more. Duties will include meeting a pair of undergraduates in the program, attending and demystifying a day of talks with them, joining them for a meal, introducing them to colleagues and in general befriending them in ways that show that evolutionary biology is a welcoming discipline. No costs for travel, housing or registration are covered.

If you are interested in serving as a mentor, please send an email to either Rich Kliman (rmkliman@cedarcrest.edu) or Scott Edwards (sedwards@fas.harvard.edu). Please also indicate your broad field of interest, so that we can pair you with appropriate students. And please help spread the word about this very rewarding activity.

Thanks! Rich

Richard Kliman <Rmkliman@cedarcrest.edu>

Taxonomy discussion list

The Open Biomedical Ontologies project (OBO; <http://obofoundry.org>) has created a new mailing list for the discussion of ontological representation of taxonomies and phylogenies. The OBO Foundry supports the development of orthogonal, interoperable reference ontologies for biological science.

The Phenoscape project (<http://phenoscape.org>) is funded by NSF-BDI and supported by the National

Evolutionary Synthesis Center (NESCent; <http://nescent.org>) to develop methods and tools for using ontologies to integrate comparative morphological data with mutant phenotypes of genetic model organisms. As such we are very interested in participation from members of the evolutionary biology community to explore how best to integrate taxonomy into an ontological framework. Issues include proper semantics of the relationship between taxonomic groups, and between specimens and species.

Join the mailing list: <https://lists.sourceforge.net/lists/listinfo/obo-taxonomy> James P. Balhoff, Ph.D.
Research Programmer National Evolutionary Synthesis Center 2024 West Main St., Suite A200 Durham, NC 27705 USA

balhoff@nescent.org

ThermalAdaptation call for postdoc grants

***** PERMANENT CALL FOR POST-DOC GRANT APPLICATIONS *****

In 2006 we launched a new ESF Programme on “Thermal adaptation in ectotherms: Linking life history, physiology, behaviour and genetics” (ThermAdapt); see <http://www.esf.org/thermadapt>. The Objective of this ESF Programme is to foster a multidisciplinary European network of scientists working on thermal adaptation. We particularly aim to integrate research at multiple levels of investigation, including genetics, physiology, ecology, behaviour or theory. Interested persons or groups are encouraged to join our activities. These include advertising their expertise via our web site, and participation in various activities to be announced separately and regularly over the next 5 years such as workshops, training courses, short and long exchange grants, exchange of specimens and expertise, sharing of facilities, and scientific collaboration of any kind.

We PERMANENTLY call for applications for

==> Short Visit (< 15 days) and Exchange Grants (15 days - 3 months)

There is no particular deadline. Instead, submission of grant proposals is now PERMANENTLY OPENED, as explained on our web site <http://www.esf.org/thermadapt> under > Grants, where the application pro-

cedure is also outlined. We shall periodically review submissions about every 3 to 4 months.

Proposals should be broadly related to the scientific objectives of the Programme. Short Visits may serve for planning collaborative research projects, brief data gathering or data analysis. The longer-term Exchange Grants typically involve planning and execution of a larger collaborative research project (under special circumstances stays longer than 3 months may be possible).

Grant applications will be chosen based on scientific quality, and priority will be given to applicants who come from or intend to visit countries supporting the programme (Austria, Belgium, Czech Republic, Denmark, Estonia, Finland, Germany, Hungary, Netherlands, Portugal, Slovenia, Spain, Switzerland), but other European nations can be involved.

For further inquiries, or if you wish to be included in the ThermAdapt e-mail list to receive regular updates on Programme activities, please contact:

Ellen Degott (ESF office liaison; Email: edegott@esf.org) Wolf Blanckenhorn (chair; Email: wolf.blanckenhorn@zm.uzh.ch) Mauro Santos (co-chair; Email: mauro.santos@uab.es)

Dr. Wolf Blanckenhorn Chairman ESF ThermAdapt Programme Zoological Museum University of Zurich-Irchel 34 (building)-J (floor) -98 (office) Winterthurerstrasse 190 CH-8057 Zurich

Phone: +41 44 635.47.55 Fax: +41 44 635.47.80 e-mail: wolf.blanckenhorn@zm.uzh.ch <http://www.esf.org/-thermadapt> wolfman@zm.uzh.ch wolfman@zm.uzh.ch

ThermalAdaptation call for workshop grants

**** PERMANENT CALL FOR WORKSHOP GRANT APPLICATIONS ****

In 2006 we launched a new ESF Programme on “Thermal adaptation in ectotherms: Linking life history, physiology, behaviour and genetics” (ThermAdapt); see <http://www.esf.org/thermadapt> . The Objective of this ESF Programme is to foster a multidisciplinary European network of scientists working on thermal adaptation. We particularly aim to integrate research at multiple levels of investigation, including genetics,

physiology, ecology, behaviour or theory. Interested persons or groups are encouraged to join our activities. These include advertising their expertise via our web site, and participation in various activities to be announced separately and regularly over the next 5 years such as workshops, training courses, short and long exchange grants, exchange of specimens and expertise, sharing of facilities, and scientific collaboration of any kind.

We PERMANENTLY call for applications for local organization of

==> WORKSHOPS, SCIENCE MEETINGS or TRAINING COURSES on specific topics within the realm of the ThermAdapt Programme

There is no particular deadline. Instead, submission of workshop proposals is now PERMANENTLY OPENED, as explained on our web site <http://www.esf.org/thermadapt> under > Science Meetings, where the application procedure is also outlined. We shall periodically review submissions about every 3 to 6 months.

Such workshops, financed by our ESF programme if approved, bring together between 10 and 50 participants for 2 to 4 days to focus on a specific issue and are planned to occur on an annual basis over the coming years.

Workshop grant applications will be chosen based on scientific quality, and priority will be given to applicants who come from or intend to visit countries supporting the programme (Austria, Belgium, Czech Republic, Denmark, Estonia, Finland, Germany, Hungary, Netherlands, Portugal, Slovenia, Spain, Switzerland), but other European nations can be involved.

For further inquiries, or if you wish to be included in the ThermAdapt e-mail list to receive regular updates on Programme activities, please contact:

Ellen Degott (ESF office liaison; Email: edegott@esf.org) Wolf Blanckenhorn (chair; Email: wolf.blanckenhorn@zm.uzh.ch) Mauro Santos (co-chair; Email: mauro.santos@uab.es)

Dr. Wolf Blanckenhorn Chairman ESF ThermAdapt Programme Zoological Museum University of Zurich-Irchel 34 (building)-J (floor) -98 (office) Winterthurerstrasse 190 CH-8057 Zurich

Phone: +41 44 635.47.55 Fax: +41 44 635.47.80 e-mail: wolf.blanckenhorn@zm.uzh.ch <http://www.esf.org/-thermadapt> wolfman@zm.uzh.ch wolfman@zm.uzh.ch

UV for sterilization

I am based in a molecular ecology laboratory and am planning to extract DNA from and genotype modern and museum specimens of the same species. So, obviously there is potential for cross-contamination here.

I work under a UV hood and so all my equipment is

sterilised under a UV crosslinker before use. I also UV sterilise my extraction buffer and ddH₂O, I was wondering if enzymes (such as proteinase K and Taq) and other PCR reagents (i.e. dNTPs) can also be treated in this way or would their efficacy be adversely affected? Some people have suggested that as proteinase K is so stable it should be able to withstand UV but that dNTPs could not, others disagree!

Any suggestions?

Many thanks, Claire

claireraisin@hotmail.com

PostDocs

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EmoryU HostParasiteEvolution

Reminder: Application Deadline May 15th

Insect-Pathogen Postdoctoral Position Emory University, Atlanta, GA USA Laboratory of Dr. Nicole Gerardo

There is funding available for one postdoctoral re-

searcher in the laboratory of Dr. Nicole Gerardo. Our lab's focus is on the evolutionary ecology of microbial host-parasite interactions.

We combine molecular genetics, phylogenetics and experimentation to study pathogens associated with diverse insect systems. Our research is centered on understanding how insect hosts adapt to defend against pathogens and how pathogens then adapt to overcome these host defenses. We also study how mutualistic microbes may play a role in defending their hosts against pathogens. Initial projects will focus largely on the interactions of aphids, their bacterial symbionts and microbial pathogens, though there may be opportunities to work on fungus-growing ants and other systems as well. For more information, go to www.biology.emory.edu/-research/Gerardo/Gerardohome.html. The lab is part of Emory's Population Biology, Ecology and Evolution program, which has a strong focus on host-parasite interactions and disease ecology. For more information on the program and the researchers at Emory, go to: www.biomed.emory.edu/-PROGRAM_SITES/PBEE/ Candidates should have a background in host-parasite interactions or symbioses, as well as an interest in research combining experimental and molecular approaches to understanding the interaction of insects and their microbial communities. Background in experimental biology of insects and or microbes, molecular ecology, and/or bioinformatics strongly preferred. Postdocs must have strong communication skills and be willing to help with lab maintenance and training of undergraduate students. If interested, please send a CV, along with a brief statement of interests and experiences in the above-mentioned areas, to Nicole Gerardo by May 15, 2008. After May 15th, Nicole will begin to review the applications and will ask for references from some candidates. Candidates must be able to start the position no later than January 2009.

Dr. Nicole Gerardo Emory University Department of Biology

nicole.gerardo@emory.edu

INRA Dijon France WeedPopulations

Post-doctoral fellowship: *Spatio-temporal processes underlying the structure of weed communities*.

We are looking for a highly motivated post-doctorate associate with a solid mathematical/analytical background to join a research team on investigating the spatio-temporal processes underlying the structure of weed communities.

Recent studies over several European countries have shown the dramatic decrease of the specific weed diversity in industrialized agriculture over the last decades. On the basis of extensive regional and national long-term datasets, the post-doctorate will investigate the mechanisms that shape weed community structure in various crop types in France. The research will focus on quantifying the relative importance of temporal (i.e. crop rotations) and/or spatial (i.e. landscape structure and fragmentation) heterogeneities on the composition of weed communities and their associated biodiversity value. The relative effects of other mechanisms such as environmental properties (climatic, soil, topographic), plant functional traits and agriculture practices could also be investigated. The post-doctorate will work in the Biology and Management of Weeds lab, as a member of the research unit consisting of research staff, technical assistants, Ph.D., masters and undergraduate students and postdoctoral fellows. The lab is located in INRA Dijon in a scientifically rich environment for agro-ecology. The position will provide with excellent opportunities for publications.

The post-doctorate position requires an independent and highly motivated researcher with excellent English writing and data analysis skills (advanced knowledge of statistics under R platform), who has a keen interest in population and community dynamics, evolution and spatio-temporal modelling. The applicant should have a PhD in evolution or applied statistics, and experience in theoretical and applied studies. Experience in community evolution will be an asset.

The post is open from 1st September 2008, for one year. It may be renewable for a second year subject to availability of funds and satisfactory performance. The position is open to all nationalities with the exception of French citizen. PhD thesis should have been defended less than 5 years ago. The fellowship amount is of 2000 after taxes per month (health care is included). Dijon offers the pleasant environment of the Burgundy region, with gastronomy, historical interest and nice natural environmental surroundings. Paris is at around 1 h 40 min by TGV train.

Deadline for application: 30 June 2008. Please send by e-mail your application, including CV, names of two reference persons and a brief statement of research interest to:

Sabrina Gaba (sabrina.gaba@dijon.inra.fr)

<mailto:sabrina.gaba@dijon.inra.fr>

Sandrine Petit (sapetit@dijon.inra.fr
<mailto:sapetit@dijon.inra.fr>.) UMR INRA-
ENESAD-Université de Bourgogne Biologie et
Gestion des Adventices 17 rue Sully BP 86510,
21065 Dijon Cedex, France

Tel: +33 (0)3 80 69 31 87

Sabrina Gaba <sabrina.gaba@dijon.inra.fr>

KansasStateU EvolutionaryGenomics

POSTDOCTORAL RESEARCH FELLOWSHIP IN EVOLUTIONARY GENOMICS AT KANSAS STATE UNIVERSITY

To view the following announcement on a webpage, please visit: <http://www.k-state.edu/ecogen/Recruit-Postdoc-EcogenVS.htm>. A postdoctoral research fellowship is available through the Ecological Genomics Institute (www.k-state.edu/ecogen) at Kansas State University (K-State). Our interdisciplinary Institute seeks to understand responses of organisms to their natural environment by combining functional genomic and ecological/evolutionary approaches. The postdoctoral fellow will have access to excellent university resources including the Konza Prairie Biological Station, a core Long-Term Ecological Research (LTER) site (www.climate.konza.ksu.edu), the K-State Gene Expression Facility (www.k-state.edu/gene-exp), and infrastructure of the Division of Biology and Departments of Entomology, Agronomy and Plant Pathology. For additional information about the Ecological Genomics Institute please visit the Ecogen website!

Candidates must have excellent oral and written communication skills, demonstrate evidence of past research achievement, and have completed requirements for a Ph.D. by the start date. This full-time position provides a competitive salary and benefits. The anticipated start date is summer or fall 2008.

Full applications must include: 1. A cover letter detailing your qualifications and proposed start date. 2. A research proposal (three page maximum, not including references). *Proposals utilizing genetic and/or genomic approaches to examine evolutionary relevant traits or interactions will receive highest priority. 3. A current curriculum vitae. 4. Two letters of recommendation from referees who are familiar with the appli-

cant's research. Major advisor or members of supervisory committee preferred.

Completed applications can be e-mailed to Doris Merrill at dmerrill@ksu.edu. Applications can also be sent by regular mail to: Ecological Genomics Kansas State University Division of Biology, Ackert Hall Manhattan KS 66506-4901

Review of applications will begin July 1, 2008. This position is sponsored by a Kansas State University Targeted Excellence Award in Ecological Genomics.

K-State is an Equal Opportunity Employer, and actively seeks diversity among its employees.

PLAN NOW to attend.... the 6th Annual "Genes in Ecology, Ecology in Genes" Ecological Genomics Symposium, November 14 - 16, 2008, at the InterContinental Hotel on the Plaza in Kansas City.

Doris Merrill, Program Coordinator Ecological Genomics Institute Kansas State University, Division of Biology 116 Ackert Hall, Manhattan, KS 66506-4901 (785) 532-3482, dmerrill@ksu.edu www.ksu.edu/ecogen dmerrill@k-state.edu

LeibnizInst EvolutionaryGenetics

PostDoc-Position in Evolutionary Genetics

The Leibniz-Institute for Zoo and Wildlife Research (IZW) is one of eight research institutes forming the Forschungsverbund Berlin e.V. and member of the Leibniz-Gemeinschaft. They are jointly funded by the German federal and state governments.

The research group "Evolutionary Genetics" offers a PostDoc-Position (beginning 01. August 2008) on the 'Immune gene expression in relation to parasite loads and human impact in wildlife species'.

Infectious diseases are very strong selective pressures that afflict wildlife populations. The capacity to develop an immune response after exposure to antigens, i.e. the immunocompetence, depends upon the host immune status and is influenced by genetic and environmental factors.

The specific goal for this position is to identify the molecular correlates of immune challenge and pathogen defence and to investigate differential expression of immune response genes in wildlife populations via quantitative real-time PCR. The successful candidate will work as part of an interdisciplinary team investigating

the effects of human impact on parasite loads, population dynamics and levels of neutral and adaptive genetic variability in small mammal populations in the Mata Atlantica/Brazil. In addition, the successful candidate will have the opportunity to establish own externally funded projects related to this topic.

An applicant should have a PhD degree in Biology. Candidates must have a strong background in population genetics, molecular biology and evolutionary ecology. We seek a highly motivated and scientifically creative scientist with an excellent literature overview and publication record in peer-reviewed journals in this field, ability to work independently, team work abilities, social, organisational and good English writing skills. Knowledge of required molecular techniques especially in quantitative expression analyses via real-time PCR is essential.

The position is limited to one year. The IZW is an equal opportunity employer. Applications from women are strongly encouraged. Preference will be given to disabled applicants with the same qualifications.

For further information please contact Prof Dr. Simone Sommer + 49 30 5168-315 or Sommer@izw-berlin.de

Applicants should submit a letter explaining their research interests and background and particular skills for this position, a CV including candidate's photo, a summary of the PhD thesis, two letters of recommendation and publication list preferentially before 31.05.2008. We will consider applications until the position is filled. Please cite reference 10/2008.

Application should be sent to:

Leibniz-Institut für Zoo- und Wildtierforschung im
Forschungsverbund Berlin e. V. z. Hd. Frau Wagner
Postfach 60 11 03 10252 Berlin

“Sommer, Simone” <SOMMER@izw-berlin.de>

LouisianaStateU ComparativePhylogeography

POSTDOCTORAL RESEARCHER Department of Biological Sciences

Required Qualifications: (Postdoc) Ph.D. or equivalent in Biology or related field. Additional Qualifications Desired: (Postdoc) Experience gathering and analyzing genetic data, particularly DNA sequences and/or microsatellites. Responsibilities: (Postdoc) conducts

comparative phylogeographic research in a plant-insect community, including molecular wet-lab work, data analysis, and some fieldwork. An offer of employment is contingent on a satisfactory pre-employment background check. Application deadline is May 16, 2008 or until a candidate is selected. Send statement of interest, CV (including e-mail address), and contact information for two professional references to:

Dr. Bryan Carstens Department of Biological Sciences
Louisiana State University Ref: #012809 Baton Rouge,
LA 70803

Phone: (225) 578-0960 E-mail: carstens@lsu.edu

LSU IS AN EQUAL OPPORTUNITY/EQUAL ACCESS EMPLOYER

–

Bryan C. Carstens Assistant Professor Department of Biological Sciences Louisiana State University

mail 202 Life Sciences Building Louisiana State University Baton Rouge, LA 70803 USA

e-mail carstens@lsu.edu bryan.c.carstens@gmail.com

web <http://www.biology.lsu.edu/webfac/Carstens/-index.htm> office A114 Life Sciences Annex (225) 578-0960

lab A153 Life Sciences Annex (225) 578-4918

fax (225) 578-2597

carstens@lsu.edu carstens@lsu.edu

McMasterU MetagenomicData

POST-DOCTORAL POSITION: Theoretical Biology/Metagenomics Department of Biology, McMaster U., Hamilton ON

We are seeking a computational biologist to work on theoretical methods for analyzing metagenomic data, and exploring the 'space' in which genomes evolve. The successful candidate will pursue collaborative research with Dr. Jonathan Dushoff, and collaborators at Georgia Tech, Princeton University, and UC Davis, and will be expected to take an active role in shaping the direction of this research.

We are looking for a candidate with a solid grounding in biology, as well as computational and mathematical skills. The candidate will be expected to help develop, and to apply, novel statistical and mathematical

methods to understanding genomic data. The position will be based in the Disease Modeling lab at the Department of Biology, where we are currently developing a state-of-the-art computer platform for collaborative multi-scale modeling. Our lab also has access to the high-performance Sharcnet computer cluster.

Hamilton, Ontario is a pleasant place to live and work, less than an hour from both the Niagara gorge and from Toronto (and convenient to the latter by public transportation). The McMaster campus is large and green; conveniently accessible by city buses; within walking distance of pleasant residential neighborhoods; and adjacent to the Cootes Paradise section of the Royal Botanical Gardens.

The position is expected to last for two years. Review of applications will begin on 1 July 2008. Anticipated starting date is 1 Oct 2008, and is negotiable. To apply, please send (by email, in PDF format, to the address below): (1) a CV; (2) a list of three scientists who can be contacted for letters of reference; (3) a one-page statement of research interests; and (4) a half-page summary of skills and experience relevant to the pursuit of computational biology.

Jonathan Dushoff McMaster U. Department of Biology
dushoff@mcmaster.ca

Jonathan Dushoff <dushoff@mcmaster.ca>

NHM LosAngeles FishSystematics

POSTDOCTORAL FELLOW IN SYSTEMATIC ICHTHYOLOGY - NATURAL HISTORY MUSEUM OF LOS ANGELES COUNTY

The Natural History Museum of Los Angeles County seeks a postdoctoral fellow in systematics and evolution of fishes. The successful candidate will be a self-motivated researcher with a PhD. in organismal biology and evolution, a strong track record in systematic ichthyological research, and a research focus that includes analysis of molecular data. Focus on marine fishes is desirable, but not required. Research plans which include use of the museum's fish collection are also desirable, but not required. This two year position begins August or September 2008. Applications should include a Curriculum Vitae, statement of research interests and proposed research project, copies of relevant publications, and names and contact information for three referees. Review of applications will begin July

15, 2008. Questions may be addressed to Dr. Christine Thacker (thacker@nhm.org), and I will also be attending the 2008 ASIH meetings in Montreal, where I encourage candidates to contact me if they are interested in the position. Submissions must be made by email to thacker@nhm.org. The Natural History Museum of Los Angeles County is an Equal Opportunity Employer.

Christine Thacker Associate Curator of Ichthyology
Natural History Museum of Los Angeles County 900
Exposition Blvd. Los Angeles, CA 90007 Voice: 213
763 3210 Fax: 213 748 4432

thacker <thacker@nhm.org>

NorthCarolinaStateU DiseasePopulationGenetics

NC State University Vector/disease genetic models

Postdoctoral Fellowship

Vector/disease genetic models: We need a mathematically oriented biologist (or biologically oriented mathematician) with experience in population genetics and/or epidemiology to work on an NIH- and Gates Foundation-funded project.

The project is aimed at building stochastic, spatially explicit, simulation models that link insect population dynamics, disease epidemiology, and population genetics in a way that can contribute to improving strategies for releasing transgenic mosquitoes to reduce the incidence of human disease. The fellowship is for 2 years but could be extended for a third year pending additional funding. In addition to working on model development and analysis, the person in this position will collaborate in an interdisciplinary group composed of mosquito ecologists, disease epidemiologists, molecular biologists, biomathematicians, ethicists, and scientists from disease-endemic countries, in efforts to develop novel transgenic strategies for disease reduction. The person in this position will work the PIs (Fred Gould & Alun Lloyd) and another postdoc in organizing a workshop to teach other researchers how to use the models.

There will be an opportunity for some empirical research (if desired), and for interactions with other members of the lab who are working on other ecological and evolutionary research. NCSU has just begun development of an interdisciplinary graduate program in Genetic Pest Management, so there are likely to be teach-

ing opportunities.

An overview of the area of research and an entry point to relevant literature can be found in:

Gould, F. K. Magori, and Y. Huang. 2006. Genetic strategies for controlling

mosquito-borne diseases. *Am. Sci.* 94:238-246.

Sinkins, S. P., and F. Gould. 2006. Gene-drive systems for insect disease

vectors. *Nat. Rev.* 7:427-435.

North Carolina State University is a leading research institution with a strong commitment to the study of quantitative and population genetics. The University is situated in Raleigh, NC and is within 30 miles of Duke University, UNC-Chapel Hill, NIEHS, an EPA research unit, and the Research Triangle Park. NC State University is an equal opportunity and affirmative action employer.

To apply: Send to Fred_Gould@NCSU.edu 1) A one or two page letter of intent. 2) CV,

and 3) Names of 3-4 references. Closing date for applications is July 15, 2008, or until a suitable candidate is found. For further information call Fred Gould at 919-515-1647 or email to above email address.

fred_gould@ncsu.edu fred_gould@ncsu.edu

Paris MemoryEvolutionaryBiol

POSTDOC EVOLUTIONARY BIOLOGY OF MEMORY CNRS Gif Sur Yvette, France

A 3 year postdoctoral position is available in the Laboratory of Evolution, Genomes, and Speciation (LEGS, CNRS) in Gif sur Yvette (France) to work on the evolutionary biology of memory. The starting date of the position is programmed for September 1st 2008. In *Drosophila*, 4 different memory phases have been described (short-term, middle-term, anesthesia-resistant and long-term). Using selection experiments, population comparisons and conditioning assays, we are addressing issues such as: Genetic and environmental variations of learning and memory among *drosophila* species and populations, fitness benefits and costs of the different memory phases, effect of ecologically-relevant stress on the memory phases. The successful candidate should be highly motivated and will develop his/her own project in this area. Candidates should have a

PhD in Evolutionary Biology, Animal Behavior or Neuroscience. Some experience with *Drosophila* behavior, genetics or molecular methods would be helpful but are not required. The application is open to all nationalities and is funded by the European Research Council (the salary is around 2100 Euro/Month taxes included). No pre-existing knowledge of French is required to work in the lab, although some knowledge makes living in France easier. Gif sur Yvette is located 40 min from downtown Paris. To apply, send your CV, a letter describing your research interests and some ideas for a project to Frederic.mery@legs.cnrs-gif.fr. Arrange for one or two letters of recommendation to be sent to the same address.

The review of applications will begin on June 15, 2008.

Frederic Mery Laboratoire Evolution, Genomes et Speciation CNRS - Bat 13 Avenue de la Terrasse F-91198 Gif sur Yvette Cedex France E-mail: Frederic.Mery@legs.cnrs-gif.fr Phone (Office): (33) 1 69 82 37 32 Phone (Lab): (33) 1 69 82 38 63 Fax: (33) 1 69 82 37 36 Web: <http://www.legs.cnrs-gif.fr/> Frederic Mery Laboratoire Evolution, Genomes et Speciation CNRS - Bat 13 Avenue de la Terrasse F-91198 Gif sur Yvette Cedex France

E-mail: Frederic.Mery@legs.cnrs-gif.fr Phone (Office): (33) 1 69 82 37 32 Phone (Lab): (33) 1 69 82 38 63 Fax: (33) 1 69 82 37 36

Web: <http://www.legs.cnrs-gif.fr/perso.php?id=3D106&lang=3Dfr> Frederic Mery <Frederic.Mery@legs.cnrs-gif.fr>

PennsylvaniaStateU 3 ViralEvolution

Up to three postdoctoral positions are available to work with Professor Eddie Holmes at The Pennsylvania State University on various aspects of virus evolution. Particular areas of research interest include (i) the basic mechanisms of RNA virus evolution (mutation, recombination etc.), (ii) macroevolutionary processes in RNA viruses, (iii) the evolutionary biology of emerging viruses, and (iv) the molecular epidemiology of influenza virus. One position will focus on the emergence and evolution of parvoviruses in animals in a collaborative project with Professor Colin Parrish at Cornell University, and this position will most likely be based at Cornell University.

Each position requires a Ph.D. and a record of published research in areas related to molecular evolution, computational biology and/or virology. Candidates with a strong background in mathematics, statistics and/or computing are particularly encouraged to apply. Each postdoctoral position will be for an initial period of two years. The positions are currently open, and the starting date is negotiable.

All qualified applicants should submit a cover letter, a curriculum vitae, and the names and email addresses of three references by email to:

Eddie Holmes, Center for Infectious Disease Dynamics, Department of Biology, The Pennsylvania State University, Mueller Laboratory, University Park, PA 16802. USA. Email: ech15@psu.edu URL: http://www.cidd.psu.edu/people/bio_holmes.html Women and minorities are encouraged to apply. We encourage applications from individuals of diverse backgrounds. Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

Eddie Holmes, Center for Infectious Disease Dynamics, Department of Biology, The Pennsylvania State University, Mueller Laboratory, University Park, PA 16802. USA. Tel. 1 814 863 4689 Fax. 1 814 865 9131 URL: http://www.cidd.psu.edu/people/bio_holmes.html Eddie Holmes <ech15@psu.edu>

Scotland Ornithology

Research Evolutionist BTO Scotland (£25,051 - £27,834 plus pension) 2-year contract The British Trust for Ornithology is seeking an enthusiastic and innovative evolutionist to further enhance its ornithological research in Scotland.

Candidates should have a PhD in evolutionary biology or a related subject (or equivalent experience), three years post-doctoral experience, and a proven track record of research development and scientific publication. Applications from researchers with experience of applied issues in upland, woodland/forestry, or urban habitats, of seabirds or raptors, or of spatial modelling/GIS-based approaches are particularly welcome.

Closing date for receipt of applications is Monday 9 June 2008.

Further details on the post are available from Sophie Foulger, BTO, Thetford, Norfolk, IP24 2PU (Tel:

01842 768247; email jobs@bto.org) or from our website: <http://www.bto.org/> Please quote reference UN/08-2.

Rupert Marshall <rmm@aber.ac.uk>

SwanseaU SalmonEvolution

Postdoctoral Position in Salmon Evolutionary Ecology

An EU-funded (SALSEA-MERGE) postdoctoral position is available for 20 months starting on September 2008 at the Department of Environmental and Molecular Biosciences (Swansea University; <http://www.swan.ac.uk/biosci/>) in collaboration with the Institute of Biological, Environmental and Rural Sciences (Aberystwyth University; <http://www.aber.ac.uk/-biology/>).

SALSEA-MERGE combines genetic and ecological investigations to infer the migration and distribution of Atlantic salmon at sea, and seeks to understand the reasons for the high marine mortality and widespread decline of Atlantic salmon across its range.

The successful candidate will work on the development of a genetic database to support the identification of the region and river of origin of Atlantic salmon captured at sea, and will undertake a molecular analysis of growth patterns and natural selection at different time scales. The work will involve microsatellite typing, as well as the development of a suite of SNP markers for mitochondrial DNA in collaboration with partners at the FRS Freshwater Laboratory (Pitlochry, Scotland).

Required qualifications: - PhD in evolutionary biology, population genetics, molecular ecology or a related topic - Research experience and first-authored publications on the above mentioned topics

Salary will be in the range £24,403 to £27,466 per annum, depending on experience and qualifications.

Informal enquiries can be directed to Dr. Carlos Garcia de Leaniz c.garciadeleaniz@swansea.ac.uk

<http://www.swan.ac.uk/staff/academic/-EnvironmentSociety/BiologicalSciences/-deLeanizcarlosgarcia/>

or to Dr. Sonia Consuegra skc@aber.ac.uk; <http://www.aber.ac.uk/biology/dept/sonia.consuegra.html>).

Applicants should send a covering letter summarizing their research background and interests, a recent CV, and contact details of three referees. An

application form and further details may be obtained from the Personnel Department, Swansea University, Singleton Park, Swansea, SA2 8PP, tel. (01792) 295136 (24 hours) or at <http://www.swan.ac.uk/personnel/Vacancies/> < <http://www.swan.ac.uk/personnel/Vacancies/> >. The closing date for applications is Thursday July 3rd. Interviews are expected to be carried out on July 2008.

Dr. Carlos Garcia de Leaniz Swansea University Biological Sciences Singleton Park, SA2 8PP Swansea, UK Tel. +44 (0) 1792 295383 Fax. +44 (0) 1792 295447 email. c.garciadeleaniz@swansea.ac.uk

"GarciaDeLeaniz C." <C.GarciaDeLeaniz@swansea.ac.uk>

portunity employer. Female, minority and handicapped candidates, as well as veterans of the Vietnam era are encouraged to apply. Information on benefits for Postdoctoral Researchers at Tulane may be found at: <http://www.tulane.edu/~wfmo/postdoc/postdoc.html>. Henry L. Bart, Jr., Ph.D. Director, Tulane University Museum of Natural History Curator, Royal D. Suttkus Fish Collection 3705 Main Street Belle Chasse, LA 70037 <http://www.museum.tulane.edu/-hank> E-mail address: hank@museum.tulane.edu Voice: 504-394-1711 Fax: 504-394-5045

Hank Bart <hank@museum.tulane.edu>

TulaneU GrowthHormoneGeneEvolution

Postdoctoral Research Associate

The Department of Ecology and Evolutionary Biology at Tulane University seeks a Postdoctoral Research Associate to coordinate all aspects of molecular biological research in the laboratory of < <http://www.museum.tulane.edu/hank/> >Dr. Henry L. Bart, Jr. associated with the Cypriniformes Tree of Life Project (< <http://www.cypriniformes.org/> ><http://www.cypriniformes.org/>). Bart's lab is sequencing the nuclear growth hormone gene across the diversity of Order Cypriniformes, examining expression and functional divergence of duplicate copies of the gene in tetraploid cypriniforms, identifying paralogs of other nuclear genes in these fishes, and using the results to understand the role of genome duplication as a force of evolutionary change. Candidates must have a Ph.D. and should have experience with a variety of molecular biology laboratory techniques and computer software, including primer design, reverse-transcription and real-time PCR, sequence editing and alignment, and data analysis methods. The successful candidate will be expected to participate in research conferences and assist with report writing and publication of results. Send Curriculum Vitae, reprints of published papers, a statement of relevant experience and three letters of recommendation (including one from the dissertation advisor) to Hank Bart, Department of Ecology and Evolutionary Biology, 400 Boggs Hall, Tulane University, New Orleans, LA 70118, or by e-mail to hank@museum.tulane.edu. Tulane University is an Affirmative Action, Equal Op-

UAlaska EvolutionaryBiol

POST-DOCTORAL FELLOWSHIP IN EVOLUTIONARY BIOLOGY AT THE UNIVERSITY OF ALASKA

A post-doctoral student is sought to study the evolution and adaptive value of color polymorphism in coastrange sculpins under the University of Alaska's International Polar Year program. The coastrange sculpin is a particularly well-suited species for examining adaptive responses to newly available habitat following glacial retreat. Sculpins colonize new habitat quickly due to the high dispersal ability of larvae, whereas adults tend to be relatively sedentary once established within streams and show a strong tendency to match stream substrate color. The project will focus on candidate genes involved in color change and the adaptive value of color plasticity using molecular, experimental, and field methods.

The position will be based in Juneau, Alaska, under the guidance of David Tallmon and Tony Gharrett. Start date is early September 2008. The successful applicant will have a PhD in evolutionary biology or a closely related field, along with a strong background in population, quantitative, and/or molecular genetics. An interest in combining lab, experimental, and field data is necessary.

The position will run for one year and may be extended pending the availability of funds. Salary is \$50,000/yr plus benefits with at least a \$5,000 research budget.

For further information or to apply, please email a CV, 1 page cover letter, and contact information for three referees to david.tallmon@uas.alaska.edu. Applicant reviews will begin on June 15th until the position

is filled. Person(s) hired by the University must comply with the provisions of the Federal Immigration Reporting and Control Act of 1986 and must possess a valid Social Security card. All non-resident aliens must provide proof of eligibility to work. The University of Alaska is an equal employment opportunity/affirmative action employer and educational institution. Your application for employment with the University of Alaska is subject to public disclosure under the Alaska Public Records Act. Women and minorities are encouraged to apply.

David Tallmon University of Alaska Southeast 11120
Glacier Hwy Juneau, AK 99801 USA (907) 796-6330

david.tallmon@uas.alaska.edu
david.tallmon@uas.alaska.edu

UAlaska StatisticalPhylogeography

Postdoctoral Fellow in Landscape Genetics We are searching broadly for a Postdoctoral Fellow to work in the general research area of Landscape Genetics and Statistical Phylogeography. The successful applicant will address questions regarding past and current genetic diversity in relation to migration history, past climate change and migration routes within Arctic and Boreal regions including Alaska and the former Beringian landmass. We are particularly keen on research proposals that link GIS-based hypothesis generation with molecular-based hypothesis testing. The organismal focus is open, but the successful applicant will have identified a faculty member at the University of Alaska (Fairbanks-Anchorage-Juneau) who is participating in the current Alaska EPSCoR Initiative in Landscape Genetics. These faculty include the following: Matt Carlson <http://aknhp.uaa.alaska.edu/staff_home_pages/-MattCarlson/mcarlson_home.htm> Kris Hundertmark <www.iab.uaf.edu/~kris_hundertmark/> Steffi Ickert-Bond <<http://www.iab.uaf.edu/~stefanie.bond/>> Link Olson <http://www.uaf.edu/museum/mammal/Link_Olson/> Matt Olson <http://users.iab.uaf.edu/~matt_olson/> Sanjay Payare <http://www.uas.alaska.edu/envs/faculty_staff.html> Derek Sikes <http://www.uaf.edu/museum/ento/sikes_lab/sikes_lab.htm> Naoki Takebayashi <<http://www.faculty.uaf.edu/ffnt/>> David Tallmon <<http://www.uas.alaska.edu/biology/faculty/index.html>> Lee Taylor <http://mercury.bio.uaf.edu/~lee_taylor/> Diana Wolf <<http://www.faculty.uaf.edu/ffdew2/>>

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This position is funded through an NSF-funded Alaska EPSCoR initiative. The fellowship is for 2 years and will include an annual salary of \$42,000 US with benefits. Research funds of \$24,000 are included. Start date is negotiable.

TO APPLY: Applicants are strongly encouraged to first contact participating faculty about potential projects prior to submission of an application. Applicants must apply to posting number 0054683 at the University of Alaska Human Resources website www.uakjobs.com. Applications must include the following: 1) Cover letter referencing the position number 921390, 2) Statement of research interests (up to 2 pages), 3) a current curriculum vitae, 4) three letters of reference, and 5) a UA Applicant Form. Review of applicants will begin June 15 and continue until the position is filled. Person(s) hired by the University of Alaska Fairbanks must comply with the provisions of the Federal Immigration Reporting and Control Act of 1986 and must possess a valid Social Security card. All non-resident aliens must provide proof of eligibility to work. The University of Alaska Fairbanks is an equal employment opportunity/affirmative action employer and educational institution. Your application for employment with the University of Alaska is subject to public disclosure under the Alaska Public Records Act. Women and minorities are encouraged to apply.

Matt Olson <matt.olson@uaf.edu>

UCaliforniaDavis FishDiversification

Postdoctoral position in fish diversification

I am looking to fill a two-year postdoc position in my laboratory to participate in a study of morphological and ecological diversification in several groups of teleost fishes. Experience with phylogenetic reconstruction and comparative methods are the most desired skills, but I will consider people with other backgrounds. Expertise with fish and morphology would be advantageous but is not required. This project is funded by an NSF grant and involves a collaboration with Tom Near at Yale University and Leo Smith at the Field Museum of Natural History.

If you are interested in this position, please send me an email with a summary of your interests and background, and include a copy of your cv.

pcwainwright "at" ucdavis.edu

Peter Wainwright Department of Evolution & Ecology University of California Davis, CA 95616
Phone: 530-752-6782 Fax: 530-752-1449 <http://www.eve.ucdavis.edu/~wainwrightlab/> pcwainwright@ucdavis.edu pcwainwright@ucdavis.edu

UCaliforniaSanDiego ViralEvolution

Postdoctoral position

MODELING SEQUENCE EVOLUTION IN VIRUSES

School of Medicine

University of California San Diego

DESCRIPTION: A fully funded postdoctoral position is available starting June 1, 2008 to work on statistical models of sequence evolution and their application to viral organisms, such as HIV-1 and Influenza A virus. Specific goals include:

- (1) The development of statistical methods and algorithms that estimate properties of evolutionary processes from coding sequence alignments
- (2) Design of new metrics to compare evolutionary properties inferred from different genes in order to develop the concept of evolutionary BLAST
- (3) Analysis of evolutionary patterns in large collections of viral sequence alignments using machine learning, data mining and other statistical techniques

The position will be for one year in the first instance, with the possibility of extension to up to three years, dependent on progress and funding. Salary will be according to NIH-recommended payscales, and commensurate with experience.

RESEARCH GROUP: The position is based in the laboratory of Dr. Simon DW Frost. The successful candidate will work closely with Dr. Sergei Kosakovsky Pond (<http://www.hyphy.org/sergei/>). There is a potential to develop and co-supervise undergraduate and graduate research projects.

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

REQUIREMENTS: A Ph.D. in statistics, population

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

APPLICATION: Please send letter of interest, C.V., and the names and contact details of three referees by June 1st, 2008 to: Postdoctoral Position in Statistical Evolutionary Models, Dr. Simon Frost, UCSD Antiviral Research Center, 150 W. Washington St., San Diego CA 92103, USA. Electronic application materials (PDF, Word) are preferred - please email to sdfrost at ucsd.edu. Review of applications will begin immediately, and continue until the position is filled.

spond@ucsd.edu spond@ucsd.edu

UCollegeCorkIreland PlantFunctional EvoGenetics

Postdoctoral Fellow (Arabidopsis functional evolutionary genetics)

Genetics & Biotechnology Lab, University College Cork, Ireland

The lab of Dr. Charles Spillane is seeking a highly motivated postdoc to work on functional evolutionary genomics of rapidly evolving genes within the Arabidopsis genome. The successful applicant will work within a small team of Arabidopsis researchers investigating genetics and epigenetics of reproduction/seed development. We seek enthusiastic and highly motivated candidates with excellent and proven (as evidenced by publications) skills in plant (Arabidopsis) molecular genetics, functional genomics, molecular evolution, bioinformatics, DIC/fluorescence microscopy and/or in situ hybridisation in Arabidopsis thaliana. The project is funded for three years, and will build on ongoing collaborations with other Arabidopsis groups, including the group of Prof. Karl Schmid (Dept of Plant Biology and Forest Genetics, Swedish University of Agricultural Sciences (SLU), Uppsala, Sweden). Salary for the position will be ~ 40,000 per annum.

Prospective applicants should send an e-mail outlining your research interest and motivations, including; (a) your C.V. (please list publications and experimental skills) & (b) contact details and e-mail addresses for 3 referees to: Dr. Charles Spillane, Genetics & Biotechnology Lab, Biochemistry Dept & Biosciences Institute, University College Cork, Cork, Ireland. E-mail: c.spillane@ucc.ie

Deadline: June 16th 2008 (or until suitable applicant is recruited). Lab website: www.ucc.ie/spillane UCC is an equal opportunities employer

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

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

UColorado ComparativeGenomics

Comparative Genomics Laboratory Postdoctoral Positions U. Colorado School of Medicine

The Consortium for Comparative Genomics at the University of Colorado School of Medicine has an opening for postdoctoral researchers in its high-throughput genomics laboratory. These are full-time position funded by the Consortium for Comparative Genomics and the UC Cancer Center. Successful candidates would be expected to perform major and minor facets of molecular biology laboratory work required for running and maintaining the Roche-454 FLX ultra-high throughput genome sequencer operated by the Consortium, and contribute intellectually to the comparative genomic research conducted through the consortium. Successful candidates would be expected to subdivide time-effort to maintain an independent genomics-based research program in addition to maintaining the effective sequencing throughput of the consortium. The position is an excellent opportunity for interested persons to become heavily involved with diverse cutting-edge comparative genomics research (medical and otherwise) in a highly collaborative setting. The position will be supervised by David Pollock and Todd Castoe, and the postdoc would also be joining the evolutionary genomics research group led by David Pollock (www.evolutinarygenomics.com).

The position would be located at the new UC-Health Sciences Center Anschutz Medical Campus in Aurora, Colorado, on the outskirts of Denver. (<http://www.uchsc.edu/>)

Specific Duties: The duties of the position holder will center around performing and managing technical laboratory aspects required to run experiments on a 454-FLX high-throughput automated genome sequencer housed in the School of Medicine, as well as data analysis. Specifically, this will involve assessing sample quality and quantity from users, communicating with users and other directors regarding sample diagnosis and project design, and carrying out molecular biology laboratory work including PCR, oligo ligation, quality control, and other steps within the 454-FLX sample preparation protocol. This position requires close intellectual interaction with various project directors as well as smooth integration with other laboratory work housed in the UC Cancer Center Core facility. There is excellent potential, if desired, for the position to expand into experimental design and grant-writing related to the postdocs own interests, as well as collaborative work with participating scientists. The successful candidate will be expected to maintain an academic research career as part of their efforts with the Consortium.

Requirements: A Ph.D. degree in a relevant field is required, and further research experience is preferred. The candidate must be a highly motivated, self-organizing and independent worker with the ability to also collaborate in a team setting. Computer literacy is required, and additional computer experience with Unix, and/or programming experience is a plus. Any genomics, DNA sequencing, molecular evolution, or statistical experience is also a strong plus. A deep and broad understanding of molecular biology is essential.

Salary: The salary range for this position is between \$35,000 and \$65,000 per annum, depending on qualifications.

To apply: Please forward a cover letter, CV/Resume and names of three references to Kathy R. Thomas, Administrative Coordinator, Computational BioScience Program, PO Box 6511, Mailstop 8303, Aurora, CO 80045-0511, or email to HYPERLINK "mailto:Kathy.R.Thomas@uchsc.edu" Kathy.R.Thomas@uchsc.edu

Review of applicants will begin immediately and continue until the position is filled. Multiple openings may be available.

The University of Colorado is committed to diversity and equality in education and employment.

Todd.Castoe@UCHSC.edu Todd.Castoe@UCHSC.edu

UGeorgia GeneticsComplexTraits

A postdoctoral position studying the genetic basis of complex traits in sunflower is available in the Burke lab at the University of Georgia. This position will involve the development of association mapping resources in sunflower, characterization of the structure of linkage disequilibrium across the sunflower genome, and candidate gene analyses aimed at associating molecular polymorphisms with variation in traits such as flowering time and seed dormancy.

Funds are currently available to support this position for up to three years. Applicants should have a strong background in population and/or quantitative genetics. Experience with association mapping approaches is desirable.

To apply, please send your CV, a statement of research interests, and contact information for three references to:

John M. Burke, PhD University of Georgia Department of Plant Biology Athens, GA 30602

or (preferably) via e-mail to: jmburke@uga.edu

Informal inquiries are also encouraged. Review of applications will begin immediately and continue until the position is filled.

For more information about the UGA Department of Plant Biology, please visit:

<http://www.plantbio.uga.edu/> Information on the Burke lab can be found at:

<http://www.theburkelab.org/> – John M. Burke, Ph.D. Tel: 706.583.5511 Fax: 706.542.1805 <http://www.theburkelab.org/> University of Georgia Department of Plant Biology Miller Plant Sciences Athens, GA 30602

jmburke@uga.edu jmburke@uga.edu

UGlasgow PlantMatingSystems

University of Glasgow, Faculty of Biomedical and Life Sciences Division of Environmental and Evolutionary

Biology

Postdoctoral Research Assistant in Plant Mating Systems

Ref: 14269/DPO/A3 Salary: £24,403 to £27,466 (grade 6) £30,013 - £33,780 (grade 7) per annum. This post is available at either grade 6 or grade 7 depending upon qualifications and experience. The post is available for up to two years, starting in September 2008.

We are seeking a Post-Doctoral Research Assistant to work on a project entitled “Leveraging the genome sequences of two Arabidopsis relatives for evolutionary and ecological genomics”, funded by a grant from the Biotechnology and Biological Sciences Research Council, as part of an international consortium assembled under the ERA-plant genomics initiative. The goals of the project are to evaluate how the mating “decisions” that plants make affect their potential to respond to environmental change, as a result of changes in genetic diversity resulting from different levels of inbreeding. This project will address this question by examining naturally occurring populations of a species that is normally outcrossing (i.e., is only able to breed with unrelated individuals), but for which populations have been identified that have experienced a change in the genetic machinery required to maintain this mating strategy. The project will be designed to meet the overall goals of the consortium project, which is geared towards understanding how genomic changes affect adaptation in natural plant populations.

For details about the application process, please visit: www.gla.ac.uk/jobs/vacancies Informal enquires should be made to Dr Barbara Mable (B.Mable@bio.gla.ac.uk). Further details about the research environment can be found at: <http://www.gla.ac.uk/departments/eeb/researchinterests/-academicstaff/barbaramable/> Applications should be submitted to: FBLS Staffing Office, Rm 353B, West Medical Building, University of Glasgow, Glasgow, G12 8QQ, quoting the reference number. Closing date: 6 June 2008

Dr. Barbara Mable Senior Research Fellow Division of Environmental and Evolutionary Biology Rm 404 Graham Kerr Building University of Glasgow Glasgow, Scotland G12 8QQ email: b.mable@bio.gla.ac.uk Phone: +44 (0)141 330 3532 Mobile: +44(0)7910 833 819 Fax: +44 (0)141 330 5971

b.mable@bio.gla.ac.uk b.mable@bio.gla.ac.uk

UHawaii Insect Evolutionary Functional Morphology

Note: The closing date for this postdoc has been extended to May 13, 2008, due to some administrative errors. There is no need to reapply if you have already done so.

Thanks, Marguerite Butler

Begin forwarded message:

2 POSTDOCTORAL RESEARCHERS: VISUAL TARGET DETECTION IN HAWAIIAN DAMSELFLIES and WING VEIN EVOLUTION IN FLYING INSECTS

UNIVERSITY OF HAWAII. I am seeking two highly motivated postdocs to work on:

Visual target detection behavior, morphology, and visual performance in damselflies: The Hawaiian damselfly genus *Megalagrion* is an endemic adaptive radiation with extensive color variation and extreme ecological diversification in terms of breeding habitat (light environment). Vision is important for foraging (identifying insect prey), identifying sexual partners (females are often cryptic), as well as avoiding predators. Thus, learning the fundamental mechanisms by which these animals with simple visual systems accomplish very difficult visual tasks may have broad implications for their ecology and evolution, in addition to possible practical applications.

Wing Vein Evolution in Flying Insects: The material properties of insect wings are widely believed to be conferred by the structure and organization of wing veins. We will conduct a broad-based comparative study to quantify wing vein diversity, model how the morphological features of the veins contribute to the material properties of the wing, and how this in turn affects the aerodynamic performance of the wing in flight. Data collected will include confocal microscopy, SEM, and estimates of fluid flow via light microscopy. Morphological data will be used to inform computational models using genetic algorithms to “evolve” wing vein patterns subject to “fitness” imposed by aerodynamics. Models will be validated by field tests of wing damage and flight performance.

Candidates should have the following: Drive and mo-

tivation to solve difficult scientific problems. Good communication/interpersonal skills, good experimental skills and experience in either animal behavior, visual or neurophysiology, or kinematic analysis using high-speed video for postdoc 1 and candidates for postdoc 2 should have good experimental skills and experience with microscopy, kinematic analysis using high-speed video, or morphometrics with experience with image analysis. Demonstrated ability to do field and lab work. Self-starter and creative problem-solver. Both postdocs must have some familiarity with scientific computer programming and excellent quantitative skills.

Desirable qualifications: Candidates experienced in the R programming language and with solid data analysis skills are preferred. Candidates interested in extending the project to address major questions in behavior, sensory physiology, or evolutionary ecology are particularly welcome. Fabrication skills. Experience with insects a plus.

Candidates interested in extending the project to address major questions in behavior, sensory physiology, or evolutionary ecology are particularly welcome.

The Butler lab is in the Department of Zoology at the University of Hawaii, studies the evolution of morphology from functional, structural, and adaptive (evolutionary) perspectives. Other projects in the lab include: the evolution of sexual dimorphism in lizards and damselflies, locomotor biomechanics and the physical effects of pregnancy in lizards, opsin evolution in damselflies, and direct modeling approaches to phylogenetic comparative methods.

We have a dynamic network of colleagues and resources available via: the Bishop Museum, Pacific Biomedical Research Center, Hawaii Institute of Marine Biology, Kewalo Marine Laboratory, Pacific Center for Emerging Infectious Diseases Research, as well as the Bekesy Laboratory of Neurobiology.

Appointment is initially for one year, renewable for second year based on satisfactory performance. Competitive stipend. Start date flexible. Positions subject to availability of funds.

E-mail inquiries are welcome to mbutler@hawaii.edu Applications (preferably by e-mail) should include cover letter, CV, names and contact info for 3 references, pdf's of two most significant publications or manuscripts.

Review of applications begins February 1, 2008 and will continue until filled.

Marguerite Butler <http://www2.hawaii.edu/~mbutler>
<http://www.hawaii.edu/zoology/> Marguerite A. But-

ler Department of Zoology University of Hawaii 2538
McCarthy Mall, Edmondson 259 Honolulu, HI 96822

Phone: 808-956-4713 Lab: 808-956-5867 FAX: 808-
956-9812 Dept: 808-956-8617 <http://www.hawaii.edu/zoology/faculty/butler.html>

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To read the entire message look it up at <http://life.biology-mcmaster.ca/~brian/evoldir.html>

UillinoisUC EvolDevo

POSTDOCTORAL POSITION in Evolutionary Developmental Biology, University of Illinois at Urbana-Champaign

The Sears Lab at the University of Illinois at Urbana-Champaign (UIUC) seeks a highly motivated postdoctoral researcher to study the developmental mechanisms that shape morphologic evolution in mammals. The actual project will be tailored to the specific interests and research skills of the successful applicant, but may include study of marsupial development and evolution, bat development and evolution, mammalian girdle development and evolution, or other topics. For more information regarding the Sears Lab, please see the lab website at www.life.uiuc.edu/sears.

Minimum requirements for this position include a PhD in a related field (e.g., paleontology, developmental biology, evolutionary biology, etc.). Preferred requirements include training in some combination of comparative anatomy, paleontology, developmental biology, and genetics. However, applications are encouraged from anyone interested in uniting the study of genetics, developmental biology and paleontology to study mammalian evolution, regardless of training.

Funding is available for a minimum of 1 year, and may be extended pending availability of funds. Preference will be given to applicants with a high probability of applying for (with PI help) and obtaining independent funding (e.g., NIH-NRSA fellowship, NSF postdoctoral fellowship, etc.).

The preferred starting date is Fall 2008, however, this is flexible. Applications will be considered in a rolling fashion, and the position will remain open until filled. For primary consideration, applications should be received by July 1st. Although candidates may be inter-

viewed before July 1, hiring decisions will not be made until this date. Informal inquiries are welcomed, prior to formal application. To apply, please send the following:

1. Curriculum vitae
2. Names of 3 referees willing to provide a letter of recommendation upon request
3. Brief statement of your research goals and how they fit with those of the Sears Lab

E-mail applications are preferred: ksears@life.uiuc.edu.

Mailed applications are also acceptable to: Karen Sears
515 Morrill Hall 505 South Goodwin Avenue School
of Integrative Biology University of Illinois at Urbana-Champaign Urbana, IL 61801

UIUC is an Equal Opportunity / Affirmative Action Employer.

ksears@life.uiuc.edu ksears@life.uiuc.edu

ULausanne EvolutionaryConservationBiol

Available:

Postdoc position (2 years, elongation up to 5 years in total possible)

Department of Ecology and Evolution, University of Lausanne, Switzerland.

Start: summer 2008 or later

Our group studies the selective forces that act on freshwater fish, i.e. the effects of human activities in interaction with natural and sexual selection. We are also exploring the link between cooperation theory and conservation issues. See <http://www.unil.ch/dee/page21537.html> for further information.

We are seeking candidates with an interest in evolution, conservation genetics, life history, and/or game theory.

Please send your application by email (all material in one attached file please) to Claus Wedekind (claus.wedekind@unil.ch). Include your Curriculum vitae, a short description of your research interests and research experience, and names and email addresses of one or two references who could be contacted. Review of applications will begin June 15th, 2008, but applications will be accepted until the position is filled.

Claus Wedekind <Claus.Wedekind@unil.ch>

Steve Paterson <s.paterson@liverpool.ac.uk>

ULiverpool EntamoebaGenomics

A post-doctoral position is available in the School of Biological Sciences, University of Liverpool.

Entamoeba histolytica is the agent responsible for amoebic dysentery and kills tens of thousands of people every year, mostly in the developing world. However, far greater numbers are infected but are asymptomatic. This project will use massively parallel sequencing and SNP genotyping to understand pathogen population structure and identify genes responsible for virulence. This is an exciting opportunity to explore the biology of an understudied pathogen using new genomic methods.

The project is funded by The Wellcome Trust for 3 years under the direction of Prof Neil Hall (Liverpool), Dr Graham Clark (London School of Tropical Medicine) and Dr Steve Paterson (Liverpool).

You should have a PhD in a biological subject and have experience of sequence analysis. Knowledge of bioinformatics or parasitology would be advantageous.

Applications and further details through the University of Liverpool: http://www.liv.ac.uk/working/-job_vacancies/research/R-567720.htm Closing date 13th June

Informal enquiries to Neil Hall, neil.hall[at]liv.ac.uk

Clark CG, ... Hall N. (2007) Structure and content of the *Entamoeba histolytica* genome.. *Adv. Parasitol* vol 65 pp 51-190

Clark C G, Ali I K, Zaki M, Loftus B J and Hall N (2006) Unique organisation of tRNA genes in *Entamoeba histolytica*. *Mol Biochem Parasitol* vol 146 issue 1 pp 24-9

Loftus B J and Hall N (2005) *Entamoeba*: still more to be learned from the genome. *Trends Parasitol* vol 21 issue 10 pp 453

Loftus B, ... Hall N (2005) The genome of the protist parasite *Entamoeba histolytica*. *Nature* vol 433 issue 7028 pp 865-8

Dr. Steve Paterson School of Biological Sciences University of Liverpool LIVERPOOL, UK L69 7ZB

Tel. 0151 795 4521 Mob. 0151 794 7668 Fax. 0151 795 4408 email s.paterson[at]liv.ac.uk Rm. 202 Biosciences Building

ULouvainlaNeuve ButterflyEvolution

Job offer for a postdoc at the University of Louvain-la-Neuve (Universite catholique de Louvain, UCL, Belgium):

“Behavioural evolution of butterfly movements: a matter of perception?”

We are looking for a postdoctoral researcher who could join us for a period of 12 months starting in 2008 (exact starting date is negotiable). We aim to develop new and stimulating behavioural research on the significance of perceptual range within a context of insect dispersal in fragmented landscapes. Butterflies are used as model system for a series of experiments in the lab and in the field. Earlier work on speckled woods (*Pararge aegeria* L.) has suggested intriguing differences in the response distance to target habitat in individuals from continuous forest and individuals from fragmented agricultural landscape (Merckx & Van Dyck 2007. *Anim. Behav.* 74: 1029-1037). We want to better understand the nature of environmental cues butterflies respond to during traveling across the landscape matrix. Therefore we want to develop a challenging evolutionary ecological research program with a strong emphasis on perceptual differences relative to landscape type. We will also explore some eco-physiological aspects. Another postdoc will also join our team to work in this field, so it will be a collaborative project. There will be frequent interactions with the lab-members of other lines of research. You will earn a postdoc grant from our University (UCL).

Candidates should have excellent CV (i.e., several publications in outstanding behavioural, ecological, conservation or evolutionary journals, experience with observational and experimental behavioural research). Only researchers who have been outside Belgium for at least the last two years can apply for this position. You will work within a cluster of two young research teams at the Biodiversity Research Centre of the Université catholique de Louvain (UCL) in Belgium. The Behavioural Ecology and Conservation Group headed by Hans Van Dyck (www.ecol.ucl.ac.be/ecco/en) and the Quantitative Conservation Biology Group headed by Nicolas Schtickzelle (www.uclouvain.be/quant-cons-biol). Van Dyck's lab addresses several issues within

the broad field of evolution in anthropogenic landscapes (combining behavioural ecology, life history biology, thermal ecology, landscape ecology and conservation). Schtickzelle's lab addresses conservation issues using quantitative approaches like population viability analysis. Both labs have a common and complementary interest in the process of dispersal and in resource-based habitat approaches. Our university is in the French-speaking part of Belgium (Louvain-la-Neuve, close to Brussels). Lab meetings and other scientific meetings are in English, some knowledge of French would be easy.

If you are interested, please send an e-mail message (to both Hans Van Dyck or Nicolas Schtickzelle) in which you explain why you would like to join us and attach your CV (including a full publication list and a reference person) as a separate document.

Please submit your file no later than September, 15 2008. The application will, however, be closed as soon as we have a suitable candidate.

Prof. Hans Van Dyck, Behavioural Ecology & Conservation Group (hans.vandyck@uclouvain.be) Prof. Nicolas Schtickzelle, Quantitative Conservation Biology Group (nicolas.schtickzelle@uclouvain.be)

nicolas.schtickzelle@uclouvain.be
las.schtickzelle@uclouvain.be

nico-

UmeåU Evolutionary Modeling

Postdoctoral fellow, Umeå University, Sweden

Numerical methods and computational tools for evolutionary ecology vegetation models based on integro-partial differential equations

We are looking for a postdoctoral fellow to take on the numerical and computational challenges arising in an international research collaboration that aims to develop an evolutionary ecology vegetation model capable of predicting vegetation structures favored under different environmental conditions. The model is physiologically structured and represented mathematically by an integro-partial differential equation, i.e., by a PDE in which coefficients depend on properties of the solution such as the light availability at a given height above ground.

A major objective of your work will be the development of a fast solver for integro-partial differential equations and the development of related computational tools required for simulations. There is also scope for devel-

oping algorithms and methods for studying phenotypic evolution in physiologically structured population models. Ume University hosts a center for high-performance computing, HPC2N, and we expect that you can make use of these computing resources if needed. Depending on the direction in which you take your work, the position may lead to publications in computational mathematics, mathematical/theoretical ecology, or both. In addition, there is a good opportunity that your contributions will become incorporated in the next generation of world vegetation models.

The position is available for one year with a possible prolongation for another period of one year. The postdoc will be based at the Department of Mathematics and Mathematical Statistics and will work in close collaboration with our international partners, including the International Institute for Applied Systems Analysis (IIASA) in Laxenburg, Austria, and Macquarie University, Sydney, Australia. The position is expected to entail visits and secondments to one or both of these institutions, possibly for durations of up to several months. To qualify for this position, you need a PhD degree in computational mathematics or a quantitative science related to the project, preferably not older than five years. Experience of programming in C++, parallel computing, or mathematical ecology will be an advantage, but is not required. Proficiency in written and spoken English is essential.

Umeå university in northern Sweden is a dynamic university with ca 3 900 employees and more than 29 000 students, of which 1 300 are in PhD programs. The department of Mathematics and Mathematical Statistics has about 65 employees including 25 PhD students. The department of Ecology and Environmental Science has about 170 members including 65 PhD students. For further information, please contact assistant professor Åke Brännström, +46-90-786 78 62, ake.brannstrom@math.umu.se, professor Mats Larson, +46-90-7865502, mats.larson@math.umu.se or Head of department Anders Fällström anders.fallstrom@math.umu.se. For a general presentation of the department, see www.math.umu.se. The International Office, http://www.umu.se/-/international_office provides a general presentation of Umeå and the University.

The application should contain a curriculum vitae, copies of degree certificates, names and contact details of at least two references, and short accounts of scientific and teaching activities. Reprints of your most relevant publications and other documents that you wish to refer to should be attached.

Union information is available from SACO, +46-(0)90-

786 53 65, SEKO civil, +46-(0)90-786 52 96 and ST, +46-(0)90-786 54 31.

Your complete application, marked with reference number 315-1620-08, should be sent to jobb@umu.se or to the Registrar, Umeå University, SE-901 87 Umeå, Sweden to arrive June 2, 2008 at the latest.

We look forward to receiving your application!

Ake BRANNSTROM <brnstrom@iiasa.ac.at>

tawa 30 Marie-Curie Priv. Ottawa, Ontario, K1N 6N5 CANADA

Office: +1 613-562-5800 x2835; Fax: +1 613-562-5486; Lab: +1 613-562-5800 x6837 Email: hrundle@uottawa.ca; Skype: howarddrundle <http://www.science.uottawa.ca/~hrund050/> hrundle@uottawa.ca

UOttawa EvolutionaryBiology

Postdoctoral fellowship in Evolutionary Ecology at the University of Ottawa, Canada

uOttawa has announced a competition for four Vision 2010 postdoctoral fellowships for outstanding researchers in a diversity of fields (for details, see: <http://www.grad.uottawa.ca/Default.aspx?tabid=-3D2247>). These fellowships provide \$50,000/year for two years, with this amount covering salary, fringe benefits, and a maximum research allowance of \$5,000. These fellowships are open to Canadian and international candidates.

The Department of Biology at uOttawa (<http://www.biology.uottawa.ca/>) has growing strengths in evolutionary ecology, and we are actively seeking an outstanding candidate to put forward for a fellowship. Potential applicants with research interests that coincide with one or more of our members are encouraged to contract the relevant faculty member(s) directly:

Howard Rundle (<http://www.science.uottawa.ca/~hrund050/>) Rees Kassen (<http://www.science.uottawa.ca/~rkass574/>) Risa Sargent (<http://www.science.uottawa.ca/~rsargent/>)

Fellowships require the support of a faculty member at uOttawa. To this end, we will be screening applicants to choose someone to put forward for a fellowship. Interested candidates should provide a copy of their C.V, a list of 2-3 references, and a brief statement (1 page max) of their research interests and accomplishments. These should be sent via email, preferably as a pdf attachment, directly to the relevant faculty member above by June 20, 2008 (final fellowship applications are due by Aug. 1, 2008).

Sincerely, Howard

Howard D. Rundle Assistant Professor & Canada Research Chair Department of Biology University of Ot-

UParisSud PhylogeneticLanguage

We propose a postdoctoral opportunity in the group of Dr. Ch. Froidevaux at the University of Paris-Sud on the following theme: Towards a language to query phylogenetic data

Please send a motivation letter, a resume, and the name of collaborators/advisors able to recommend your application by June 10th, 2008 to Christine Froidevaux (chris@lri.fr) and Sarah Cohen-Boulakia (cohen@lri.fr)

More information is available below and at <http://www.lri.fr/~cohen/phylo.html> * Advisors Sarah Cohen-Boulakia (Assistant Professor), Christine Froidevaux (Professor) * Collaborators Bernard Labeledan, Olivier Lespinet (Institut de Genetique et de Microbiologie, Universite Paris-Sud, Orsay, France) Val Tannen (University of Pennsylvania, USA) * Location Bioinformatics group at LRI (Laboratoire de Recherche en Informatique), Universite Paris-Sud, Orsay, France

* Topic Understanding the relationships between different species may have consequences both at practical level (e.g., history of a pathogen agent involved in a disease), and at fundamental level (e.g., construction of the tree of life: finding the history of all organisms). The study of evolution requires various and numerous pieces of data such as morphological characteristics of a set of specimens or, more importantly, genomic and proteomic sequences of a group of species, functional and structural annotations. For several years now, there has been an avalanche of data available. Combining and integrating masses of phylogenomics data is of paramount importance for better understanding evolution.

* Background More specifically, this subject is part of two projects, pPOD and Microbiogenomics.

** On the one hand, pPOD is an international project, in which data are collected throughout the world by research groups having distinct interests (specialized on

different groups of species). Data collected by those various groups are available in a variety of formats (relational, tabulated files, and so on.).

** On the other hand, partners of the the French project “ANR masses de donnees” Microbiogenomics study evolution by building phylogenetic trees based on families of proteins, part of their data is currently stored in flat-files format (trees) and within a relational warehouse (sequences, annotations).

In both projects, phylogeneticists need to ask complex questions involving all the data, both produced and consumed by the various steps of the generation and analysis of phylogenetic trees, including the trees themselves or families of trees. Examples of queries include: What are the differences between those two trees? If I modify the alignment by adding gaps, what would be the impact on the final generated tree; or

”Among the available trees, what are the subtrees whose proteins are all involved in a given metabolic pathway? Which are the protein modules appearing in trees in which a given group of species is monophyletic; or

* Work The aim of this work is to enable various phylogeneticists to make use of all these data in a unified way, in the context of a relational database. One of the main challenges lies in that the relational model does not fit with hierarchical (tree-based) data.

As a first step, queries frequently asked by major pPOD and Microbiogenomics partners should be identified. Queries may be increasingly complex and can be expressed using different kinds of language (relational algebra, SQL and so on). In particular, queries may involve families of trees, comparison and clustering algorithms, and topological features of the trees.

A classification of queries should then be proposed.

The third step would consist in exploring the limitations of current relational standards (latest versions of SQL) to represent phylogenetic data and express queries. This study should provide the building blocks for a more expressive high-level query language.

More information on the pPOD project: <http://-phyldata.seas.upenn.edu> More information on the Microbiogenomics project: <http://microbiogenomics.u-psud.fr> More information on the Bioinformatics group at LRI: <http://www.lri.fr/bioinfo>

Sarah Cohen-Boulakia and Christine Froidevaux

Sarah Cohen-Boulakia Assistant Professor University of Paris Sud 11 Computer science department, Bioinformatics group Orsay 91405 cedex France +33 1 69 15 32 16

Sarah Cohen Boulakia <Sarah.Cohen_Boulakia@lri.fr>

UPennsylvania InferringSelection

An NIH-funded postdoctoral fellowship (2 years, renewable for another 2) is available in the computational biology group of Hannenhalli and Plotkin at the University of Pennsylvania. The research project aims to understand the evolutionary forces that shape genetic variation at regulatory and protein-coding sites in eukaryotic genomes. A primary focus will be the development of methods that quantify natural selection on and epistasis among regulatory and protein-coding SNPs. Open questions include the relationship between selection pressures on sites and their role in either regulation, structure, or function of proteins.

Areas of interest in the Plotkin and Hannenhalli group include mathematical population genetics, the evolution of gene regulation, and the computational identification of regulatory sites. Requirements for the position include: a proven record of self-motivated research; a PhD in computer science, mathematics, statistics, physics, biology or related area; excellent quantitative skills. The candidate must be familiar with scientific programming, and should ideally have experience with analyzing sequence data, SNP data, and protein structural information.

The fellowship provides a competitive annual stipend plus benefits and health insurance. Start date and term are negotiable. Highly motivated applicants, of any nationality, are encouraged to email a statement of research interests, CV, and contact details for three references to [jplotkin\[at\]sas.upenn.edu](mailto:jplotkin[at]sas.upenn.edu) or [sridharh\[at\]pcbi.upenn.edu](mailto:sridharh[at]pcbi.upenn.edu).

URochester Computational Population Genomics

Post-Doctoral Research Associate: Computational Population Genomics

A postdoctoral position in computational population genomics is available in the laboratory of Dan Gargigan in the Biology Department at the University of

Rochester, with an anticipated start date of September 2008.

Applicants will hold a Ph.D., preferably in either Biological Science or Computer Science. Individuals with training in population genetics and evolutionary computer simulations are encouraged to apply. The successful candidate will develop simulation software for massively parallel computing systems, with the aim of analyzing large population genomic datasets. Familiarity with computer languages like C/C++ and the ability to work with large genetic databases are both necessary. Major research themes of the laboratory include development of novel Markov chain Monte Carlo techniques, examining models of population structure, and the efficient implementation of recombination into coalescent-based algorithms. There will be an excellent opportunity to develop extensive skills in parallel programming that take advantage of emerging computational technologies.

The Biology Department at the University of Rochester offers a collaborative, highly productive research environment (<http://www.rochester.edu/College/BIO/index.php>). The successful candidate will be an integral part of a new faculty laboratory that will be starting in September 2008. The initial appointment will be for two years and the start date is negotiable. Review of applications will begin immediately and continue until the position is filled. Salary and benefits are competitive. Interested applicants should send a cover letter stating their previous research experience and future directions, a CV, and contact information for three references to Dan Garrigan at dgarrigan@oeb.harvard.edu.

The University of Rochester is an Equal Opportunity Employer and actively seeks diversity among its employees.

dgarrigan@oeb.harvard.edu
dgarrigan@oeb.harvard.edu

dgarrigan@oeb.harvard.edu

USaoPaulo CulicidaeSystematics

Postdoctoral Position - Faculdade de Sade Publica, Universidade de Sao Paulo The Culicidae Systematic Laboratory at the University of Sao Paulo, Brazil, seeks a highly motivated and productive postdoctoral researcher to work on FAPESP Temtico-funded research on historical demographics of Anopheles darlingi mosquito populations, divergence times, and rates of molecular evolution.

The position requires an individual with a PhD and experience in phylogenetic systematics, population genetics, or related fields. Outstanding molecular, computational and/or statistics skills are particularly advantageous. It is expected the candidate collaborate in discipline, field work in Brazil, and training undergraduate and graduate students in molecular techniques employed in systematic.

Funding is available for a minimum of 1 year, and may be extended upon both mutual and FAPESP agreement. Preference will be given to candidates with a high probability of applying for and obtaining independent funding; for example through Conselho Nacional de Desenvolvimento Cientifico e Tecnoligico (CNPq), TDR/WHO, or other funding agencies.

The starting date is flexible, and the position will remain open until filled. For primary consideration, applicants should apply by June 1, 2008. Informal inquiries are welcomed, prior to formal application. To apply, please send the following:

1. A curriculum vitae
2. Names of 3 referees willing to provide a letter of recommendation upon request
3. A brief statement of how your research goals fit with research of Culicidae lab
4. A brief statement of interest, ideas, and qualifications for independent grant applications

E-mail applications are preferred: masallum@usp.br

Mailed applications are also acceptable to: Maria Anice Mureb Sallum Faculdade de Sade Publica Universidade de Sao Paulo Avenida Doutor Arnaldo 715 sala 200 01246-904 Sao Paulo Sao Paulo, Brasil

Maria Anice Mureb Sallum <masallum@usp.br>

UTours 2 InsectViralEvolution

2 POSITIONS: Postdoctoral Research Associate and Postgraduate Research Assistant

The Insect Biology Research Institute (IRBI) is seeking to recruit a postdoctoral research associate and a postgraduate research assistant to join a new team lead by Dr Elisabeth Herniou and funded by the European Research Council (ERC) to work on the adaptation of virus genomes to insect immunity. A solid background in bioinformatics and comparative genomics is required for the postdoctoral research associate as his project will consist in analysing the genomes of 2 polyd-

naviruses and comparing them to insect viruses. The postgraduate research assistant will be in charge of setting up insect cultures and running selection and bioassay experiments with baculoviruses.

Comparative genomics of polydnviruses and insect viruses Postdoctoral Research Associate Starting Salary 30,000 p. a.; Starting from January 2009; initially 2 years funding Closing date 31st October 2008

Baculovirus Adaptation to Insect hosts Postgraduate Research Assistant / Ingénieur d'étude Starting Salary 23,180 p. a.; Starting date: October 2008; initially 4 years funding Closing date 31st July 2008

Fluency in French is not essential but would be a bonus.

For more information please contact: Dr Elisabeth Herniou (e.herniou@imperial.ac.uk); Institut de Recherche sur la Biologie de l'Insecte, Université de Tours, Faculté des Sciences et Techniques, Parc Grandmont, 37200 TOURS France

Carlos.Lopez-Vaamonde@orleans.inra.fr Carlos.Lopez-Vaamonde@orleans.inra.fr

UUtah Coevolution DarwinsFinchesParasites

Co-evolution of Darwin's Finches and parasites

The Clayton Lab (darwin.biology.utah.edu) at the University of Utah in Salt Lake City is seeking a highly motivated postdoc for an NSF-funded project concerning Darwin's Finches and their parasites. The project, which is based in Utah and the Galapagos Islands, is at the interface of co-evolutionary ecology, immunology, behavior, and conservation biology. Although Darwin's Finches are one of the most famous examples of adaptive radiation, we know relatively little about the role of parasites and pathogens in their ecology, behavior and evolution. Unfortunately, finch populations have recently come under serious threat from the introduced tropical nest fly *Philornis downsi*. A better understanding of this parasite is urgently needed because of the danger it poses to these iconic birds. The overriding goals of this project are: 1) to conduct rigorous tests of the impact of *P. downsi* and other parasites on Darwin's Finches; and 2) to determine the ability of the finches to defend themselves against parasites. The project will focus on interactions between *P. downsi* and the Medium ground finch (*Geospiza fortis*) on Santa Cruz Island; however, we will also study interactions between

other species of finches and their parasite communities. We hope that this work will help conservation biologists protect Darwin's Finches from invasive parasites and pathogens in the future.

The postdoctoral position is renewable annually for up to three years, depending on performance and funding. The salary starts at \$35,000 per year, plus benefits. We are interested in candidates with experience working under physically demanding field conditions. A background in experimental design and statistical analysis is essential, and some experience with population or epidemiological modeling is a plus. Experience with birds and parasites/pathogens is desirable, but not essential. Strong communication skills and experience mentoring graduate and undergraduate students are also desirable. Proficiency in Spanish (spoken and written) is a definite plus.

To apply, send a single email file with the items listed below to Dr. Dale Clayton, c/o Alyssa Farley at: alyssafarley@bioscience.utah.edu 1) CV including info on publications, field experience, and analytical skills 2) One page statement of research interests and future goals 3) Names & contact info (incl telephone numbers) of 3-5 referees who are familiar with the applicant's past research and skills.

Review of applications will start in mid-June and continue until a suitable candidate is found. The position could start as early as August, 2008. The University of Utah is an Affirmative Action/Equal Opportunity Employer.

Dale H. Clayton, Ph.D. Professor, Dept. of Biology, Univ. of Utah 257 South 1400 East Salt Lake City, Utah 84112 Voice: 801-581-6482; Fax: 801-581-4668

Dale Clayton <clayton@biology.utah.edu>

UWesternOntario AshBorerPopulationBiol

Please post this on EvolDir, as I'm hoping for an audience of creative evolutionary biologists. Thanks, brent
POSTDOC: Plasticity of Overwintering in Emerald Ash Borer A motivated, creative postdoc is sought to work on an NSERC-funded project on phenotypic plasticity in overwintering biology of the Emerald Ash Borer.

Emerald Ash Borer is an invasive buprestid beetle that

is devastating North American ash (*Fraxinus* spp.). The applicant will join an interdisciplinary team of physiologists, ecologists, foresters and modellers in examining the potential impacts of changing winter conditions on the spread and success of this species. As well as the applied aspects of this work, there is strong opportunity for the candidate to develop experiments to address fundamental questions about the evolution of physiological plasticity in an invasive insect.

The position will be based in Dr Brent Sinclair's lab at the University of Western Ontario (see < <http://publish.uwo.ca/~bsincla7/> ><http://publish.uwo.ca/~bsincla7/>), and can start any time after July 1 2008 for a period of approximately 20 months. The successful applicant will have a PhD and a background in organismal evolution, evolutionary ecology or ecophysiology. Prior experience with insects or forest biology is desirable, but not necessary, but an interest in combining field and lab work and working with whole organisms is essential.

For further information (informal enquiries are encouraged), please email Dr Brent Sinclair (bsincla7@uwo.ca). To apply, please email a CV, and cover letter, and the names and contact details of three referees. Review of applications will begin June 1 2008, and continue until the position is filled.

Brent J. Sinclair, PhD

Assistant Professor of Invertebrate Biology Department of Biology Room 2078, Biological & Geological Sciences Building 1151 Richmond Street North The University of Western Ontario London, ON N6A 5B7 Canada

Tel: + 1-519-661-2111 ext 83138 Fax: + 1-519-661-3935 bsincla7@uwo.ca <http://www.uwo.ca/biology/Faculty/sinclair/index.htm>

Brent Sinclair <bsincla7@uwo.ca>

ary processes from microsatellite and single nucleotide polymorphism (SNP) data. The successful candidate will compare the properties of these different classes of variation and develop statistical methods that combine them to improve population genetic inference. Potential topics include (but are not limited to): the detection and characterization of natural selection operating on different timescales, the measurement of population structure, and genome-wide association mapping of complex traits. Research will involve computer simulations and analyses of genome-wide patterns of variation in human populations. Salary and benefits are competitive. The term of the position is flexible.

The Laboratory of Genetics features a strong historical tradition in population genetics, which includes Sewall Wright, Motoo Kimura, and James Crow. UW-Madison has a thriving community of evolutionary biologists from departments across campus. The university is also very strong in related fields, such as statistical genetics. Madison is consistently ranked as one of the best U. S. cities in which to live.

Required qualifications: - Ph.D. in evolutionary biology, bioinformatics, computer science, statistics, genetics, applied mathematics, or a related field. - Research experience (with first-authored publications) in population genetics - Proficiency in programming, including C/C++, as well as scripting languages such as perl or R. Experience with a linux environment and large (genome-scale) datasets is preferred. - Highly motivated, with strong ability to work independently.

Applicants should send a cover letter summarizing their research background and interests, a recent CV, and contact information for three references (all as pdfs) to Bret Payseur at payseur@wisc.edu. Review of applications will begin immediately and continue until the position is filled.

Bret Payseur <payseur@wisc.edu>

UWisconsinMadison PopulationGenetics

Postdoctoral Position in Population Genetics at the University of Wisconsin V Madison

A NIH-funded POSTDOCTORAL POSITION is available in the laboratory of Dr. Bret Payseur in the Laboratory of Genetics (Department of Medical Genetics) at the University of Wisconsin (Madison, WI). The research focus will be the inference of evolution-

UWyoming StructuralBioinformatics

Postdoctoral Researcher in Evolutionary Structural Bioinformatics

A position is currently available for a postdoctoral researcher in evolutionary structural bioinformatics in the Liberles Research Group at University of Wyoming in the beautiful Rocky Mountains. Applicants should

have skills in programming, knowledge of statistics, an interest in protein structure and/or physical chemistry, as well as interest in evolutionary biology and population genetics. Research will involve work at the interface of structural and evolutionary bioinformatics to understand how structure constrains sequence evolution as well as how and why the genome-specific distribution of structures changes between species.

For more details on research in the Liberles Research Group, please see <http://www.wyomingbioinformatics.org/LiberlesGroup>.

To apply, please send a CV, contact information for three references, and 2 .pdf copies of your favorite (significant) papers you have published together with a cover letter to liberles@uwyo.edu.

David Liberles <liberles@uwyo.edu>

WoodsHole BacterialGenomeEvolution

Postdoc Position Bacterial genome evolution, Woods Hole, Mass.

A postdoc position is available Jennifer Wernegreen's lab at the Marine Biological Lab in Woods Hole, Mass. Potential postdoc projects include empirical and/or computational studies of bacterial genome variation, population genetics, and molecular evolution.

Our work explores the impacts of basic evolutionary processes (mutation, selection, genetic drift, recombination) on DNA sequences and full genomes. We're comparing the effects of these processes in host-dependent versus free-living bacterial species, using lab-based and computational approaches. We're especially interested in understanding how symbiotic lifestyles influence effective population sizes, and then testing the effects of Ne on rates and patterns of bacterial evolution. Much of our work focuses on bacterial endosymbionts of insects.

Our lab is part of the MBL's Josephine Bay Paul Center in Woods Hole, a vibrant and collaborative group exploring microbial diversity, molecular evolution, and comparative genomics (<http://jbpc.mbl.edu/>). The Center has strong expertise and facilities in computational biology and high-throughput molecular biology (including 454 pyrosequencing).

This position requires a Ph.D. in biology, evolution, bioinformatics, or a related field, and a demonstrated

publication record. Computational skills are strongly preferred, including knowledge of UNIX/LINUX, PERL programming, phylogenetic and population genetic programs, and experience with full genome analyses. Molecular biology expertise and some exposure to high-throughput methods would be helpful.

The application consists of three items: (i) a cover letter describing your current interests, your goals for a postdoc position, and your specific motivation to join our lab, (ii) your CV, and (iii) contact information for three referees.

The application website for this postdoc position is:

mbl.simplehire.com/applicants/Central?quickFindP515

or, go to: mbl.simplehire.com > click '\Scientist'] > '\Postdoctoral Scientist- Genome Evolution']

Please contact Jen Wernegreen (jwernegreen@mbl.edu) with any questions.

Jennifer Wernegreen <jwernegreen@mbl.edu>

WoodsHole BacterialGenomeEvolution correction

Postdoc Position Bacterial genome evolution, Woods Hole, Mass.

Correction:

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To apply, please go to [mbl.simplehire.com](http://mbl.simplehire.com) (see instructions at top of this notice).

For more information about the lab, please see: <http://jbpc.mbl.edu/labs-wernegreen.html> Please contact Jen Wernegreen ([jwernegreen@mbledu](mailto:jwernegreen@mbledu)) with any questions about projects or the position.

Jennifer Wernegreen <[jwernegreen@mbledu](mailto:jwernegreen@mbledu)>

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## WorkshopsCourses

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| Frauenchiemsee Germany EvolSexChromosomes Sep14-19 . . . . . 89 | UMinnesota LifeHistoryStatistics Jun25-26 . . . . . 91 |
| LaFouly Switzerland AdaptiveGeneticVariation Sep3-6 90          | UMuenster EvolutionaryBiol Summer 2 . . . . . 92       |

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### CzechRepublic ConservationGenetics Sep1-7

we would like to announce Conservation Genetics Summer School which is organized within the ESF ConGen Research Networking Programme. The school web page is:

<http://www.natur.cuni.cz/zoologie/ConGen/index.htm> Conservation Genetics Summer School: Assessing populations structure and dynamics through the use of molecular markers and novel computational models, Château Liblice, Czech Republic, 1-7 September 2008 ... and a link to the web page

Thank you.

Sincerely

Pavel Munclinger

Pavel Munclinger Department of Zoology Charles University in Prague Vinicna 7, Praha 2, CZ 128 44  
Czech Republic e-mail: [muncling@natur.cuni.cz](mailto:muncling@natur.cuni.cz) <http://www.natur.cuni.cz/~muncling/> Pavel Munclinger <[muncling@natur.cuni.cz](mailto:muncling@natur.cuni.cz)>

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### Frauenchiemsee Germany EvolSexChromosomes Sep14-19

Sorry for cross-posting.

The Munich Graduate Program for Evolution, Ecology and Systematics (EES) invites applications for the international EES Summer School on 'the Evolution of Sex Chromosomes' held at Frauenchiemsee (80 km east of Munich) from 14 - 19 September 2007.

The 5-day Summer School will consist of lectures, discussions and exercises provided by the invited teachers as well as oral and/or poster contributions by the more advanced student participants. Arrival of participants is scheduled for Sunday 14 September evening, departure for Friday 19 September early afternoon.

Confirmed teachers:

Deborah Charlesworth (University of Edinburgh)  
Sander van Doorn (Santa Fe Institute) Judith Mank (Uppsala University) Daven Presgraves (University of Rochester)

Local organizers: John Parsch, Susanne Renner, Bart Kempnaers, Pleuni Pennings (Ludwig-Maximilians-University Munich and Max Planck Institute for Ornithology Seewiesen)

The instructors will cover theoretical aspects of sex chromosome evolution and present empirical results from diverse systems including plants, insects and birds. Specific topics will include the origin of sex chromosomes, the expression and molecular evolution of sex-linked genes, and the role of sex chromosomes in speciation.

The summer school is open to students at the PhD and Master/advanced Diploma levels. The course language will be English. Students who are involved in research related to the topic of the summer school are encouraged to prepare short oral contributions or posters highlighting their research interests and/or achievements.

Thanks to support from the Volkswagen Foundation, the University of Munich's EES program will cover costs for housing and meals during the Summer School. Participants will have to cover their travel expenses and must pay a 50 Euro registration fee. A limited amount of funding is available to partly subsidize travel expenses for students from the most distant localities.

Applicants should provide a full CV, a statement about your research interests/current projects (max. half page), a statement about why you want to attend the Summer School, explicitly addressing how you expect to benefit and what you can contribute (max. half page). Application deadline is 24th of June.

Questions can be addressed to Ms Pleuni Pennings (pennings@lmu.de). Please send your application by e-mail, preferably as a single pdf file, to Ms Pleuni Pennings (pennings@lmu.de). Further informa-

tion is available at [http://www.eeslmu.de/eeswiki/index.php?title=Summer\\_school\\_2008](http://www.eeslmu.de/eeswiki/index.php?title=Summer_school_2008). Best wishes,  
Pleuni Pennings

–

Pleuni S. Pennings

\* Program Coordinator of the Munich Graduate School for Evolution, Ecology, and Systematics

\* Postdoc in theoretical evolutionary biology

Evolutionary Biology, Department Biologie II University of Munich (LMU) Großhaderner Str. 2 D-82152 Planegg-Martinsried

Tel: 0049 89 2180 74 234 <http://www.eeslmu.de/eeswiki> <http://www.biologie.uni-muenchen.de/ou/theopogen/index.htm> pennings@lmu.de

pennings@lmu.de

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## LaFouly Switzerland Adaptive Genetic Variation Sep3-6

A workshop on "Managing adaptive genetic variation in conservation biology" will be held in La Fouly, Valais, Switzerland, from September 3rd to September 6th 2008.

Workshop summary: Current population management concentrates very much on demographics, local adaptation, and on the maintenance of genetic variation. Recent developments in theory and on some model organisms suggest, however, that there can be significant variation in heritable viability within a population. So-called 'good genes' models of sexual selection predict, for example, that reproductive skew in the wild are positively linked to heritable viability. Conservation management should try to minimize any variance in reproductive success that is not linked to viability traits. However, including 'good genes' effects in, for example, captive or supportive breeding could increase the average viability in the next generation. This positive effect would have to be balanced with the management of overall genetic variation. So far, neutral markers were mainly used to study the genetic make up of wild populations, but new methods and analyses can now give insights into adaptive genetic variation. We will discuss the advancements in these fields and their possible relevance for population management. Invited speakers:

Juha Merilä (University of Helsinki, Finland); Wayne

Potts (University of Utah, USA); Jon Slate (University of Sheffield, UK); Jay Storz (University of Nebraska, USA); Pierre Taberlet (CNRS & University of Grenoble, France). In addition to invited speakers, participants will also have the opportunity to present their own research. Ample time will be allowed for discussions.

Registration fees are CHF 300, including local accommodation and food. Fees are waived for students from the Swiss universities affiliated to the CUSO (Geneva, Lausanne, Neuchatel, Fribourg and Berne), which will be given priority.

Deadline for registration is July 15th 2008.

Please register directly on our web site: <http://www.unil.ch/dee/page11644.en.html> Note that the workshop is limited to 35 participants, and a final selection will be done at the end of July.

Organizers : G. Evanno, L. Fumagalli & C. Wedekind, University of Lausanne.

Workshop location: <http://www.dolent.ch/>

Luca.Fumagalli@unil.ch Luca.Fumagalli@unil.ch

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### Switzerland LifeHistoryEvolution Aug25-27

Workshop on “Maternal effects: Underlying mechanisms and implications for life history evolution”, 25-27 August 2008. The workshop will be held in Adelboden, Switzerland, a picturesque mountain village at 1400 m sea level amidst the High Alps of the Berner Oberland.

The study of maternal effects is a rapidly growing field with important implications for questions concerning life history evolution and population biology. This workshop aims to further our understanding of maternal effects by bringing together leading scientists of the field working at different levels, namely the causation of maternal effects, their adaptive function and their long-term consequences for population dynamics and evolution.

The workshop will include lectures by invited speakers representing a wide range of disciplines including physiology, developmental biology, evolutionary biology, behavioural ecology and mathematics. The major part of the workshop will be devoted to discussions in small groups to induce intensive interactions between students and more advanced researchers and the in-

vited experts. Participants will get an overview about the current approaches used to study maternal effects, both at the ultimate and proximate levels, and they are encouraged to discuss potential future directions of this field among each other and with the invited speakers.

Invited Speakers:

Kathryn Arnold, University of Glasgow

Ton Grootuis, University of Groningen

Rufus Johnstone, University of Cambridge

Virpi Lummaa, University of Sheffield

Allen Moore, University of Exeter

Tobias Uller, University of Oxford

For more information please visit: <http://behav.zoology.unibe.ch/index.php?pp=56&pf> Registration: Please register as soon as possible. There is no registration fee. The deadline of registration is 30 June 2008, and there is an upper limit of 40 participants. Participants of CUSO-Universities (Bern, Fribourg, Geneva, Lausanne and Neuchatel) can be reimbursed for their expenses (travel and subsistence; see details on our workshop web site).

Please register at the CUSO web site: <http://www.cuso.ch/3e-cycle/biologie.html> and at the same time notify us of your interest to participate at: [marlis.gerteis@esh.unibe.ch](mailto:marlis.gerteis@esh.unibe.ch)

We are looking forward to see you in Adelboden! Barbara and Michael Taborsky, Organizers of the workshop

Dr. Barbara Taborsky

Zoological Institute, Behavioural Ecology, University of Bern, Wohlenstrasse 50A, CH-3032 Hinterkappelen, Switzerland Tel: +41/ 31/ 6319 157, Fax: +41/ 31/ 6319 141

[barbara.taborsky@esh.unibe.ch](mailto:barbara.taborsky@esh.unibe.ch)

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### UMinnesota LifeHistoryStatistics Jun25-26

Aster Summer Workshop - June 25th and 26th, 2008  
Aster Models for Life History Analysis

Instructors: Charles J. Geyer, Professor, Sch. of Statistics, University of Minnesota Ruth G. Shaw, Professor, Dept. of Ecology, Evolution, and Behavior, University of Minnesota

A two day workshop on aster models will be offered on June 25th and 26th, 2008 in the School of Statistics at the University of Minnesota, Minneapolis Campus. The workshop will meet from 9 am to 4 pm each day. There are no fees.

Aster is a newly developed statistical approach that is designed to address longstanding problems associated with the joint analysis of life history data (e.g. measures of survival to reproductive age and fecundity). Aster can be applied to comparing fitness measures between groups, estimating fitness landscapes, and estimating population growth rates.

Aster is implemented in the R statistical computing environment, which is free software and can be downloaded from <http://www.r-project.org>. When R is installed, the aster package is installed using the "packages" menu. The site <http://www.stat.umn.edu/-geyer/aster/> provides further information on Aster including tutorials, technical reports, and publications.

The goal of the workshop is to provide participants with hands on experience using the aster statistical package. The majority of workshop activity will be dedicated to using aster to analyze several pre-selected data sets in a computer lab setting. If participants have data that may be appropriate for aster models, we can try that too. Each phase of the analyses will be covered from formatting and loading data to analyzing results. Workshop participants will also be introduced to as much of the theory of aster models as ordinary users need to know to set up scientifically sensible aster models, interpret hypothesis tests, and construct confidence intervals. Aster's applicability to specific research questions and data sets of the participants will also be addressed.

Lab space is limited. Please register soon by sending a brief email to Marcus Warwell at [mwarwell@um.edu](mailto:mwarwell@um.edu) that includes your name and contact information.

[warw0017@umn.edu](mailto:warw0017@umn.edu)

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## UMuenster EvolutionaryBiol Summer 2

Dear EvolDir members

there are still three places left!! Please feel free to distribute this information among Master students and early PhD students that you might think maybe interested. Thanks a lot!

Ignacio G. Bravo ---

The school The Bernhard-Rensch Summer School on Evolutionary Biology is organised by the Institute of Evolution and Biodiversity (<http://www.uni-muenster.de/Evolution/>) of the University Muenster (<http://www.uni-muenster.de/de/index.html>), and sponsored by the Volkswagen Foundation (<http://www.volkswagen-stiftung.de/>).

The aim The interest of the Bernhard-Rensch Summer School is Evolutionary Biology, in an open and broad sense. Interaction between students from different fields/orientations is explicitly wanted and encouraged.

The topic The specific topic this year will be phylogenetic reconstruction and deep phylogenetic relationships. Students working in a related topic will be invited to present their research in a short talk.

Evolution and the philosophy of biology The Summer School also wants to be a meeting point for students interested in the philosophy of science. Since evolution is the integrative framework for biology as a science, we could say that evolution is the philosophy of biology. We will discuss and share views on the structure of science and scientific theories, the paradigms of evolution and the position of evolutionary theory in present times.

The work during the summer school Each student should bring the own laptop. Tasks will include training in interdisciplinary components, improving transferable skills (writing, presenting, planning projects), team-work, working with scientific literature, developing a concept of philosophy of science.

The place The Summer School will take place at the marine biological station in Carolinensiel (<http://www.uni-muenster.de/-Biologie.Zoophysiologie/Station/>), located in the Wadden Sea National Park in Lower Saxony ([http://www.nationalpark-wattenmeer.niedersachsen.de/-master/C5912120\\_L20\\_D0.html](http://www.nationalpark-wattenmeer.niedersachsen.de/-master/C5912120_L20_D0.html)). Carolinensiel is not too easy to reach by public transportation. We will try to arrange a bus or to pick you up at Wittmund (details to be specified later on with the participants).

The timing From June 30th (Monday) to July 11th (Friday). Arriving date June 29th (Sunday) and leaving date July 12th (Saturday).

The faculty Herve Philippe (Montreal) Olaf Bininda-Emonds (Oldenburg) Walter Salzburger (Basel) Thorsten Reusch (Muenster) Erich Bornberg-Bauer (Muenster) Joachim Kurtz (Muenster) Ignacio G. Bravo (Muenster, Summer School coordinator)



The costs There will be a fee of approximately 200 euros per person, including accommodation and food. Travel expenses are not covered. Exact price will depend on the final number of participants, but will not differ much. Price will be paid in advance. Details will be later on specified with the participants.

The students The summer school is open for students from the MSc in Biologie at the University Muenster as a Masters Module. Master students and early PhD students from anywhere else are welcome to apply (final number of students around 22).

The application Deadline is April 30th. Please send an email including a short description of your scientific career and interests to [igbravo@uni-muenster.de](mailto:igbravo@uni-muenster.de). Please include all the relevant informa-

tion in the body of the email. Do not include attachments. Shortlisted students will be contacted by May 15th. Definitive participation will be subject to payment of course fees.

Ignacio González Bravo

Experimental Molecular Evolution Institute for Evolution and Biodiversity Westfaelische Wilhems University Muenster Hüfferstrasse 1 48149 Münster Germany

phone +49 251 83 21637 +49 251 83 21027 (Secretary Ms Hitziger) fax +49 251 83 24668

email address: [igbravo@uni-muenster.de](mailto:igbravo@uni-muenster.de)

<http://www.uni-muenster.de/evolution/expmolevol/>  
“Ignacio G. Bravo” <[igbravo@uni-muenster.de](mailto:igbravo@uni-muenster.de)>

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## Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to [Golding@McMaster.CA](mailto: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](mailto:Golding@McMaster.CA). In addition, if it originates from ‘blackballed’ addresses it will be sent to me at [Golding@McMaster.CA](mailto: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](mailto: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](mailto:evoldir@evol.biology.McMaster.CA). Do not include encoded attachments and do not send it as Word files, as HTML files, as  $\LaTeX$  files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at [Golding@McMaster.CA](mailto: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  $\text{\LaTeX}$  do not try to embed  $\text{\LaTeX}$  or  $\text{\TeX}$  in your message (or other formats) since my program will strip these from the message.