
E v o l D i r

December 1, 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.



Forward	1
Conferences	2
GradStudentPositions	10
Jobs	33
Other	55
PostDocs	71
WorkshopsCourses	84
Instructions	87
Afterward	88

Conferences

CardiffU PopGroup2008 Dec16-19 Reminder	2	UMichigan UsingPhylogenies Mar14 2	7
Hinxton ProteinEvolution Jan26-27	2	UNebraskaLincoln MEEC Mar27-29	7
HumboldtU MetazoanPhylogeny Mar3-6	3	UOxford AvianEvolution Jan7-9	7
IrvineCA InTheLightOfEvolution Jan15-17	3	Uruguay VertebrateDiversity Jul26-31	8
Luxembourg Biodiversity Mar26-28	4	UWisconsinMadison StatisticalGenetics May4-6	8
NaturalisMuseum Leiden IslandEvolution Feb12-13 2 4	4	Wageningen ConservationGenetics Dec8	9
Norwich Genetics Sept9-11	6		
Seville Darwin Feb25-27	6		

CardiffU PopGroup2008 Dec16-19 Reminder

Reminder - PopGroup 2008

Details of this year's PopGroup meeting can be found at: www.popgroup.org

Registration is available at standard rates until 24th November 2008, thereafter a late fee of £50 will apply.

Plenary speakers for this year's meeting are: Bryan Clarke (Nottingham), Mark Blaxter (Edinburgh), Francois Balloux (Imperial) and Mark Jobling (Leicester). There will be a special session on human population genetic variation and molecular evolution, sponsored by the Wales Gene Park, and accordingly we are inviting talks from those working in these areas. Please contact Mike Bruford (BrufordMW@Cardiff.ac.uk) if you would like to offer a talk in this session.

For general enquiries, please email PopGroup2008@Cardiff.ac.uk

Mike Bruford

sbimwb@groupwise.cf.ac.uk
sbimwb@groupwise.cf.ac.uk

Hinxton ProteinEvolution Jan26-27

Protein Evolution: Sequences, Structures and Systems
 26th - 27th January 2009 Wellcome Trust Conference
 Centre, Hinxton, Cambridge, UK A Biochemical Society/Wellcome Trust Focus Meetings

For registration and further information please visit http://www.biochemistry.org/meetings/-programme.cfm?Meeting_No=SA099 With kind regards Lucy Criddle

* Office Days: Monday, Tuesday, Wednesday & Thursday

Mrs Lucy Criddle Conference Organiser, Event Management The Wellcome Trust Conference Centre The Wellcome Trust Genome Campus Hinxton Cambridge CB10 1RQ

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www.wellcome.ac.uk

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Lucy Criddle <l.cridde@wtconference.org.uk>

HumboldtU MetazoanPhylogeny Mar3-6

Dear evolutionary biologists,

the “Deep Metazoan Phylogeny” Program of the German Science Foundation (DFG) invites you to the international conference **“Celebrating Darwin: From /The Origin of Species/ to Deep Metazoan Phylogeny”*.*

Registration is open: *<http://www.dmp2009.org>*
SCOPE:

Darwin’s 1859 book “On the Origin of Species” contained only a single figure depicting a tree diagram of species origins and relationships. This little scheme was nevertheless the starting point for the ubiquity of phylogenetic trees in today’s zoology. Every week numerous cladograms representing animal relationships at all levels are published. An increasing number of these articles deal with the phylogeny of the major groups of multicellular animals (Metazoa). However, these publications show that neither sequence data nor available morphological character sets produce phylogenies that converge to a widely accepted consensus. It is obvious that some traditional views cannot be maintained and that a new framework of animal phylogeny is emerging. Nevertheless, the large number of contradicting trees indicates that some fundamental problems of phylogenetic studies have not been discovered or resolved.

The international conference **“Celebrating Darwin: From /The Origin of Species/ to Deep Metazoan Phylogeny”** brings together mathematicians, theorists, molecular systematists, and morphologists interested in a critical review of known pitfalls and in the presentation of new analytical tools, new types of characters, and a synopsis of molecular and morphological characters. It is intended to get a critical and constructive view of the state of the art.

On behalf of the organising committee we would like to invite you to this conference, which will take place from *3th - 6th March 2009* at the Humboldt-University and the Museum of Natural History in Berlin, Germany. The meeting will consist of sessions with several invited speakers and open sessions with short presentations. In addition, there will be the possibility to show posters. The meeting focuses on three major themes:

*1) Innovations in analyses of molecular and morpho-

logical data*

2) Molecular phylogeny: new markers and phylogenomic analyses

*3) The indispensability of morphology *

The conference is organised by the Priority Program “Deep Metazoan Phylogeny” of the German Science Foundation (DFG). The project is a joint effort of more than 20 participating workgroups bringing together molecular, morphological and bioinformatic expertise with the goal to establish a robust (hopefully) backbone tree of metazoans. Details on the priority project “Deep Metazoan Phylogeny” can be found at: <http://www.deep-phylogeny.org/> . For more information and to register please visit our website (above).

– Zoologisches Forschungsmuseum Koenig Leibniz-Institut für die Biodiversität der Tiere

Susanne Düngelhoef Sektion Coleoptera Adenauerallee
160 53113 Bonn

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www.zfmk.de Werden Sie Mitglied in der Alexander Koenig Gesellschaft: <http://www.zfmk.de/web/-Foerderer/Freunde/index.de.html> Susanne Duengelhoef <s.duengelhoef.zfmk@uni-bonn.de>

IrvineCA InTheLightOfEvolution Jan15-17

January 15-17, 2009 In the Light of Evolution III: Two Centuries of Darwin Organizers: John C. Avise and Francisco J. Ayala Beckman Center of the National Academies, Irvine, CA The year 2009 will mark the 200th anniversary of Charles Darwin’s birth and the 150th anniversary of his most influential publication, On the Origin of Species, in which he developed the equally revolutionary concept that a natural but non-random process - ‘natural selection - yields biological adaptations that otherwise can give a superficial impression of intelligent conscious design.

This colloquium will bring together leading evolutionary biologists and science historians to reflect upon and commemorate the Darwinian Revolution. One goal of this symposium will be to canvass modern scientific thought and research approaches regarding each of the three main categories of selection (natural, artificial, and sexual) that Darwin addressed during

his career. Although Darwin is associated most often with his elucidation of natural selection in the Origin, he also thought and wrote extensively about artificial and sexual selection, as reflected for example in two other books titled, respectively, *The Variation of Animals and Plants Under Domestication* (1869) and *The Descent of Man and Selection in Relation to Sex* (1871). Other goals of this colloquium will be to place Darwin's seminal contributions in historical perspective, and in general to celebrate Darwin's ongoing scientific legacy. A preliminary program can be viewed at < http://www.nasonline.org/SACKLER_Darwin_program > http://www.nasonline.org/SACKLER_Darwin_program

\$250 EARLY REGISTRATION BY DECEMBER 15, 2008 Attendance at the Colloquium is limited to 230 registered individuals. Registrations will be accepted only when the registration fee is included and in the order in which they are received. The EARLY registration fee (\$250) includes the cost of meals, reception, and banquet.

\$150 STUDENT / POST DOC REGISTRATION BY DECEMBER 15, 2008 - TRAVEL/HOTEL AWARDS AVAILABLE A reduced all-inclusive (meals, reception, and banquet) registration fee of \$150 is offered to Graduate Students and Postdocs who register by December 15, 2008. The NAS has provided funds to supplement the expenses of participating graduate students and postdocs up to \$125 for hotel costs and up to \$300 for air travel (see award qualification details on the registration page). Awards will be approved on a first come basis when accompanied by the registration fee. Reimbursements will be paid after the Colloquium, upon documentation of qualifying expenses.

After December 15, 2008 - All Registrations are \$350

Register at < http://www.nasonline.org/SACKLER_Darwin > http://www.nasonline.org/SACKLER_Darwin >

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

Luxembourg Biodiversity Mar26-28

Call for contributions Symposium on Biodiversity Hotspots 26-28 March 2009, MNHN Luxembourg

Focus:

One of the key objectives of nature conservation is the

protection of biodiversity hotspots - centres of high numbers of ecosystems, species and/or genes. This meeting focuses on the development and status of areas with particularly high diversity, most of them not being adequately protected.

Programm and Registration:

The previewed programm is online available. Oral contributions and posters can become registered under the following website:

<http://www.symposium.lu/hotspots/default.aspx> –
Dr. Jan Christian Habel Musée national d'histoire naturelle Luxembourg 25, rue Münster L-2160 Luxembourg

++49 (0)651-2079116 ++49 (0)176-40123699

Axel Hochkirch <hochkirch@uni-trier.de>

NaturalisMuseum Leiden IslandEvolution Feb12-13 2

Reminder

Places still available, please do not forget to register for the:

International Congress

Island Evolution 150 Years After Darwin

www.naturalis.nl/darwin2009 150 Years after Darwin's *On the Origin of Species*, island evolution is entering a new phase. By habitat fragmentation, we humans create more and more islands, while at the same time, by transporting species from their native biomes, we remove the dispersal barriers that kept habitats isolated.

To explore the implications of this new era of island evolution, the National Museum of Natural History in Leiden, the Netherlands, together with the Darwin Center for Biogeology in Utrecht, the Netherlands, will organise an international congress on

"Island Evolution 150 Years After Darwin"

11-13 February 2009 Museum Naturalis Leiden, the Netherlands

The meeting will bring together traditional students of island biotas, experimental/theoretical community ecologists, and evolutionary biologists, to explore the role of island-biological processes in a world in which the "island processes" of isolation and dispersal are being drastically altered.

Registration fee:

Early (before 15 January 2009): EUR 150 (regular participants); EUR 100 (students)

Late (15 January 2009 and later): EUR 175 (regular participants); EUR 125 (students)

The registration fee covers book of abstracts, ice-breaker, free entry to the museum, lunches, buffet dinner, Darwin Year opening reception, and refreshments.

Registration closes on January 28th, 2009. Abstracts for posters (A0 format, 84 x 119 cm) should be submitted to Jeremy Miller (miller@naturalis.nl) before December 15th, 2008.

For more information and registration: <http://www.naturalis.nl/darwin2009> Scientific Programme:

Wednesday February 11, 2009

16.00-18.00 Early registration and ice-breaker.

Thursday February 12, 2009

Keynote Address: Mark Lomolino, New York Univ. On the Origin, Evolution and Preservation of Island Life: an Historical and Prospective Overview

Session I. Evolution in Island Systems (organisers: Jeremy Miller & Lars Chatrou)

on: What are evolutionary islands, why are they good model systems for evolutionary studies, and what was Darwin's role in developing island evolutionary biology?

Keynote lecture: Robert Whittaker, Univ. Oxford. Dynamic oceanic island biogeography: development and initial evaluation of a general model

Lecture 1: Peter Linder, Univ. of Zürich on the evolution and diversity of South Africa's Cape flora [exact title to be announced]

Lecture 2: Menno Schilthuizen, Naturalis. Evolution on a block of rock; land snail speciation on limestone outcrops

Lecture 3: Nicole de Voogd & Leontine Becking, Naturalis, and Katja Peijnenburg, Univ. of Amsterdam. Anchialine lakes: hidden islands within islands

Session II. Evolutionary ecology of isolated ecosystems (organisers: Menno Schilthuizen & Frank Berendse)

on: How do isolated ecosystems function and how do they evolve in the face of extinction and invasion?

Keynote lecture: Peter J. Morin, Rutgers Univ. The ecology and evolution of island communities in a changing world

Lecture 1: José Montoya, Univ. London. Unravelling Darwin's entangled bank: The architecture of ecologi-

cal fragility

Lecture 2: Han Olf, Groningen Univ. Dynamics of metacommunities and metaecosystems

Lecture 3: Kostas Triantis, Univ. Oxford. Evolutionary species-area curves

Reception and Opening of the Dutch Darwin year programme of events (All conference participants are invited)

Buffet dinner in the restaurant

Friday February 13, 2009

Session III. Evolutionary islands through time (organisers: Frank Wesselingh & Henry Hooghiemstra)

on: To show that island ecosystems are of all times and that the nature, context and extent of evolutionary processes on islands can be gleaned from the fossil record

Keynote lecture: Matthias Harzhauser, Natural History Museum Vienna. Evolutionary lessons from ancient long-lived lakes

Lecture 1: Henry Hooghiemstra, Univ. Amsterdam. Evolution of high tropical Andean endemic floras

Lecture 2: John de Vos et al. Naturalis. The island ecosystem of the Hobbit

Lecture 3: Isaac Cananovas-Vilar, Institut Català de Paleontologia: Neogene micromammal evolution and turnover between isolation and continuity.

Session IV. Human perspectives of evolutionary islands (organisers: Martien van Oijen & Kenneth Rijdsdijk)

on: Is there a future for evolutionary islands? How do island ecosystems respond to the pressures from human society and how does human society respond to the demise of island ecosystems?

Keynote lecture: Tijs Goldschmidt, Amsterdam. Temporary and perpetual effects of unplanned and calculated introductions

Lecture 1: Kenneth Rijdsdijk, Naturalis, Leiden and Julian Hume, the Natural History Museum, London. The message of the Dodo

— / —

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>

Norwich Genetics Sept9-11

Genetics 100 Years On John Innes Centre, Norwich, UK, 9-11 September, 2009 <http://www.jic.ac.uk/-centenary/events/Genetics100YearsOn/> < <http://www.jic.ac.uk/-centenary/events/Genetics100YearsOn/> >

To help celebrate 100 years of genetics at John Innes, join us for a very special symposium. Paul Nurse will open with the Bateson Lecture and Sydney Brenner will close with "Genetics 100 Years On". Sandwiched in between will be reflections on areas of human interest that have been transformed by a genetic approach, examining where they are now, and where they might be in the next 100 years. Come and listen to David Stern, Stewart Cole, Michael Ashburner, Jonathan Hodgkin, John Doebley, Walter Bodmer, Linda Partridge, Michael Stratton, Chris Tyler-Smith, Leena Peltonen-Palotie, Rico Coen, Eric Wieschaus, Rich Losick, Mark Patshne, Daniel St Johnson, David Baulcombe and Caroline Dean.

Student Funding There will be fully funded PhD student places available covering registration for the Symposium and three nights bed and breakfast accommodation. To apply for a place please send a covering letter of application, a CV and a letter of support from your supervisor to dawn.barrett@bbsrc.ac.uk <mailto:dawn.barrett@bbsrc.ac.uk> by Thursday 30th April 2009.

If you are interested in the history of genetics there is a one day meeting immediately preceding the symposium <http://www.jic.ac.uk/-centenary/events/historyofgenetics/programme.htm> < <http://www.jic.ac.uk/-centenary/events/historyofgenetics/programme.htm> > , and if you have ever worked at JI there is an Alumni Day following the symposium where you can meet up with old friends. <http://www.jic.ac.uk/-centenary/events/alumniaday/programme.htm> We would be very grateful if you could please forward to all your colleagues - thank you.

on behalf of the Organising Committee Professor Keith Roberts (Chair, JIC Emeritus Professor), Professor Chris Lamb (Director JIC), Professor Sir David Hopwood (JIC Emeritus Professor), Professor Enrico Coen, (JIC), Dr Sarah Wilmot (JIC), Professor Sir Paul Nurse (Rockefeller, NY, USA), Sir Walter Bodmer (Oxford, UK).

Dee Rawsthorne, PhD Outreach Coordinator Norwich

BioScience Institutes Norwich Research Park Colney Norwich NR4 7UA

Direct Line: 44 (0)1603 251457 Fax: 44 (0)1603 255168 E mail: dee.rawsthorne@bbsrc.ac.uk <<mailto:dee.rawsthorne@bbsrc.ac.uk>>
www.ifr.ac.uk < <http://www.ifr.ac.uk/> >
www.jic.ac.uk < <http://www.jic.ac.uk/> > <
<http://www.jic.bbsrc.ac.uk/sainsbury-lab/> > <http://www.tsl.ac.uk> < <http://www.tsl.ac.uk/> >

Need a meeting venue? Visit www.venue-norwich.info < <http://www.venue-norwich.info/> >

Want to find out first hand what's going on in world leading science research centres then join for free Friends of the John Innes Centre and IFR in the City <http://www.jic.ac.uk/corporate/friends/-index.htm> < <http://www.jic.ac.uk/corporate/friends/-index.htm> >

Are you a former employee, student, post-doc or project leader? If so, make sure we have your details on our Alumni Database and keep up to date with news from John Innes <http://www.jic.ac.uk/corporate/friends/-alumni-association.htm> < <http://www.jic.ac.uk/corporate/friends/-alumni-association.htm> >

www.plantsandus.org.uk < <http://www.plantsandus.org.uk/> > - Plants and Us - an innovative new charity devoted to promoting understanding about plants and plant science

"dee rawsthorne (TOC)"
 <dee.rawsthorne@bbsrc.ac.uk>

Seville Darwin Feb25-27

Just to be added to the plethora of conferences celebrating the Darwin bicentenary, there will be another one in Seville, Spain, next February 2009. You can find details at: <http://institucional.us.es/darwin09/> Regards Juan Arroyo

Dr. Juan Arroyo Dept Biología Vegetal y Ecología Universidad de Sevilla Apartado 1095, E-41080 Sevilla, Spain tel +34 95 455 7058 fax +34 95 455 7059 arroyo@us.es < <http://www.grupo.us.es/grnm210> >
<http://www.grupo.us.es/grnm210>

Juan Arroyo <arroyo@us.es>

UMichigan Using Phylogenies Mar14 2

NOTE: Nominations have been extended to December 1 and are now open to early stage assistant professors (in their first or second year in a tenure-track position).

CALL FOR NOMINATIONS

5th ANNUAL UNIVERSITY OF MICHIGAN EARLY CAREER SCIENTISTS SYMPOSIUM:

USING PHYLOGENIES IN ECOLOGY

The Ecology and Evolutionary Biology department at the University of Michigan invites the nomination of outstanding scientists early in their careers to take part in a symposium focused on using phylogenies to address ecological questions. This symposium will be held in Ann Arbor, Michigan on Saturday, March 14, 2009. Eight scientists will be selected to present their work. All research related to the use of phylogenetic information to interpret and understand ecological processes and patterns will be considered, and we particularly encourage nomination of researchers who are attempting to elucidate general principles or novel approaches.

Early career scientists are defined as senior graduate students (will receive their Ph.D. within one year), postdoctoral researchers, and early stage assistant professors (in first or second year in a tenure-track position). Graduate students or postdoctoral researchers should be nominated as potential speakers by their advisor or a senior colleague. Assistant professors may nominate themselves.

Nominations must include a brief letter of recommendation addressing both the nominee's scientific and communication skills, a copy of the nominee's curriculum vitae, and a brief abstract of the proposed presentation (< 200 words, written by the nominee). Nominations can be sent electronically (in a single file) to kuhnlein@umich.edu with the subject line: ³Nominee for ECSS² or by mail to ³Early Career Scientists Symposium, Department of Ecology and Evolutionary Biology, 2019 Natural Science Bldg., 830 North University, Ann Arbor, MI 48109-1048². More information is available at <http://sitemaker.umich.edu/ecss2009> All nominations must be received by December 1, 2008. Selected participants will be contacted by December 15, 2008.

For more information, contact Gail Kuhnlein (kuhnlein@umich.edu).

2009 ECSS organizing committee: Dr. Deborah Goldberg (degold@umich.edu), Dr. Chris Dick (cwick@umich.edu), Brian Sedio (bse-dio@umich.edu), Celia Churchill (celiakc@umich.edu). <http://www.eeb.lsa.umich.edu> Christopher Dick <cwick@umich.edu>

UNebraskaLincoln MEEC Mar27-29

The *Midwest Ecology and Evolution Conference (MEEC) *will be hosted at the University of Nebraska-Lincoln from March 27-29, 2009. This conference is for graduate and undergraduate students to present research via oral paper and poster presentations. Keynote speakers will include David Quammen, David Hillis, and Svata Louda. For more information about MEEC 2009, please visit midwesteec.org < <http://midwesteec.org> >.

While faculty and post-docs are not allowed to present at MEEC 2009, they are strongly encouraged to attend to support and network with top students from throughout the Midwest. All MEEC attendees must register for the conference.

Abstract submission and meeting registration should be completed online at midwesteec.org < <http://midwesteec.org> >.

* Abstract Submission Deadline: *February 15, 2009*
* Conference Registration Deadline*: February 15, 2009*
* Hotel Special Rate Deadline*: February 15, 2009*

Sincerely,

MEEC 2009 Steering Committee

TJ Bliss, Chair Matthew Giovanni Travis Hinkelman

Travis Hinkelman <travis.hinkelman@gmail.com>

UOxford Avian Evolution Jan7-9

International Ornithological Student Conference

Organised by the Edward Grey Institute, Department of Zoology, University of Oxford

Theme: Avian Evolution, Oxford, 7-9.01.2009

Closing date for submission of abstracts: 5th December 2008. Closing date for conference registration and fee payment: 15th December 2008.

Plenary Speakers:

- Camille Bonneaud, Harvard University, USA - Ian Brown, Avian Virology and Mammalian Influenza, VLA-Weybridge, UK - Lukas Keller, Zoological Museum, University of Zurich, Switzerland - Judith Mank, Dept of Zoology, University of Oxford, UK - Nick Mundy, Dept of Zoology, University of Cambridge, UK

Conference Format:

- 5 Speaker sessions - Talks: 12 + 3 minutes - Posters with 1 minute oral pitch by presenters - 2 Workshop sessions - Conference banquet and full social programme

The conference is opened to students (both undergraduate and graduate level) and early career post-docs. The guest speakers will be presenting talks relevant to the general theme of avian evolution. However, student talks and posters are open to any ornithological topic.

For further details, please visit our website:

<http://www.zoo.ox.ac.uk/egi/newsevents/-conference.htm> - Marta Szulkin, Magdalen College Research Fellow Edward Grey Institute, Dpt of Zoology University of Oxford, Oxford OX1 3PS, U.K.

marta.szulkin@zoo.ox.ac.uk

marta.szulkin@zoo.ox.ac.uk

Uruguay Vertebrate Diversity Jul26-31

Dear vertebrate morphologists

We are most pleased in inviting you to Punta del Este, Uruguay, to gather at the 9th International Congress of Vertebrate Morphology (ICVM 9). The Congress will take place from the 26th to the 31st July 2010 at the Conrad Hotel & Spa.

Past and present South American vertebrate diversity will be celebrated in this meeting, although we are confident that it will be as ecumenic as the previous eight, with scientists from all over the world conveying the joy of morphological discovery in its widest sense.

Visit the web page <http://icvm-9.edu.uy/> Estimados morfólogos de vertebrados

Tenemos el mayor placer en invitarlos a Punta del Este, Uruguay, para participar del 9 Congreso Internacional de Morfología de Vertebrados (ICVM 9). El Congreso se desarrollará entre el 26 y el 31 de julio de 2010 en el Conrad Hotel & Spa.

En este evento, serán abordados el pasado y el presente de la diversidad sudamericana de vertebrados. No obstante, estamos seguros que será tan universal como los ocho que le precedieron, con científicos de todo el mundo reunidos por el deleite del descubrimiento morfológico en su sentido más amplio.

Visite la página <http://icvm-9.edu.uy/> Prezados morfólogos de vertebrados

Temos o maior prazer em convidá-los a Punta del Este, Uruguai, para participar do 9º Congresso Internacional de Morfologistas de Vertebrados (9th International Congress of Vertebrate Morphology ICVM 9). O congresso será realizado entre os dias 26 e 31 de julho de 2010 no Conrad Hotel & Spa.

A diversidade passada e atual dos vertebrados sul-americanos será abordada neste evento. Porém, temos certeza de que será tão abrangente quanto as oito edições anteriores, com cientistas de todo o mundo reunidos para compartilhar o prazer da descoberta morfológica no mais amplo sentido.

Visite o site <http://icvm-9.edu.uy/> passer@fcien.edu.uy

UWisconsinMadison StatisticalGenetics May4-6

SYMPOSIUM:

STATISTICAL GENETICS OF LIVESTOCK FOR THE POST-GENOMIC ERA

The Symposium "Statistical Genetics of Livestock for the Post-Genomic Era" will be held at the University of Wisconsin - Madison, USA, on May 4-6, 2009 (please notice the new dates!). This meeting will provide an important opportunity to share and discuss state-of-the-art bioinformatics and statistical genomics methodologies as applied to livestock and companion animals. The symposium will be structured around four themes (Animal Functional Genomics, Systems Biology, Whole Genome Enabled Animal Selection, and Whole Genome Association Analysis), each with top-notch invited speakers covering contemporary topics

in statistical genetics, data mining and bioinformatics approaches applied to animal genomics. Additionally, there will be a poster session for delegates to present their latest research results.

The symposium will feature an outstanding list of invited speakers!

Dr. James Crow (Univ. of Wisconsin, USA; Opening Keynote Lecture)

Dr. David Allison (Univ. of Alabama - Birmingham, USA)

Dr. Agustin Blasco (Universidad Politecnica de Valencia, Spain)

Dr. Alicia Carriquiry (Iowa State Univ., USA)

Dr. Rohan Fernando (Iowa State Univ., USA)

Dr. Jean-Louis Foulley (INRA, France)

Dr. Ben Hayes (DPI-VIC, Australia)

Dr. Bjorg Heringstad (Norwegian University of Life Sciences, Norway)

Dr. William Hill (University of Edinburgh, UK)

Dr. Sunduz Keles (Univ. of Wisconsin, USA)

Dr. Ignacy Misztal (Univ. of Georgia, USA)

Dr. William Muir (Purdue University, USA)

Dr. Dan Nettleton (Iowa State Univ., USA)

Dr. Miguel Perez-Enciso (ICREA - UAB, Spain)

Dr. Max Rothschild (Iowa State Univ., USA)

Dr. Henner Simianer (University Goettingen, Germany)

Dr. Moshe Soller (Hebrew University, Israel)

Dr. Daniel Sorensen (University of Aarhus, Denmark)

Dr. Robert Tempelman (Michigan State Univ., USA)

Dr. Miguel Toro (INIA, Spain)

Please mark in your calendars! Additional information will be sent out soon.

Sincerely,

Dr. Kent Weigel and Dr. Guilherme Rosa

Symposium co-chairs

The Symposium organization acknowledges funding support from the USDA-NRI 43.0 Animal Genome Program.

–

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Wageningen Conservation Genetics Dec8

International symposium:

New opportunities for conservation genetics with genome wide information

Monday 8th December 2008, 09.00-17.00, Hotel De Nieuwe Wereld, Wageningen, the Netherlands

Genetic diversity is of vital importance to cope with changing environments and human demands. Currently genetic diversity is under threat, both in the wild and in crops and domestic animals. With the rapid development of molecular biology, methods to measure genetic variability in detail across the entire genome are available. This symposium explores the new possibilities for genetic conservation opened up by the latest molecular technologies.

Program

In the morning various invited speakers will give an overview of conservation genetics research, related to plant and animal genetic resources, including the (potential) use of new molecular techniques. Amongst them are:

Professor John Woolliams (Roslin Institute, UK): From animal genetic resources to the animal genomic revolution

Dr. Theo van Hintum (CGN, NL): Conserving and mining plant genetic resources using knowledge of the genome

Dr. Richard Crooijmans (WUR, NL): New molecular technologies in animal biodiversity

In the afternoon, short presentations will be given by researchers and PhD students who are working in the area of conservation genetics.

Organisation

This symposium is organized by the working group Biodiversity within the Animal Breeding and Genomics

Centre (ABGC) of the Animal Sciences Group, in collaboration with the Graduate School Wageningen Institute of Animal Sciences (WIAS), the Graduate School for Production Ecology and Resource Conservation (PE&RC) and the Centre of Genetic Resources The Netherlands (CGN).

Kor Oldenbroek (WIAS, CGN)

Krista Engelsma (ABGC,CGN)

Admission is free, after registration. For further information and registration please contact:

Krista.Engelsma@wur.nl

GradStudentPositions

ChicagoBotanicGarden PlantConservation	10	UGeorgia InvasiveSpecies	22
ColoradoStateU BehavioralEvolution	11	UGeorgia PlantEvolution	23
ColoradoStateU EvolBiol	11	UGottingen ChemoautotrophicEvolution	23
Do bacteria have sex	12	UHelsinki EvolutionaryGenetics	24
EastCarolinaU SticklebackEvolution	12	UHelsinki ParastoidEvolution	25
GhentU EvolutionaryRobots	13	UKentucky EvolutionaryBiology	25
LeibnizInst 2 AsexualReproduction	13	UMassachusettsAmherst CiliatePhylogeography ...	26
Leipzig PrimateEvolution	14	UMinnesota IntroducedSpecies	26
Madrid TreeEvolution	14	UNevadaLasVegas BirdEvolution	27
MasseyU MicrobialGeneticsEvolution	15	UNewOrleans ConservationBiology	50
MasseyU MolecularEvolution	15	UOregon MolecularSystemEvolution	27
MaxPlanckGottingen PopulationGenomics	16	UOulu ArabidopsisSpeciation	80
Munich 2 DinoflagellateEvolution	16	UppsalaU ProtistEvolutionaryGenomics	28
OregonStateU ParasiteHost EvolutionaryGenet ...	17	USalzburg EvolutionaryBiology	29
RiceU PlantEvolution	17	USaskatchewan AdaptationGenomics	30
SAfrica PopGenInvasionBiology	18	USouthCarolina EvolutionaryBiol	30
Salzburg EvolutionOfSex	18	UToronto EvolutionaryBiology	31
StonyBrookU EvolutionaryBiol	19	UUtah HostParasiteEvolution	31
SyracuseU Fish EvoDevo	19	UWesternOntario Phylogenetics Sociobiology	32
TexasAMU EvolBiol	20	UWisconsinMilwaukee PopulationGenetics	32
UArkansas EvolutionaryBiol	21	Wellington NZ MusselFitnessDifferences	32
UCaliforniaLosAngeles EvolutionaryBiology	21		

ChicagoBotanicGarden PlantConservation

DOCTORAL FELLOWSHIPS IN PLANT CONSERVATION AND BIOLOGY NORTHWESTERN UNIVERSITY AND THE CHICAGO BOTANIC GARDEN

Northwestern University and the Chicago Botanic Garden announce a joint doctoral program in Plant Biology and Conservation. Support will be provided for five years through fellowships and teaching and research assistantships with a competitive stipend. The Chicago Botanic Garden and Northwestern University offer exciting opportunities for graduate student research in ecology, restoration ecology, soil ecology, climate change, invasive biology, paleobotany, paleoecology, conservation genetics, evolution, and systematics. For more information about the program and faculty

research interests, please visit our website: <http://www.plantbiology.northwestern.edu> Or contact: Nyree Zerega Director of Graduate Program Plant Biology and Conservation n-zerega@northwestern.edu

nzerega@chicagobotanic.org

ColoradoStateU BehavioralEvolution

Graduate Position in Behavioral Evolution

A PhD position is available in the lab of Lisa Angeloni at Colorado State University. Motivated students interested in evolutionary ecology, sexual selection, and animal mating behavior are encouraged to apply. We are investigating the mating strategies of Trinidadian guppy populations that experience different levels of predation pressure in their natural habitats. Predation can affect guppy life history strategies, male color patterns, male mating behavior and female preferences for male traits. This project focuses on the interaction between reproductive behavior and predation pressure, but there are many possible questions to ask with this system, and a new graduate student will have the opportunity to help shape the scope of the project. Applications can be submitted through the Graduate Degree Program in Ecology (<http://www.ecology.colostate.edu>) or the Department of Biology (<http://www.colostate.edu/Depts/Biology>). Prior to applying, please send a preliminary statement of interest (along with a CV or resume) describing previous research experience, research interests, GPA, and GRE scores by January 5, 2008 to Lisa Angeloni (angeloni@lamar.colostate.edu). Applications will be reviewed as they come in, and may also be reviewed after the target date if the position has not been filled.

Lisa Angeloni Assistant Professor Department of Biology and Graduate Degree Program in Ecology Colorado State University Fort Collins, CO 80523-1878 (970) 491-0562 angeloni@lamar.colostate.edu <http://rydberg.biology.colostate.edu/angelonilab> angeloni@lamar.colostate.edu

Hi all,

Several of the below have an evolutionary focus (or core).

Best, Ruth

Graduate Research and Teaching Assistantships Available

The Department of Bioagricultural Sciences and Pest Management (BSPM) at Colorado State University has several graduate student research and teaching assistantships available in fields ranging from ecology to genomics. Projects focus on insects, plants or plant pathogens and the focus ranges from the molecular to the ecosystem level. Faculty seeking students and the general research areas are listed below.

Lou Bjostad (louis.bjostad@colostate.edu): Natural products chemistry in agriculture Cini Brown (cynthia.s.brown@colostate.edu): Invasive plants range limits and expansion, the role of plant community and ecosystem restoration in invasive plant control Stephen Chisholm (chisholm@colostate.edu): Molecular host-microbe interactions Boris Kondratieff (boris.kondratieff@colostate.edu): Insect biodiversity Andrew Norton (apnorton@lamar.colostate.edu): Plant-insect interactions and biological control of weeds. John McKay (j.mckay@colostate.edu): Evolution of plant genomes; physiology and genomics of drought adaptation; drought adaptation of emerging biofuels crops. Paul Ode (paul.ode@colostate.edu): Parasitoid behavioral ecology; ecology of multitrophic interactions Paul Opler (paul.opler@colostate.edu): Lepidoptera systematics, taxonomy and ecology Frank Peairs (frank.peairs@colostate.edu): Insect pest management

Students can enter through BSPM or through the Graduate Degree Programs in Ecology or Molecular Plant Biology. Join the outstanding students and faculty at Colorado State University! See us at: <http://www.colostate.edu/Depts/bspm/> <http://www.ecology.colostate.edu/> <http://www.plantbiology.colostate.edu/> <http://www.NREL.colostate.edu/> For more information and application instructions, please email our graduate secretary Janet Dill (dillj@lamar.colostate.edu) and the individual faculty listed above.

CSU is an EO/AA employer.

Ruth Hufbauer <hufbauer@lamar.colostate.edu>

Do bacteria have sex

Dear EvolDir,

I have an opening for a graduate student interested in using molecular tools to investigate the evolution of natural competence in bacteria. This is a very controversial problem that's also at the heart of a bigger problem - whether any of the bacterial processes that cause recombination have been selected to do so.

Interested students can read more about our work in the papers, proposals and blogs on our web pages (see especially the 2007 grant proposal on DNA uptake). The ideal applicant would have some experience with both evolutionary biology and molecular biology, but strengths in one area could compensate for weaknesses in the other.

Vancouver is frequently ranked as the most livable city in the world, but it's also a great environment for molecular and evolutionary biologists (see for example <http://www.lsi.ubc.ca/> and <http://www.zoology.ubc.ca/veg/VEG/Welcome.html>)

Rosie

Dr. Rosemary J. Redfield redfield@interchange.ubc.ca

Associate Professor Department of Zoology Office: (604) 822-3744 Univ. of British Columbia Lab: (604) 822-6323 Vancouver, B.C. V6T 1Z4 Fax: (604) 822-2416 Canada

We're now in the Life Sciences Centre (RJR office 2551, lab 2520; email us for directions)

Web site: <http://www.zoology.ubc.ca/~redfield>
 Research blog: <http://rrresearch.blogspot.com> redfield@zoology.ubc.ca redfield@zoology.ubc.ca

EastCarolinaU SticklebackEvolution

Dear colleagues,

I would add to our departmental announcement below that I am particularly keen to recruit students to work on female color evolution in sticklebacks and color poly-

morphism evolution in the telmatherinid fishes of Sulawesi.

Cheers, Jeff http://www.ecu.edu/cs-cas/biology/-mckinnon_jeff.cfm GRADUATE STUDIES IN EVOLUTION AND ECOLOGY AT EAST CAROLINA UNIVERSITY

The Department of Biology at East Carolina University (the third largest campus in the North Carolina University System) invites inquiries and applications from prospective graduate students for Fall 2009. We have an active and well-supported group of faculty in Evolution and Ecology and will guarantee accepted PhD students (to the Interdisciplinary Doctoral Program in Biological Sciences) at least two years of support with no teaching obligations and at least five years of support total, at a very competitive level. We also offer two MS programs (with Teaching Assistant-ships readily available) and participate in ECU's PhD program in Coastal Resources Management.

Situated in the attractive and affordable community of Greenville, we are in easy reach of North Carolina's Research Triangle (including the National Evolutionary Synthesis Center) as well as the diverse natural communities of the Coastal Plain and the Outer Banks. Thus excellent opportunities exist for collaboration and to work in terrestrial, aquatic, wetland and marine systems. A readily available 454 sequencer at ECU's Brody School of Medicine facilitates genomic research. Travel is convenient through Raleigh-Durham International Airport and our faculty are engaged in research on every continent but Antarctica.

Please visit <http://www.ecu.edu/biology/> to find out more about our department. Information on our graduate programs is available here: <http://www.ecu.edu/-biology/graduate.cfm> Review of graduate applications generally begins in March (though the formal deadline is later).

Our Evolution and Ecology faculty (<http://www.ecu.edu/biology/faculty.cfm>) include: Jason Bond: Arthropod systematics. Mark Brinson: Wetland restoration ecology, ecosystem ecology. David Chalcraft: Population and community ecology; ecological aspects of biodiversity. Robert Christian: Systems and network theory; ecology of coastal ecosystems. Lisa Clough: Marine benthic ecology (Arctic and Atlantic). Carol Goodwillie: Plant mating system evolution. Jinling Huang: Evolutionary genomics, bioinformatics; horizontal gene transfer. Claudia Jolls: Plant evolutionary ecology and conservation. Dave Kimmel: Plankton ecology. Trip Lamb: Systematics and phylogeography. Joe Luczkovich: Food web ecology and fish bioacoustics. Jeff McKinnon: Sexual

selection, speciation in fish. Sue McRae: Behavioral ecology and social evolution in birds. Anthony Overton: Larval fish ecology, fisheries biology. Enrique Reyes: Landscape ecology, ecological modeling, coastal management. Roger Rulifson: Fisheries Biology and management. Jean-Luc Scemama: Post-duplication gene evolution. Matt Schrenk: Biofilm ecology, microbiology. Ed Stellwag: Vertebrate evo-devo and cis-regulatory network evolution. John Stiller: Plant comparative genomics. Kyle Summers: Evolution of color, behavior in poison frogs; evolutionary medicine. Heather Vance-Chalcraft: Predation and community ecology. Terry West: Human impacts on coastal ecosystems. Baohong Zhang: MicroRNA evolution, comparative genomics, and molecular genetics.

In addition to visiting the websites, please contact prospective mentors directly for more information, or graduate studies director Terry West: westt@ecu.edu

Jeffrey S. McKinnon, Chair Dep. of Biology, N108 Howell Science Complex East Carolina University Greenville, NC 27858-4353 Phone 252-328-5258 mckinnonj@ecu.edu http://www.ecu.edu/cs-cas/biology/mckinnon_jeff.cfm MCKINNONJ <mckinnonj@ecu.edu>

GhentU EvolutionaryRobots

The Research Group Bioinformatics and Evolutionary Genomics of the Department of Plant Systems Biology at VIB/Ghent University is currently looking for a

PhD student

To work on a European FP7 Project entitled SYMBRION (Symbiotic Evolutionary Robot Organisms) - scientific research towards a PhD degree (4 year period, starting asap) - perform scientific research on the evolvability of symbiotic robot organisms, develop a robot genome and bio-inspired evolutionary strategies - interpret the characteristics and behaviour of the resulting robot organisms in an evolutionary context - regular interaction with an established network of top-level researchers - requirement of attending and presenting your work at international scientific meetings - publish in peer-reviewed international journals

Profile

- you have a master in Engineering - you have a strong interest in robotics and evolution - good knowledge of Java and C - good communication and writing skills -

proficient in English - prepared to go abroad for several months for training purposes

Further information SYMBRION website: <http://www.symbrion.org/> Visit us at <http://bioinformatics.psb.ugent.be/> Send your CV by email to Prof. Dr. Yves Van de Peer (yves.vandeppeer@psb.ugent.be <mailto:yves.vandeppeer@psb.ugent.be>). Applications will be accepted until the position is filled.

- Yves Van de Peer, PhD.

Professor in Bioinformatics and Genome Biology Group Leader Bioinformatics and Evolutionary Genomics VIB Department of Plant Systems Biology, UGent Ghent University Technologiepark 927 B-9052 Ghent Belgium

Phone: +32 (0)9 331 3807 Cell Phone: +32 (0)476 560 091 Fax: +32 (0)9 331 3809 email: yves.vandeppeer@psb.ugent.be

<http://bioinformatics.psb.ugent.be/> Yves Van de Peer <yves.vandeppeer@psb.ugent.be>

LeibnizInst 2 AsexualReproduction

Dear EvoDir,

I have two 10 month "diplom" positions (German equivalent of an MSc) to study expression of house-keeping genes from microdissected tissues taken from sexual and asexual plants of the genus *Boechera* (wild relative of *Arabidopsis*). The goal of the project(s) will be to validate gene expression profiles across different analysis platforms, and to examine the effects of asexual genome variability on validation results.

If possible, I'm looking for students with some experience with PCR, DNA sequencing and RNA extractions. The working language of my group is english.

Please don't hesitate to contact me if you are interested.

Best wishes, Tim

Dr. Tim Sharbel Apomixis Research Group Leader Dept. of Cytogenetics and Genome Analysis Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstraße 3, D-06466 Gatersleben Germany

Apomixis Group Webpage <http://www.ipk-gatersleben.de/Internet/Forschung/-CytogenetikGenomanalyse/Apomixis> International Max Planck Research School (IMPRS) faculty member <http://imprs.ice.mpg.de/people/>

Faculty_Members.htm?mp=3D12 IPK Webpage
www.ipk-gatersleben.de tel: +049 (0)39482 5608 fax:
 +049 (0)39482 5137

sharbel@ipk-gatersleben.de sharbel@ipk-gatersleben.de

Leipzig PrimateEvolution

Applications invited for a Ph.D position in Molecular Primatology.

I am looking for a PhD student to conduct a project aimed at using DNA sequence analysis to improve our understanding of the evolutionary histories of primate populations. Primates in the wild exist in populations with very varied distributions. For example, some primates may occur in fragmented patches in a restricted area, whereas others may be quite widespread. Some closely-related species occupy widely separated ranges, while others occur adjacent to one another and may even hybridize along their contact zone. The wealth of nuclear genome sequence information newly available from chimpanzees, macaques, and other primates enable us to ask questions concerning the long-term histories of primate populations. By using high-throughput methods to resequence multiple segments of the nuclear genome of small numbers of representatives of different populations, we seek to understand when and how populations diverge, how they remain separate in the presence of gene flow, and the social, ecological and demographic factors that ultimately underly the patterns observed.

Candidates with experience in relevant molecular biology lab techniques, population genetics theory, and skills in genetic data analysis are encouraged to apply. The student will be a member of the genetics group of the primatology department of the Max Planck Institute for Evolutionary Anthropology (see <http://www.eva.mpg.de/primat/files/genetics.htm>) and receive a degree through the Leipzig School of Human Origins, an International Max Planck Research School of the University of Leipzig and the Max Planck Institute for Evolutionary Anthropology (see <http://www.leipzig-school.eva.mpg.de/start.html>). Students are supported by fellowships.

Applicants will ideally already have a masters degree in a relevant subject (e.g., Biochemistry, Molecular Biology, Genetics, Anthropology). Alternatively, an excellent bachelors degree (e.g., first, with high honors)

may be acceptable but please enquire prior to applying. Candidates should also have good organizational skills, be interested in behavioral ecology, genetics and evolution, be able to work independently as well as in a team and enjoy working in an interdisciplinary environment.

The application deadline is January 31, 2009 and the student should begin by September 1, 2009. Applications should be filed following the instructions at <http://www.leipzig-school.eva.mpg.de/start.html>. For additional information please contact me via email: Dr. Linda Vigilant Max Planck Institute for Evolutionary Anthropology Deutscher Platz 6 04103 Leipzig Germany tel. ++49-341-3550-222 fax. ++49-341-3550-299 email vigilant@eva.mpg.de

Linda Vigilant <vigilant@eva.mpg.de>

Madrid TreeEvolution

PhD offer (FPI program 2009):

Ecological and genetic responses to environmental change in forest systems

Associated to projects: VaMPiro (Molecular Variation and Pyrophytism, Spanish National Science Foundation) and LinkTree (Linking genetic variability with ecological responses to environmental changes: forest trees as model systems, EU BiodivERsA)

The research Project will focus on the response of Mediterranean and Sub-saharian African forests to natural selection mediated by environmental change, including forest fires and drought. To achieve this objective, we will combine ecological research in the field with molecular analyses. Lab work will be done at the Forest Genetics and Ecophysiology Lab, Forest Research Institute (CIFOR-INIA, www.inia.es), Madrid (Spain) as well as in various other European and North American labs. The research environment in our group is dynamic and multidisciplinary and European doctorates are encouraged.

Applicants requirements:

Citizenship or legal residence in the European Union
 Master Degree in Life Sciences, Biology or Forestry
 Excellent academic records
 Expertise in molecular techniques will be appreciated
 Knowledge of population genetics and evolutionary biology disciplines
 Language skills (high level of written and spoken English abso-

lutely required) Amenability for travelling and doing research stays in different labs of Europe and North America Full time dedication to pursuing PhD studies at a Spanish University

Applicants can send a CV and a motivation letter to:

Dr. Santiago C. Gonzalez Martinez CIFOR-INIA
santiago[no sp@m]inia.es www.plantevol.arrakis.es/~scgonzalez.htm Deadline: January 8th, 2009

MasseyU MicrobialGeneticsEvolution

PhD opportunity

Molecular epidemiology / microbial genetics and evolution

We offer a 3-year Marsden-funded PhD programme examining the molecular evolution of New Zealand's most prominent human pathogen: *Campylobacter*. We are looking for someone with an interest and background in population genetics or statistics who would like to develop skills applying phylogenetics, molecular epidemiology and coalescent-based genealogical modelling to genome-scale data. You will be based at Massey University in Palmerston North and will be supervised by a team of scientists based at the Hopkirk Research Institute, the Allan Wilson Centre, ESR Ltd, and the Universities of Oxford and Lancaster. You must be willing to spend some time working in the United Kingdom during the PhD programme.

For further information please contact:

Professor Nigel French

Hopkirk Institute, Institute of Veterinary, Animal and Biomedical Sciences College of Sciences, Massey University, Palmerston North

Email - N.P.French@massey.ac.nz Phone - +64 (06) 356 9099 extn 81188

brhollan@googlemail.com

MasseyU MolecularEvolution

We offer a 3-year Marsden-funded PhD programme examining the molecular evolution of New Zealand's most prominent human pathogen: *Campylobacter*. We are looking for someone with an interest and background in population genetics and/or statistics who would like to develop skills applying phylogenetics, molecular epidemiology and coalescent-based genealogical modelling to genome-scale data. You will be based at Massey University in Palmerston North, North Island, New Zealand and will be supervised by a team of scientists based at the Hopkirk Research Institute, the Allan Wilson Centre, the Institute for Environmental Science and Research Ltd and the Universities of Oxford and Lancaster in the United Kingdom. You must be willing to spend some time working in the United Kingdom during the PhD programme.

For further information please contact: Professor Nigel French Email - N.P.French@massey.ac.nz , Phone - +64 (06) 356 9099 extn 81188

Further details of the research programme:

Cows, starlings and *Campylobacter* in New Zealand: unifying phylogeny, genealogy and epidemiology to gain insight into pathogen evolution

Summary: The introduction of European wildlife has had a devastating effect on New Zealand's flora and fauna. Yet these historical events, coupled with the importation of domestic livestock, have provided us with a unique opportunity to study the evolution of a globally important human pathogen: *Campylobacter*. Using analytical tools recently developed by our research team, together with detailed sequencing studies, we aim to exploit the newly-discovered host specificity of *C. jejuni* and *C. coli* strains and the well-characterised historical separation of both NZ and European host and bacterial populations, to improve our understanding of *Campylobacter* species evolution. We have unprecedented access to isolates, and their multilocus gene sequences, cultured from humans, domestic animals and wildlife in NZ and Europe - and will gather additional isolates and more detailed sequence data from NZ. We will discover how often, and how much, genetic material is exchanged between natural populations; how important recombination is relative to mutation for the emergence of new strains; and in which host species these events are most likely to occur. Ultimately we can learn how and why *C. jejuni* emerged to become such a prominent human pathogen; anticipate further evolution and restrict the emergence and spread of new strains.

p.fearnhead@lancaster.ac.uk

MaxPlanckGottingen PopulationGenomics

PhD Student Position - Population Genomics

A 3-year PhD student position in Population Genomics is available in the newly formed lab of Dr. Oskar Hallatschek at the Max-Planck-Institute for Dynamics and Self-Organization in Göttingen. The student will join a young and interactive research group in evolutionary dynamics and biophysics, including theoreticians and experimentalists. We cultivate an international atmosphere and the everyday working language is English. The Max-Planck-Institute for Dynamics and Self-Organization is located close to the center of the medieval town of Göttingen. More information about the group is available on the web at: <http://www.fas.harvard.edu/~ohallats/>

The goal of the P.h.D. project is to quantify genetic footprints of natural selection and demographic revolutions, and how they can be disentangled from one another: Kimura's neutral theory dominated the field of population genetics as long as sequence data was a rare commodity. The recent years of whole genome sequencing revealed quite surprisingly that standard neutral models rarely explain observed polymorphism data well. Many researchers take these deviations as ubiquitous signatures of acting natural selection. However, although standard neutral models seem to be a poor null model, the new interpretation in terms of natural selection is far from straight forward. Most models of natural selection make even more stringent assumptions than neutral models, such as panmixia, demographic equilibrium and negligible epistatic interactions. These simplifications could well have dropped the baby with the bath water.

The situation clearly indicates that genetic data mining is ahead of our theoretical understanding of the how molecular evolution works ("population genetics was much more fun in lack of genetic data", Whitlock). What could replace the neutral theory as a null model of molecular evolution? The P.h.D. student will join our group effort to develop a new null model, which could well dependent on the species. Specifically, he or she will search for new sensible ways to disentangle natural selection from a typically unsteady demographic history. The project will pay attention to spatial aspects of evolution, epistatic selection and the previously unseen

types and amounts of data of the coming years. Prior experience in population genetics modeling, molecular evolution or comparative genomics is helpful but not necessary.

The appointment will be on a temporary basis for a maximum of 4 years. The gross salary starts at approximately 1400,- per month depending on age and experience (TVöD 13/2, Stufe 1). The student will be enrolled in the Göttingen Graduate School for Neurosciences and Molecular Biosciences (GGNB, <http://www.ggnb.uni-goettingen.de/>). Applicants should have a master's degree or equivalent in biology, math, physics, or related fields. If you hold an excellent BSc (1st class honors) please contact us about possible accession. German is not required but international students will be offered opportunities to take German courses. Interested candidates should send a cover letter summarizing their research background and interest in the position, CV, and contact information of two potential referees as a single PDF file to: oskar.hallatschek.applications@gmail.com

Applications will be reviewed beginning December 1, 2008. Interviews will be held in January. Starting date is February 1 2009 or later. If you have any specific questions (e.g. details of the project), feel free to email me.

The Max-Planck-Institute for Dynamics and Self-Organization is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled.

oskar.hallatschek.applications@googlemail.com

Munich 2 DinoflagellateEvolution

Job announcement

The Departments of Palaeontology (FU Berlin), Systematic Botany (LMU Munich), Historical Geology & Palaeontology (University Bremen), and the Museum of Natural History (Berlin) invites applications for 2 Ph.D. Studentships in Systematics, Evolution and Biogeography of Dinoflagellates Salary: approx. 29,000 gross per annum (employment according to German BAT IIa/2 / E13/2), funded by the Deutsche Forschungsgemeinschaft (DFG, project title: "Evolution of calcareous dinoflagellates producing benthic cysts", Ref. KE 322/36-1) Duration: 2009-2011 (2 x 36 months) Starting date: January 1st, 2009, or as soon

as possible thereafter

Essentials We are looking for two motivated candidates holding a Masters degree (or equivalent) in a relevant subject. One Ph.D. project requires expertise in molecular systematics (DNA extractions, PCR, sequencing, bioinformatics; biochemists are also welcome to apply), and the other project involves research, for which light and electron microscopy (SEM/TEM) skills are essential. Both Ph.D. projects will be located at the Ludwig-Maximilians-University in Munich, and successful candidates will demonstrate interest in the fields of taxonomy and systematics, broader questions in evolutionary biology, and biogeography and molecular clock studies. Good communication skills, the ability to work independently in an interdisciplinary team, and the willingness to conduct fieldwork in Europe and South America are essential. A working knowledge of English, and possibly also Spanish, is desirable.

Job duties The two Ph.D. students will interact closely, combining molecular and morphological approaches to expand the currently fragmentary knowledge about the extant diversity of calcareous dinoflagellates. Such micro algae belonging to the Alveolata are excellently preserved in the fossil record and have received increased attention over the past three decades as regards their use in biostratigraphy, climate, and environmental reconstruction. Supposed "living fossils" have been described, but not been brought into culture so far. The project will thus include fieldwork to expand the World's largest living culture collection of calcareous dinoflagellates held at Bremen. Detailed morphological and anatomical investigations of the different life cycle stages will result in additional characters for phylogenetic analyses and will provide a deeper understanding of morphology and function of coccoid stages in calcareous dinoflagellates. Multi-gene phylogenetic trees will be set in a temporal context by fossil calibrations or constraints, and you will address questions about the timing and setting of divergence events as well as the association of divergence events with habitat requirements and the establishment of new ecological niches.

Applications should be sent to Prof. Dr. Helmut Keupp, Freie Universität Berlin, Geologische Wissenschaften, Fachrichtung Paläontologie, Malteserstrasse 74-100, D - 122 49 Berlin, and include: 1) a cover letter outlining relevant background and work experience, 2) a full curriculum vitae, including a list of publications and copies of certificates, 3) names and addresses of two referees. The Freie Universität Berlin supports gender equality and particularly encourages women to apply. Equally qualified, severely handicapped applicants will be given preference.

For informal enquiries, please contact Dr. Marc Gottschling (gottschling@biologie.uni-muenchen.de). The deadline for receipt of all applications is December 1st, 2008.

gottschling@biologie.uni-muenchen.de

OregonStateU ParasiteHost EvolutionaryGenet

Mike Blouin at Oregon State University is encouraging applications from students interested in doing PhD work in the area of host-parasite evolutionary genetics.

Our lab works in the general area of population genetics and molecular evolution, but with a major focus on parasites (see website below).

Feel free to email or call Mike for more information. – Michael Blouin Dept. Zoology, Oregon State University Corvallis, OR 97331-2914 <http://oregonstate.edu/~blouinm/> Tel: 541-737-2362 Fax: 541-737-0501

blouinm@science.oregonstate.edu

blouinm@science.oregonstate.edu

RiceU PlantEvolution

Ph.D. Students Wanted: Ecology and evolution of plants and plant-animal interactions

My lab is broadly interested in the ecology and evolution of plants and their communities, often focusing on plant-animal interactions such as herbivory, seed predation, and seed dispersal. Major questions include how genetic diversity is maintained in nature, how invasive plant species acquire their invasive traits, and how genome size might affect plant ecology and evolution. We use a combination of field, greenhouse, phylogenetic and molecular genetic approaches. Students are expected to develop their own independent projects but will also have opportunities to collaborate on an NSF-funded investigation of hybridization and adaptation to herbivory in wild sunflowers.

Rices Ecology and Evolutionary Biology (EEB) program boasts an exceptionally active faculty and a dynamic group of graduate students. We also have great

facilities, including new molecular labs and a new 3600 sq. ft. greenhouse. Areas of emphasis include interspecific interactions, mutualism, cooperation, herbivory, and invasion biology. Outstanding fellowship-based financial support is available for Ph.D. students.

For more info please contact:

Ken Whitney

email: kwhitney@rice.edu
 <<mailto:kwhitney@rice.edu>> personal webpage:
<http://www.ruf.rice.edu/~kwhitney/> < <http://www.ruf.rice.edu/~kwhitney/> > lab webpage:
<http://www.ruf.rice.edu/~planteco/index.html> <
<http://www.ruf.rice.edu/~planteco/index.html> >

Please also check out the research pages for other Rice EEB faculty, many of whom are also accepting students: <http://eeb.rice.edu/faculty.html> – Ken Whitney, Asst. Professor Dept. of Ecology and Evolutionary Biology, MS 170 Rice University, 6100 Main St., Houston, TX 77005 (713) 348-3057 ph. (713) 438-5232 fax

Safrika PopGenInvasionBiology

Postgraduate Bursaries in Ecological Genetics of Invasive Species. Several opportunities at Honours, MSc and PhD level at the Centre for Invasion Biology, Stellenbosch University Please note: these bursaries are only for South Africans.

The C*I*B is a dynamic, internationally leading agency which undertakes research to reduce the rate and impacts of biological invasions. We are looking for several postgraduate students interested in ecological genetics and molecular ecology, to form part of a major 5 year collaborative project with the Working for Water Programme and the University of Adelaide / Herbarium of South Australia.

Project details: The projects form part of a broader project to improve our understanding and management of alien plant invasions using molecular techniques. Component 1 focuses on the phylogeography of Australian plants invasive in South Africa (more than 20 species of wattles and hakeas). We want to understand how, why, and from where exactly plants were introduced. This information is of direct applied benefit to classical biological control efforts. Population genetics analysis using microsatellite markers will also be used to compare levels of genetic diversity; the occurrence of admixture and hybridization; studying for

evidence of local adaptation; and potentially exploring epigenetic differences; we will address one of the most exciting and topical questions in biology: how quickly can species evolve under new selection pressures? In the second component we will extend the analysis to include insect and fungi introduced for classical biological control. Finally, in component 3, we want to combine mathematical models and ecological studies with analyses of gene flow to understand dispersal distances and invasion pathways of major invasive alien species in South Africa.

The projects are flexible, allowing students to focus on issues that interest them and, after preliminary analysis, would identify additional research questions.

Requirements: Hons: excellent marks at undergraduate level * a keen interest in molecular ecology * excellent communication skills (speaking, reading, writing) in English and sound mathematical literacy * ability to work independently and take initiative * an interest of some of the main issues in conservation * ability to work within a team * willingness to work extended hours when required * knowledge of basic laboratory etiquette * willingness to travel overseas for training.

MSc (in addition to the above): experience in working in a molecular lab

PhD (in addition to the above): evidence of producing work published or publishable in international journals * presentations given at national and/or international meetings.

Recommendations: Experience in working with microsatellite markers * experience of working with and analysing population genetic data * experience of ecological field-work * papers published in international journals * an interest in botany, ecology and/or evolutionary biology/genetics. Closing date: 30 November 2008 to start January 2009. Enquiries: Dr John Wilson, jrwilson@sun.ac.za More information about the DST-NRFCentre for Invasion Biology can be found at <http://www.sun.ac.za/cib> jrwilson@sun.ac.za jrwilson@sun.ac.za

Salzburg EvolutionOfSex

Institute for Limnology (Mondsee) of the Austrian Academy of Sciences

PhD position in Evolutionary Ecology (evolution of sex)

Application deadline: 15. December 2008

A 3-year PhD position is available in the lab of Dr. Claus-Peter Stelzer at the Institute for Limnology in Mondsee (near Salzburg, Austria), to study the causes and consequences of transitions to obligate parthenogenesis in monogonont rotifers. The project is a combination of laboratory experiments, molecular techniques, and field sampling. The summary of the project funded by the Austrian Science Foundation (FWF), as well as further information on the lab can be found at <http://www.oeaw.ac.at/limno/personnel/stelzer/stelzer.htm>. Applicants should have a Master's or diploma degree in biology, or a related field. Experience in experimental design, statistics and PCR-based molecular genetic methods would be advantageous, as well as some "affinity towards using technical equipment" (e.g. our automated culture systems).

The Institute for Limnology is located in the Salzkammergut lake area, 30 km east of the City of Salzburg - which is also the location of the nearest university. The Institute has a staff complement of approximately 25, including 10 research scientists, who work on various areas in ecophysiology and evolutionary ecology of aquatic organisms.

The PhD student will receive a salary according to the FWF pay scale. Applicants should send a cover letter summarizing their research background and interest in the position, a CV, and contact information for two referees (everything as one PDF document) to claus-peter.stelzer@oeaw.ac.at, by 15. Dec. 2008. The ideal starting date would be 1. Feb. 2009.

Dr. Claus-Peter Stelzer Institute for Limnology Mondseestrasse 9 A-5310 Mondsee Austria

claus-peter.stelzer@oeaw.ac.at

claus-peter.stelzer@oeaw.ac.at

StonyBrookU EvolutionaryBiol

GRADUATE OPPORTUNITIES IN ECOLOGY AND EVOLUTIONARY BIOLOGY

The Department of Ecology and Evolution at Stony Brook University is recruiting graduate students for Fall 2009. Our graduate program trains students in Ecology, Evolution and Biometry. The following faculty are seeking graduate students for their labs:

H. Resit Akcakaya <http://life.bio.sunysb.edu/~ee/akcakayalab/> Stephen B. Baines <http://life.bio.sunysb.edu/~sbaines/> Michael A. Bell <http://life.bio.sunysb.edu/ee/belllab/> David O. Conover <http://www.msrc.sunysb.edu/~conover> Liliana M. Dávalos <http://life.bio.sunysb.edu/~ee/davaloslab/Welcome.html> Daneil Dykhuizen <http://life.bio.sunysb.edu/dykhuizenlab/> Walter F. Eanes <http://life.bio.sunysb.edu/ee/eaneslab/> John G. Fleagle <http://gibbon.anat.sunysb.edu/Department/jfleagle.html> Lev Ginzburg <http://life.bio.sunysb.edu/ee/people/ginzbindex.html> Jessica Gurevitch <http://life.bio.sunysb.edu/gurevitchlab/> Jeffrey Levinton <http://life.bio.sunysb.edu/~marinebio/levinton.main.html> Steve Munch <http://msrc.sunysb.edu/people/munch.htm> Dianna K Padilla <http://life.bio.sunysb.edu/ee/~padillalab/padilla/index.htm> Massimo Pigliucci www.genotypebyenvironment.org Joshua Rest <http://life.bio.sunysb.edu/ee/restlab/> F. James Rohlf <http://life.bio.sunysb.edu/morph> John J. Wiens <http://life.bio.sunysb.edu/ee/wienslab/homepage.html> Pat C. Wright <http://icte.bio.sunysb.edu> For more information regarding the Graduate Program in Ecology and Evolution see: <http://life.bio.sunysb.edu/ee> and <http://life.bio.sunysb.edu/ee/programs.htm>

The deadline for receipt of all application materials is January 15. For additional assistance, e-mail our Graduate Program Coordinator, Iris Roth, iroth@notes.cc.sunysb.edu

lmdavalos@gmail.com lmdavalos@gmail.com

SyracuseU Fish EvoDevo

Graduate research assistantship (Ph.D.) to work on the development and evolution of skeletal adaptations in Antarctic icefish.

Albertson Lab, Department of Biology, Syracuse University

The highly successful evolutionary radiation of Antarctic notothenioid fish involved several structural changes in the musculoskeletal system to accommodate a pelagic lifestyle. These include the evolution of bone loss to increase buoyancy, and craniofacial adaptations to accommodate shifts in diet and foraging strategies. Up to four years of funding (via research assistantship) are available to study the genetic and developmental mechanisms that underlie these skeletal adaptations.

The successful applicant will interact with other students in the lab (undergraduate, graduate, and post-doctoral) participating in a variety of projects using a number of systems including zebrafish, African cichlids and Antarctic icefish. The approach of the lab is to integrate studies in a laboratory model (i.e., zebrafish) and natural populations (i.e., cichlids) to understand the evolution of animal form and function. Methods of study include comparative embryology, developmental and molecular genetics, quantitative genetics, and morphometric shape analysis.

For more information about ongoing projects in the lab please visit my website at <http://albertsonlab.syr.edu/research.html>. Faculty in the Biology Department at Syracuse University have a broad array of interests ranging from molecular, cellular and developmental biology to ecology and evolution. Furthermore, the close proximity of SU to several other excellent institutions including SUNY Environmental Science and Forestry, SUNY Upstate Medical Center, Cornell University and the University of Rochester, contributes to a strong and vibrant intellectual community that will facilitate a great graduate experience.

All prospective students are encouraged to contact Dr. Craig Albertson via e-mail (rcalbert@syr.edu) and to complete a free on-line pre-application form available at <http://biology.syr.edu/graduatestudies/graduatepreapp.html>. For Fall 2009 admittance, formal graduate applications should be received in early January 2009.

R Craig Albertson <rcalbert@syr.edu>

TexasAMU EvolBiol

The labs of Drs. Mariana Mateos and Luis Hurtado at Texas A&M University are looking for highly motivated talented graduate students to work on the following projects:

-Phylogeography of Gulf of California-Baja Peninsula marine isopods. This project is funded by NSF and is aimed at studying the evolutionary histories of a set of isopods to unravel the geological processes that occurred during the formation of this megadiverse region. The project includes collecting in the Baja Peninsula, mainland Mexico and California coast.

-Conservation genetics of endemics of the Gulf of California islands

-Host-symbiont association of *Drosophila* flies and *Spiroplasma* bacteria. This project is aimed at understanding the evolution of symbiotic associations. The project involves field collecting in Mexico and the US. The project includes fitness experiments, molecular evolution, functional genomics (funded by NIH), and comparative genomics.

-Evolution of sexual and asexual Mexican freshwater fishes. This project is focused on phylogeography, population genetics, conservation genetics, evolution of reproductive isolation (speciation), and evolution and maintenance of asexuality.

-Population genetics of invertebrate fisheries. We are studying population genetics of commercially important aquatic species using various genetic markers.

Several of our projects utilize next generation massive sequencing technologies. Students would have the option of conducting research in the above projects and/or pursue other projects of their choice in the areas of conservation genetics, phylogeography, host-symbiont evolution, sexual evolution, and molecular evolution.

Financial support is available through research assistantships, teaching assistantships, and several Texas A&M University fellowships (Merit, Diversity and Regents; see <http://ogs.tamu.edu/prospective/financial-expenses-and-financial-aid>). In addition, Dr. Mateos and Dr. Hurtado are Faculty Mentors under the Alfred P. Sloan Foundation Minority Ph. D. Program, which offers generous scholarships to Ph. D. students from underrepresented groups in science (see <http://www.nacme.org/sloan/MPHDP/apply/>).

Interested individuals should contact us at mmateos@tamu.edu and/or lhurtado@tamu.edu to discuss research interests and background. Check <http://wfsc.tamu.edu/mateoslab/> for more information. We are particularly interested in students who can contribute to enhancing the diversity of our department, university and discipline. The application deadline for students wishing to be considered for Texas A&M fellowships is January 1 2009.

- Mariana Mateos, Ph.D. Assistant Professor and Sloan Faculty Mentor Section in Ecology and Evolutionary Biology Department of Wildlife and Fisheries Sciences Texas A&M University 320B Heep Laboratory Building 2258 TAMUS College Station, TX 77843-2258 Phone: 979-847-9462 Fax 979-845-4096 Email: mmateos@tamu.edu <http://wfsc.tamu.edu/mateoslab/> Mariana Mateos <mmateos@tamu.edu>

UArkansas Evolutionary Biol

Doctoral Fellowships - University of Arkansas

The Department of Biological Sciences at the University of Arkansas is actively recruiting Distinguished Doctoral Fellows (DDF) and Doctoral Academy Fellows (DAF) to begin graduate work in August 2009. The Distinguished Fellowships have a minimum 12-month stipend of \$30,000, and the DAFs have a minimum 12-month stipend of \$20,000. Both are available for up to 4 years of support based on satisfactory progress. Fellowships will require research and/or teaching depending upon the major professor chosen. In addition, fellowships include a full waiver of tuition and most fees. Selection will be based on undergraduate GPA, GRE scores, letters of recommendation, and undergraduate (B.S.) research experience or graduate (M.S.) research experience. Applicants should contact faculty members in the Department of Biological Sciences whose research they may be interested in directly at <http://biology.uark.edu/> or <http://comp.uark.edu/~wetges/EEpage.html>. For more information on departmental requirements, see <http://biology.uark.edu/1255.htm> or <http://www.uark.edu/depts/gradinfo/recruit/funding/fellowships.html> for general requirements. DAF applications can be made at any time and will be reviewed as received. Review of DDF applications will begin on 16 January 2009 with decisions made by the end of February. Those qualified applicants not chosen for a DDF will be offered a DAF.

William J. Etges Department of Biological Sciences
SCEN 632 1 University of Arkansas Fayetteville, AR
72701 USA wetges@uark.edu <http://comp.uark.edu/~wetges/wetges.html> office: (479) 575-6358 lab: (479) 575-7437 FAX (479) 575-4010

wetges@uark.edu

UCaliforniaLosAngeles EvolutionaryBiology

UCLA Graduate Program in Ecol & Evol Biology in-

vites applications

We are pleased to announce that the The Department of Ecology and Evolutionary Biology at UCLA has raised its graduate support packages to \$26,000 per year with opportunities for research seed money. With the hire of eight new faculty in the last five years, the graduate program has exciting opportunities in many subdisciplines of Ecology and Evolutionary Biology. Visit our website <http://www.eeb.ucla.edu> and learn about our departments interdisciplinary strengths animal behavior, conservation biology, ecology, evolutionary biology, marine biology, paleobiology, plant biology, physiological ecology, theoretical biology and tropical biology.

This announcement is to remind you that our deadline is 1 December. Applications can be submitted on-line. If you will miss this deadline, we encourage you to contact a potential faculty advisor or send inquiries to Jocelyn Yamadera, Student Affairs Officer, jocelyn@lifesci.ucla.edu . Please encourage applications from individuals in underrepresented groups in Science. We are committed to the recruitment and education of underrepresented minorities.

FACULTY

Michael Alfaro, Vertebrate macroevolution (especially coral reef fishes)

Priyanga Amarasekare, Mathematical ecology, diversity maintenance in variable environments

Paul Barber, Evolutionary and conservation biology of marine ecosystem

Daniel Blumstein, Evolution of behavior and conservation biology

Clifford Brunk, Molecular evolution

Donald Buth, Ichthyology and parasitology, phylogenetic systematics

Peggy Fong, Marine ecology of coastal ecosystems

Arthur Gibson, Functional plant anatomy and ecophysiology of plants

Malcolm Gordon, Comparative ecological physiology of lower vertebrates

Patricia Gowaty, Evolutionary ecology and behavior

Gregory Grether, Evolutionary behavior and sexual selection

Stephen Hubbell, Community ecology; biodiversity

David Jacobs, Evolution/Development of Invertebrates

James Lloyd-Smith, Ecological and evolutionary dynamics of infectious diseases

Glen MacDonald, Biogeography

Peter Narins, Auditory Behavior and Neurophysiology

Peter Nonacs, Behavioral ecology and social evolution

John Novembre, Population genetics and computational biology

Philip Rundel, plant ecology of desert, Mediterranean, and tropical ecosystems

Lawren Sack, Ecology and physiology of plant species coexistence.

Barney Schlinger, hormonal control of brain and behavior in tropical bird species

Rebecca Shipe, Marine phytoplankton ecology, physiology and biogeochemistry

Thomas Smith, Evolutionary ecology, speciation, and conservation of tropical vertebrates

Victoria Sork, Plant evolutionary ecology, molecular ecology, conservation genetics

Charles Taylor, population genetics; population structure of malaria vectors

Blaire Van Valkenburgh, Paleobiology, ecology, and functional morphology of vertebrates

Robert Wayne, Application of molecular genetic techniques to questions in systematics, population genetics, and conservation

Cheryl Ann Zimmer, Population ecology of marine organisms, especially the role of hydrodynamic processes

Richard Zimmer, Ecology and sensory biology of aquatic organisms; chemical signals and communication

For more information, contact Jocelyn Yamadera, Student Affairs Officer, jocelyny@lifesci.ucla.edu.

Victoria Sork <vsork@ucla.edu>

UGeorgia InvasiveSpecies

PHD STUDENT FELLOWSHIPS ECOLOGICAL GENETICS OF INVASIVE SPECIES

UNIVERSITY OF GEORGIA

Graduate Student Fellowships are available starting in Fall 2009 to study the ecological genetics of invasive species, including plant pathogens. Fellowships offer a highly competitive stipend as well as funds for research

and travel.

The University of Georgia has received a Partnerships for International Research and Education (PIRE) grant from the National Science Foundation to support research on the genetics and ecology of invasive plant and pathogen species exchanged between the southeastern US and China, Taiwan and Hong Kong. Successful applicants will develop research projects that will study the population genetics, ecology and/or demography of invasive species that are native to the southeastern US and to China. A significant proportion of each student's research project must be conducted in China in collaboration with Chinese research scientists. Students will receive training in Chinese language and culture as well as appropriate biology courses.

Students can work with any senior personnel on the UGA-PIRE program (see list below and at http://www.genetics.uga.edu/pire/people_senior_US.html).

Students should contact a prospective major adviser directly and apply through that department. For additional information concerning the application process, interested students should refer to our web site (<http://www.genetics.uga.edu/pire>).

Questions? Contact Dr. Rodney Mauricio, UGA-PIRE Program Director, via email (mauricio@uga.edu).

Current List of Senior Personnel on the UGA PIRE:

Michael Arnold (Department of Genetics, University of Georgia) Jeff Bennetzen (Department of Genetics, University of Georgia) John Burke (Department of Plant Biology, University of Georgia) Donald Champagne (Department of Entomology, University of Georgia) Shu-Mei Chang (Department of Plant Biology, University of Georgia) G. Keith Douce (Department of Entomology, University of Georgia, Tifton) John Drake (Odum School of Ecology, University of Georgia) Qinfeng Guo (Research Ecologist, USDA-Southern Research Station) James Hamrick (Department of Plant Biology, University of Georgia) Paul Hendrix (Professor of Ecology, University of Georgia) Lissa Leege (Department of Biology, Georgia Southern University) John Maerz (Department of Forestry and Natural Resources, University of Georgia) Rodney Mauricio (Department of Genetics, University of Georgia) Richard Meagher (Department of Genetics, University of Georgia) Karin Myhre (Department of Comparative Literature, University of Georgia) Andrew Paterson (Departments of Crop and Soil Sciences, Plant Biology, and Genetics, University of Georgia) Harald Scherm (Department of Plant Pathology, University of Georgia) William Vencill (Department of Crop and Soil Sciences, University of Georgia) Ronald Walcott (Department of Plant Pathology, University of Georgia) John Wares (Assistant Pro-

fessor of Genetics, University of Georgia) Susan Wessler (Department of Plant Biology, University of Georgia) Lorne Wolfe (Department of Biology, Georgia Southern University)

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Rodney Mauricio, Ph.D. Department of Genetics Phone: (706) 542-1417 University of Georgia FAX: (706) 542-3910 Athens, GA 30602-7223 e-mail: mauricio@uga.edu

Lab Web Page: <http://www.genetics.uga.edu/-mauriciolab> PIRE Grant Web Page: <http://www.genetics.uga.edu/pire> Evolution at UGA: <http://www.genetics.uga.edu/evolution> Rodney Mauricio <mauricio@uga.edu>

UGeorgia PlantEvolution

The Department of Plant Biology at the University of Georgia in Athens, GA seeks highly motivated Ph.D. students to join our graduate program in evolutionary biology. Ongoing research in the Department investigates fundamental questions in organismal and molecular evolution using a range of approaches including population and quantitative genetics, molecular systematics, and comparative genomics.

Graduate fellowships, assistantships, research support and travel grants are available for qualified candidates. Application information can be found on the web at:

<http://www.plantbio.uga.edu/graduate.html> Plant Biology-affiliated faculty with evolutionary interests include:

Mike Arnold (http://www.genetics.uga.edu/-people.bio_arnold_m.html) Jeff Bennetzen (<http://www.genetics.uga.edu/jlblab>) John Burke (<http://www.theburkelab.org/>) Shu-Mei Chang (<http://www.plantbio.uga.edu/~chang/chang.html>) Katrien Devos (<http://www.cropsoil.uga.edu/-personnel/faculty/devos.html>) Lisa Donovan (<http://www.plantbio.uga.edu/~donovan/donovan.html>) Mark Farmer (<http://www.uga.edu/cellbio/farmer.html>) Jim Hamrick (<http://www.plantbio.uga.edu/~hamrick/hamrick.html>) Jim Leebens-Mack (<http://www.plantbio.uga.edu/~jleebensmack/JLMmain.html>) Russell Malmberg (<http://www.plantbio.uga.edu/~russell/index.html>) Rodney Mauricio (<http://www.genetics.uga.edu/mauriciolab>) Andy Paterson (<http://www.plantgenome.uga.edu/>)

Sue Wessler (<http://www.plantbio.uga.edu/~suew>) Xiaoyu Zhang (<http://www.plantbio.uga.edu/~xiaoyu/>) Wendy Zomlefer (<http://www.plantbio.uga.edu/~wendyz/wendyz.html>)

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

UGöttingen ChemoautotrophicEvolution

Could you please post the following ad for a PhD position (research topic: evolution of chemoautotrophic symbioses)?

Thank you very much for your help!

Best wishes, Sharmishtha

The newly formed junior research group “Geomicrobiology and Biosignatures in the Deep Biosphere” headed by Dr. Sharmishtha Dattagupta in the Courant Research Centre Geobiology at the University of Göttingen invites applications for one Ph.D. position

The CRC Geobiology (Coordinator: Prof. Reitner, Department of Geobiology; www.uni-goettingen.de/-crc.c) is one of five interdisciplinary research centres (www.uni-goettingen.de/crc) recently established by the University of Göttingen as part of its institutional strategy “Tradition - Innovation - Autonomy”.

Our research group focuses on the microbial ecology and evolution of chemoautotrophic ecosystems, with emphasis on animal-bacterial symbioses. Ecosystems sustained by chemoautotrophy are found at deep-sea hydrothermal vents, cold seeps and some sulfide-rich limestone caves. Terrestrial sulfide-rich caves are easier to access than deep-sea habitats and offer an excellent opportunity to study the interplay between geochemistry, microbes and macrofauna. Our primary research field site is the actively forming sulfide-rich Frasassi cave complex of central Italy that hosts an ecosystem sustained entirely by microbial chemoautotrophy. We have recently discovered a symbiosis between a Frasassi-endemic amphipod and filamentous chemoautotrophic bacteria. Future projects will address the potential benefits of the bacterial symbionts to the amphipod host, and examine the evolution of this symbiosis.

Candidates should hold either a Master's degree or a German "Diplom" in Molecular Biology, Microbial Ecology or Geomicrobiology. Fieldwork experience is desired. The working language of the group is English, and applicants from abroad are encouraged to apply. The University of Göttingen seeks to increase the participation of women in areas in which they are currently underrepresented and therefore explicitly urges women to apply. Disabled persons with equivalent aptitude will be favored.

The position is initially available for two years starting immediately and can be extended to three years following favorable reviews. Salary is in accordance with the German state regulated public service salary scale (TV-L 13).

For informal enquiries please contact sdattag@uni-goettingen.de Please submit your application online under the given link: www.uni-goettingen.de/positions-exini. Application deadline is November 21, 2008.

Sharmishtha Dattagupta Junior Professor Georg-August-Universität Göttingen Courant Research Centre Geobiology Goldschmidtstr. 3 37077 Göttingen, Germany Phone (office): +49 551 39 12910 Mobile: (+49) 0157 75823206 Email: sdattag@uni-goettingen.de

Sharmishtha Dattagupta <sdattag@uni-goettingen.de>

UHelsinki EvolutionaryGenetics

Department of Biological and Environmental Sciences, University of Helsinki, invites applications for

Doctoral Student Position

The Doctoral Student will be a part of the Evolutionary Genetics Research Unit (EGRU) in their project "Long term phenotypic trends of migratory whitefish (*Coregonus lavaretus*): evolutionary and genetic perspectives". The assignment will begin on the early 2009 (start date is flexible) and end in the end of 2011. EGRU is part of the Finnish Centre of Excellence in Evolutionary Genetics and Physiology (<http://www.coe.fi>). Supervisors of the project are Dr. Anna Kuparinen and Prof. Juha Merilä. The research work is done in collaboration with Finnish Game and Fisheries Research Institute (<http://www.rktl.fi>).

The aim of this PhD project is to investigate the trends

in growth, age and size at maturation as well as genetic structuring of the whitefish populations spawning in two Finnish rivers. The specific aims are to investigate temporal phenotypic trends, to assess how these coincide with possible changes in the genetic structure of the populations, and to gain insights into possible genetic basis of the phenotypic trends. The analyses will be based on scale samples collected over two decades from the spawning stock. The work includes aging and back-calculation of growth trajectories from scale growth layers, population genetic and statistical analyses of the data.

A successful candidate for this position is interested on conservation and population genetics problems, and/or problems in ecological and evolutionary genetics in general. A background in population genetics/genomics and/or evolutionary biology is desirable.

We are looking for an individual with a Masters Degree or equivalent degree in Biology or Genetics, who is highly self-motivated and can work both independently and in a team. The working language will be English. Proven skills in English are required for admission to post graduate study program (minimum 550 points from TOEFL PBT, or grade A, B or C from CAE/CPE).

An overview of our past and current research can be found at <http://www.helsinki.fi/biosci/egru> and <http://www.coe.fi>.

The salary will be based on level 2 of the demands level chart for teaching and research personnel in the salary system of Finnish Universities. In addition, the appointee will be paid a salary component based on personal work performance (the total salary will vary between 1785 - 2197 EUR per month).

The application should include a complete - CV - Publication list (if available) - A scanned academic transcript (list of grades in university courses) - A statement of research interests and motivation for applying this position not exceeding two pages - Two references.

Applications should be addressed to the Faculty of Biosciences and sent to Department of Biological and Environmental Sciences, Johanna Paananen, P. O. Box 65 (Viikinkaari 1), FIN-00014 University of Helsinki, to arrive no later than 1st December 2008, by 3:45 p.m. (local Helsinki time). More information on the Doctoral Student Position from the supervisor Dr. Anna Kuparinen (tel. +358 9 191 57708, email. anna.kuparinen@helsinki.fi).

More information about Finland, University of Helsinki, and Department of Biological and Environmental Sciences can be found from the follow-

ing links: <http://www.helsinki.fi/en/index.html> (city) <http://www.helsinki.fi/university/> (university) <http://www.helsinki.fi/bio/english/> (department) Further information about University of Helsinki International Staff Services: <http://www.helsinki.fi/intstaff/> Johanna Paananen <johanna.paananen@helsinki.fi>

UHelsinki ParastoidEvolution

Open position for one evolutionary PhD student in one of two possible projects (A) PARASTOID METACOMMUNITY EVOLUTION or (B) PARASITOID BEHAVIORAL EVOLUTION. Apply for one or the other.

A) PARASTOID METACOMMUNITY EVOLUTION- This is work based on the metacommunity of insects associated with the Glanville fritillary butterfly (*Melitaea cinxia*) in the Åland islands, Finland. Your research will address patterns of metacommunity structure and mechanisms behind them, such as (1) the prediction that food-chain length decreases with habitat fragmentation because the adverse effects of habitat fragmentation increase with trophic level, and (2) the landscape level effects of indirect interactions between butterflies mediate by parasitoids. The applicant must have a strong interest in community evolution and a Masters Degree or equivalent. For information about the research system see: http://www.helsinki.fi/science/metapop/metacom/-research/metacom_structure.htm B) PARASITOID BEHAVIORAL EVOLUTION- There is a history of conceptually linking behaviour of parasitoids with resulting predator-prey population dynamics. So far biologists know about what parasitoids do over short time-scales foraging in small areas, but this is only part of the picture. The student would work on an ongoing project using the parasitoids of the Glanville fritillary (*Melitaea cinxia*) in Åland, Finland to understand evolutionary relevant parasitoid foraging behaviour. This includes study of spatial learning, competition among adult female parasitoids, and measures of foraging success in a natural landscape. The applicant must have a strong interest in and experience with behavioural evolution, and a Masters Degree or equivalent. For information about the research system see: http://www.helsinki.fi/science/metapop/metacom/-research/parasitoid_foraging.htm The successful applicant will be a PhD student in the metacommunity evolution group, a subgroup of the Metapopulation

Research Group, at the University of Helsinki (<http://www.helsinki.fi/science/metapop/>). We are a Centre of Excellence supported by the Academy of Finland. We have an international research environment with opportunities for mixing among evolutionists, molecular biologists and mathematicians. The position is for completion of a PhD within four years, and includes a salary of about 2,300 /month plus social benefits. Please send your application and any enquiries to Saskya van Nouhuys (saskya@cornell.edu). Include a short CV, a one page explanation of your motivation and suitability for the project (be clear about which project), and the e-mail addresses of three researchers who can document that you are self-motivated and can do productive independent work. Consideration of applications will begin mid November 2008 and continue until the position is filled. The position could start as soon as January 2009.

sdv2@cornell.edu sdv2@cornell.edu

UKentucky EvolutionaryBiology

Graduate positions (M.S. or Ph.D) for Fall 2009 are available in the recently established laboratory of David Weisrock in the Department of Biology at the University of Kentucky.

Work in the Weisrock Lab centers on using genetics to resolve the geographic boundaries of species in nature, reconstruct the relationships among these lineages, and address the mechanisms that have led to their formation. There is great enthusiasm to continue building a research team focused on the evolution and diversification of North American salamanders and Malagasy lemurs. However, students that find a home in the Weisrock Lab are ultimately encouraged to pursue research projects that meet their personal research interests.

For further information regarding research in the lab prospective students can contact David Weisrock directly at dweis2@uky.edu or they can consult the Weisrock Lab webpage:

<http://sites.google.com/site/weisrocklab/> Dave Weisrock

Department of Biology University of Kentucky
101 Thomas Hunt Morgan Building Lexington,
KY 40506 859-257-2249 dweis2@uky.edu <http://sites.google.com/site/weisrocklab/> David Weisrock

<dweis2@uky.edu>

UMassachusettsAmherst CiliatePhylogeography

GRADUATE STUDENT POSITION Phylogeography
Of Ciliates In Near-Shore Environments Smith College
/ UMass Amherst

We are looking for a highly motivated student to join our project, which aims to elucidate the patterns of diversity of ciliates near-shore environments and to explore the ecological processes that underlie this diversity. The project is collaborative between Laura Katz's lab at Smith College and marine ecologist George McManus at the University of Connecticut. Work on the project combines culture-independent approaches with analyses of targeted morphospecies. Techniques include analyses of clone libraries, DGGE, and both light and fluorescence microscopy.

Graduate students in Laura Katz's laboratory join either through MS program at Smith College or the Organismic and Evolutionary Biology program at the University of Massachusetts Amherst. Interested individuals should visit the web sites below and contact Dr. Laura Katz directly (lkatz@smith.edu)

Laura Katz, Smith College <http://www.science.smith.edu/departments/Biology/lkatz/> OEB at UMass Amherst <http://www.bio.umass.edu/oeb/> <http://www.bio.umass.edu/oeb/admissions> Smith College MS in biology <http://www.science.smith.edu/departments/Biology/graduate.html> <http://www.smith.edu/gradstudy/> Collaborator George McManus, University of Connecticut <http://microzooplankton.uconn.edu/> -

++ Laura A. Katz, Elsie Damon Simonds Professor Department of Biological Sciences Smith College Northampton, MA 01063 Phone: 413-585-3825 Fax: 413-585-3786 lkatz@smith.edu <http://www.science.smith.edu/departments/Biology/lkatz/> <http://www.us.oup.com/us/catalog/general/subject/LifeSciences/EvolutionaryBiology/?view=usa&ci=9780198569749> +

lkatz@smith.edu lkatz@smith.edu

UMinnesota IntroducedSpecies

NSF IGERT PhD Traineeships for Risk Analysis of Introduced Species and Genotypes

The Risk Analysis for Introduced Species and Genotypes IGERT at the University of Minnesota seeks applicants to enter the program in Fall 2009. This Integrative Graduate Education and Research Traineeship (IGERT) Program is supported by the National Science Foundation and focuses on policy-relevant research.

The program educates Ph.D. students to conduct research to improve Ecological Risk Analysis and contribute workable solutions to policy questions and problems affecting management of introduced species and genotypes. Trainees will complete a graduate minor in Risk Analysis for Introduced Species and Genotypes and typically receive two years of NSF funding which includes a stipend of \$30,000 and an annual allowance of \$10,500 to cover tuition and health insurance.

Areas of research interest include: Invasive plant evolution Ecology of GMOs and other novel genotypes Prevention of invasion Confined ecological risk assessment Restoration ecology Science and technology policy Biological control of invasives

For a complete list of faculty, their interests and more information about the program see: <http://isg-igert.umn.edu> . Applications are due 15 December 2008. Apply online at: <http://isg-igert.umn.edu/application/default.htm> The ISG-IGERT program promotes the value of a diverse scientific community. We are committed to making the ISG-IGERT at the University of Minnesota a welcoming environment in which graduate students and faculty work together in a diverse setting for science education, research, and service to society. This program provides equal access to educational opportunities through recruitment, admission, and support programs that promote diversity, foster successful academic experiences, and cultivate the leaders of the next generation.

shawx016@umn.edu

UNevadaLasVegas BirdEvolution

GRADUATE OPPORTUNITIES IN NEOTROPICAL RESEARCH (M.S. or Ph.D.) I am seeking 1-2 graduate students to develop thesis (dissertation) projects that use modern molecular methods combined with field work, to study the evolution of neotropical birds in Middle America. Students will be a part of a team that is studying the comparative biogeography of select avian taxa. Individual research topics may differ in focus but must involve a systematic framework. Spanish-speaking ability and prior neotropical experience are preferred. A strong work ethic and an interest in specimen-based (museum) ornithology are required. Assistantship stipends are \$16,000 - 18,000 for 12 month appointments and include a tuition waiver. Some additional funding is available for research expenses. UNLV has a growing program in the fields of phylogenetic systematics and comparative biogeography with three professional vertebrate systematists (an ornithologist, a herpetologist, and a mammalogist) on campus. Successful applicants will begin September 2009 (or sooner). Students from Latin America are especially encouraged to apply. Interested persons should send GRE scores, transcripts, a CV, names and phone numbers of three personal references, and a letter of interest to: John Klicka, UNLV, Marjorie Barrick Museum, 4505 Maryland Parkway, Box 454012, Las Vegas, Nevada 89154 94012 [klicka@unlv.nevada.edu / (702) 895-2749].

John Klicka Curator of Birds Barrick Museum of Natural History Box 454012, University of Nevada Las Vegas Las Vegas, NV 89154

e-mail: klicka@unlv.nevada.edu phone:(702)895-2749 fax:(702)895-3094

John Klicka <klicka@unlv.nevada.edu>

UNewOrleans ConservationBiology

DOCTORAL FELLOWSHIPS IN CONSERVATION BIOLOGY UNIVERSITY OF NEW ORLEANS

The Department of Biological Sciences at the University of New Orleans announces two Doctoral Fellowships in Conservation Biology. One is available in Spring 2009 and the other begins in Fall 2009. The fellowships provide support for four years with an annual stipend of \$25-26,000 and a full tuition waiver. The Department of Biological Sciences offers exciting opportunities for graduate student research in ecology, evolution, systematics, genetics, physiology, molec-

ular biology, and biochemistry. For more information on the Department, faculty research interests, and other resources, please see the website: <http://biology.uno.edu/>. Applicants should indicate the semester they wish to enter the program and that they wish to be considered for a Fellowship on the standard application form for the Graduate Programs in Biological Sciences, which can be obtained online at <http://biology.uno.edu/phdprogram.aspx> or by writing to:

Graduate Coordinator Department of Biological Sciences University of New Orleans New Orleans, LA 70148

Applicants must also file a graduate application with University of New Orleans admissions (see <http://admissions.uno.edu/app.cfm>). Applicants must be U.S. citizens or permanent residents. Applications from minority groups under-represented in the sciences are especially encouraged. Review of applications for Spring 2009 will begin on November 1, 2008. Review of applications for Fall 2009 will begin on January 15, 2009. UNO AA/EEO.

Nicola Mary Anthony <nanthony@uno.edu>

UOregon MolecularSystemEvolution

We seek highly motivated graduate students to join an integrated group of biologists in the Center for Ecology and Evolutionary Biology (CEEB) at the University of Oregon. Our members have a broad range of interests such as host-pathogen interactions, the evolution of molecular systems, global climate change, microbial ecology, biogeochemistry, the evolution of phenotypes in the wild, theoretical ecology and many others. More details on our group can be found at <http://ceeb.uoregon.edu/>.

CEEB is an integrated component of a highly interactive group of scientists in the Department of Biology, and our research Centers and Institutes also facilitate robust interactions among members of the Anthropology, Chemistry, Computer Science, Geology, Geography and Psychology Departments (see <http://biology.uoregon.edu/lifesci/>). Many of our faculty share funded research programs across disciplines, and perform work all over the world. Our integrative approach to graduate education is supported by numerous NIH and NSF training grants, as is exemplified by our very successful NSF IGERT training grant in Evolution, Development and Genomics (<http://>

evodevo.uoregon.edu/).

The University of Oregon is one of the top research institutions in the country, with outstanding laboratory facilities on campus, and easy access to numerous field sites from the Pacific Ocean to the Cascade Mountains and the high desert of Eastern Oregon. Eugene is a very livable city that is consistently voted one of the top ten greenest and most active in the U.S.

Applications to the Department of Biology can be submitted online through <http://biology.uoregon.edu/-graduate/apply.php> For more information on CEEB contact Brendan Bohannon (bohannon@uoregon.edu) or Bill Cresko (wcresko@uoregon.edu), or individual faculty members in whose research you are interested. Specific inquiries about the graduate application process can be directed to the Biology Department Graduate Recruiting Coordinator, Lynne Romans (lromans@uoregon.edu).

CEEBC FACULTY & RESEARCH INTERESTS

Brendan Bohannon Microbial ecology and evolution
 William Bradshaw Experimental and evolutionary genetics of seasonal and climatic adaptations
 Scott Bridgham Ecosystem and community ecology, biogeochemistry, wetlands, climate change, restoration
 George Carroll Mycology and ecology
 Dick Castenholz Microbial aquatic ecology, physiological ecology of photosynthetic microbes
 William Cresko Evolutionary developmental genetics, population genomics, vertebrate evolution
 Jessica Green Biodiversity and biogeography, theoretical ecology, microbial ecology, community genomics
 Patrick Phillips Evolutionary genetics of sex, aging and behavior
 Barbara (Bitty) Roy Plant-fungus interactions, pollination ecology, and invasive species.
 Joe Thornton Evolution of gene function, ancestral gene resurrection, evolution of molecular complexity
 Dan Udovic Dynamics of pollination mutualisms, population modeling, science education
 Michelle Wood Microbial ecology and evolution, biological oceanography

William A. Cresko Assistant Professor of Biology Center for Ecology and Evolutionary Biology University of Oregon #5289 Eugene, Oregon 97403-5289
 wcresko@uoregon.edu www.uoregon.edu/~wcresko ph: 541-346-4779

wcresko@uoregon.edu

UOulu Arabidopsis Speciation

Doctoral student position in genomics of speciation in *Arabidopsis lyrata* available in the plant genetics group, Department of Biology, University of Oulu, Finland,

Arabidopsis lyrata is an outcrossing relative of the *A. thaliana*. The genome sequence of *A. lyrata* has just been completed. The project examines the genetics of incipient reproductive isolation between subspecies of *A. lyrata*, (e.g. Kuittinen et al. 2004 Genetics, Leppälä et al. 2008 Heredity), and its ecological consequences, exploiting the methods applicable in a fully sequenced species.

The doctoral student will be able to influence the shaping of the thesis work with the project. The student will interact with doctoral students already working on related issues, and with partners of an ERANET Plant genomics project Arelatives <http://www.erapg.org/everyone/9587/18624/18614/18626>

The funding for the doctoral thesis can be up to four years, depending on the starting date. The project is funded by the Biosciences and Environment Research Council of Finland.

The salary is based on the Finnish Universities scales for teaching and research personnel, which include a component based on personal work performance.

The application should include a CV, a publication list, a statement of research interests and a short description of the motivation for applying for this position, and the names of two references.

The applications should be sent to Outi.Savolainen@oulu.fi, preferably by e-mail, before December 15, (or until position is filled). For further information, please contact Outi.Savolainen@oulu.fi (phone +358-8-5531782).

Outi Savolainen <outi.savolainen@oulu.fi>

UppsalaU Protist Evolutionary Genomics

Department of Evolution, Genomics and Systematics, Uppsala University, Sweden, invites applications for

Doctoral student position in molecular evolution with the focus on genome evolution of microbial eukaryotes

The doctoral student will be part of a comparative genomics project on the protist group diplomonads under the supervision of

Dr. Jan Andersson (jan.andersson@ebc.uu.se <<mailto:jan.andersson@ebc.uu.se>>). The information below can be found at http://www.personalavd.uu.se/-ledigaplatser/2693dorand_eng.htm. Project description: * * Diplomonads are a group of anaerobic microbial eukaryotes that have two cell nuclei. The human intestinal parasite /*Giardia lamblia* /belongs to diplomonads, but there are also free-living members of the group. The project will study how genetic information is transferred between the two nuclei, among diplomonads, and between diplomonads and other organisms, over evolutionary time. The aim is an understanding how these and other evolutionary processes interact with various lifestyles within the group.

* *

*Comparative genomic methods will be used on data generated with next-generation sequencing methods from a diversity of diplomonads. The project will have a strong bioinformatic component, but also molecular biology methods may be included. The results from this project are relevant for epidemiological studies, although the main focus will be on a deeper understanding of genome evolution of microbial eukaryotes. *

The position will be within a creative international research environment at the Department of Genomics, Evolution and Systematics (<http://www.egs.uu.se/>) at Uppsala University (<http://www.uu.se/en/>). The project is in collaboration with research groups in Sweden and Canada.

* *

Qualifications: We are looking for an excellent, strongly motivated candidate with a keen interest in microbial evolution. The PhD position requires a Master of Science, or equivalent, in bioinformatics, microbiology, molecular biology, or in a field which is relevant for the topic of the project. *Your application* should include a short description of research interests and relevant experiences, curriculum vitae, copy of relevant exam and notes, master's thesis or an outline thereof, and other relevant information you wish to include. Candidates are asked to provide names of at least two reference persons or to include letters of recommendation.

For appointment as PhD student it is required that the PhD student is accepted to the researcher's education. The position may include departmental duties at a level of at most 20% (typically teaching). Local guidelines for the salary class are applicable. Starting date as soon as possible.

Information concerning the PhD position

can be obtained from Associate Professor Jan Andersson, e-mail: jan.andersson@ebc.uu.se <./jan.andersson@ebc.uu.se>. Web page: <http://www.egs.uu.se/molev/staff/xxJA.html>. Representatives of the labor unions are Anders Grundström, SACO, phone +4618-471 5380, Carin Söderhäll, TCO/ST, phone +4618-471 1996, and Stefan Djurström, SEKO, phone +4618-471 3315.

You are welcome to submit your written application *the latest on December 1, 2008*, to the address: Registrar, UFV-PA 2008/2693, Uppsala universitet, Box 256, S-751 05 Uppsala, Sweden; or via fax: +4618-471 2000 or via e-mail, to: _registrator@uu.se <<mailto:registrator@uu.se>>. If an application is sent by fax or e-mail, it has to be completed by a written application within a week's time after the deadline of the application period.**

Jan.Andersson@ebc.uu.se Jan.Andersson@ebc.uu.se

USalzburg EvolutionaryBiology

THREE-YEAR PHD POSITION IN PLANT EVOLUTIONARY BIOLOGY

A Ph.D. position in Plant Evolutionary Biology is available at the Dept. of Organismic Biology, Division of Plant Ecology & Diversity, University of Salzburg, Austria, with Prof. Hans Peter Comes and Dr. Gunter Fischer to study the ecology and evolution of reproductive traits in the orchid genus *Bulbophyllum* from the Southwest Indian Ocean region (Madagascar, Comores, Mascarenes)

This research project will focus on micro-evolutionary studies of a previously identified sister species pair, *B. bicoloratum* Schltr. and *B. occultum* Thouars, both with supposedly outcrossing populations in Madagascar (the mainland±), but with exclusively auto-pollinating populations of *B. occultum* also occurring in La Runion, Mauritius, and the Comores. We will employ population genetic surveys of cpDNA haplotype sequence variation, single-copy nuclear genes, and nuclear microsatellites at both the intra- and interspecific level, complemented by detailed floral-trait measurements and pollination experiments, to determine the reproductive, floral-morphological and population genetic consequences associated with remote oceanic island colonization of *B. occultum*.

The ideal applicant has a strong interest in plant evo-

lution and a strong background in population genetics and statistical analyses. Laboratory experience is required and experiences in pollination experimental work would be an advantage. An MSc, diploma degree or equivalent in Botany, Genetics or Evolutionary Biology is required. Fluent English is a must.

Funding is for three years by the Austrian National Science Fund (FWF). The University of Salzburg (<http://www.uni-salzburg.at/>) offers excellent facilities, and a very pleasant working and living environment in one of the most beautiful landscapes in Austria.

Please send a letter of application together with a full CV, a copy (pdf) of your master/diploma certificate and thesis, and the addresses of three referees to:

peter.comes@sbg.ac.at or gunter.fischer@sbg.ac.at

Prof. Hans Peter Comes

Department of Organismic Biology

Division of Plant Ecology & Diversity Paris-Lodron-University Salzburg Hellbrunnerstr. 34, A-5022 Salzburg Austria Tel.: ++ 43 (0) 662 8044-5505 Fax: ++43 (0) 8044-142

The position will be filled as soon as a suitable applicant is found.

gunter.fischer@sbg.ac.at

USaskatchewan AdaptationGenomics

PhD Student Position V Genomics of adaptation and speciation.

A PhD student position in Genomics of adaptation and speciation is available in the newly formed lab of Dr. Jose A. Andres at the University of Saskatchewan, Saskatoon, Canada. Potential areas of research include: linking ecologically relevant phenotypic and genotypic variation, and detecting candidate speciation genes (e.g. Andres et al. 2006, Andres et al 2008). Study systems include host-plant races (i.e. ecotypes) of phytophagous insects and closely related species of field crickets. However, I am always looking for new and interesting questions. Candidates who wish to combine theoretical/computational approaches with experimental biology are highly encouraged to apply.

Currently some of my research projects are run in collaboration with Dr. Richard Harrison (Department of

Ecology and Evolutionary Biology, Cornell University) and the though the successful applicant would expend most of her time in my lab, she/he is expected to work at Cornell for short periods of time. Three years of funding are already available, including tuition, an annual allowance of approx. \$16,000 CAN and benefits (health insurance plus basic dental and eye care).

Qualifications: I am looking for an excellent, strongly motivated candidate with a strong interest in evolutionary genetics/genomics. Successful candidates should have some prior experience with DNA-based genetic analysis, molecular biology, bioinformatics, or related fields. Applications consisting of brief cover letter, CV, description of research interests and relevant experiences, and contact information for two references, should be sent to: jose.andres [at] usask.ca. The review of applications will begin immediately and will remain open until the position is filled.

Jose Andres <jose.andres@usask.ca>

USouthCarolina EvolutionaryBiol

I am recruiting graduate students who are interested in how evolutionary processes operate in natural environments. Ideal candidates will have research goals that include some mixture of ecology, evolution and genetics. Students working with me are expected to develop their own research projects that integrate with the overall themes of the lab. Currently, these themes include adaptive divergence, ecological speciation, consumer-resource interactions, population connectedness, life history evolution (particularly aging), and the molecular/regulatory basis of adaptation. Our lab uses *Daphnia* as a model system, and employs fieldwork, laboratory experiments, quantitative genetics and emerging tools in ecological genomics. Additional details on current projects can be found at <http://www.biol.sc.edu/faculty/dudycha.html>. Year-round support (including health benefits & tuition) is provided through a mixture of teaching and research assistantships. Interested individuals should contact me via email (dudycha [at] biol.sc.edu) to discuss their background and research interests.

–Jeff Dudycha

Jeffrey L. Dudycha Assistant Professor Dept. of Biological Sciences University of South Carolina Columbia, SC 29208 dudycha [at] biol.sc.edu <http://www.biol.sc.edu/faculty/dudycha.html>

UToronto EvolutionaryBiology

GRADUATE STUDENT POSITIONS IN EVOLUTIONARY & ECOLOGICAL GENETICS University of Toronto, Department of Ecology & Evolutionary Biology <http://www.eeb.utoronto.ca> We are pleased to announce graduate student positions in EVOLUTIONARY AND ECOLOGICAL GENETICS in the Department of Ecology and Evolutionary Biology (EEB) at the University of Toronto (St. George campus). EEB is home to over 30 outstanding scientists in the fields of ecology and evolution. Research in evolutionary and ecological genetics is one of the strengths of EEB, comprised of an innovative community of faculty and students studying topical problems in population genetics, molecular evolution, quantitative genetics, experimental evolution, and comparative genomics. Faculty research uses both non-model systems and the classic model organisms *A. thaliana*, *C. elegans*, and *D. melanogaster*. Graduate student positions are available in the labs of:

Aneil Agrawal (<http://labs.eeb.utoronto.ca/agrawal/>)
 Belinda Chang (<http://labs.eeb.utoronto.ca/chang/>)
 Asher Cutter (<http://labs.eeb.utoronto.ca/cutter/>)
 John Stinchcombe (<http://labs.eeb.utoronto.ca/-stinchcombe/>) Stephen Wright (<http://labs.eeb.utoronto.ca/wright>)

and many others (<http://www.eeb.utoronto.ca/people/faculty/eeb>)

The graduate program in EEB provides training for students toward both M.Sc. and Ph.D. degrees and promotes excellence in research. The EEB department is located on the St. George campus of the University of Toronto in downtown Toronto, Ontario. Toronto is a vibrant, multicultural city on the shore of Lake Ontario, and is home to rich cultural options in the arts, music and film, ethnic cuisine, and a high quality of life.

Interested students should contact faculty with a brief cover letter and curriculum vitae indicating their academic background and research interests, and should file an application with the department. Additional information about faculty research programs and graduate studies, as well as application instructions, is available on the EEB website (<http://www.eeb.utoronto.ca/graduate>). We welcome strong applicants from any country, but particularly encourage

Canadian citizens with NSERC predoctoral fellowships and US citizens with NSF predoctoral fellowships, both of which can be supported at the University of Toronto. The deadline for new applicants in EEB is January 15, 2009.

–
 Asher D. Cutter Assistant Professor & Canada Research Chair in Evolutionary Genomics Department of Ecology & Evolutionary Biology University of Toronto 25 Willcocks St. Toronto, ON, M5S 3B2

tel: 416-978-4602 email: asher.cutter@utoronto.ca
<http://www.eeb.utoronto.ca/people/faculty/-cutter> <http://labs.eeb.utoronto.ca/cutter>
asher.cutter@utoronto.ca asher.cutter@utoronto.ca

UUtah HostParasiteEvolution

Ph.D. Research: Host-parasite evolutionary ecology, Clayton Lab, Dept. of Biology, University of Utah

I am seeking one or two highly motivated Ph.D. students interested in the evolutionary ecology of host-parasite systems. More specific topics of study in my lab include parasite specificity, speciation, co-speciation, competition, adaptive radiation, and ecological immunology. Study systems range from experimental work with captive pigeons and lice, to fieldwork on invasive parasitic flies of Darwin's Finches in the Galapagos. For additional information see: darwin.biology.utah.edu.

Positions are available for Fall Semester, 2009. Students in my lab are supported by a combination of fellowships, research assistantships, and teaching assistantships. Support is guaranteed for five years, contingent upon performance.

Please visit www.biology.utah.edu for departmental information, admission requirements, and application information. The application deadline is January 9th, 2009.

Inquiries are welcome via email to Dr. Dale Clayton (clayton@biology.utah.edu).

Dale Clayton <clayton@biology.utah.edu>

UWesternOntario Phylogenetics Sociobiology

MSc position in molecular phylogenetics. I have an opening for an MSc student with an interest in computational biology and its application to the evolution of insect social behaviour. The project will focus on the analysis of large amounts of nucleotide sequence data within a phylogenetic context. The ultimate goal is to develop a statistically well-founded phylogeny of a clade of social insects (termites; Isoptera) and use this phylogeny to develop and test alternative hypotheses regarding the evolution of insect social behaviour (and other character sets).

Prospective students should have an interest in computational biology (bioinformatics, in silico analyses, evolutionary algorithms) and/or evolutionary biology (molecular evolution, phylogenetics, sociobiology, insect biodiversity). For more context and information about our general research theme, please see our lab web site:

<http://www.uwo.ca/biology/Faculty/thompson/-index.htm> . The University of Western Ontario has a large and vibrant Department of Biology (<http://www.uwo.ca/biology/>) and hosts the SHARCNET high- performance research computing facility (<http://www.sharcnet.ca/>).

Candidates must meet the entry requirements for Graduate Studies at Western: <http://www.uwo.ca/biology/-graduate/graduate.htm>. To inquire, submit (via email) a cover letter with a brief summary of your research interests and a CV to: graham.thompson@uwo.ca - Graham Thompson Department of Biology, University of Western Ontario, London Ontario. The anticipated start date is May or September 2009.

Graham Thompson Assistant Professor Department of Biology University of Western Ontario 1151 Richmond Street North London, Ontario N6A 5B7 CANADA

519 661 2111 (ext 86570) 519 615 6066 (cell)
graham.thompson@uwo.ca <http://www.uwo.ca/-biology/Faculty/thompson> Graham Thompson
<graham.thompson@uwo.ca>

UWisconsinMilwaukee PopulationGenetics

Graduate position (MS or PhD) in Population Genetics in the lab of Dr. Emily Latch, Department of Biological Sciences, University of Wisconsin-Milwaukee.

I am seeking a highly motivated and enthusiastic PhD or MS student interested in the evolution, conservation, and management vertebrate populations. Research in my lab employs molecular genetic tools and statistical genetic methods to address fundamental questions in vertebrate population genetics and evolutionary ecology. Many projects have an applied focus, helping to design, implement, and monitor conservation and management programs. Members of the lab are encouraged to develop independent research within this scope. Current research in the lab includes molecular investigations of hybrid zone evolution, landscape genetic structure, population establishment following translocation, and mating systems. Successful candidates should have some prior experience with DNA-based genetic analysis. Funding in the form of assistantships, research support, and travel grants are available for qualified candidates.

For more information about my lab, visit: <http://www.uwm.edu/People/latch> To learn more about graduate studies in the Department of Biological Sciences at UWM, visit: <http://www.uwm.edu/Dept/-Biology/Docs/Grad/gradindex.html> For more information, or to apply, email a CV (including GPA and GRE scores), letter of interest, and contact information for 3 references to Dr. Emily Latch (latch@uwm.edu). The review of applications will begin immediately and will remain open until the position is filled. Anticipated start date is August 2009.

latch@uwm.edu latch@uwm.edu

Wellington NZ MusselFitnessDifferences

A fully-funded 3-year PhD position is available to work with Dr Jonathan Gardner in Wellington (NZ)

on the genetic basis of fitness differences among individuals and families of the New Zealand greenshell mussel (*Perna canaliculus*). The research will involve the application of genetic markers to assess the evolutionary basis of fitness differences among mussels, and may include construction of a linkage map, determinations of aneuploidy, chromosomal preparations and fluorescent in-situ hybridisation. This position is funded through the NZ Foundation for Research, Science and Technology, and is part of a long-standing collaboration between The Cawthron Institute of Nelson (NZ) and Victoria University of Wellington (NZ). The position is available immediately and is open to

all nationalities. Candidates with a background in molecular/chromosomal techniques (e.g. microsatellites, RAPDs, AFLPs, flow cytometry, karyotyping) and an interest in evolutionary biology and shellfish genetics are encouraged to apply.

Further details and application forms are available from <http://www.fis.org.nz/BreakOut/vuw/schols.phtml?detail+600579> . Information about life in Wellington and the terms of the Scholarship can be found at www.victoria.ac.nz < <http://www.victoria.ac.nz/> > and then following the “scholarships” button in the quicklinks box.

Jonathan Gardner <Jonathan.Gardner@vuw.ac.nz>

Jobs

Amsterdam ComputationalBiology	33	UCaliforniaRiversie EvolutionaryMicrobiol	45
BatesCollege Chair EvolutionaryBiology	34	UColoradoBoulder BotanyCurator	46
BrighamYoungU PlantEvolution	35	UKwaZuluNatal PopulationGenetics	46
BrockU EvolutionaryBiol	35	UMaryland ChairBiology	47
CornellU PopulationComparativeGenomics	36	UMassAmherst ConservationGenetics	47
Durham NC NESCent Director	36	UMichigan ResTech FungalEvolution	48
FloridaIntlU 2 PopulationGeneticist	37	UMinnesotaRochester EvolutionaryBiology	48
GeorgeWashingtonU EvolutionaryMolBiol	38	UNebraska ViralEvolution	49
HarvardU Behavior	38	UNewOrleans 2 ConservationBiol	50
LosAngeles ResTech CopepodSpeciation	39	UNewOrleans ConservationBiology	50
LouisianaStateU ComputationalBiology	39	UNewSouthWales Genetics Lectureship	50
MemorialU Bioinformatics	40	UNSW Sydney EvolutionLecturer	51
MississippiStateU EvolutionaryGenetics	41	UParis6 IntegrativeEvolution	52
SimonFraserU ResTech QTL	41	UQueensland PlantSystematics	52
Smithsonian FieldAssist PlantMammalEvolution ..	41	US EPA Cincinnati PopulationGenetics LabTech ..	53
Smithsonian ResTech PoriferaTreeOfLife	42	US FishWildlife 2 Tech FishPopulationGenetics ...	53
Sydney EvolutionBiol	42	Vienna LabTech MolecularGenetics	54
Trento Italy Biodiversity	43	VirginiaCommonwealthU PlantMolecularSystematics	54
UAlberta LabTech VertebrateBiol	44		
UAlgarve Director MarineEvolBiol	44		

Amsterdam ComputationalBiology

In the context of its recently initiated priority research theme, ‘Earth and Life Sciences’, the Centrum voor Wiskunde en Informatica (CWI) invites applications for the position of a

scientific staff member (tenure track).

CWI is the national research institute for mathematics and computer science in the Netherlands. CWI performs frontier research in mathematics and computer science and transfers new knowledge in these fields to society in general and trade and industry in particular (see <http://www.cwi.nl/>).

The opening is a research position within the field of
* bio-statistics and/or * bio-informatics/computational biology and/or * bio-mathematics

CWI intends to extend its activities in these fields and to initiate new research groups that focus on computer science and/or mathematics for the life sciences. Additional support is available for the new research groups in the form of postdoc positions supplied by CWI.

Profile * The applicant is an independent researcher who has a demonstrated record of high-quality research * He or she has experience in collaborating with scientists working in the life sciences. * The applicant also has the intention and ability to search for project funding, and to build up a research group.

Terms of employment The vacancy concerns a tenure-track position, with an initial appointment for three years. Depending on the candidate's experience, different terms of appointment can be discussed. The salary and terms of employment are in accordance with the "CAO-onderzoekinstellingen" and are based on qualifications. Moreover, CWI offers attractive working conditions, including flexibility and initial help with housing for foreigners.

Information and application Further information on this position can be obtained through Nada Mitrovic (Nada.Mitrovic@cwi.nl).

An application should consist of a cover letter, a curriculum vitae, a list of publications, a research statement, and the names of three references. The research statement should in any case include the applicant's perspective, experience and plans regarding: the relevance of the applicant's research in the life sciences, the applicant's contacts with researchers in the life sciences, and the mathematical and computer science theory and techniques the applicant develops for and applies to the life sciences.

The deadline for applications is set on 16 December 2008. Please send the application to the following address:

CWI Personnel & Organisation (P&O) PD@cwi.nl P.O. box 94079 1090 GB Amsterdam The Netherlands

"Gunnar W. Klau" <Gunnar.Klau@cwi.nl>

BatesCollege Chair EvolutionaryBiology

Evolutionary Biologist, Chair of Biology

The Department of Biology at Bates College (<http://abacus.bates.edu/acad/depts/biology/>) seeks an Evolutionary Biologist at the Associate or Full Professor rank who will also serve as Chair of the Department. This is the first of two positions the Department hopes to fill in the next two years as a result of recent retirements. Courses to be covered collectively by the two positions include evolution, comparative vertebrate anatomy, molecular biology, and genetics, plus courses within the candidates' specialties. Familiarity with genomics/proteomics approaches or the comparative and functional morphology of vertebrates is expected of this appointee. Individuals whose courses and/or research mentorship can contribute to interdisciplinary programs such as biological chemistry, environmental studies, neuroscience or women's studies will be given preference. Candidates for Chair should be able to readily establish an active research program involving undergraduates and have experience in the recruitment and retention of students, faculty, and staff from underrepresented groups. Chair roles and responsibilities include, but are not limited to, leadership in departmental development and effective communication with College administration. Salary and distribution of time devoted to teaching, research and chair duties are negotiable.

The successful candidate must have a Ph.D. in one of the biological sciences and several years of teaching, research, and leadership/administrative experience in academia. Review of applications begins October 15, 2008 and will continue until the position is filled. A cover letter, curriculum vita, statements on teaching, research, and academic leadership, and the names and contact information for at least four evaluators who have agreed to write letters of recommendation should be addressed to:

Chair of Biology Search Committee #R2377 c/o Bates College Academic Services 2 Andrews Rd., 7 Lane Hall Lewiston, ME 04240

Bates College values a diverse college community and seeks to assure equal opportunity through a continuing and effective Affirmative Action Program.

Academic Services <academicservices@bates.edu>

Brigham Young U Plant Evolution

The Department of Biology at Brigham Young University seeks to fill a full time, continuing status position in plant biology. Qualified applicants with a PhD, postdoctoral experience, and expertise in evolutionary or organismal biology (including, but not limited to, modern applications such as molecular ecology, systematics, genomics, evolutionary development, and so forth) are encouraged to apply. The successful candidate is expected to maintain an externally funded research program involving both undergraduate and graduate students. Excellence in teaching is required; teaching responsibilities will include general biology, plant diversity, and a graduate course in the candidate's area of expertise. The department offers competitive start-up packages and reduced teaching loads for new faculty. Interested persons should send a CV, statements of teaching and research interests, and a completed BYU faculty application form to: Dr. Leigh Johnson, Plant Biology Search Committee Chair, 401 WIDB, Department of Biology, BYU, Provo, UT 84602 - electronic applications, preferred, may be sent to bio@byu.edu.

The review process will begin December 10, 2008 for this position and continue until the position is filled. Faculty application forms can be found at: <https://yjobs.byu.edu>. Additional department and college information is available at website: <http://biology.byu.edu/home>. Brigham Young University, an equal opportunity employer, does not discriminate on the basis of race, color, gender, age, national origin, veteran status, or against qualified individuals with disabilities. All faculty are required to abide by the university's honor code and dress and grooming standards. Preference is given to qualified candidates who are members in good standing of the affiliated church, The Church of Jesus Christ of Latter-day Saints.

leigh_johnson@byu.edu leigh_johnson@byu.edu

BrockU Evolutionary Biol

BROCK UNIVERSITY St. Catharines, Ontario*

* Assistant Professor Ecology and/or Evolution*

* *The Department of Biological Sciences is seeking applications for a probationary tenure track position in Ecology and/or Evolution at the rank of Assistant Professor, effective July 1, 2009, subject to final budgetary approval. Research can be in any area of ecology or evolution, and emphasize field, lab, or theoretical approaches. A Ph.D. degree and postdoctoral experience are required, and teaching experience would be an asset. Teaching requirements will include both undergraduate and graduate courses. The establishment of an externally funded research program with supervision of undergraduate and graduate students is expected. Review of applications will begin on January 12, 2009 and continue until suitable candidates have been identified. Further information about the Department can be found at www.brocku.ca/biology < <http://www.brocku.ca/biology> >/. Please submit a letter of application with a research plan, a statement of teaching philosophy, a CV, reprints of several recent publications, and three letters of reference to Dr. Gary Pickering, Chair, Department of Biological Sciences, Brock University, St. Catharines, Ontario, CANADA L2S 3A1. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. More information on Brock University can be found on the University's website www.BrockU.ca < <http://www.BrockU.ca> >. Brock University is actively committed to diversity and the principles of Employment Equity and invites applications from all qualified candidates. Women, Aboriginal peoples, members of visible minorities, and people with disabilities are especially encouraged to apply and to voluntarily self identify as a member of a designated group as part of their application. Candidates who wish to be considered as a member of one or more designated groups should fill out the Self-Identification Form available at <http://www.brocku.ca/hr/careers/-SelfIdentification.pdf> and include the completed form with their application.

– Miriam Richards Associate Professor Dept. Biological Sciences Editor, J. Entomol. Soc. Ontario

Address: Dept. Biological Sciences Brock University
500 Glenridge Ave. St. Catharines, Ontario L2S 3A1
Canada

Phone: +1 905 688 5550 x4406 Fax: +1 905 688 1855
Email: miriam@brocku.ca

Miriam Richards <miriam@brocku.ca>

CornellU PopulationComparativeGenomics

We wish to identify talented candidates for a tenure-track Assistant Professor position in Population and/or Comparative Genomics in the Department of Biological Statistics and Computational Biology (BSCB) at Cornell University in Ithaca, NY. We are seeking to fill this position with a creative individual who is focusing on developing and applying statistically rigorous methods to large-scale data analysis in population and/or comparative genomics. The successful candidate will join an outstanding and interactive group of faculty at Cornell with core interests in population, comparative and evolutionary genomics including Andy Clark, Carlos Bustamante, Adam Siepel, Jason Mezey, Rick Durrett, Brian Lazzaro, Dan Barbash, Mariana Wolfner, Ed Buckler, Steve Kresovich, Steve Tanksley, Susan McCouch, Zhenglong Gu, Kerry Shaw, Matt Hare, Irby Lovette, Rick Harrison, Nelson Hairston, Jr., Kelly Zamudio, Monica Geber, Michael Stanhope, Ruth Ley, Steve Zinder, Nate Sutter, Bryan Danforth, Jeff Doyle, myself, and others. An advertisement, which is attached, appeared in the Oct. 10, 2008 issue of Science describing this position together with three other faculty searches in related areas (<http://scjobs.sciencemag.org/jobs/-default.aspx?job=31709>). These other positions include Assistant/Associate Professor in the genomics approaches to the study of gene regulation (including comparative and evolutionary approaches), Assistant/Associate Professor of cellular systems biology, and two positions (open rank) in computational biology/genomics.

The Department of Biological Statistics and Computational Biology is dedicated to the application of statistical, computational, and mathematical approaches to problems in modern biology. The department has broad strengths in statistics and computational biology, including comparative, evolutionary, quantitative, and population genomics, Bayesian and computationally intensive statistics, and machine learning. The department occupies a key position at the interface between the quantitative and biological sciences at Cornell and offers rich opportunities for collaborations with other investigators on the Ithaca campus, and at the Weill Cornell Medical College in New York City. Some of the research areas with particularly high potential for

collaboration include: human genetics, agricultural genomics, canine genomics and other aspects of veterinary medicine, and evolutionary genomics of diverse organisms. Members of the department are physically located in one of three adjacent buildings that also house the Department of Molecular Biology and Genetics, Entomology, and the Weill Institute for Cell and Molecular Biology. The Departments of Ecology and Evolutionary Biology, and of Neurobiology and Behavior, are in an adjacent (connected) building, with faculty being placed most closely to relevant colleagues in these other departments.

This is a very exciting time at Cornell as the University has specifically targeted comparative and population genomics for expansion, and has just launched a new Cornell Center for Comparative and Population Genomics (<http://www.news.cornell.edu/stories/Oct08/-PopGenCtr.kr.html>). The University is making a concerted investment in these and other interdisciplinary studies that bridge existing strengths in the University (see <http://www.cornell.edu/lifesciences/>).

Please bring this great opportunity to the attention of outstanding junior scientists your group and department. If you have any questions, please do not hesitate to contact me at CFA1@cornell.edu.

Best regards,

Chip Aquadro Chair of the Search Committee Professor of Population Genetics, Dept of Molecular Biology and Genetics Co-Director, Cornell Center for Comparative and Population Genomics

Chip Aquadro <cfa1@cornell.edu>

Durham NC NESCent Director

Director, National Evolutionary Synthesis Center
Durham, NC, USA

Applications and nominations are invited for the position of Director of the National Evolutionary Synthesis Center, NESCent (www.nescent.org), a research center in Durham, North Carolina. The Center is supported by the National Science Foundation, and is jointly sponsored by Duke University, the University of North Carolina at Chapel Hill and North Carolina State University. The position of Director will be a faculty appointment at the senior level made by Duke University.

NESCent promotes collaborative research on funda-

mental synthetic questions in evolutionary biology by supporting visiting scientists in working groups and catalysis meetings (>500 scientists/year) and resident sabbatical and visiting scholars and postdoctoral fellows. The Center also has a large Informatics group and an active program in Education and Outreach in evolutionary biology.

The Director has overall responsibility for administration of the Center, in collaboration with Associate Directors from the co-sponsoring Universities. The Director reports annually to NSF and to administrators of the associated universities and is advised by a Senior Advisory Board (SAB). The Director provides scientific leadership and fosters an environment that inspires collaboration. The Director should have a clear and imaginative scientific vision that serves the larger scientific community, receptiveness to alternative scientific views, an understanding of the key role that technology plays in fostering collaborative and synthetic science, and an unwavering commitment to the highest possible quality research. The Director should have an outstanding record of research in evolutionary biology with demonstrated organizational and management and interpersonal skills, and a fully articulated commitment to the goals of the Center. Experience in working with various funding agencies, including NSF, would be advantageous.

Subject to approval by the relevant disciplinary department, and provided the successful candidate meets the university's criteria for scholarly excellence, Duke University will appoint the candidate to a faculty position at the senior level. Evaluation of candidates, and selection of the Director, will be done by faculty from the collaborating Universities as well as a representative of NESCent's SAB; the final decision requires NSF approval.

Applications and nominations should be submitted electronically to nescent-director@duke.edu. Review of applications will begin December 1, 2008 and continue until the position is filled. *Applications should be formatted as a single pdf document and include a letter of interest, CV, and names of three people who have agreed to provide letters of recommendation.* The letter of interest should include a vision statement for the Center and the applicant's career goals. Inquires regarding the search and/or Center function should be addressed to nescent-director@duke.edu.

The Center is especially interested in candidates who can contribute to the diversity and excellence of the academic community through research, teaching and service.

Duke University is an Equal Opportunity/Affirmative

Action Employer

noon@duke.edu noon@duke.edu

FloridaIntIU 2 PopulationGeneticist

The Department of Biological Sciences at Florida International University in Miami, FL, now has two positions open that are of interest to Evolutionary Biologists. We require all of our undergraduates to take a one-semester upper division course on Evolution and participation in that course would be welcome, though not required, from the successful applicant for either position. At present the course is offered in spring and fall academic terms and teaching responsibilities rotate among several faculty members to permit diversity in teaching assignments. Feel free to contact Joel Trexler (trexlerj@fiu.edu), or the search committee Chairs indicated on each advertisement, with questions about either position.

Vertebrate Functional Morphologist. Florida International Univ. Biological Sciences Dept. invites applications for a tenure track, rank open, faculty position, for Fall 2009. Candidates must have a PhD, demonstrated record of research excellence, potential for independent research, commitment to teaching at the undergraduate and graduate levels. Post-doctoral experience required, and the successful candidate is expected to develop a competitive extramurally-funded research program. The Biological Sciences Dept. has 900+ undergraduate majors, 135 graduate students, 16 post-doctoral fellows and 40 faculty members. Our website is www.fiu.edu/~biology < <http://www.fiu.edu/~biology/> >. Applications will be accepted until the position is filled. Send curriculum vitae, summary of research and teaching interests, 3 reprints, names and addresses of recommenders to: Ophelia I. Weeks, Chair, Vertebrate Functional Morphologist Search & Screen Committee, Department of Biological Sciences, Florida International University, University Park Campus, OE 167, Miami, Florida, 33199. Florida International University is an Equal Opportunity Educator and Employer.

Population Geneticist. The Department of Biological Sciences at Florida International University is seeking a scientist for an open rank position in population genetics. Our department has a strong multidisciplinary emphasis; we are looking for a colleague to strengthen our programs in evolutionary biology, ecology, and molec-

ular and cellular biology. We seek applicants with a Ph.D. and an exceptional research record in population genetic studies. All areas of empirical or theoretical population genetics will be considered. Candidates will contribute to our undergraduate and graduate teaching programs in population genetics and general genetics. Interested applicants should send their CV, including a bibliography of published work, a brief description of research accomplishments and objectives, a statement of teaching interests, selected reprints, and the names, addresses, and contact information for at least three references to: Tim Collins, Chair, Population Genetics Search, Dept. Biological Sciences, FIU, 11200 SW 8th St., Miami, Florida 33199 (collinst@fiu.edu). Review of applications will begin December 1, 2008, and continue until position is filled. Florida International University is an Equal Opportunity Educator and Employer.

Joel Trexler <trexlerj@fiu.edu>

George Washington U Evolutionary Mol Biol

TENURE TRACK FACULTY POSITION in MOLECULAR BIOLOGY

The Department of Biological Sciences invites applications for a tenure track Assistant Professor for September, 2009. We are seeking a broadly trained scientist interested in the *molecular biology of organismal interactions*. Research could include, but is not limited to, immunology, parasitology, plant-microbe interactions or symbiosis. Research conducted in an evolutionary context will be preferred. We seek a scientist who will strengthen and expand the research and teaching within the department (see www.gwu.edu/~biology). The successful candidate will develop or maintain an externally funded research program that involves graduate and undergraduate students. Teaching will include an undergraduate lab course in molecular biology and second course within the candidate's area of expertise. A completed PhD and postdoctoral experience is required.

Review of applications will begin November 16, 2008 and will be ongoing until the position is filled. Application procedure: interested candidates should submit electronically 1) a letter of application, 2) a CV, 3) a brief description of research interests including past accomplishments and future plans, 4) a statement of teaching plans including a description of courses that

could be taught, and 5) up to three publications. Candidates should arrange for three letters of recommendation to be sent to:

Molecular Biology Search Chair Department of Biological Sciences 340 Lisner Hall 2023 G Street NW The George Washington University Washington DC 20052 e-mail: mbsearch@gwu.edu Phone: 202 994-6090

Only complete applications will be considered.

GWU is an equal opportunity/affirmative action employer. The search committee seeks to attract an active, culturally and academically diverse faculty of the highest caliber.

"L. Courtney Smith" <lcourtneysmith@gmail.com>

HarvardU Behavior

Evolutionary biologists working on behavior are particularly encouraged to apply for this recently advertised position:

ASSISTANT PROFESSOR OF BIOLOGY HARVARD UNIVERSITY

Department of Organismic and Evolutionary Biology
Center for Brain Science

The Department of Organismic and Evolutionary Biology and the Center for Brain Science at Harvard University are seeking an Assistant Professor in the area of animal behavior, behavioral genetics and neuroethology. We are especially interested in individuals who conduct rigorous, field and/or laboratory-based tests of general problems in behavior using genetic, genomic, neurobiological, and/or endocrinological approaches.

As a member of the Center for Brain Science, the successful candidate will have opportunities to interact with faculty from other departments in the Faculty for Arts and Sciences and Harvard Medical School. Aims of the Center include mapping neural circuits that underlie experimentally accessible behaviors in diverse species, and elucidating the biological bases of individual differences in behavior. CBS fosters interactions across disciplinary boundaries. Faculty from several academic departments are housed in common research space, contiguous with that of the Department of Organismic and Evolutionary Biology, and its connections reach out across the University.

Candidates should have demonstrated excellence in both research and teaching. Teaching duties will

include offerings at both undergraduate and graduate levels. Applications from, or nominations of, women and minority candidates are encouraged. Questions regarding the position can be addressed to Joshua R. Sanes, Center for Brain Science, Harvard University, 7 Divinity Ave., Cambridge, MA 02138 (sanesj@mcb.harvard.edu) or Naomi E. Pierce, Department of Organismic and Evolutionary Biology, 26 Oxford Street, Cambridge, MA 02138 (npierce@oeb.harvard.edu).

To apply, please send a cover letter, curriculum vitae, and statements of research and teaching interests, and arrange for submission of 3 letters of recommendation.

Application materials should be submitted electronically to: cbs@fas.harvard.edu. Review of applications will begin December 15, 2008 and will continue until the position is filled.

Further information about the Department of Organismic and Evolutionary Biology and the Center for Brain Science is available at their respective websites: <http://www.oeb.harvard.edu>, and <http://cbs.fas.harvard.edu/>. Harvard University is an Affirmative Action/Equal Opportunity Employer. –

Naomi E. Pierce Museum of Comparative Zoology Labs
26 Oxford Street Cambridge, Massachusetts 02138-2902
USA TEL: (617) 495-2576 (office) (617) 495 4012 (lab)
FAX: (617) 495-5667 npierce@oeb.harvard.edu

naomi.pierce@googlemail.com

LosAngeles ResTech CopepodSpeciation

Laboratory Research Technician University of Southern California, Los Angeles

The Edmands lab seeks a full-time research technician for studies of the genetics of speciation in a marine copepod. Duties would include 1) development and maintenance of a large breeding study, 2) assistance with molecular assays, 3) data analysis and preparation for publication (including co-authorship) and 4) general lab management. The position is for 6-12 months, beginning approximately March 2009, and requires work on the weekends. For more information on the range of research projects conducted in our lab, please see our website at <http://college.usc.edu/labs/edmands/home/index.cfm>. Applicants should have a bachelor's degree in biology or a related field, and a strong back-

ground in genetics and/or evolution. Other qualifications include excellent organizational skills, the ability to work independently, a high tolerance for microscope work, and above average manual dexterity. Previous experience in a lab environment, particularly with molecular tools, is also desirable but not required.

Salary is commensurate with experience and a full benefits package is included. Please apply via email to Suzanne Edmands (sedmands@usc.edu) and include a resume, contact information for three references and a cover letter describing your experience, your interest in the position, and your desired start date. Applications will be considered until the position is filled.

– Suzanne Edmands Associate Professor Department of Biological Sciences 3616 Trousdale Parkway, AHF 316 University of Southern California Los Angeles, CA 90089 (213)740-5548 <http://college.usc.edu/labs/-edmands/home/index.cfm> edmandss@gmail.com

LouisianaStateU ComputationalBiology

ASSISTANT/ASSOCIATE/FULL PROFESSOR IN
COMPUTATIONAL BIOLOGY

Department of Biological Sciences/Center for Computation & Technology

Louisiana State University

The Department of Biological Sciences and the Center for Computation & Technology (CCT) at Louisiana State University invite applications for a joint faculty position in Computational Biology, broadly defined. Required Qualifications: Ph.D.; a successful track record of independent research; areas of interest include, but are not limited to: genomics, systems biology modeling, biomolecular structure/function, and computational neuroscience. Responsibilities: maintains and has a vigorous, extramurally funded research program and contributes to undergraduate and graduate teaching; works closely with faculty in Biological Sciences and other departments at LSU, as well as the CCT faculty to foster the development of a center of excellence in Computational Biology at LSU.

LSU anticipates hiring several additional faculty in computational biology in the future. The CCT offers an innovative and interdisciplinary research environment for advancing computational sciences, including a

highly competitive computing environment with access to 100 TFlops of computing resources in conjunction with the Louisiana Optical Network Initiative (LONI). This position is also offered in conjunction with the LONI Institute (<http://institute.loni.org/>), a bold new inter-university collaboration aiming to fill a dozen new faculty positions in related areas. LSU is part of the national TeraGrid. For additional information visit our departmental website: <http://www.biology.lsu.edu>, and the CCT website: <http://www.cct.lsu.edu/home>. We encourage applications from women and minorities. An offer of employment is contingent on a satisfactory pre-employment background check. Application deadline is January 30, 2009 or until a candidate is selected. Send curriculum vitae (including e-mail address), statements of research & teaching interests, three letters of recommendation, and no more than three representative publications to:

Charyl Thompson

Department of Biological Sciences

202 Life Sciences Bldg.

Louisiana State University

Ref: Log #2041

Baton Rouge, LA 70803

LSU is an Equal Opportunity/Equal Access Employer

Robb Brumfield, PhD Museum of Natural Science 119
Foster Hall Louisiana State University Baton Rouge,
LA 70803

brumfld@lsu.edu brumfld@lsu.edu

MemorialU Bioinformatics

MEMORIAL UNIVERSITY Tenure-Track Faculty Position in Bioinformatics

The Departments of Computer Science and Biology at Memorial University have each embarked on multi-year renewal programs. Each department currently has more than 20 tenure-stream faculty members, and supports M.Sc., Ph.D. and collaborative graduate programs. For more details, see <http://www.mun.ca/biology/Home/> and <http://www.mun.ca/computerscience/>. Both departments invite applications for a tenure-track position in Bioinformatics, starting no later than September 1, 2009. This will be a joint appointment between the de-

partments. The appointment will be made at the level of Assistant Professor, with the primary appointment in Computer Science, and equal responsibility in both departments, in accordance with the terms of Memorial's Collective Agreement. A Ph.D. in Computer Science, Computational Science, Biology, or related fields is required and postdoctoral or equivalent experience is desirable. Applicants should have experience in Bioinformatics, and be keen to do interdisciplinary work between the departments. Applicants should possess a strong research record with outstanding promise for future research, and be able to demonstrate the potential for excellent undergraduate and graduate teaching in Bioinformatics. Applicants should submit a Curriculum Vitae, statements of research interests, teaching interests and philosophy, and up to three reprints of publications. The application should be accompanied by names of at least three referees of international standing, who are willing to provide letters of recommendation (include details on affiliations, plus phone numbers and email addresses). All material must be received by January 15, 2009; refer to position VPA-COSC-2007-001 in all correspondence, and submit materials to:

Dr. Wolfgang Banzhaf, Head Department of Computer Science Memorial University St. John's, NL, Canada, A1B 3X5 Email: chair@cs.mun.ca

Memorial University is the largest university in Atlantic Canada. As the Province's only university, Memorial plays an integral role in the educational and cultural life of the Province of Newfoundland and Labrador. Offering diverse undergraduate and graduate programs to almost 18,000 students, Memorial provides a distinctive and stimulating environment for learning. St. John's is a very safe and friendly city with great historic charm, a vibrant cultural life, and easy access to a wide range of outdoor activities. Memorial University is committed to employment equity and encourages applications from qualified women and men, visible minorities, aboriginal people and persons with disabilities. All qualified candidates are encouraged to apply; however, Canadian citizens and permanent residents will be given priority. Partners of candidates for positions are invited to include their resumes for possible matching with other job opportunities.

Dr Steven M Carr, Professor of Biology Department of Biology Memorial University of Newfoundland St John's NL A1B 3X9 CANADA

e-mail: scarr@mun.ca <http://www.mun.ca/biology/-scarr/Research.html> (709) 737 - 4776 office / -4713 lab / -3018 FAX

scarr@mun.ca

MississippiStateU EvolutionaryGenetics

TENURE-TRACK FACULTY POSITIONS IN BIOLOGICAL SCIENCES

The Department of Biological Sciences at Mississippi State University invites applications for two tenure-track Assistant Professor positions to begin August 16, 2009. Successful candidates will be expected to develop externally funded research programs that complement the existing strengths of the department. Desired areas of expertise include, but are not limited to: molecular, cellular and evolutionary genetics; ecological, environmental and industrial microbiology; molecular ecology; infectious diseases and pathogenesis. Additionally, successful candidates will be those who can direct graduate students and contribute to both the undergraduate and graduate teaching missions of the department. Minimum requirements for consideration include a Ph.D. in a related biological sciences field. Post-doctoral experience is preferred.

Scientific infrastructure at Mississippi State University supports focus areas in proteomics, genomics, and computational sciences. University centers that house these facilities include the Life Sciences & Biotechnology Institute, the Electron Microscopy Center, the Geosystems Research Institute, and the Center for Computational Sciences. For more information on the department or these entities, please visit the Department of Biological Sciences website (www.msstate.edu/dept/-biosciences).

Applicants should submit a curriculum vitae, reprints of three representative publications, a concise statement of current and future research interests (one page), and a brief statement of teaching philosophy including relevant areas of teaching competence. Also, arrange for at least 3 letters of reference to be sent to the address below. Send applications (hard copy or electronic) to Dr. Nancy Reichert, Professor and Head, Department of Biological Sciences, P.O. Box GY, Mississippi State University, Mississippi State, MS, 39762, nar1@msstate.edu. Screening will begin January 15, 2009 and will continue until the positions are filled.

Mississippi State University is an Affirmative Action/Equal Opportunity Employer

Mark E. Welch, Ph.D. Assistant Professor Dept. of Bi-

ological Sciences Mississippi State University P.O. Box GY Mississippi State, MS 39762

E-mail: mark.welch@msstate.edu Phone: 662.325.7564
Fax: 662.325.7939

Mark Welch <welch@biology.msstate.edu>

SimonFraserU ResTech QTL

Recently funded NIH position for QTL mapping and positional cloning of genes responsible for vertebral curvature in guppy and closely-related species. Come to beautiful Vancouver and participate in research on the first genetic model of human idiopathic scoliosis. available ASAP contact:

Felix Breden/Kristen Gorman Department of Biological Sciences Simon Fraser University Burnaby, BC V5A 1S6 778-782-5647/5641 breden@sfu.ca/kfg@sfu.ca

breden@sfu.ca breden@sfu.ca

Smithsonian FieldAssist PlantMammalEvolution

Field Assistant Position, Rainforest Plant-Mammal Interactions

We have a position for one field assistant to help with NSF funded research on interactions between mammals (agoutis) and palm seeds. This work will focus on radio-tracking both the agoutis as well as the seeds they disperse, but will also include helping with monitoring projects using camera traps and plant surveys. The assistant will work as part of a team that includes post-docs, students, volunteers, and other assistants involving a broad collaboration between the New York State Museum, Princeton University, the Max Plank Institute, University of Groningen, University of Wageningen, and the Smithsonian Tropical Research Institute.

TIME PERIOD: One year, starting late March 2009, with possible extension for a second year.

LOCATION: Barro Colorado Island, a research station in central Panama administered by the Smithsonian Tropical Research institute.

PAYMENT: \$24,000 per year plus benefits through the NY State Museum, one round-trip plane ticket. Assistant will be responsible for their living fees in Panama. Applicants must be a US citizen or have a valid work visa for the United States.

QUALIFICATIONS: Applicant must have a BS or MS degree and experience in field ecology. A background in tropical ecology, radio telemetry, or animal-handling skills would also be beneficial. Applicants must be a US citizen or have a valid work visa for the United States.

APPLICATION DEADLINE: 29 December 2008

TO APPLY: Send a CV, names of 3 references, and a cover letter to rkays@mail.nysed.gov

“Hirsch, Ben” <HirschB@si.edu>

Smithsonian ResTech PoriferaTreeOfLife

I will be looking to fill a contract position for a research technician in molecular biology and biodiversity.

The contractor will provide support services to the multi-institutional, NSF-funded Porifera Tree of Life (PorToL) project, and will be located at the Smithsonian's National Museum of Natural History (NMNH) and Laboratory of Analytical Biology (LAB). Duties will include:

1. Extracting DNA from a variety of sponge (Porifera) specimens using extraction kits and the high throughput capabilities of LAB. Results to be checked for quantity and quality of yield and success in downstream applications.
2. Conducting DNA amplification of barcode and phylogenetic markers (including nuclear 18S and 28S and mitochondrial COI and 16S) from DNA extracts.
3. Troubleshooting, optimizing, and editing molecular sequence results and data.
4. Post-processing trace and sequence data and assembling “barcode compliant” metadata for upload to Genbank, the Sponge Barcoding Project, and the PorToL database.
5. Backing up all DNA extractions via archival system with new technologies.
6. Assisting in documentation (databasing and vouchering) of specimens from which sequence data are generated.

7. Providing feedback to automated LIMS (Laboratory Information Management System) to improve efficiency and advance throughput procedures for data creation and management.

8. Integrating new collections and 2D barcoding methodologies into LAB workflow (via Matrix tube, plates, scanners and software).

9. As necessary operating, monitoring, and assisting users on key pieces of robotic equipment (Automated DNA Extractors, Automated capillary DNA sequencers, etc.).

If interested, please contact Allen Collins (202-633-0645; collinsa@si.edu) with a CV and contact information for references, at which point we can discuss compensation with benefits.

Dr. Allen G. Collins - phone: (202) 633-0645, fax: (202) 633-8848 Invertebrate Zoologist with Curatorial Responsibilities for Medusozoa and Hexactinellida National Systematics Laboratory of NOAA Fisheries Service National Museum of Natural History, MRC-153 Smithsonian Institution, P.O. Box 37012, Washington, DC 20013-7012 USA

For FedEx (or other couriers), please use: Smithsonian Institution, MRC 0163, Natural History Building, West Loading Dock 10th and Constitution Avenue, Washington, DC 20560

The contents of this message are mine personally and do not necessarily reflect any position of the Government or the National Oceanic and Atmospheric Administration.

“Collins, Allen” <COLLINSA@si.edu>

Sydney EvolutionBiol

Please note two lecturer positions at UNSW - an Evolution position (advertised previously on Evoldir) with a closing date of Monday 1 December, and a Marine Ecology position (closes 31 January). Our strengths are at the interface of evolution and ecology, and both positions are broad searches looking for the strongest possible applicant. Lecturer in Australia is a research and teaching position equivalent to tenure-track Assistant Professor in the USA. 31 October 2008 Lecturer in Evolution Faculty of Science SCHOOL OF BIOLOGICAL, EARTH & ENVIRONMENTAL SCIENCES REF. 6226NET

The School of Biological Earth and Environmental Sciences (BEES), in conjunction with the Evolution & Ecology Research Centre (E&ERC) is seeking a Lecturer in Evolution. BEES is a large and multi-disciplinary school in the Faculty of Science at the University of New South Wales. The school incorporates a range of disciplines within the broad fields of Biology, Marine Science, Geography and Geology.

The appointment will enhance UNSW's research profile in Evolutionary Biology and Evolutionary Ecology and the appointee will be a member of the UNSW Evolution & Ecology Research Centre. The successful candidate will be required to establish an internationally recognized, externally funded research program in Evolutionary Biology and to teach undergraduate courses in Evolution, Ecology, Genetics and/or Biology. Applicants should have a strong research record and should outline in their application their capacity to contribute to the existing research areas in the Centre and the School. Candidate's research should be focussed on adaptive processes and the testing of theory, and should not be entirely descriptive. Candidates whose research involves the experimental study of adaptation and its links to genetic, genomic, behavioural and/or physiological processes may be preferred

This is a continuing appointment

Salary range for Lecturer A\$73,573 - A\$86,734 per year (plus 17% employer superannuation and leave loading)

Candidates holding existing ARC/NHMRC fellowships and/or research grants are encouraged to apply as well as those who are able to form synergistic interactions with existing researchers and groups within the E&ERC. Women and people from equity groups are also encouraged to apply.

Applicants should systematically address the selection criteria in their application.

For the Information Package click < <http://www.hr.unsw.edu.au/services/recruitment/jobs/-/services/recruitment/jobs/info/pd31100808.pdf> >HERE

Enquiries may be directed to Associate Professor David Cohen on telephone + 61 2 9385 8084 or email d.cohen@unsw.edu.au or Associate Professor Rob Brooks on +61 2 9385 2065 or email rob.brooks@unsw.edu.au Further information on the School, please visit: < <http://www.bees.unsw.edu.au/> ><http://www.bees.unsw.edu.au/>

Applications close : 01 December 2008

Lecturer in Applied Marine Ecology & Conservation Faculty of Science SCHOOL OF BIOLOGICAL,

EARTH & ENVIRONMENTAL SCIENCES REF. 6228NET

The School of Biological Earth and Environmental Sciences (BEES) is seeking a Lecturer in Applied Marine Ecology and Conservation. BEES is a large and multi-disciplinary school in the Faculty of Science at the University of New South Wales. The school incorporates a range of environmentally relevant disciplines enabling the School to undertake comprehensive education and research in the broad fields of Biology, Marine Science, Geography and Geology. Members of the School of BEES form a core part of the Sydney Institute of Marine Science.

The position will enhance the research profile in applied marine ecological research. It will also contribute to the expansion of the School's profile within the Sydney Institute of Marine Science and in the Evolution & Ecology Research Centre, in marine ecology and conservation research and education. The successful candidate may be required to coordinate the Master of Conservation Biology or similar programs. Applicants should have a strong research record in applied marine ecology and conservation and the capacity to contribute to the school's existing and emerging research areas.

This is a full-time and continuing position.

Salary range for Lecturer A\$73,573 - A\$86,734 per year (plus 17% employer superannuation and leave loading)

Applicants should systematically address the selection criteria in their application. Women and people from equity groups are also encouraged to apply.

Please direct any enquiries to Associate Professor David Cohen on telephone (61 2) 9385 8084 or email d.cohen@unsw.edu.au or Professor Iain

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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>

Trento Italy Biodiversity

Two positions are open to work at Centro di Ecologia Alpina (Fondazione E. Mach) in the project ACE-SAP (Alpine Ecosystems in a Changing Environment: Biodiversity Sensitivity and Adaptive Potential), funded by the Autonomous Province of Trento, Italy.

-Post-doctoral position in Vertebrate Molecular Ecology (Cod. 024_AS_VME): A 33 months contract is available to work in the molecular and data analyses on neutral and adaptive markers in common frog (*Rana temporaria*), yellow-necked field mouse (*Apodemus flavicollis*) and black grouse (*Tetrao tetrix*). Main duties include: coordination of sampling activities; adequate storing of tissue samples collected; DNA extraction and amplification via PCR; optimisation of PCR reactions for amplifying both neutral markers (mainly mtDNA and nuclear microsatellites) and adaptive markers (e.g. MHC genes and/or other loci involved in immunitary response); preparation of cycle sequencing DNA reaction; cloning of PCR products; editing of DNA sequences; maintenance of database; data analyses with population genetics/evolutionary specific softwares; drafting scientific papers and reports; attending national and international conferences, workshops; supervision of young researchers activity. Details about salary, application and other can be found at: http://www.fondazioneedmundmach.it/-sperimentazione.context2.jsp?ID_LINK=3143&area=6
Deadline for application: December, 31, 2008 Starting date: from mid-January 2009

-Laboratory and field research assistant in molecular ecology (Cod. 025_AS_RAME): A 33 months contract is available to work in field sample collection and molecular analyses of amphibian and reptile species. Main duties are: Non-invasive sampling of amphibian and reptile species from mountain areas of Trentino; adequate storing of tissue samples collected; DNA extraction and amplification via PCR; preparation of cycle sequencing DNA reaction; editing of DNA sequences; maintenance of database. Further details (how to apply, salary, etc.) can be found at: http://www.fondazioneedmundmach.it/-sperimentazione.context2.jsp?ID_LINK=3143&area=6
Deadline for application: December, 31, 2008 Starting date: from mid-January 2009

For any additional information please send an e-mail to: risorseumane.centroricerca@iasma.it

Cristiano Vernesi Centro di Ecologia Alpina Fondazione Edmund Mach Viote del Monte Bondone - 38040 Trento - Italy tel +390461939523 (NEW) - fax +390461948190 skype name: cvernesi

vernesi@cealp.it

UAlberta LabTech VertebrateBiol

The Department of Biological Sciences, University of Alberta is advertising for a Lab Coordinator / Biology Technologist in Vertebrate Biology. This is a full-time position with a generous benefits package. For details and application instructions, see:

< <http://www.careers.ualberta.ca/Support/Competitions.aspx?key=1004> >
< <http://www.careers.ualberta.ca/Support/Competitions.aspx?key=1004> >
Closing date is November 20th. A mid-December start date is anticipated.

A. Richard Palmer, FRSC Systematics and Evolution Group Department of Biological Sciences University of Alberta Edmonton, Alberta T6G 2E9 CANADA phone: (780) 492-3633 message: (780) 492-3308 FAX: (780) 492-9234

<http://www.biology.ualberta.ca/palmer/palmer.html>
(biological asymmetries, software, course notes) Founding Chair, Comparative Morphology & Development section, Canadian Society of Zoologists. For info. see: <http://www.biology.ualberta.ca/CMD/home.htm>
rich.palmer@ualberta.ca

UAlgarve Director MarineEvolBiol

The following director position is open for a scientist in any field of biology or related sciences, but it would be of great interest to the research center (CCMAR) to have a director that would foster the development of current and novel evolutionary research areas concerning marine life (e.g. marine chemical ecology and co-evolution, metagenomics, genomics of adaptive responses, conservation genetics)

Director Position The Centre of Marine Sciences (CCMAR, www.ccmар.ualg.pt) invites applications to fill the position of Science & Research Director. CCMAR is located at the University of Algarve, Faro, Portugal, and is part of the Centre of Marine and Environmental Research, (CIMAR V Associated Laboratory, <http://www.cimar.org/>), a centre of excellence for marine science research in Portugal. The salary will be commensurable with experience at the rank of Full Professor. The appointment will start as early as possible in 2009.

Position description: We are seeking an individual with an outstanding scientific career, developed leadership, good knowledge of international networks, well-organized and self-directed who is team oriented and

has the capability to define strategy and provide innovative leadership in the research and outreach functions of CCMAR. The candidates will demonstrate a strong commitment to diversity and be an active international fundraiser both from the public and private sectors.

Duties and responsibilities: The new director is expected to manage the overall policy of CCMAR, and carry out inherent duties within the CIMAR-AL; provide leadership towards scientific excellence; define master lines of strategic development; make recommendations about appropriate new appointments; and consolidate interdisciplinary exchange and interaction within the centre and at international level.

Application materials: The application should include a letter describing qualifications and highlighting motivation and leadership experience relevant to the distinctive environment of CCMAR, curriculum vitae and complete contact (including name, address, telephone fax numbers, and e-mail addresses) of at least four references. Interviewees will be expected to make a presentation to the CCMAR members as part of the selection process.

Application address: Ms. Filipa Queiroz, Centre of Marine Sciences, Campus de Gambelas, University of Algarve, 8005-139 Faro, Portugal.

Informal enquiries: Professor K. Erzini (Interim Director) tlf/ fax: + 351 289 800 051, e-mail: kerzini@ualg.pt

The screening process will begin December 15, 2008 and will continue until the position is filled.

CCMar has an equal employment policy.

Ester Serrao <http://www.ccmар.ualg.pt/maree/> CCMAR, CIMAR-Lab. Assoc. FCMA, Universidade do Algarve Gambelas, 8005-139 Faro, Portugal telef: (+351) 289 800 928 fax: (+351) 289 800 069

Ester Serrao <eserrao@ualg.pt>

UCaliforniaRiversie EvolutionaryMicrobiol

UNIVERSITY OF CALIFORNIA, RIVERSIDE

Faculty Position Evolutionary Microbiologist

Position Description: The Department of Plant Pathology and Microbiology, University of California, Riverside, invites applicants for a 9-month, tenure-track Open Rank position. The position will be available

July 1, 2009, and carries a 50% research appointment in the Agricultural Experiment Station and a 50% teaching appointment in the College of Natural and Agricultural Sciences. The Department of Plant Pathology and Microbiology currently has 17 ladder-rank faculty and four Cooperative Extension Specialists.

Research: This position will carry out studies of microbial gene or genome evolution, phylogenetic reconstructions of microbe evolution, comparative genome analysis, comparative structural biology, and/or evolution of metabolic pathways. The research will be primarily basic in nature, and may focus on eukaryotic or prokaryotic microbes that are saprophytes, pathogens, organisms important in industrial microbiology, etc. The research methodology may be largely theoretical or integrate both theoretical and experimental approaches.

The position will join a vibrant community of researchers studying microbe-plant, microbe-animal, and microbe-environment interactions from evolutionary, ecological, molecular and biochemical perspectives. The successful applicant will have access to modern campus facilities in genomics, bioinformatics, proteomics and microscopy to support their research. A competitive start-up package is available.

Teaching: The successful candidate will advise both graduate and undergraduate students and contribute to both graduate and undergraduate teaching in microbiology and evolutionary biology, and possibly bioinformatics and statistics.

Application: A Ph.D. in a relevant field and a proven ability to conduct innovative research are required. Evaluations of applications will begin January 5, 2009, but the position will remain open until filled. Applicants should send curriculum vitae, statements of research and teaching interests, a complete list and selected reprints of publications, and three letters of reference to:

Dr. Katherine A. Borkovich Chair, Search Committee
c/o Marie Gaton, marie.gaton@ucr.edu Department of Plant Pathology and Microbiology University of California Riverside, California 92521-0415

Additional information about the department can be found at <http://www.plantpathology.ucr.edu> The University of California is an Affirmative Action/Equal Opportunity Employer

Greg Douhan <gdouhan@ucr.edu>

UColoradoBoulder BotanyCurator

The University of Colorado Museum of Natural History and Department of Ecology and Evolutionary Biology (EEB), University of Colorado Boulder invite applications for a joint, tenure-track appointment as Curator of Botany and Assistant or Associate Professor. Primary responsibilities will be to curate and develop the Museum's botany collections, use phylogenetic and systematic approaches as a core part of their research program on any group of plants (including bryophytes and lichens), and teach in Museum and Field Studies and EEB. The successful individual will be expected to take a leadership position in advancing the role of the Herbarium. The Herbarium houses a diverse collection of approximately a half million specimens of vascular plants, bryophytes, and lichens and has strong holdings from the southern Rocky Mountain region. This regional strength is enhanced by collections from western North America, the American Arctic, the Altai and the Caucasus Mountains of Central Asia, the European alpine, and the Sierra Madre Occidental of Mexico. Additional information about EEB and the CU Museum and Herbarium can be found on the web at: <http://www.cumuseum.colorado.edu> and <http://www.colorado.edu/eeb>.

Applicants must have a doctoral degree; curatorial experience is important. Apply at <http://www.jobsatcu.com/>, Posting# 805528, beginning November 1. The application package should include curriculum vitae, representative publications, statements of research, teaching, and curatorial experience and vision, along with names and addresses of four references. Contact: Robert.Guralnick@colorado.edu. Review of applications begins January 1, 2009 until a successful candidate is identified. The University of Colorado is committed to diversity and equality in education and employment.

robgur@gmail.com

UKwaZuluNatal PopulationGenetics

All appointments will be in terms of the prevailing Uni-

versity Employment Equity Policy and the Employment Equity Plan of the faculty/division (available at <http://www.ukzn.ac.za/ESU>). The University reserves the right not to make an appointment or to stop the process at any stage to headhunt or re-advertise the post to meet its equity goals. Candidates who do not meet the minimum criteria will not be considered.

LECTURER IN POPULATION/ CONSERVATION GENETICS SCHOOL OF BIOLOGICAL & CONSERVATION SCIENCES FACULTY OF SCIENCE AND AGRICULTURE PIETERMARITZBURG CAMPUS REFERENCE NO.: SA08/2008

The School of Biological and Conservation Sciences is well established with a very active research profile and a substantial postgraduate programme. It has excellent research facilities and modern equipment, including access to the University research farm, a comprehensive herbarium and botanical gardens. The successful applicant should have a background in Population and/or Conservation Genetics, and be able to integrate with the existing expertise in Ecology and Conservation Biology. The appointee will be required to contribute to the delivery of the programmes in Genetics (in collaboration across several Schools), teach at undergraduate and postgraduate levels, supervise research students and establish a research programme.

MINIMUM REQUIREMENTS: \$B!|(B MSc in a relevant field; \$B!|(B Evidence of current research activity with published papers in the peer-reviewed scientific literature in Population and/ or Conservation Genetics. ADVANTAGE: \$B!|(B PhD in a relevant field.

For further information see the School website at <http://www.ukzn.ac.za/biology> or contact Prof. Kevin Kirkman at kirkmank@ukzn.ac.za

The closing date for receipt of applications is 14 November 2008. The University however, reserves the right in special circumstances to accept late applications or to extend the above date in order to facilitate further searches.

Applicants are required to submit a covering letter highlighting their experience in, and providing evidence for, each of the minimum requirements and advantage as listed above, together with a detailed CV including the names, full addresses, fax numbers and e-mail addresses of three referees, to Ms Sharon Ireland, Human Resources Administration, University of KwaZulu-Natal, Private Bag X01, Scottsville, 3209, Fax. No. +27 (0)86 516 8321 or e-mail: recruitment-agsc@ukzn.ac.za quoting the relevant reference number.

Please find our Email Disclaimer here: <http://www.ukzn.ac.za/disclaimer/> Brothers@ukzn.ac.za

UMaryland ChairBiology

Chair: Department of Biology University of Maryland, College Park

We seek a distinguished senior scientist with a vigorous research program, commitment to excellence in graduate and undergraduate education, and broad vision, experience, and energy to chair the Department of Biology in the College of Chemical and Life Sciences at the University of Maryland. Biology is a broadly based and cohesive Department with research strengths in cellular biophysics, developmental biology, ecology, evolutionary biology, genomics, and neurobiology. Faculty research laboratories are located in the new Bioscience Research Building and adjoining Biology- Psychology Building. The Departments academic programs include undergraduate and graduate programs that span the College and campus. Recruitment of both senior and junior faculty is expected as part of an ambitious drive to enhance the life sciences. These efforts are focused in the College on ecological sustainability, genomics, host-pathogen interactions, nanoscience/biomaterials, and sensory neuroscience, and at the campus level on broad initiatives in areas such as climate, energy, health, and nanoscience. For more information please visit www.chemlife.umd.edu. Apply electronically to <http://chemlife.umd.edu/biologychairsearch.html> with an application letter and the following: (1) curriculum vitae, (2) statement of research interests, (3) statement of academic vision and administrative experience, and (4) names and addresses of at least four references. Review of credentials will continue until the position is filled. Review of applications will begin on November 3, 2008.

The University of Maryland, College Park is the flagship campus of the University System of Maryland and one of the most rapidly advancing public research universities in the country. Close proximity to Washington, Baltimore, and the Maryland Biotechnology Corridor facilitates interactions with an extraordinary range of major research institutions, including the NIH, FDA, Smithsonian Institution and the USDA.

The University of Maryland is an equal opportunity affirmative action employer. Minorities and women are encouraged to apply.

Thanks!

Eric S. Haag, Ph.D. Assistant Professor Department of Biology 0256 Biology/Psychology Building University of Maryland College Park, MD 20742 phone: (301) 405-8534 fax: (301) 314-9358 ehaag@umd.edu <http://www.life.umd.edu/biology/faculty/haag/index.html> "I'd rather be here now."

Eric Haag <ehaag@umd.edu>

UMassAmherst ConservationGenetics

ASSISTANT PROFESSOR IN CONSERVATION GENETICS Department of Natural Resources Conservation University of Massachusetts Amherst

The Department of Natural Resources Conservation at the University of Massachusetts Amherst seeks applications for a 9-month, tenure-track appointment as Assistant Professor in Conservation Genetics. A doctoral degree in Conservation Genetics or closely related field is required with a strong background in genetic and evolutionary applications to problems of conservation biology, landscape ecology and resource management involving terrestrial and aquatic organisms. Duties include teaching an undergraduate conservation genetics course, a graduate-level course in applied conservation genetics, and contribution to a graduate-level sequence of courses in the design and analysis of ecological data; and developing independent and collaborative research programs.

Earliest start date is September 1, 2009. Review of applications will begin January 5, 2009. The position will remain open until filled. Applicants should submit curriculum vitae, statements of research and teaching goals, and the names, addresses and contact information of three references to:

Kevin McGarigal, Chair Conservation Genetics Search Committee Department of Natural Resources Conservation Holdsworth Natural Resources Center University of Massachusetts, Amherst MA 01003 (413) 577-0655 mccgarigalk@nrc.umass.edu

The full position description is available on the web at:

<http://nrc.umass.edu/index.php/positions-in-nrc/>

The College and the Department are committed to increasing the diversity of the faculty, student body and the curriculum. The University of Massachusetts is an Affirmative Action/Equal Opportunity Employer. Women and members of minority groups are

encouraged to apply

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 Ana L. Caicedo, Ph.D. Assistant Professor 221 Morrill Science Center phone: (413) 545-0975 Biology Department fax: (413) 545-3243 University of Massachusetts email: caicedo@bio.umass.edu Amherst, MA 01003 <http://www.bio.umass.edu/biology/caicedo>
 caicedo@bio.umass.edu caicedo@bio.umass.edu

UMichigan ResTech FungalEvolution

Research technician in fungal ecology and evolution Department of Ecology and Evolutionary Biology University of Michigan Ann Arbor, MI 48109-1048 USA

We seek a highly motivated and organized scientist to help manage a new lab in the Department of Ecology and Evolutionary Biology at the University of Michigan, Ann Arbor. The research group is a joint laboratory shared between Dr. Tim James and Dr. Jeri Parrent that broadly pursues ecological and evolutionary investigations of fungi. The full-time research technician will be expected to participate in ongoing research projects and oversee daily operation of the lab. The technician will be actively engaged in a wide range of research projects, such as population genetics of the frog pathogen *Batrachochytrium*, evolution of carbon/nutrient exchange in plant-fungal symbioses, and molecular ecology of mycorrhizal communities. Projects in the lab utilize the following techniques: fungal cultivation, greenhouse experiments using plants and plant-associated fungi, DNA sequencing and genotyping, quantitative PCR, genetic transformation, and microscopy.

The ideal applicant would have a bachelor's or masters degree in biology or related field, familiarity with culturing microorganisms or cell lines, and research experience using molecular and computational methods. Experience with PCR, cloning, and other nucleic acid manipulation is desirable. Responsibilities will include active participation in research projects, ordering and maintaining equipment and supplies, and maintenance of databases and culture collections.

Pay will scale with experience. Women and minorities are encouraged to apply. The University of Michigan is an equal opportunity/affirmative action employer.

Descriptions of ongoing research projects may be found

at these websites: <http://www.duke.edu/~tyj2/> http://www.uoguelph.ca/~jnklab/Jeri_Parrent.htm Information on the department and life in Ann Arbor can be found here: <http://www.eeb.lsa.umich.edu/-eeb/index.html> <http://arborweb.com/> For questions and informal inquiries please contact: Tim James, Department of Biology, McMaster University, jamesti@mcmaster.ca

Applications should be submitted by email to jamesti@mcmaster.ca. Please prepare a cover letter, complete curriculum vitae and contact information for three references.

The anticipated starting date is January 2009 but is flexible. Review of applications will begin immediately and continue until the position is filled.

jamesti@univmail.cis.mcmaster.ca

jamesti@univmail.cis.mcmaster.ca

UMinnesotaRochester EvolutionaryBiology

/* Faculty Position at the University of Minnesota Rochester*/

The University of Minnesota Rochester (UMR) invites applications for open-rank, tenure-track faculty positions for its degree program, the Bachelor of Science in the Health Sciences (BSHS) in the area of Life/health sciences (preferred area is evolutionary biology and comparative anatomy). This program will provide education and experiential learning for students interested in Health Professions career programs, graduate education, or professional degrees.

Faculty will join the newly established Center for Learning Innovation (CLI) as Design Faculty. CLI leads the development of an integrated curriculum for a baccalaureate degree in the health sciences. It promotes a learner-centered, competency-based learning environment in which ongoing assessment guides and monitors student learning and is the basis for data-driven research on learning. Design Faculty are responsible for the development of the curriculum, including learning objectives, development of learning objects, assessment, and mentoring of postdoctoral fellows. They are expected to significantly contribute to advancing the field of inquiry of student learning, especially as it pertains to understanding principles and concepts in the life, physical, and quantitative sciences and the social

sciences/humanities.

The successful candidate has a Ph.D. in the area mentioned above with a deep interest in science-based learning and has experience in the design of new curricula, assessment, and technology-enhanced education at the undergraduate level. The successful candidate works well in interdisciplinary teams, is comfortable working in an uncertain and unstructured environment, and exhibits creativity, innovation and

/*Application Information */ Review of applications will begin December 1, 2008 and will continue until all positions are filled. Applications must be submitted online at <https://employment.umn.edu> <<https://employment.umn.edu/>>.

For application instructions and links, click on "Search Postings" and use the following job requisition numbers: #158918

In addition to the Faculty/Academic Application for Employment form, applicants must attach to the online application a description of teaching experience and philosophy, summary of research interests, curriculum vitae, and names and contact information (including e-mail addresses) for three references.

For more information, contact Andrea Wilson, University of Minnesota Rochester, 300 University Square, 111 S. Broadway, Rochester, MN 55904; fax 507-281-7794, phone 507-280-4650, e-mail wils1236@umn.edu <<mailto:wils1236@umn.edu>>. For more information about the University of Minnesota Rochester, please visit our website: <http://www.r.umn.edu/> /The University of Minnesota is committed to the policy that all persons shall have equal access to its programs, facilities, and employment without regard to race, color, creed, religion, national origin, sex, age, marital status, disability, public assistance status, veteran status or sexual orientation./

– Claudia Neuhauser Vice Chancellor for Academic Affairs Director of the Center for Learning Innovation Director of Graduate Studies, Biomedical Informatics and Computational Biology

HHMI and Distinguished McKnight University Professor Morse-Alumni Distinguished Teaching Professor

University of Minnesota Rochester 300 University Square 111 South Broadway VOICE 507-281-7791 Rochester, MN 55904 FAX 507-280-2820

<http://www.cbs.umn.edu/eeb/faculty/-NeuhauserClaudia/> Claudia Neuhauser <neuha001@umn.edu>

UNebraska ViralEvolution

VIRAL EVOLUTION Tenure track Assistant Professor at the University of Nebraska Center for Virology and the School of Biological Sciences. Candidates will be expected to develop a nationally recognized research program emphasizing a broad biological or system approach, preferably working on the evolution of prokaryotic and eukaryotic viruses. Specific area of research is open; appropriate examples of research interests include viral evolutionary genetics, comparative genomics and proteomics, pathogenesis or epidemiology of diseases. Candidates must show excellent capacity to develop and coordinate interdisciplinary collaborative research with other Center and departmental researchers. Candidates will be expected to teach courses at the undergraduate and graduate levels. A Ph.D. or equivalent and post-doctoral experience in related area is required. Start date is Fall 2009. The position will remain open until a suitable candidate is selected. The University of Nebraska has an active National Science Foundation ADVANCE gender equity program, and is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers. To apply log on to <http://-employment.unl.edu> requisition #080880 and complete the Faculty/Administrative information Form and attach CV, cover letter, statement of research interests and teaching interests and philosophy; representative publications; names, addresses and phone numbers of three references. Arrange for three letters of reference to be sent by January 12, 2009 to Dr. Alan Kamil, School of Biological Sciences, University of Nebraska-Lincoln, 348 Manter Hall, Lincoln, NE 68588-0118. Review of applications will begin January 12, 2009 and continue until the position is filled or the search is closed.

JayF.Storz SchoolofBiologicalSciences University-ofNebraska Lincoln,NE68588 Phone:402/472-1114 E-mail:jstorz2@unl.edu

<http://www.biosci.unl.edu/labs/storz/index.html> Jay F Storz <jstorz2@unlnotes.unl.edu>

UNewOrleans 2 ConservationBiol

The Department of Biological Sciences at the University of New Orleans invites applications for two Endowed Chairs:

The Freeport-MacMoRan Endowed Chair in Conservation Biology, with a focus on the biology and conservation of terrestrial vertebrates.

The Greater New Orleans Foundation Endowed Chair in Aquatic or Terrestrial Resource Conservation. Preference will be given to those candidates whose focus is on the biology and conservation of aquatic populations, communities, or landscapes.

The two Chairs will assume leadership roles in the doctoral program in Conservation Biology within the Department of Biological Sciences. Chairs will teach in their areas of expertise, advise graduate and undergraduate students, and conduct dynamic and innovative research generating significant advances in basic biology and conservation of their study systems.

The Department of Biological Sciences is currently planning to expand the Conservation Biology program. Over the next five years we anticipate additional hires at the level of Assistant Professor and new investment in departmental facilities.

Candidates should have a distinguished record of publication and funding consistent with appointment at the rank of Professor, but exceptional candidates at the rank of Associate Professor will be considered. For more information, see <http://biology.uno.edu/> or contact Dr. Jerome Howard at jjhoward@uno.edu.

Applicants should send a letter of application, curriculum vita, statement of research interests, and contact information for five references by January 5, 2009 to:

Endowed Chair Search Committee Department of Biological Sciences University of New Orleans New Orleans, LA 70148

The University of New Orleans in an Equal Opportunity/Affirmative Action employer.

Nicola Mary Anthony <nanthony@uno.edu>

UNewOrleans ConservationBiology

The DEPARTMENT OF BIOLOGICAL SCIENCES, UNIVERSITY OF NEW ORLEANS invites applications for a tenure-track position at the rank of ASSISTANT PROFESSOR.

We seek an ORGANISMAL BIOLOGIST using experimental, theoretical, or field approaches to investigate problems in terrestrial or aquatic systems. Applicants with an evolutionary or comparative perspective on processes at the organismal level are encouraged to apply. Candidates should have research interests with a clear relationship to conservation biology.

Applicants must have a Ph.D. and postdoctoral experience. Successful candidates will develop extramurally funded research programs, direct graduate students, and teach at the undergraduate and graduate levels. For information about the department, see <http://biology.uno.edu/>. Applications will be accepted electronically as a single PDF file that combines: a curriculum vitae, statement of research interests and teaching philosophy, and names and contact information of three references. Send application materials to Dr. Jerome Howard, jjhoward@uno.edu, Ecology & Organismal Biology Search Committee, Department of Biological Sciences, University of New Orleans, LA 70148, Telephone 504-280-6741, FAX 504-280-6121. Review of applications will begin December 1, 2008.

Nicola Mary Anthony <nanthony@uno.edu>

UNewSouthWales Genetics Lectureship

Associate Lecturer in Genetics Faculty of Science SCHOOL OF BIOTECHNOLOGY AND BIOMOLECULAR SCIENCES University of New South Wales, Sydney, Australia

REF. 6229NET

Applications are invited for the appointment of a position of Associate Lecturer in the School of Biotechnology and Biomolecular Sciences.

We are seeking an enthusiastic teacher with skills in genetics to contribute to the undergraduate teaching in the School. The successful candidate will be expected to contribute significantly to the School's teaching programs.

Subject to the approval of the Head of School, the appointee may undertake a limited amount of research work.

This is a 5 year fixed-term appointment.

The salary range for Associate Lecturer is A\$65,503 - A\$70,062 per annum (plus 17% employer superannuation plus leave loading).

Applicants should systematically address the selection criteria in their application. Women and people from equity groups are encouraged to apply.

For the Information Package <http://www.hr.unsw.edu.au/services/recruitment/jobs/31100807.html>

Enquiries may be directed to Head of School, Professor Bill Ballard, email: w.ballard@unsw.edu.au

Applications close : 18 November 2008

Professor Bill Ballard Head of School School of Biotechnology and Biomolecular Science Faculty of Science University of New South Wales NSW 2052 Australia Tel: +61 2 9385 2029 FAX: +61 2 9385 1483 PH: +61-2-9385-2587 FAX: +61-2-9385-1558

a.wilton@unsw.edu.au a.wilton@unsw.edu.au

UNSW Sydney EvolutionLecturer

Lecturer in Evolution Faculty of Science SCHOOL OF BIOLOGICAL, EARTH & ENVIRONMENTAL SCIENCES and EVOLUTION & ECOLOGY RESEARCH CENTRE REF. 6226NET

The School of Biological Earth and Environmental Sciences (BEES, www.bees.unsw.edu.au), in conjunction with the Evolution & Ecology Research Centre (E&ERC, www.eerc.unsw.edu.au) is seeking a Lecturer in Evolution. BEES is a large and multi-disciplinary school incorporating a range of disciplines within the broad fields of Biology, Marine Science, Geography and Geology.

The appointment will enhance UNSW's research profile in Evolutionary Biology and Evolutionary Ecology and the appointee will be a member of the UNSW Evolu-

tion & Ecology Research Centre. The successful candidate will be required to establish an internationally recognized, externally funded research program in Evolutionary Biology and to teach undergraduate courses in Evolution, Ecology, Genetics and/or Biology. Applicants should have a strong research record and should outline in their application their capacity to contribute to the existing research areas in the Centre and the School. Candidate's research should be focussed on adaptive processes and the testing of theory, and should not be entirely descriptive. Candidates whose research involves the experimental study of adaptation and its links to genetic, genomic, behavioural and/or physiological processes may be preferred.

UNSW is one of the Group of Eight research intensive universities, and Evolution and Ecology are among our recognized research strengths.

This is a continuing appointment. North American applicants should note this is equivalent to a tenure-track assistant professor position.

Salary range for Lecturer A\$73,573 - A\$86,734 per year (plus 17% employer superannuation and leave loading)

Candidates holding existing ARC/NHMRC fellowships and/or research grants are encouraged to apply as well as those who are able to form synergistic interactions with existing researchers and groups within the E&ERC. Women and people from equity groups are also encouraged to apply.

Applicants should systematically address the selection criteria in their application.

For the Information Package click < <http://www.hr.unsw.edu.au/services/recruitment/jobs/-/services/recruitment/jobs/info/pd31100808.pdf> >HERE

Enquiries may be directed to Associate Professor Rob Brooks on +61 2 9385 2065 or email rob.brooks@unsw.edu.au or Associate Professor David Cohen on telephone + 61 2 9385 8084 or email d.cohen@unsw.edu.au . Further information on the School, please visit: < <http://www.bees.unsw.edu.au/> ><http://www.bees.unsw.edu.au/>

Applications close : 01 December 2008

Evolution & Ecology Research Centre www.eerc.unsw.edu.au School of Biological, Earth and Environmental Sciences The University of New South Wales Kensington, Sydney 2052 NSW, Australia PH: +61-2-9385-2587 FAX: +61-2-9385-1558 <http://www.bees.unsw.edu.au/school/staff/-brooks/brooksresearch.html> rob.brooks@unsw.edu.au rob.brooks@unsw.edu.au

UParis6 IntegrativeEvolution

An assistant professor position at the Universite Pierre and Marie Curie (UPMC) in Paris, France, is available to work in integrative ecology, i.e. at the interplay between physiology, evolution and ecology. Candidates must hold a PhD diploma in animal ecology, population ecology, behavioral ecology or evolutionary ecology and have solid skills in ecology and animal physiology, and some basic knowledge in French. Those of you who are interested can contact the group leader Manuel Massot by email for further information (mmasot@snv.jussieu.fr). A full description of the teaching and research experience required (unfortunately in french) is available at <http://jf.legalliard.free.fr/>. The job will start in september 2009 with the gross salary of an assistant professor in France (ca. 2000 a month) but candidates should apply for this position as soon as possible. Indeed, candidates who hold a PhD and would like to apply must first obtain a "qualification" before late december 2008 at the GALAXIE portal (<https://-antares.orion.education.fr/antares/can/index.jsp>). For those who do not know about this french bizarerie, this is the normal procedure to obtain the right to apply for any assistant professor position all over France during four years. If you get the qualification, you will then be able to apply in spring 2009 to this position in our laboratory. Of course, I can provide assistance for those of you who would like to apply from abroad and are highly motivated by the prospect of a position in our research group.

Do not hesitate to contact me!

Best regards, Jean-Francois.

Dr. Jean-Francois Le Galliard <http://jf.legalliard.free.fr/> CNRS - UMR 7625 Fonctionnement et evolution des systemes ecologiques Universite Pierre et Marie Curie Case 237, Batiment A, 7 Quai St Bernard 75005 Paris FRANCE

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Jean-Francois Le Galliard <galliard@biologie.ens.fr>

UQueensland PlantSystematics

LECTURER IN PLANT SYSTEMATICS - UNIVERSITY OF QUEENSLAND

The School of Integrative Biology is one of the largest Schools of its type in Australia, with 47 full-time academic staff. The School provides outstanding opportunities for research in plant and animal biology, with research programs spanning ecology, molecular plant sciences, marine biology, entomology, and genetics & evolution.

The role: The School is seeking to develop its program in plant molecular ecology, systematics and conservation. The position involves teaching undergraduate and postgraduate courses in one or more areas covering plant ecology, molecular ecology, conservation biology, evolution and systematics, in addition to the supervision of honours and postgraduate research students. You will be expected to develop a vibrant, externally-funded research program. A competitive start-up package will be negotiated with the successful applicant.

The person Applicants should possess qualifications in the relevant disciplines and should have expert knowledge in the area of plant molecular ecology, systematics and conservation and its applications. Evidence of publication in high-ranking refereed journals and the ability to work collaboratively with colleagues are essential. Experience in teaching, and evidence of success in obtaining competitive research funding will be an advantage.

Remuneration: This is a full-time, fixed term appointment for five years at Academic level B. The remuneration package will be in the range \$70,968 - \$84,275 p.a., plus employer superannuation contributions of 17% (total package will be in the range \$83,033 - \$98,602 p.a.).

Contact: Obtain the position description and selection criteria online . To discuss the role contact Prof. Hugh Possingham, telephone + 61 07 3365 9766 or email h.possingham@uq.edu.au or Dr. Gordon Guymer, telephone +61 7 3896 9325 or email gordon.guymer@epa.qld.gov.au

Send applications to the PA to the Head of School, School of Integrative Biology, The University of Queensland, St Lucia, Qld 4072, or email a.mckee@uq.edu.au

Applications close 5 January 2009.

Reference No. 3019409.

For further details and application instructions: <http://seek.com.au/users/apply/index.aspx?Sequence=-3D18&PageNumber=3D1&jobid=14336326>
c.riginos@uq.edu.au c.riginos@uq.edu.au

US EPA Cincinnati Population Genetics LabTech

The Molecular Ecology Research Branch, US Environmental Protection Agency, Cincinnati, OH is looking for a recent graduate to provide technical laboratory support under a contract mechanism for research projects focusing on development of molecular techniques to inventory and quantify organisms collected from stream, lake, and ballast samples and to assess population genetic patterns that contribute to an understanding of population processes of fish, aquatic invertebrates, and terrestrial insects. Work involved with the tasks may include, but is not limited to: (1) tissue and sample collection and organization; (2) DNA extractions; (3) PCR amplification and purification; (4) molecular cloning; (5) microsatellite genotyping; (6) DNA sequencing; (7) analysis of genotype and DNA sequence data; and (8) other general laboratory and field duties necessary to carry out research (e.g., sample collection and transport, routine equipment maintenance).

Contact Mark Bagley (513-569-7455, bagley.mark@epa.gov) for further information on the research and see <http://www.epa.gov/oamrtplc/q0900011/index.htm> for details on the application process.

US Fish Wildlife 2 Tech Fish Population Genetics

Position Title: Fish Biologist / Fish Geneticist (Term position)

Agency / Location: USFWS, Abernathy Fish Technology Center, Longview, WA

Responsibilities: Ensure data standardization, con-

sistency, and quality control to identify information and prevent duplication of efforts. Reconstruct pedigrees in hatchery and natural populations to assist in estimating relative reproductive success. Collect genotypic, gene frequency, and DNA sequence data for hatchery and natural populations. Maintain database of genetically marked fish released into the wild. Collect tissue and/or blood samples from fish in natural environments, live traps, and hatchery structures. Analyze genetic data and incorporate into written reports and scientific publications. Present data at workshops, symposia, and other scientific meetings.

Qualifications: MS (or BS with work experience) in genetics, fisheries, or a related discipline. Knowledge of population genetics principles and demonstrated writing skill required.

Salary: \$45,040 - \$54,494

Closing Date: Wednesday, November 19, 2008

Contact: Additional information regarding this position is available at USA JOBS (<http://www.usajobs.gov/>). Applications must be submitted online via USA JOBS by the closing date. The Federal Government is an Equal Opportunity Employer. For questions about the position please contact Dr. Denise Hawkins, Program Head, at 360-425-6072, x339.

Position Title: Biological Science Technician / Geneticist (Term position)

Agency / Location: USFWS, Abernathy Fish Technology Center, Longview, WA

Responsibilities: - Preparing laboratory solutions, extracting DNA from fish tissue samples, and conducting polymerase chain reaction (PCR) of extracted DNA; - Conducting data collection, entry, and assisting with basic statistical and genetic analysis as part of larger complex genetic studies; - Operating and assisting with the maintenance of specialized genetic laboratory equipment such as thermal cyclers, automated DNA sequencers, and centrifuges; - Maintaining work and storage spaces, ensuring laboratory supplies are stocked, and assisting in maintaining samples repositories; - Preparing tabular and graphic data and descriptions of laboratory methods for use in reports; - Training students, volunteers, and visiting scientists in methods and techniques.

Qualifications: BS (or equivalent work experience) in genetics, fisheries, or a related discipline. Experience with microsatellite analysis and use of DNA sequencers advantageous.

Salary: \$29,726 - \$38,639

Closing Date: Wednesday, November 12, 2008

Contact: Additional information regarding this position is available at USA JOBS (<http://www.usajobs.gov/>). Applications must be submitted online via USA JOBS by the closing date. The Federal Government is an Equal Opportunity Employer. For questions about the position please contact Dr. Denise Hawkins, Program Head, at 360-425-6072, x339.

Christian.Smith@fws.gov

Vienna LabTech MolecularGenetics

** High Priority **

Laboratory Technician: Molecular Genetics/Bioinformatics Konrad Lorenz Institute of Ethology, Vienna, Austria

We seek a highly organized laboratory technician with excellent bench skills using molecular genetic techniques (PCR, Real-Time PCR, DNA capillary sequencing, microsatellite typing, fragment analysis, SSCP, Southern and Western blotting, etc.) and preferably with data analysis/bioinformatics experience. Duties require helping with general laboratory maintenance, such as making stock solutions, ordering supplies, autoclaving, overseeing waste disposal, etc. Opportunities for collaborative research are possible. The institute is international and communication is in English, but German would be very useful. We are located in the Vienna Woods, and 30 min from the city center. We have a well-equipped genetics laboratory (www.oeaw.ac.at/klivv), and we are next door to the Research Institute of Wildlife Ecology, University of Veterinary Medicine Vienna (www.fwiw.at). Vienna offers exceptional public transportation, schools, cultural activities, and outdoor recreation (www.virtourist.com/europe/vienna/index.html). The position is initially for one year and can be made permanent depending upon performance. Salary depends upon experience. Review of applications starts immediately and ends January 15, 2009. Application deadline is Dec. 31, 2008. To apply, please send via email: (1) a brief cover letter; (2) CV, (3) any publications, (4) names of scientists who can be con-

tacted for letters of reference to the address below.

Dustin Penn, Director Konrad Lorenz Institute of Ethology Austrian Academy of Sciences Savoyenstrasse 1a A-1160 Vienna, Austria Tel: +43 51581 2700 Fax: +43 51581 2800 office@klivv.oeaw.ac.at

Alexandra Katzer <A.Katzer@klivv.oeaw.ac.at>

VirginiaCommonwealthU PlantMolecularSystematics

Virginia Commonwealth University

PLANT MOLECULAR SYSTEMATIST

The Department of Biology invites applications for a faculty position in the area of molecular systematics. Primary teaching responsibilities will include an undergraduate and a graduate plant related course. This is a nine-month, tenure-track position at the rank of Assistant Professor. Anticipated start date is August 16, 2009, pending funding. The successful applicant will be expected to develop a productive, externally funded research program and direct graduate students through the Ph.D. level. Postdoctoral experience is expected and demonstrated evidence of excellence in scholarship and teaching is required. Competitive start-up funds and excellent core facilities are available.

Virginia Commonwealth University has an enrollment of 32,000 students, including over 1,500 undergraduate and approximately 100 graduate students in Biology. The Department of Biology (www.has.vcu.edu/bio) has 32 faculty members with diverse research interests. Additional research opportunities are available through the Center for Environmental Studies and at the Rice Center, VCU's nearby field station on the James River. Submit vitae, statements of research and teaching interests, and three letters of reference by December 15, 2008 to: Stephanie Millican, Department of Biology, Virginia Commonwealth University, Richmond, VA 23284-2012.

Virginia Commonwealth University is an equal opportunity/affirmative action employer. Women, minorities and persons with disabilities are encouraged to apply.

Rodney Dyer <rjdyer@vcu.edu>

Other

Ancient Naturalists from Asia	55	Multplex PCR	63
Arlequin mismatch question	55	Nuclear and mitochondrial phylogeny	64
Basic tasks	56	Outsourcing microsat development	64
BioTek Precision XS Micropipettor answers	56	Outsourcing microsat development answers	64
Book changes	57	Parallel evolution speciation studies	65
Crustacean Intron primers	57	Pooling samples for disease prevalence	65
Evanno Method Structure answers	58	Problems microsatellite development	65
Evanno Method Structure answers 2	59	Reducing microsatellite stutter paper answers	66
Evanno Method Structure answers 3	59	Scat DNA in DMSO	67
Evolutionary Applications Journal	60	Sharing 454	67
GCG SeqLab extensions	60	SmithsonianPanama FrogEvolution	67
Ghrelin evolution	60	Software BAPS upgrade available	68
Grant for early-stage researchers	60	Software Champuru online tool	68
Haplotype software	61	Software DAMBE update	68
Haplotype software answers	61	Software SeqPHASE online tool	68
Is old acrylamide usable	62	Software SeqVis1 4	69
Linkage map programs answers	62	Software TESS	69
LinkageMaps Recombination software	62	TajimasD analysis answers	69
Measuring selection coefficients	63	Undergraduate Core Curriculum	70
MrBayes non-matching headers bugfix	63		

“Jorge I. Mena-Ali” <jorge.mena-ali@fandm.edu>

Ancient Naturalists from Asia

Dear EvolDir Members,

I am preparing a course on the History of Natural History, from ancient times to the 21st century. Unfortunately, I haven't been able to find any leads on Ancient Accounts of Natural History from Asia, particularly names of significant or noteworthy individuals in ancient Eastern societies. This is in sharp contrast with the vast amount of information on Greek and Roman philosophers/naturalists.

If anyone can suggest specific references or provide names of prominent Ancient Naturalists from Asia, it will be greatly appreciated. Also welcome is information regarding any knowledge of remarkable, yet-relatively unknown naturalists that I should investigate.

Best regards,

Jorge

Jorge Mena-Ali, PhD <jmenaali@fandm.edu> Dept of Biology, Franklin & Marshall College Lancaster PA

Arlequin mismatch question

Hi all

I have a question about the calculation of the mismatch distribution using the Arlequin 3.11 software package.

In their article, Schneider and Excoffier (1999), strongly suggest to take into account rate heterogeneity and nucleotide mutation correction models when calculating a mismatch distribution. Especially in the case where the parameters Tau and Theta is going to be used and the validity of inferring a demographic expansion is tested.

However, in Arlequin it seems that the only distance option available is a Pairwise difference with no gamma correction.

Although, I have seen articles that say that they used correction models such as K2P and modified alpha values when calculating mismatch distributions in Ar-

lequin.

Is there a way that one can incorporate these corrections in your data using Arlequin?

Any suggestions will be much appreciated

Thank you

Carina Schlebusch cschlebu@yahoo.com

Carina Schlebusch <cschlebu@yahoo.com>

Basic tasks

Dear all,

I am doing some basic population genetics analysis and I need to perform some basic tasks automatically to speed data processing. I need softwares to do automatically the following tasks:

a) to output unique haplotypes, sorting haplotype frequencies per population b) a spreadsheet software that allows the exclusion of a population from a pairwise matrix, reorganizing cells of the remaining comparisons. And also allows the inversion of a pairwise matrix to put it as a mirror of another pairwise matrix (so I will have two different indices analyzed for the same populations in a square matrix) c) A software that output the differentiation index S_{nn} (Hudson, 2000) from several pairwise comparison in a single matrix (I can do pair by pair in DNAsp)

Any help would be greatly appreciated.

Thanks

Daniel

Daniel Toffoli Ribeiro Laboratório de Genética de Populações e Evolução Universidade Federal de São Carlos <http://www.ufscar.br/~evolucao/> tel: ++55 (16)33518787

toffolidan@yahoo.com.br

BioTek Precision XS Micropipettor answers

Recently I inquired about experience anyone has had with the Biotek Precision XS automatic pipettor. The

original inquiry and two informative responses are posted below. I have since fiddled with our instrument considerably, and have a few follow up points to offer as well. Generally, it seems as though this instrument can handle volumes down to 2ul, but is more accurate with volumes ≥ 5 ul (don't count on using it to set up real-time PCR assays). Spotting small volumes on the bottom of wells is difficult, but it can be done. The flexibility of the platform is not quite as advertised, but is adequate. For instance, we had to purchase several very expensive adapters to fit our plates and microfuge tubes. We also had to purchase separate adapters in order to install our plates on the rear row of docking stations. With all this said, we are pleased (overall) with the performance of the instrument so far. Thanks to all who responded.

Original Inquiry:

> Hi all- > > I am wondering if anyone that uses this forum has a BioTek Precision > XS Micropipettor in their lab. If so, for what applications do you > use it, what kind of volumes are typically exchanged, and how > satisfied are you as far as the instrument meeting your > needs/expectations? In particular, our lab has just purchased one and > we are interested in using it to set up PCRs, combine samples for > multiplexing, clean samples for sequencing, etc. I would like to get > in contact with somebody who uses it for these and other functions.

Replies:

Hi Joel,

We have a different BioTek model, the Precision 2000. We've had it for about 6 years and it's still going strong. I have only had to replace the o-rings. The only thing we use it for is pooling pcrs for multiplexing on gels or capillary injections (96 well microplate format). It is very useful and quick for that application—and we could probably use it for other post-pcr apps as well—but its use is somewhat limited by the minimum pipetting volume of 3 ul. We use it to transfer volumes of 3-10 ul, and although it does okay with 3, it seems to be more accurate/uniform in the 5-10 ul range. Hope this helps, and let me know if you have any other questions.

Libby Gilbert-Horvath NOAA Fisheries Service 110 Shaffer Road Santa Cruz CA 95060

Joel, We bought a Precision last year, and I was not impressed with the initial communication with the company in getting us set up with the necessary plate and tip holders. It took us several months to get it set up properly, and they were quite disorganized. In the end they continued to help until we got things sorted out, and we have been using the instrument only for making

replicate plates for genotyping or DNA quantification. Unfortunately, we didn't buy the XS model, which I now think we could use, so we only have 8-channel capability. I have found that the minimum reliable volume for transferring to empty plates is about 4 μ l, but at that volume it seems to work very well. What I like about the instrument is that it is quite easy to program once you understand the basics, and once programs are set up, it is very reliable. We haven't had any problems with our standard programs, and we use the instrument fairly often. Assuming you have all of the parts you need for your applications, I think the instrument is a good value, and very flexible. One other thing I just remembered. We tried to use a variety of other tips, and ended up buying the tips from BioTech because others didn't work well with it. If you already have a brand you want to use, make sure to test them out on the robot first.

I hope this helps. If you get good responses about using the instrument for the applications you mentioned in your Evoldir posting, I would appreciate it if you would forward them to me, or post them on Evoldir.

Sincerely, Phil Morin

Phillip A. Morin, Ph.D. Southwest Fisheries Science Center

Joel Anderson Natural Resource Specialist Perry R. Bass Marine Fisheries Research Station Coastal Fisheries Division, Texas Parks and Wildlife ph: (361) 972-5483 fax: (361) 972-6352

Joel Anderson <Joel.Anderson@tpwd.state.tx.us>

Book changes

"Treasure Your Exceptions". The Science and Life of William Bateson (Springer, September 2008) by Alan G. Cock & Donald R. Forsdyke

A list of errors (mainly typographical) may be accessed at: <http://post.queensu.ca/~forsdyke/-book04corrections.htm> Details of the book are at: <http://post.queensu.ca/~forsdyke/book04> Sincerely, Donald Forsdyke, Department of Biochemistry, Queen's University, Canada

forsdyke@queensu.ca forsdyke@queensu.ca

Crustacean Intron primers

Dear colleagues,

I posted a request on evoldir a few months ago trying to find out if anyone working on decapod crustaceans is aware of primers for intron-containing nuclear genes other than those for Elongation Factor 1-alpha (which seem to work only for insects). Although the response was negative, Paul Sunnucks pointed out some universal coelomate primers for low-copy nuclear genes (Jarman et al. 2002).

Those didn't work for our species either, but we got motivated to design our own primers for one of the genes in that paper, the Adenine Nucleotide Transporter (ANT). Although our primers were designed using penaeids and are not universal (they don't seem to work for anomurans and freshwater crayfish), they amplify PCR product in a number of other decapod groups, including the Achelata, Brachyura, Caridea, Dendrobranchiata, Eryonoidea and Thalassinoidea. PCR products tend to have a good concentration, single bands were obtained in all cases, and both primers are also good for sequencing. Most sequences contained an intron, which was more than 834 bp long in one of the crabs, and no shorter than 150 bp in most other species.

The region amplified also contains a large chunk of exon, so this may be useful for multi-locus phylogenetic studies, in addition to the usual mtDNA+18S/28S/H3 combination.

The primer note is (almost) in press: Teske PR, Beheregaray LB. Intron-spanning primers for the amplification of the nuclear ANT gene in decapod crustaceans, Molecular Ecology Resources. If you'd like a pdf, please contact me at Peter.Teske@bio.mq.edu.au

We've only tested these in decapods, but I'd be very interested to hear if anyone gets them to work in other crustacean orders. And of course I'm still very keen to find out if anyone is aware of other primers for crustacean introns.

Thanks, Peter

Dr Peter R. Teske Postdoctoral Researcher Molecular Ecology Lab Dept. of Biological Sciences, E8C Macquarie University Sydney, NSW 2109 Australia Phone: +61 2 9850 8190 Fax: +61 2 9850 8245 E-mail: Peter.Teske@bio.mq.edu.au Web-

site: <http://www.bio.mq.edu.au/molecularecology/people.htm> Publications: http://www.ru.ac.za/academic/departments/botany_research/peter/ Peter.Teske@bio.mq.edu.au Peter.Teske@bio.mq.edu.au

Evanno Method Structure answers

I have been away from lab for a week, but below I finally summarize the replies that I received to my evoldir query, which was:

I have a question regarding the delta k method of inferring the most likely k value in STRUCTURE. This method is discussed in the paper Evanno G, S Regnaut, J Goudet 2005. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Mol Ecol* 14: 2611-2620.

Obviously, there is no way to validate $k = 1$. But since $k = 2$ is based on prior values (in part) generated for $k = 1$, is it also invalid? The reason I ask is that I often get the highest delta k value for $k = 2$, which for my pops makes little sense. Intuitively, $k = 2$ would seem to not be able to be validated by Evanno et al.'s method, but I need some reinforcement for this assessment! Any input will be appreciated.

First off, a number of evoldir readers affirmed my concern - they, too, have received the highest delta k values for $k = 2$, which they either found not very informative or peculiar. Below, reader responses are bracketed in quotation marks. My further comments are without quotes.

“There’s no reason I can think of why evaluating at $K=2$ would be invalid. You may be finding that $K=2$ is most probable because you have hierarchical structure in your data set – the Evanno method finds the uppermost level of structure in a given data set. You may want to subset your data based on the results of the individual assignments for $K=2$, and run STRUCTURE on those subsets, and evaluate them with the Evanno method. See Coulon et al 2008 (*Mol Ecol* 17, 1685-1701) for more details.”

This did occur to me, i.e., that STRUCTURE was capturing the highest level of hierarchy, thus it would be appropriate to then test each cluster independently for substructure. However, I noted that the vast majority of my original 45 populations were being assigned to cluster 1 with high probabilities, and only one pop was almost completely admixed. What disturbed me, how-

ever, was that one subpopulation from a cluster of three very closely related populations from a previous published paper, was being assigned to the second cluster in this mega-analysis.

“A more statistically motivated alternative to the Delta K method of evanno is the DIC. We have implemented it in TESS (similar to structure but using spatial coordinates in addition to the genetic data). You might have a look at it

TESS 2.0: <http://www-timc.imag.fr/Eric.Durand/soft.html>.”

My doctoral student is in fact using TESS. Meanwhile, realizing that a minority of my 45 pops were at HWE, and a many were in fact inbred, I began using InStruct, which drops STRUCTURE’s HWE assumption and also estimates inbreeding in each inferred population. InStruct also implements the DIC (Deviance Information Criteria) to assess the optimal k value. In fact finds $k = 7$ to be most likely. Interestingly, after the large peak of delta k at 2, 6 and 7 have next highest scores and are statistically equal.

“In your case it might be better to follow the common sense approach advocated in the STRUCTURE manual, which as far as I remember is to pick the K where the likelihood, $L(K)$, stops making large improvements, and to combine this with prior biological knowledge. The delta K method is designed to find this K objectively by calculating something close to the maximum retardation, ΔK [or $\text{abs}(L'(K))$], of the $L(K)$ vs K curve. In cases where the answer isn’t obvious from the $L(K)$ plot (it’s always worth looking at the plots), then I’d guess that the delta K plot will also be hard to interpret.

“For example, if the “true“ K is 1, then the delta K plot should be approximately flat because there should be no K around which $L(K)$ rises substantially from $K-1$ to K and then rises much less from K to $K+1$ (this is the signal that max delta K is trying to find). Of course the delta K plot won’t be exactly flat, but if there is no clear spike (e.g. the spike at $K=5$ in Fig. 2D of Evanno et al.) then max delta K will reflect noise. Perhaps this is what you have? It would be nice to have an objective way to tell signal from noise, but for now it’s best to include a large dose of common sense (but see the PLoS Genetics paper below).

”Other cases where the answer might not be obvious are where the model of discrete admixed populations doesn’t represent very well the true population, or where the number of loci or samples is too small. Imagine a situation with no prior information on population membership where there is clear structure reflected in

the L(K) plot, but it isn't obvious which of a range of K is best. In this case the delta K method at least has the advantage of objectivity, although reporting a plausible range of K might make more sense than giving a point estimate.

“One thing I don't understand about the delta K method is the motivation

— / —

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>

Evanno Method Structure answers 2

I neglected to include Jerome Goudot's response to my query on the Evanno delta k method last week, and include as well, a more recent reponse.

“I see no reason why our method would not work for K=2. It does in computer simulations (this is the case for our "hybrid zone" scenario, Fig 1C and Fig 4, G, H of our paper). It is based on the rate of change of the slope in Ln(K), and this can be estimated for K=2. What do you mean when you say K=2 makes little sense for your data? It might be that you have only one cluster, but the nearest best solution is K=2? What does Ln(K) says? I should also emphasize that our method is ad hoc, and needs to be complemented by looking at how well individuals are assigned to the different clusters. If all or most individuals at K=2 share ancestry in the two clusters, then K=2 is likely wrong.”

“have you tried running AMOVAs on your dataset using the K - values Structure suggests? In my case I indeed had the highest Fst values when using K = 2.”

Alan

PLEASE NOTE THE NEW PHONE NUMBER!

Alan W. Meerow, Ph.D., Research Geneticist and Systematist USDA-ARS-SHRS, National Germplasm Repository 13601 Old Cutler Road, Miami, FL 33158 USA voice: 786-573-7075; FAX: 786-573-7110 email: alan.meerow@ars.usda.gov

Evanno Method Structure answers 3

Yet another informative reply to my query on estimating k in STRUCTURE:

“I hesitated to add what I felt was an obvious answer to your K problem - but it seems those responsible for a solution are being shy. Within one run, STRUCTURE, and its relatives, do not compare different values of K - instead the user is left to do this posthoc. From an inference point of view, this would be why section 4 of the structure manual (Estimating K) says: 'In our paper describing this program, we pointed out that this issue should be treated with care for two reasons: (1) it is computationally difficult to obtain accurate estimates of $\Pr(X | K)$, and our method merely provides an ad hoc approximation....'

“A rigorous (non-adhoc) inference approach to estimating K would, within each run, compare not only a) different memberships of individuals in clusters and b) different genetic compositions of clusters but also c) different numbers of clusters.

“STRUCTURE does (a) and (b), but not (c). That is STRUCTURE does not mix over K. Its authors are correct that mixing over K is computationally difficult BUT there are at least two model-based Bayesian clustering algorithms which do mix over K, and thus are in principle better suited for estimating K.

“1) Partition, by Dawson and Belkir - an approach which was conceived independently of, and at the same time as, STRUCTURE, but (perhaps unfortunately) has not received the same attention.

“2) The more recent Geneland, by Gilles Goullot - which not only mixes over K, but also allows geographic information to aid the clustering of individuals.

“For those who have no geographic information in their dataset, or do see it as relevant, the spatial component of Geneland can be switched off, leaving us with a clustering algorithm that mixes over K.

“I think it is great that you have provoked discussion of K estimation, but I don't think that discussion should play out solely within the framework of posthoc bandages on methods which are poorly adapted to the estimation in question.”

Alan

Alan W. Meerow, Ph.D., Research Geneticist

and Systematist USDA-ARS-SHRS, National Germplasm Repository 13601 Old Cutler Road, Miami, FL 33158 USA voice: (786) 573-7075 email: alan.meerow@ars.usda.gov

alan.meerow@ars.usda.gov

Evolutionary Applications Journal

Free! Evolutionary Applications full volume available to download. All issues of Evolutionary Applications are now freely available to download at: www.evolutionaryapplications.org. Highlights include: *Adaptation, extinction and global change (Bell & Collins) *Consequences of sexual selection for fisheries-induced evolution, (Hutchings & Rowe) *Invasion thresholds and the evolution of nonequilibrium virulence (Bull & Ebert) *Evolutionary origins of invasive populations (Lee & Gelembiuk) *Turner syndrome and the evolution of human sexual dimorphism (Crespi) *How well can captive breeding programs conserve biodiversity? (Fraser)

Journal Aims and Scope: Evolutionary Applications publishes papers that utilize concepts from evolutionary biology to address biological questions of health, social and economic relevance. Papers are expected to employ evolutionary concepts or methods to make contributions to areas such as (but not limited to): agriculture, aquaculture, biomedicine, biotechnology, climate change, conservation biology, disease biology, fisheries and wildlife management, forestry, and invasion biology. Theoretical, empirical, synthesis or perspective papers are welcome.

Submit your papers today at: <http://mc.manuscriptcentral.com/eva> Evolutionary Applications has been accepted for full ISI indexing!

ISI have confirmed that Evolutionary Applications will be fully indexed in the ISI Current Contents/Agriculture, Biology & Environmental Sciences and SCIE indexes in 2009, and all 2008 content will be included in the coverage. The journal will receive its first Impact Factor in 2010.

We would like to thank the scientific community for their continued support of Evolutionary Applications.

Louis Bernatchez <Louis.Bernatchez@bio.ulaval.ca>

GCG SeqLab extensions

We use legacy GCG software to launch EMBOSS programs. Has anybody built SeqLab extension configuration files to launch EMBOSS programs?

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

Steve Thompson <stevet@bio.fsu.edu>

Ghrelin evolution

Dear colleagues

I am interesting to study ghrelin protein sequence in sturgeon to find its evolutionary relationship with this protein in other animals and also its expression in gonads and its impact on sturgeon reproduction. I would like to introduce scientists who study on ghrelin. I would appreciate receiving reply.

Best wishes Mahtab

mahtab yarmohammadi
<mahtab_yarmohammadi@yahoo.com>

Grant for early-stage researchers

Hi folks,

I am looking for early-stage researchers that might be interested in applying for a grant. It is called a Starter Investigator Research Grant (SIRG). The criteria are:

* Candidate must be between 3-8 years post PhD experience * Candidates should have a proven record of internationally recognised independent research accomplishments V to this end candidates must have 3 peer reviewed publications as senior author AND be named on an average of 1 other per year since the PhD was awarded * Candidates should NOT have previously held a research award of greater than 100K or 1 years duration (bursaries, postdoctoral fellowships or travel awards of greater than 1 year ARE permissible) * Candidates must no hold or have held a faculty position * Candidates must have a nominated mentor from within the host institution

Programme:

* Programme is for 4 years * Direct costs up to £4500,000 * Salary is set with a starting figure of £463,819 (inclusive of PRSI) rising to £469,737 over the 4 years for the SI * The remainder of the budget must be used to fund a PhD Student and costs for consumables, equipment and travel * Overheads will be paid but are not to be included in the budget

For further information please go to: http://www.sfi.ie/content/content.asp?section_id=-739&language_id=1

If you are or you know somebody that fits these criteria, would like to move to Ireland (Maynooth) and is interested in molecular evolution research, then I would be interested in hearing hearing from them.

There is a deadline of next Wednesday for an internal selection competition, so replies must be made early next week.

Kindest regards,

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 – Work — <http://bioinf.nuim.ie/>

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

Haplotype software

Dear all,

I would thank anybody who could point me towards some kind of software that can read a bunch of se-

quences (mtDNA) and identify, count and group together same haplotypes (identical sequences).

Thanks in advance,

Luis

Luis M. Márquez, Ph.D. Investigador Asociado Centro de Biotecnología Fundación Instituto de Estudios Avanzados, IDEA Carretera Hoyo de la Puerta. Sartenejas. Caracas 1080. Venezuela Tel +58-212-9035085 Fax +58-212-9035086

Luis Marquez <luismarquez-gomez@yahoo.com>

Haplotype software answers

Hi all,

Thank you very much for the overwhelming response to my query about a program that can identify, count and group together same haplotypes.

Below I paste the suggestions with the names of people who sent them (please excuse me anybody who could have been left out).

Thanks again,

Luis

Fabox softwares: <http://www.birc.au.dk/fabox/> Sandrine Sebastien Palle Villesen Fredsted

DAMBE (<http://dambe.bio.uottawa.ca/dambe.asp>) or collapse (<http://darwin.uvigo.es/software/-collapse.html>)

Paulo Anna Francesco Nardi Yael Kisel Diana Catarino Natalia Martinkova Maarten Vonhof Joel Anderson John Switzer

TCS will do this. http://biology.byu.edu/Faculty/-kac/crandall_lab/docsdata/pdf_files/2000/TCS-ME1.pdf Amber David Posada Judith Fehrer Romina Piccinalli

DNAsp (<http://www.ub.edu/dnasp/>).

Cornelya Kluetsch Sibelle Torres Vilaça

Bioedit could probably also be made to fit the bill quite easily (Edit>Search>Find Non-unique sequences and concatenate titles) depending on the scale of the problem

Darren Obbard

DOTUR, <http://schloss.micro.umass.edu/software/->

dotur.html, can group sequences into operational taxonomic units defined by different percentage similarities

Richard

Holly Mortensen also suggested using Arlquin, but that is the program I have been using and I could not find an option for it to group same haplotypes together (it may be that I am not very good at searching, as you can tell by my original question).

Luis Marquez <luismarquez_gomez@yahoo.com>

Is old acrylamide usable

will 40% (19:1 acrylamide-bisacrylamide) that has been kept in fridge since 2006 be OK for usat electrophoresis? pls respond to mouse@lamar.colostate.edu

Ann

Ann Eileen Miller Baker
<mouse@lamar.colostate.edu>

Linkage map programs answers

These are the few replies we got to the following request: THANKS to everyone who responded.

REQUEST: We would like to get an overview over user-friendly (ideally Mac & PC based) programs to 1) make linkage maps 2) calculate recombination rates 3) allow for different recombination rates of males and females 4) ideally be usable in diploids and polyploids We would like to apply the program to pedigree data using msats in parents and F1. Thanks for your suggestions in advance. Best, Matthias

Good morning These software are not the most user friendly, in that a hidden tab or space at the end of a file can crash it but they are windows based and can handle separate Male and Female maps. They were originally developed for salmonid fish which are ancestral polyploids.

<http://www.uoguelph.ca/~rdanzman/software/Linkmfex> V mapping in male and female, allow to

examine difference in recombination between the sexes and between individuals Probmax V basic pedigree software, that will also allow you to examine if the marker panel you are using is sufficient to discern complete parentage

Enjoy

Peace D

Darrin Reid, MSc, Biologist National Research Council of Canada Institute for Marine Biosciences Halifax, NS, B3H 3Z1

No doubt you will know about 'MapMaker', which is a nightmare.

Someone recently introduced me to 'AntMap', which is interesting but doesn't do everything you request (sex differences).

<http://cse.naro.affrc.go.jp/iwatah/antmap/index.html>

Mike Ritchie School of Biology Dyers Brae House University of St Andrews St Andrews, Fife Scotland KY16 9TH

Phone 0 (44 outside UK) 1334 463495 Fax 0 (44 outside UK) 1334 463366

Website: <http://bio.st-andrews.ac.uk/staff/mgr.htm>

The animal genomics research community has used Phil Green's Cri-Map program for the best part of the last 15 years to compute linkage maps. The program will do everything that you ask (and in fact quite a bit more, since it will also construct IBD maps of the chromosomes of all individuals). It won't handle polyploids and it doesn't have a fancy GUI (it is command line driven), but it will handle very large pedigrees and large numbers of loci. We have just used the program to construct a genetic map of over 12,000 SNPs scored in 10,000 individuals.

You can get it here.

<http://linkage.rockefeller.edu/soft/crimap/> Jerry Taylor Wurdack Chair in Animal Genomics University of Missouri

Matthias Stoeck <matthias.stoeck@unil.ch>

LinkageMaps Recombination software

Dear all,

we would like to get an overview over user-friendly (ideally Mac & PC based) programs to

- 1) make linkage maps
- 2) calculate recombination rates
- 3) allow for different recombination rates of males and females
- 4) ideally be usable in diploids and polyploids

We would like to apply the program to pedigree data using msats in parents and F1.

Thanks for your suggestions in advance.

Best, Matthias

Matthias Stöck University of Lausanne Department of Ecology and Evolution (DEE) UNIL, Biophore, CH-1015 Lausanne Switzerland <http://www.unil.ch/dee/-page40038.html> email: matthias.stoeck@unil.ch Tel. +41 (0) 21 692 4186

Matthias Stöck <matthias.stoeck@unil.ch>

Measuring selection coefficients

Dear Evoldir

I want to estimate selection coefficients from a longitudinal series of diploid genotype frequencies. The gene in question encodes insecticide resistance so selection is relatively intense.

I intend to use max. likelihood to fit initial allele frequency, selection coefficient and dominance (i.e. $P(0)$, s and h in standard terminology). Given these three parameters we can predict genotype frequencies at any given time point and use the multinomial distribution to get LL of obtaining the observed number of the three genotypes.

So I have two questions

(1) Is this a sensible way of doing it, or are there hidden pitfalls and/or is there a better way? (2) Has anyone done it before and published the method so we can cite it? It seems like it should be a standard type of analysis but we haven't been able to track a previous one down yet. (3) Better still, is there a public access programme that we can download? If not, we'll write our own and make it available.

Thanks in advance for any responses.

Best wishes, Ian

Ian Hastings Liverpool School of Tropical Medicine Pembroke Place, Liverpool L3 5QA 0151 705 3183 (office) 0151 705 3147 (group secretary) Email: hastings@liverpool.ac.uk

"Hastings, Ian" <hastings@liverpool.ac.uk>

MrBayes non-matching headers bugfix

Dear all,

Does anyone have a compiled Windows .exe file for Mr Bayes 3.1.2 that includes the patch that fixes the "non-matching headers" bug? The patch was posted on Source Forge some time ago, but the recompilation is beyond my skills.

thanks Bernard Pfeil

Bernard.Pfeil@csiro.au

Muiltplex PCR

Dear Evoldir Community,

we are currently trying to establish a multiplex PCR protocol for microsatellite markers. For fragment analysis, we are using a Mega Bace sequencer. Who has successfully established a multiplex PCR protocol for a MegaBace and can give us some tips?

We appreciate your help! Susanne

– Prof. Dr. Susanne Foitzik Department Biologie II Behavioral Ecology (Verhaltensökologie) Ludwig-Maximilians-Universität München Großhaderner Str. 2 D - 82152 Planegg / Martinsried Germany

Phone: + 49 89 / 2180 74 209 Fax: + 49 89 / 2180 74 221 e-mail: foitzik@biologie.uni-muenchen.de http://-ecology.bio.lmu.de/etho_e/index.htm Susanne Foitzik <foitzik@zi.biologie.uni-muenchen.de>

Nuclear and mitochondrial phylogeny

Dear Evoldir members,

I am working with mitochondrial and nuclear sequences (cytochrome b and the intron b-fibrinogen 5) to try to delineate population structure and I am trying to do a phylogenetic tree with these two markers. But I am experiencing some problems with how to make an input for some programs (I am currently working with MrBayes and PHYML). For each individual, I have sequences of both nuclear and mitochondrial markers.

Should I analyze these two markers as two datasets? How can I do it?

Should I concatenate them and consider as a single sequence and run a modeltest to determinate the best substitution model?

In a recent paper, Cabanne et al. (2008) concatenated the nuclear and mitochondrial sequences, and used the IUPAC ambiguity code for the polymorphic sites. Since I know the phase of my nuclear sequences, is there a way that I can use it in the phylogeny with the mitochondrial data?

Any comments would be of great help.

Sibelle

– Sibelle Torres Vilaça Laboratório de Biodiversidade e Evolução Molecular ICB-UFMG Av. Antonio Carlos, 6627 CP 486 - Sala L3-244 31270-010 Belo Horizonte, MG, Brasil Tel: +55 31 3409-2566

sibelletorres@gmail.com

Outsourcing microsat development

Dear all,

I have a query about outsourcing the development of microsatellite markers. I need to have markers developed for two species for a reasonable price. Does anyone have a company to recommend?

Any help will be highly appreciated!

Best regards,

Sofia Hemmilä, PhD student sofia.hemmila@ebc.uu.se

Program in Evolutionary Functional Genomics Evolutionary Biology Centre Uppsala University Norbyvägen 18D 752 36 UPPSALA SWEDEN Phone: +46 (0)18 471 64 08

sofia.hemmila@ebc.uu.se sofia.hemmila@ebc.uu.se

Outsourcing microsat development answers

Hi all,

A couple of weeks ago I posted a question about companies to outsource microsat development to. I want to thank everyone who took the time to respond. It was very helpful! Here is a list of the different options I found:

Cornell University The Evolutionary Genetics Core Facility (EGCF) at Cornell University is offering construction and screening of genomic DNA libraries for microsatellite loci, as a service to the evolutionary community. Total cost for this service is USD 4300 per library, which includes all construction, screening, and guaranteed discovery of 32 unique clones containing SSRs.

For details, see the EvolDir post from Oct 2, or contact Steve Bogdanowicz smb31@cornell.edu, 607-254-4297, 254-4286.

Ecogenics Offers any chosen stage of microsat development. Construction of a genomic library with at least 50 SSR containing colonies costs EUR 7140. Development of a set of five markers with at least four alleles per locus in 15 unrelated individuals costs EUR 10 540, and additional markers are EUR 680 each. www.ecogenics.ch Genetic ID Services, GIS Constructs genomic libraries with 350 to 700 bp fragments, enriched for different microsatellite motifs in each of four libraries, in E. coli, with sequences that confirm the presence of at least 50% microsatellites in at least two of the libraries. Includes 100 sequences with primer design. Costs USD 10 000 for one species and a small discount is offered if more than one library is ordered. <http://www.genetic-id-services.com/-library.htm> University of Georgia Offers construction of genomic libraries (>25% positive clones) or complete microsat marker development. The price for constructing a genomic library is USD 5750. If screening for polymorphism is also ordered, the price

is in total USD 10 000 (testing 20 primer pairs on 15 individuals). Substantial discounts are offered if more than one species is ordered (for example, two species cost USD 17 000). http://www.uga.edu/srel/-Msat_Devmt/Microsatellite_Development.htm Lakehead University May offer non-advanced microsat development upon request. For details, contact renee.fratpietro@lakeheadu.ca

Do it yourself a faster protocol A new strategy for microsat development is described in Leese et al (2008) Isolation of microsatellites from unknown genomes using known genomes as enrichment templates. *Limnol. Oceanogr.*: Methods 6, 412426. Using this protocol and a template sequence from a distantly related species, development of microsat markers may be faster and cheaper.

Sofia Hemmilä Program in Evolutionary Functional Genomics Evolutionary Biology Centre Uppsala University Norbyvägen 18D 752 36 UPPSALA SWEDEN Phone: +46 (0)18 471 64 08

Parallel evolution speciation studies

Dear all,

The parallel evolution of phenotypic traits is common whenever independent populations are exposed to similar ecological conditions. This is a well know phenomenon for different forms/morphs/ecotypes of sticklebacks, lake whitefish, arctic charr and Periwinkles (*Littorina*). I plan to write an article on this subject and I would be interested to find many more examples that fits into the concept "parallel evolution/speciation" in animals. A search on ISI generates over 10.000 hits and I ask your help to find key articles, especially for taxa than I have not already mentioned

Than you in advance! /Petri

Petri Kemppainen, PhD student Tjärnö Marine Biological Laboratory, 45296, Strömstad, Sweden Tel: +46 526 686 83 Fax: +46 526 686 07 Mob: +46 709 360 124 petri.kemppainen@marecol.gu.se

Pooling samples for disease prevalence

I am looking for advice on how to pool larger specimens. I am looking to obtain an estimate of parasite prevalence from juvenile blue crabs ranging from 1-30mm in carapace width. The reason for pooling these samples is to cut back on the cost of processing a large number of juvenile crabs (100s) from a large number of sites (~30). I have found literature describing the pooling of smaller organisms, like mosquitoes and copepods, but very little concerning larger organisms. I should also add that I do not have any prevalence data for juveniles for the sites these juveniles were collected from; however, there is some adult crab prevalence information (~15% in nearby areas) and previously published studies have shown that the prevalence for this parasite is higher in juveniles (as high as 60%).

I will be extracting these pooled samples with a Qiagen DNeasy Kit. I am looking for advice on where to begin-how much tissue from each crab do I pool? How many crabs do I pool into a single sample?

Marine Molecular Genetics Laboratory Department of Environmental and Aquatic Animal Health Virginia Institute of Marine Science The College of William and Mary Rt. 1208 Greate Road Gloucester Point, VA 23062 (804)684-7926 pagenkopp@vims.edu

pagenkopp@vims.edu

Problems microsatellite development

Dear all,

I am currently in the process of developing enriched microsatellite libraries for a number of different species. But have encountered significant problems at the stage of selecting bacteria which contain inserts (i.e. blue white colour selection). The enrichment procedure follows the protocol as detailed by Kijas et al 1994 (reference below). Extremely briefly - once fragments have been preselected for specific microsatellite repeat mo-

tifs, they are digested with restriction enzymes and ligated into a specifically cleaved vector (pBluescript plasmid) and transformed into XL-2 blue supercompetent *E. coli* cells, then grown on bacteriological agar pH 7.0 containing ampicillin, IPTG and X-gal (all according to manufacturers specifications).

Transformations work fine with plenty of colonies for the control pUC-18 plasmid (blue colonies only) and for the microsatellite libraries (blue and white colonies). I decided to do a quick test to determine if ligations were successful and to determine the size of inserts. Surprisingly many of the white colonies (positives) DO NOT contain any insert at all. Even more surprisingly many of the blue colonies (negatives) actually do contain inserts. More extensive testing revealed that as many blue colonies contain inserts as do white colonies.

The digested vector has been used with great success in the past (I am using an aliquot of an existing tried and tested stock). I have redone ligations and transformations several times, each time producing a similar result. I would be very grateful for comments or suggestions regarding solutions to this problem, and I am interested to know if anyone else has experienced similar things.

Many thanks in advance

Sean

Reference

Kijas JM, Fowler JC, Garbett CA, Thomas MR (1994) Enrichment of microsatellites from the citrus genome using biotinylated oligonucleotide sequences bound to streptavidin-coated magnetic particles. *Biotechniques*, 16: 656-662.

Sean Fitzpatrick <F1502202@qub.ac.uk>

Reducing microsatellite stutter paper answers

Hello EvolDir members,

I sent the email below in October in the hopes of finding the complete reference to the described paper. I thank everybody who took the time to respond. I have not had any success in finding the reference, though I've had interest from others who would also like the reference to the described paper. I was also emailed suggested reading material, which is listed below. The technique in the Brownstein et al. (1996) paper is use-

ful to remove stutter caused by + A artifacts, though I believe the stutter in my case is not caused by this. I found the last paper listed particularly useful as a guide in reducing stutter thought to be caused by strand slippage, though the described novel technique of reducing denaturation temperature was unsuccessful in the few dinucleotide loci I attempted. I'd be interested to hear if anybody has had success (or no success) with using a reduced denaturation temperature to decrease stutter, particularly for dinucleotides as the paper only tested trinucleotides.

Brownstein, M., Carpten, J., Smith, J. (1996) Modulation of non-templated nucleotide addition by Taq DNA polymerase: primer modifications that facilitate genotyping. *Biotechniques* 20: 1004-1010

Munoz-Fuentes, V., Gyllenstrand, N., Negro, J., Green, A., Vila, C. (2005) Microsatellite markers for two stiff-tail ducks: the white-headed duck, *Oxyura leucocephala*, and the ruddy duck, *O. jamaicensis*. *Molecular Ecology Notes* 5:263-265 (which uses the technique described in the above paper)

Krzyzosiak, W., Olejniczak, M. (2006) Genotyping of simple sequence repeats - factors implicated in shadow band generation revisited. *Electrophoresis* 27: 3724-3734

Kind regards,

Catherine

Hello EvolDir members, I'm trying to find (with no luck) the original *Biotechniques* paper which describes the technique of using greatly abbreviated PCR times (e.g. 2/2/8 s) at each step to decrease microsatellite stutter. This technique was described in the response of Andrew DeWoody in 2006 (see below for quoted response) to an EvolDir member that asked about how to decrease stutter. I do not know the complete reference of this paper, and as Andrew read the paper a while ago he is also unsure of the reference though he thinks the paper might be about hymenopterans. Does anybody know the full reference of this paper or (preferentially) can they email the paper as an attachment to catherine.attard@students.mq.edu.au?

Many thanks and kind regards,

Catherine

EvolDir response: "You might try greatly abbreviated times at each step in PCR (e.g., 2 sec denaturation, 2 sec annealing, 8 sec extension). The original paper describing this was published in *Biotechniques* about 6 or 7 years ago; see also the attached reprint. [We had cited the *Biotechniques* paper in the bass reprint, but the citation was ultimately cut due to strict page limits

in PRS.] In my experience, the approach either works very well or fails completely (on a locus by locus basis). If you get amplifications, the stutter is usually greatly reduced. DeWoody et al. (2000) Proc. R. Soc. Lond. B 267:2431-2437.”

catherine.attard@students.mq.edu.au
ine.attard@students.mq.edu.au

cather-

Scat DNA in DMSO

Hi,

I am actually involved in a project that aims to provide non invasive genetic approaches (species, sex and individual identification) for the long term monitoring of jaguar (*Panthera onca*) populations in tropical areas. We are actually using a highly efficient protocol of DNA extraction from scats conserved with Silica gel beads, but we recently got some samples preserved with DMSO. I wonder whether someone has experience with this kind of storage and whether extraction protocols are available, that allow to get both sufficient quality/quantity DNA for microsatellites and mtDNA typing.

I will be very grateful to get any kind of information. Thank you very much for your collaboration.

All the best.

S everine

S everine Roques Department of Biological Conservation Estacion Biologica de Do ana, CSIC Pabellon del Per , 41013 Sevilla <http://severineroques.googlepages.com/> T el (work): 954-232340 (ext. 198/221) (Movil) 648086530

severine roques <severineroques@hotmail.com>

Sharing 454

To any and all who may be interested:

A group of collaborating researchers at Stanford University are looking for partners to share in the cost of a titanium 454 sequencing run. We are looking to purchase 1/8-1/4 of a full plate, and would like to find fel-

low researchers who are excited about the new technology, but would like a lower-cost “test-run” before committing the \$12,000-\$20,000 for a full plate. A 1/4 plate will likely cost \$3,000 - \$5,000 (depending on choice of sequencing facility), and should return ~250,000 reads, with an average length of ~ 400-500 bp, for a total of 100-125 MB of sequence. Few sequencing facilities offer partial runs at partial costs, and those that do can not guarantee rapid service unless there is enough interest in partial runs to fill a full run. We would like to find enough partners to fill a full plate within the next month or so. If you are interested please respond to Tom Oliver, (toliver@stanford.edu), and I can answer any questions you have.

Thanks,

Tom Oliver

toliver@stanford.edu toliver@stanford.edu

SmithsonianPanama FrogEvolution

Dear Colleagues,

We are recruiting US undergraduate students and Latin American undergraduates or recent graduates for NSF-funded summer internships studying ecology, evolution and behavior of red-eyed treefrogs at the Smithsonian Tropical Research Institute in Panama. This is a great opportunity for young scientists to gain research experience in a biologically rich rainforest environment, and to interact with a diverse international community of scientists. More information about the project and application process is available online at:

<http://people.bu.edu/kwarken/-KWLabInternships.html>

Please encourage any young scientist whom you believe would benefit from this experience to apply. Applications are due January 15, 2009. (We will consider later applications from students who wish to work on our project but have, or are applying for, their own funding from other sources.)

Thank you, Karen Warkentin

Dept. of Biology Boston University 5 Cummington St. Boston, MA 02215 kwarken@bu.edu people.bu.edu/kwarken

kwarken@bu.edu kwarken@bu.edu

Software BAPS upgrade available

BAPS software for population genetic analyses is upgraded to version 5.2. This version contains a number of bug fixes and new features (compared to generation 4.X) which are described in detail in the new paper:

Corander J, Marttinen P, Sirén J, Tang J. Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. BMC Bioinformatics, 2008, in press.

The BAPS website now finally contains a detailed manual describing the new features. The software is downloadable from: <http://web.abo.fi/fak/mnf//mate/jc/-software/baps.html> NB! If you have already used the version 5.0 or 5.1, the runtime component need not be re-installed when upgrading to v5.2. For details, see the software download pages.

Best, Jukka

bayesian@luukku.com

Software Champuru online tool

Dear EvolDir members,

This to inform you that Champuru [1] is now available at a new address: <http://www.mnhn.fr/jfflot/champuru>. The former address <http://134.157.186.185/champuru> will remain active for some time.

Champuru is a web program implementing a recently published method for reconstructing (deconvoluting) the haplotypes of length-variant heterozygotes. This method relies on matching and comparing the double-peaks present in the forward and reverse chromatograms obtained by direct sequencing [2].

[1] Flot J-F (2007) Champuru 1.0: a computer software for unraveling mixtures of two DNA sequences of unequal lengths. *Molecular Ecology Notes* 7:974-977

[2] Flot J-F, Tillier A, Samadi S, Tillier S (2006) Phase determination from direct sequencing of length-variable DNA regions. *Molecular Ecology Notes* 6:627-630

Best, Jean-François

– Jean-François Flot, Ph.D. UMR 7138 Systématique, Adaptation, Evolution Département Systématique et Evolution Muséum national d'Histoire naturelle CP 26, 57 rue Cuvier 75231 Paris Cedex 05 France Tel. + 33 1 40 79 38 96 Fax. + 33 1 40 79 38 44 <http://www.mnhn.fr/jfflot/publications/> jfflot@mnhn.fr

Software DAMBE update

Dear All,

DAMBE (software for data analysis in molecular biology and evolution) used to require administrator privilege to install. Now I have compiled a version that can be installed by those without administrator privileges. So now there are four versions of DAMBE (DAMBEXP, DAMBEVista, DAMBEX for Linux WINE, and DAMBE, with the last being for those without administrator privileges).

Installation packages of DAMBE for Windows are at http://dambe.bio.uottawa.ca/dambe_installation_instructions.asp Installation package of DAMBE for Linux WINE is at http://dambe.bio.uottawa.ca/dambe_installation_linux.asp.

A screen shot of DAMBE running in Ubuntu Linux is at: <http://dambe.bio.uottawa.ca/download/DAMBEScreenShot.pdf> 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

Software SeqPHASE online tool

Dear all,

SeqPHASE is a new online tool to generate PHASE input files from FASTA sequence alignments and to convert PHASE output files back into FASTA. It is freely available at <http://www.mnhn.fr/jfflot/seqphase>. Best, Jean-François

– Jean-François Flot, Ph.D. UMR 7138 Systématique, Adaptation, Evolution Département Systématique et Evolution Muséum national d'Histoire naturelle CP 26, 57 rue Cuvier 75231 Paris Cedex 05 France Tel. + 33 1 40 79 38 96 Fax. + 33 1 40 79 38 44 <http://www.mnhn.fr/jfflot/publications/> jfflot@mnhn.fr

Software SeqVis 1.4

An updated version of SeqVis 1.4 can be obtained from:

<http://www.bio.usyd.edu.au/jermin/SeqVis/-index.htm> The new version fixes a number of bugs kindly reported by some users. The bugs include incompatibility with some of the newer operative systems and reading sequences stored in the FASTA format.

Below is brief description of SeqVis:

Most phylogenetic methods assume that the sequences have evolved under homogeneous, stationary and reversible conditions. Compositional heterogeneity in data intended for studies of phylogeny suggests that the data did not evolve under these conditions. SeqVis, a Java application for analysis of nucleotide content, reads sequence alignments in several formats and plots the nucleotide content in a tetrahedron. Once plotted, outliers can be identified, thus allowing for decisions on the applicability of the data for phylogenetic analysis. The visualization of compositional heterogeneity is further supported by a matched-pairs test of homogeneity.

All the best,

Lars

— Assoc. Prof. Lars Jermin Biological Science, Bldg A08 University of Sydney NSW 2006, Australia
+61-2-9351-3717 (phone) +61-2-9351-4119 (Fax)
lars.jermin[at]usyd.edu.au

Patience is a priceless commodity...

lars.jermin@usyd.edu.au

Software TESS

A new version of TESS by Eric Durand is available on-

line at:

<http://www-timc.imag.fr/Olivier.Francois/tess.html>
or <http://www-timc.imag.fr/Eric.Durand/soft.html>

TESS 2.0 implements a Bayesian clustering algorithm for the inference of spatial population genetic structure. The new features are:

- an improved admixture model using spatial autocorrelation - inclusion of geographic distance and kinship - possibility to export to CLUMPP format directly - possibility to start from a NJ tree - computation of model choice indices: DIC - better GUI

Specifically, the new admixture model uses a CAR (conditional autoregression) model based on the Delaunay tessellation. The new version allows the user to weight the TESS spatial network by inverse geographic great circle distance or kinship. This new model could be considered more reliable than the TESS 1.x admixture model which was based on an approximation of the model implemented in STRUCTURE. The without-admixture model is unchanged.

best regards olivier

Olivier Francois, PhD Faculty of Medicine of Grenoble, Group of Math Biology TIMB, TIMC-IMAG 38706 La Tronche France <http://www-timc.imag.fr/Olivier.Francois>

Olivier Francois <olivier.francois@imag.fr>

TajimasD analysis answers

Dear All,

I have posted the following question on evoldir:

Hi to everybody, I have a question about the Tajima's D analysis implemented in DNAsp: in some papers (for instance Wheat et al. 2006, Mes et al. 2006) I found that the authors use the tajima's D analysis considering only the synonymous sites, but I don't really find the way to do it. Is there someone who knows how to do it? All answers would be very helpful.

I would like to thank all that answered me, it was really helpful. Here are all the responses I received, hope it will be helpful for someone else!

Again, thanks to everybody!

#####

Dear Erica, please note that in my methods section

(Wheat et al. 2006) I state that I used two programs for DNA summary statistic calculations. DNAsp did not do syn site Taj D calculations then, and I don't think it does it now- which is a bit of a pain. However, the other program, Proseq, does do syn site Taj D calculations- but be careful, the new program version is a bit tricky to use. I strongly recommend estimating your TajD calculations using more than one program if you are going to use the point and click GUI programs. This will ensure you are getting the numbers you really want. Cheers,

Chris

#####

This really is surprisingly difficult to do, and the work-around seems to spread slowly by word of mouth! (1) Export the synonymous polymorphic sites as a new file: generate>polymorphic/variable sites datafile>only synonymous (2) Open the new file, and do the Taj D analysis on that [If you are then using coalescent simulations with intermediate levels of recombination, remember to use the rate for the whole length of the gene, not just the subset you've generated!] Good luck! Darren

####

Hello Erica, I believe that the way to do it is to create an input file with only synonymous SNPs. In this case you will calculate TD only considering synonymous sites. Best, Luis

###

Hi, Under the Data menu, go to Remove Positions, then select which positions to include/exclude. Every analysis you do after that will only be performed on the positions you have decided to keep. I hope that helps. Brian

#####

Dear Erica: We've done it a lot. I find that looking at synonymous and nonsynonymous sites separately with Tajima's D-like statistics is very revealing. I actually use the ratio of D to the absolute value of its theoretical minimum. This latter statistic (Q) has the advantage of not being dependent on sample size (unlike D) and therefore comparable across data sets. We have done this mostly using custom-made software, some of which we are getting into a user-friendly form for publication in the not too distant future. Austin Hughes Some references: Hughes, A.L. 2005. Evidence for abundant slightly deleterious polymorphisms in bacterial populations. *Genetics* 169: 553-558.

Hughes, A.L., and Hughes, M.A. 2007. More effective purifying selection in RNA viruses than in DNA viruses.

Gene 404: 117-125.

Hughes, A.L., and Hughes, M.A.K. 2007. Coding sequence polymorphism in avian mitochondrial genomes reflects population histories. *Mol. Ecol.* 16: 1369-1376.

Hughes, A.L., and Piontkivska, H. 2008. Nucleotide sequence polymorphism in circoviruses. *Infection, Genetics, and Evolution* 8:130-138.

Dr. Erica Bortolotto Biology Dept University Of Padova Via G. Colombo 3 I-35100 Padova Italy e-mail bortolotto@unisi.it Tel 0039 049 8276222 Fax 0039 049 8276209

Erica Bortolotto <bortolotto@unisi.it>

Undergraduate Core Curriculum

In Northern California and Nevada, we are currently suffering a shortage of well-trained organismal biologists who go on to do applied work and perhaps a master's degree. Ideally, this student would have a strong undergraduate education with an emphasis in their taxonomic group of choice and advanced classes in evolution and ecology. In discussions with many colleagues, it is clear that there are two very different view points on why this is the case and how to fix the problem.

Some of us maintain that the loss of students in organismal biology, borne out by the differences in numbers of organismal biologists trained and jobs available (for example, over 100% undertraining of botanists obtained from data on # of degrees granted vs. www.bls.gov <<http://www.bls.gov/>> and other job sites) is due to the "over-integration" of undergraduate biology programs and the loss of the first year traditional biology sequence of molecular biology, botany, and zoology. We maintain that this "traditional" sequence does not negate integration and provides an introduction that simulates the upper division organismally-based courses.

Others maintain that the courses in the "traditional" freshman track are archaic and other methods for retention in organismal biology tracts are needed, or that this tract simply needs to suffer a natural death.

I would appreciate hearing about the experiences of other universities on this issue. If you reply to me off-list, I will compile the results and post them.

Thank you,

Kristina

Kristina A. Schierenbeck USDA/ARS, Research Leader
Exotic & Invasive Weeds Unit 920 Valley Road Reno,
Nevada 89512

Work: 775-784-6057 ext. 222 Cell: 530-591-9907
"Schierenbeck, Ka" <Ka.Schierenbeck@ARS.USDA.GOV>

PostDocs

Beaufort NorthCarolina ConservationGenetics	71	UNebraskaLincoln Bioinformatics MolEvol	78
CNRS France AntMolecularPhylogenetics	72	UNeuchstel EvolutionaryBotany	79
CornellU DiseaseDynamics	72	UOtago NZ Microsatellite evolution	79
DartmouthCollege EvolutionaryGenomics	73	UOulu ArabidopsisSpeciation	80
GhentU PlantSystemsBiol	73	UOxford PlantChromosomeEvolution	80
HarvardU PopulationGenetics	74	Uppsala SalixAdaptiveTraits	81
Leuven Belgium EvolutionaryGenomics	74	UQueensland MosquitoCoEvolution	81
Nice France GeneEnvironment Interactions	75	UTexas PopulationGenetics	81
NorthCarolinaStateU PopulationGenetics	76	UTuebingen EvolutionaryMarineBiology	82
RutgersU ComputationalGenomics	76	UUtah Genomics	82
UArizona VertebrateSystematics	77	UWashington PlantEvolution	83
UdeMontreal MolEvolution	77	Vienna ComputationalBiol	83
UEdinburgh StatisticalGenetics	78		

Beaufort NorthCarolina ConservationGenetics

Mary Derrickson McCurdy Visiting Scholar in
Conservation Genetics
at the Marine Laboratory, Beaufort NC

The Nicholas School of the Environment at Duke University invites applications for the Mary Derrickson McCurdy Visiting Scholar at the Marine Laboratory in Beaufort, North Carolina. The Nicholas School focuses on leadership in research, education, and service to understand basic Earth and environmental processes, to understand human behavior related to the environment, and to inform society about the conservation and enhancement of the environment and its natural resources for future generations. We seek a young scientist of outstanding promise in the field of Conservation Genetics, which we define broadly as

the use of molecular approaches to assess, protect, restore, or maintain species, communities, habitats, or ecosystems, particularly those that are threatened or endangered. We are especially interested in the application of novel molecular approaches to the conservation of marine organisms and ecosystems; in support of this research, the Marine Laboratory maintains the Marine Conservation Molecular Facility (< <http://www.nicholas.duke.edu/marinelab/molecular.html> ><http://www.nicholas.duke.edu/marinelab/molecular.html>). The McCurdy Scholar carries an appointment as Visiting Assistant Research Professor. The successful candidate is expected to engage fully in the intellectual life of the Marine Laboratory, including research, teaching, and mentoring. The term of the appointment is for one year, with potential for renewal in years 2 and 3.

Interested individuals should send curriculum vitae, summary of research interests and accomplishments, reprints of three recent papers and names of three references to the search chair. Electronic submission is strongly encouraged, but if necessary, please submit hard copy materials to the search chair:

Dr. Douglas Nowacek Chair, Search Committee, Conservation Genetics

135 Duke Marine Lab Road Beaufort, NC 28516-9721
dnp3@duke.edu

The search committee will begin reviewing applications on January 15, 2009.

The search will remain open until the position is filled.

Duke University is an Affirmative Action/ Equal Opportunity Employer.

Belinda Williford <bbw@duke.edu>

CNRS France AntMolecularPhylogenetics

Post doctoral position in population genetics at Laboratoire d'Ethologie Experimentale et Compare (LEEC-CNRS UMR 7153), France (30 minutes from the centre of Paris)

We are looking urgently for a postdoctoral researcher on the University funded project Molecular phylogenetics and evolution of social structure traits in the *Ectatomma* ants (Hymenoptera: Formicidae: Ectatomminae)±. The overall aim of this project is to understand the role of microgyny as alternative reproductive tactics in ants. The post-doctorant is expected to work with Dr C. Poteaux-Leonard and Dr J-P Lachaud to develop microsatellite markers on *E. ruidum* to analyse the fine scale population genetic structure of Mexican populations of this species (sampling has been done).

This project belongs to the research axis Organisation and phylogeny in ants societies± of the Team 1 of the Lab : Ethology of social Hymenoptera. For details of the LEECs research, please see: http://www-leec.univ-paris13.fr/accueil/accueil_en.php The position is full-time and is for a fixed term of 12 months, starting as soon as January 2009. The salary is about 2 100 net/month (including social benefits) plus an annual research bonus.

Interested individuals should have a doctorate in biology (population genetics). Full applications (including a cover letter outlining research interests, complete CV, publication list and contact details for three referees) should be sent to Dr. Chantal Poteaux-Leonard (poteaux@leec.univ-paris13.fr). Consideration of appli-

cations will begin immediately until December, 14th.

Dr. Chantal Poteaux-Leonard Laboratoire d'Ethologie Experimentale et Compare (L.E.E.C) CNRS UMR 7153 Universit Paris 13 99, avenue J.-B. Clment F-93430 - Villetaneuse

poteaux@leec.univ-paris13.fr

CornellU DiseaseDynamics

Postdoctoral Researcher: Climate Effects on Disease Ecology

A postdoctoral position is available in the Department of Ecology and Evolutionary Biology at Cornell University. This position is funded by a new award from the Cornell Center for Sustainable Future for research on climate effects on disease dynamics in three parallel systems: sea corals, amphibian populations, and mosquito-borne diseases.

Primary responsibilities of the postdoctoral researcher include 1) developing spatial and descriptive models of disease dynamics based on current datasets available for each system, and working collaboratively with climate specialists and biologists to create a climate-based forecasting tool, 2) analyzing results and writing manuscripts, 3) contributing to preparation of grant proposals for future work, and 4) coordinating projects and collaborations with other members of Cornell's ecology and evolution of infectious disease community.

To qualify, applicants should have a Ph.D. in ecology, epidemiology, or related biological field, demonstration of strong quantitative modeling and writing skills, a record of consistent and high-quality publications, and the ability to work independently and collaboratively. Preference will be given to applicants who have an understanding of ecological and population processes necessary for modeling of disease dynamics, as well as previous experience with statistical data analysis and modeling in the context of disease ecology.

Starting salary will be competitive and commensurate with previous experience/expertise; position includes Cornell University Contract College benefits. Funds are available for one year and renewable pending satisfactory progress. The position is available starting March 1, 2009; starting date is negotiable. Review of applications will begin January 1, 2009 and continue until a suitable candidate is found.

To apply, please send a cover letter, CV, statement of research interests/experiences, and names and contact information for three references who are familiar with your work. Inquiries and applications (PDF format preferred) should be e-mailed to Dr. Drew Harvell (cdh5@cornell.edu), Department of Ecology and Evolutionary Biology, Cornell University, Ithaca, NY-14853-2701.

krz2@cornell.edu krz2@cornell.edu

DartmouthCollege EvolutionaryGenomics

Postdoctoral position in evolutionary genomics at Dartmouth College

Seeking qualified applicants for a post-doctoral position with Andrew Kern in the Department of Biological Sciences at Dartmouth College. While this position is not for a particular project, some potential areas of research include: detecting functional sequence elements based on population genetic data, detecting regions of genomes that have undergone lineage-specific directional selection, identifying lineage-specific changes in mutation, linking ecologically relevant phenotypic and genotypic variation. Our two main study systems are *Drosophila* and humans, however we're always looking for new and interesting questions. Candidates who wish to combine computational approaches with experimental biology are highly encouraged to apply.

The ideal candidate would hold a Ph.D. and have a record of research achievement in genetics, molecular biology, population biology, computational biology, statistics, or a related field. A background in comparative/population/evolutionary genomics is highly desirable for this position as is fluency in programming.

Interested candidates should submit an electronic version of their CV along with a cover letter describing their qualifications and relevant experience to andrew.d.kern@dartmouth.edu

Andrew Kern Assistant Professor of Biological Sciences
Dartmouth College

andrew.d.kern@dartmouth.edu
drew.d.kern@dartmouth.edu

GhentU PlantSystemsBiol

The Bioinformatics and Evolutionary Genomics research group, part of the VIB Department of Plant Systems Biology, located in Gent, Belgium, is looking for an enthusiastic and highly motivated

Postdoctoral researcher

This 3 year full-time position is part of a large and ambitious project between the Department of Plant Systems Biology, Gent University, and CropDesign BASF.

The ultimate goal of the project is: - To identify candidate maize genes involved in various plant growth and developmental processes. Many transcriptomic experiments under different growth conditions will be performed, and the results will be analyzed and integrated using a systems biology approach. - The successful candidate will be responsible for the bioinformatics part of the project and will interact closely with the other partners involved.

Profile

- Ideal candidates for this position should have a PhD in bioinformatics with a strong publication record, and should be familiar with microarray data processing and the statistical analysis of biological data.
- A good knowledge of biological processes and pathways and a strong interest in plant biology will be an advantage.
- The candidate should be fluent in English and have good communication and interpersonal skills.

Interested candidates should submit an electronic copy of their resume or curriculum vitae, and a cover letter describing their qualifications and relevant experience to yves.vandeppeer@psb.ugent.be

- Yves Van de Peer, PhD.

Professor in Bioinformatics and Genome Biology Group
Leader Bioinformatics and Evolutionary Genomics VIB
Department of Plant Systems Biology, UGent Ghent
University Technologiepark 927 B-9052 Ghent Belgium

Phone: +32 (0)9 331 3807 Cell Phone: +32 (0)476 560 091 Fax: +32 (0)9 331 3809 email: yves.vandeppeer@psb.ugent.be

an- <http://bioinformatics.psb.ugent.be/> Yves Van de Peer
<yves.vandeppeer@psb.ugent.be>

HarvardU PopulationGenetics

Postdoc opportunity in population genetics and evolution (posted November 14, 2008)

We are searching for a motivated post-graduate researcher to join our group. The focus of the position will be on using population genetic approaches to learn about history and evolution.

The successful candidate will have a strong statistical background, as well as an interest in human history and evolution. While a background in population genetics and bioinformatics would be a strength, such a background is not necessary. Possible projects are:

(i) Estimating the dates of population mixtures using admixture linkage disequilibrium. In African Americans and Latinos, the extent of chunks of contiguous African, European and Native American ancestry are typically about 10-20 centimorgans, which shows that these populations have typically been mixing for 5-10 generations. Our goal will be to extend these methods to accurately estimate the dates of mixture events that are hundreds of generations old.

(ii) Inferring relationships of human populations using allele frequency data. No investigator believes that a simple phylogenetic tree (with populations at the leaves) is an adequate description of human history. Nevertheless, such trees are frequently published. The goal will be to develop a novel suite of analytic tools that extend the phylogenetic tree framework. To handle the presence of gene flow between populations, the project will examine mathematical models (admixture graphs) that allow a rich, but still parsimonious description of genetic relationships among populations, and develop a procedure to fit the genetic data. We will analyze genome-wide data from both SNP arrays and deep resequencing, using publicly available data and data we collect in our own lab to address the questions of highest interest.

(iii) Test whether hybridization occurred during human-chimpanzee speciation. We recently published a study (Patterson et al. Nature 2006) in which we compared about 10 million bases of the genome in humans, chimpanzees, gorillas, orangutans and macaques to show that the history of human-chimpanzee splitting was complex. We hypothesized that an explanation was hybridization during the speciation of hu-

mans and chimpanzees. While several other groups have confirmed the main observations, no one has suggested an alternative explanation for the discrepant patterns between chromosome X and the autosomes. This project will involve rigorously testing this hypothesis using whole-genome alignments and novel analysis methods.

(iv) Systematically explore whether hybridization commonly occurs during speciation. The most interesting result of analysis of human, chimpanzee and gorilla differences was the inference that speciation may not always occur in a simple way: in "allopatry". If instead we use genomic data to harken back in time to the period millions of years ago when successful speciations occurred, we might find that many speciations were complex, as reflected by a diverse and structured population ancestral to the split, and unusual patterns comparing chromosome X to the autosomes. This project will use genomic methods to study a large number of ancient speciations, and determine what pattern of speciation is most common. For this project, we will mine publicly available data and data sets that we collect in our own lab.

The position will be jointly supervised by Drs. David Reich and Nick Patterson, and will involve work at both the Department of Genetics at Harvard and the Broad Institute of Harvard and MIT. Further information about our laboratory and a list of recent papers can be found at our web page: <http://genepath.med.harvard.edu/~reich>. Please write to reich@genetics.med.harvard.edu if you are interested in this position.

David Reich <reich@genetics.med.harvard.edu>

Leuven Belgium EvolutionaryGenomics

POST-DOCTORAL POSITION IN EVOLUTIONARY BIOLOGY AND GENOMICS:

ADAPTIVE EVOLUTION OF MARINE FISHES

RESEARCH CONTEXT: Our team studies the intraspecific evolution of the fish genome and its interactions with parasites and the environment. At the moment adaptive evolution is being studied in key ecological and economic fishes (e.g., Raeymaekers et al. 2007; Maes et al. 2007; Souche et al. 2007; Chistiakov et al. 2008).

ASSIGNMENT: We have an open call for a 12-month postdoctoral fellowship in fish evolution to be funded by the Belgian Federal Science Policy (BELSPO) at the Katholieke Universiteit Leuven. The immediate task involves the in depth analysis of large-scale pyrosequencing (454) runs (annotation and polymorphism detection). Subsequently, the aim is to set-up and screen a SNP array for European eel and common sole for neutral and adaptive signatures.

PROFILE: The candidate (Ph.D. in (molecular) biological sciences, bioinformatics or biochemical sciences with excellent skills in genomics, bioinformatics and programming) will extract and interpret information from a large genetic dataset. The successful candidate originates from the following countries: non-EU Eastern Europe, new states issuing from the Russian Federation, non-EU Mediterranean region, Central and Southern Africa, Central and Southern America, India and Vietnam (see also http://www.belspo.be/belspo/-home/calls/postdoc_en.stm).

WE OFFER: You will join an expert team in ecological genetics and environmental genomics. A fully equipped medium throughput DNA lab, including a capillary sequencer, is operational. Salary is according to Belgian government standards (1600-2000 /month net). There is a possibility to extend the duration of the grant with complementary national funding opportunities. Leuven (<http://www.leuven.be>) is a pretty historical university city with a very high and pleasant standard of living. The historic university, founded in 1425 (<http://www.kuleuven.be/en>), has a top research and teaching standard.

INTERESTED? Send your CV, two letters of reference and a letter of motivation before 31 December 2008 to:

Dr. Filip Volckaert Katholieke Universiteit Leuven Laboratory of Animal Diversity and Systematics Ch. Deberiotstraat 32 B-3000 Leuven, Belgium Phone: +32 16 32 39 66 Fax: +32 16 32 45 75 E-mail: filip.volckaert@bio.kuleuven.be URL: <http://bio.kuleuven.be/dev> Disclaimer: http://www.kuleuven.be/cwis/email_disclaimer.htm Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

Nice France GeneEnvironment Interactions

POSTDOC POSITION: Gene-environment interactions in development and evolution

(Institute of Developmental Biology and Cancer, Nice, France)

A postdoc position is available to study the development and evolution of *Caenorhabditis* nematodes in variable environments. The project will focus on how developmental mechanisms respond to the environment and how such responses evolve. Research approaches will include developmental genetics, intra- and interspecific comparative analyses, and experimental evolution. The successful candidate will be highly motivated and will participate in the detailed planning of the project. Particularly encouraged are applicants with prior experience in *C. elegans* research and developmental or evolutionary genetics. The position is for 2 years and the start date is flexible, but ideally before summer 2009. The position is funded by the French National Center for Scientific Research (CNRS) and open to all nationalities.

Our new research team joins the Institute of Developmental Biology and Cancer (IBDC) in Nice at the end of 2008. The focus of our group is to apply integrative approaches to the study of development at the interface of developmental genetics, ecology and evolution. The IBDC is an international research institute hosting a large number of teams working on diverse topics in developmental and cell biology. The institute, located in the city centre, has excellent research facilities and provides an interactive scientific environment.

To apply, send a summary of your research interests and future plans, CV, names and contact information for three references to Christian Braendle (braendle@unice.fr). Informal inquiries welcome. For more information, please visit: <http://www.unice.fr/isdbc/> Christian Braendle

CIML Parc Scientifique de Marseille Luminy
Case 906 13288 MARSEILLE CEDEX 09 France
braendle@ciml.univ-mrs.fr Tel +33 (0) 4 91 26 91 13
Fax +33 (0) 4 91 26 91 65

From December 1, 2008: Institute of Developmental Biology and Cancer University of Nice Sophia-Antipolis
Parc Valrose 06108 NICE cedex 2 FRANCE <http://www.unice.fr/isdbc> braendle@unice.fr

Christian Braendle <braendle@ciml.univ-mrs.fr>

NorthCarolinaStateU PopulationGenetics

NC State University Pop. Gen./Epidemiology
Postdoctoral Fellowship

POPULATION GENETICS / EPIDEMIOLOGY / MODELING: We are searching for a postdoc who has a strong theoretical or empirical background in population ecology, population genetics, and/or epidemiology to work on an NIH- and Gates Foundation-funded project aimed at decreasing the mosquito-vectored human disease, dengue fever.

QUALIFICATIONS: Although substantial experience with building simulation models is desirable, we will consider applicants who have little experience with model building, but have a strong record of picking up new quantitative skills. In depth knowledge of statistical methods is a plus.

PROJECT DESCRIPTION: The project is aimed at assessing the potential as well as risks associated with using selfish genetic elements to drive genes into mosquito populations that render them incapable of transmitting dengue fever or malaria. We are building and testing 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. Sensitivity analysis and uncertainty analysis of model outputs will be critical in assessing reliability. We are also building simple spatial and non-spatial, deterministic models as heuristic tools for better understanding basic principles, but we are not looking for applicants who are only interested in working with simple, generic models.

The fellowship is for 2 years (starting as soon as possible) 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 with the PIs (Fred Gould & Alun Lloyd) and another postdoc in organizing a workshop to teach other researchers how to use the models.

There are opportunities for some empirical research (if desired), and for interactions with other members of the lab who are working on other ecological and evolutionary research projects. NCSU is developing an interdisciplinary graduate program in Genetic Pest Management, so there are likely to be teaching opportunities

(if desired). <http://www.ncsu.edu/project/gpm/> 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. The closing date for applications is January 1, 2009, 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

RutgersU Computational Genomics

Postdoctoral position in computational genomics at Rutgers University

A postdoctoral position is available in the lab of Kevin Chen in the Department of Genetics and BioMaPS Institute for Quantitative Biology at Rutgers University. The lab is located on the New Brunswick campus of Rutgers University, approximately 35 miles south of New York City.

We are primarily a computational group interested in the function and evolution of post-transcriptional gene regulation mediated by microRNAs and RNA-binding proteins. We develop comparative and population genomics methods and have started a small wet-lab component as well. Some potential projects include predicting targets of RNA-binding proteins, post-transcriptional control of microRNA genes, the evolution of piRNAs and variation in post-transcriptional gene regulation in natural populations. Candidates interested in combining computational and experimental approaches are especially encouraged to apply. There

are a number of groups at Rutgers interested in similar questions and joint postdocs may be possible.

The ideal candidate would have a PhD in computational biology or a closely related field such as computer science, statistics or molecular biology. However, the candidate's PhD degree program is less important than a strong record of research achievement and interest in the lab's research program. The start date must be after September 2009.

Interested candidates should email their CV and a short note describing their qualifications and interest in the position to kc1111@nyu.edu. Please include the word "postdoc" in the subject.

Kevin Chen Assistant Professor (starting 2009) Dept. of Genetics & BioMaPS Institute for Quantitative Biology Rutgers University

<http://homepages.nyu.edu/~kc1111/> http://lifesci.rutgers.edu/~genetics/?page=faculty/faculty_details&id8 kcchen@gmail.com

UArizona VertebrateSystematics

George Gaylord Simpson Postdoctoral Fellowships in Vertebrate Systematics and Evolution - University of Arizona

The Department of Ecology and Evolutionary Biology announces one postdoctoral fellowship position for Fall 2009, named in honor of G. G. Simpson's long tenure at the University of Arizona. Simpson Fellows are expected to conduct an active research program that is facilitated and complemented by the Department's extensive natural history collections in ichthyology, herpetology, ornithology, and mammalogy. The EEB collections have a strong taxonomic focus on the fauna of the southwest United States, northwest Mexico, the Gulf of California and the Eastern Pacific. The positions are part of a renewed commitment to natural history collections on the University of Arizona campus and a new initiative in biodiversity informatics (<http://loco.biosci.arizona.edu/bdii/>). Postdoctoral Fellows are encouraged to establish research collaborations with faculty in the Department of Ecology and Evolutionary Biology. Responsibilities of the positions include teaching one course per year in the Fellow's taxonomic specialty. Salary is \$37,500 plus benefits (nine-month appointment). A research stipend of \$5000 will also be included. The positions are renewable for at least two

years based on satisfactory performance.

Applicants should submit application materials online at the University of Arizona Human Resources website (<https://www.uacareertrack.com>; look for job #39290), including C.V., statement of research and teaching interests and experience, and two letters of reference. Reference letters can be emailed to sanderm@email.arizona.edu. Position is open until filled, but we anticipate reviewing applications beginning on Jan. 15, 2009. Contact Dr. Peter Reinthal (pnr@email.arizona.edu) or Dr. Michael Sanderson (sanderm@email.arizona.edu) for further information.

Michael J. Sanderson

Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721

UdeMontreal MolEvolution

Postdoctoral Position in Aquatic Population genetics and molecular evolution at Université de Montréal (GRIL)

Members from the GRIL (French acronym for Inter-University Research Group in Limnology & Aquatic Sciences) at the Université de Montréal (UdeM) are seeking to fill one postdoctoral position in aquatic ecology. The GRIL is a consortium of researchers working on a wide array of topics in aquatic sciences from different universities and research institutes in Montreal and throughout Quebec. There are 9 members of the GRIL, established at UdeM.

The research programmes of the GRIL members at UdeM are quite varied and complementary. We are seeking candidates with research experience in any of the following topics: biogeochemical cycling of N, Hg and C, cyanobacteria, food web dynamics, landscape ecology, microbial ecology, population and community ecology, population genetics and molecular evolution. Interested candidates are encouraged to consult the GRIL website <http://www.gril-limnologie.ca> and department of biology website <http://www.bio.umontreal.ca/personnel/> to identify potential future GRIL collaborators located at UdeM.

Candidates should send a CV with a statement of research interests and the contacts for 3 potential references. Université de Montréal is a French

institution; however speaking French is not obligatory for the position. The current position is for 18 months. Please send applications to Roxane Maranger (r.maranger@umontreal.ca) and Bernard Angers (Bernard.angers@umontreal.ca). The candidate must assume the position by April 2009 at the latest. We will begin consulting applications on Dec. 15 2008 and will continue receiving applications until the position is filled.

Bernard Angers Professeur agrégé Département de sciences biologiques Université de Montréal

U**Edinburgh** Statistical**Genetics**

Applications are invited for an exciting opportunity to work on a BBSRC-funded project on the genetics of cognitive ageing. The successful applicant will have a PhD and be experienced in the statistical analysis of phenotype-genotype associations, especially genome-wide analyses. The appointee will be well-organised and self-driven; computing skills and knowledge of the relevant statistical techniques are required. Experience with quantitative traits is desirable. The overall aims of the project are: to make discoveries concerning the genetic contributions to non-pathological cognitive ageing in humans; to conduct a genome-wide association study of long-term normal cognitive ageing in two UK samples; and to conduct replication studies on new, large independent samples from the same centres. The human cohorts involved in the study have unique data on cognitive ageing over several decades. The work will be in collaboration with the project investigators who have expertise in cognitive ability and ageing, genetics, and statistical genetics. The appointee will be situated within the Department of Psychology and the Centre for Cognitive Ageing and Cognitive Epidemiology. The project also has a dedicated geneticist (already appointed).

This post is full time (35 hours per week). Starting date is from the beginning of February 2008 or as soon as possible thereafter. Interviews will take place during week beginning 12 January 2009.

Informal enquiries to:

Professor Ian Deary (Psychology) ian.deary@ed.ac.uk
or Dr Albert Tenesa (Statistical genetics) albert.tenesa@ed.ac.uk

Salary Scale: BP29,704 - 35,469

– The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

eanv63@holyrood.ed.ac.uk eanv63@holyrood.ed.ac.uk

U**NebraskaLincoln** Bioinformatics Mol**Evol**

** I'm posting this postdoc ad again. The application submission process has been modified. **

POSTDOCTORAL POSITION in Bioinformatics and Molecular Evolution at University of Nebraska-Lincoln

A postdoctoral position is available in the Etsuko Moriyama lab at the University of Nebraska-Lincoln. The research project emphasizes developing methods for protein classification and functional prediction, molecular evolutionary analyses of protein functions, and elucidating evolutionary and molecular mechanisms of duplicated proteins and their functional divergence. We are currently targeting protein families including G-protein coupled receptors and nuclear receptors. The scope, however, will be expanded to other families.

Our lab has very interdisciplinary research environment. We regularly collaborate with researchers in many different fields. The postdoc will have opportunities to collaborate with researchers with diverse backgrounds, from computer science, bioinformatics, structural biology, molecular evolution, population genetics, to genomics and molecular biology.

Preference will be given to applicants who have experience in any combination of the following fields: computer science (especially machine learning), multivariate statistical analysis, bioinformatics (especially protein classification and structural analysis), comparative genomics, and molecular evolution (especially for protein functions). Strong background in biology is highly desired. Proficiency in programming (using any language) is required. Experience in MySQL database development/management will be appreciated.

To apply, go to employment.unl.edu and click on Search Job Openings and complete the Faculty/Administrative application for Requisition #080977. Then also directly send a cover letter, CV, and names and contact information for three references to emoriyama2@unl.edu. The position becomes available on January 5, 2009, and will be supported

for 2 years or longer depending on funding situation. Applications will be reviewed as they arrive. Please feel free to contact me with any questions.

The University of Nebraska has an active National Science Foundation ADVANCE gender equity program, and is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers.

Etsuko Moriyama, PhD Associate Professor School of Biological Sciences & Center for Plant Science Innovation University of Nebraska-Lincoln 403 Manter Hall Lincoln, NE 68588-0118

Email: emoriyama2@unl.edu Phone: 402-472-4979, Fax: 402-472-2083 (SBS business office)

Moriyama Lab web page: <http://bioinfolab.unl.edu/-emlab/index.html> SBS faculty page: <http://www.biosci.unl.edu/faculty/moriyama/-index.shtml> emoriyama2@unlnotes.unl.edu emoriyama2@unlnotes.unl.edu

UNeuchstel Evolutionary Botany

We seek an evolutionary botanist who will investigate the occurrence, as well as the evolutionary and ecological consequences of gene flow between wheat and its wild relatives of the genus *Aegilops*. The position is available via 2 projects funded by the Swiss National Research Program NRP 59 on the "Risks and benefits of the deliberate release of genetically modified Organisms".

The main two axes of the research are: 1) The analysis of gene flow between cultivated wheat (*Triticum* sp.) and several wild *Aegilops* relatives, as well as between wild species of Mediterranean area and North America. 2) The study of the consequences of transgene flow through a field test, where the performances of *Aegilops cylindrica* introgressants with several transgenes are compared with those of non-transgenic introgressants. This experiment is included in the jointed field test of "wheat consortium" of PNR59, located at Reckenholz, close to Zürich. The successful candidate will have a PhD in biology and collaborate with a team including a technician and several master students. Moreover, he/she will benefit from an important scientific network in Switzerland. He/she must have experience in molecular population biology and is expected to do field collection and survey.

Beginning April 1st, 2009, duration of 24 months

Please send application to:

Dr. François Felber Institute of Biology Laboratory of evolutionary botany University of Neuchâtel Rue Emile-Argand 11 Case postale 158 CH-2009 Neuchâtel Switzerland E-mail : Francois.Felber@unine.ch

FELBER François <Francois.Felber@unine.ch>

UOtago NZ Microsatellite evolution

UNIVERSITY OF OTAGO Te Whare Wananga o Otago

Dunedin, New Zealand

Postdoctoral Fellow (Fixed-term)

DEPARTMENT OF ANATOMY AND STRUCTURAL BIOLOGY OTAGO SCHOOL OF MEDICAL SCIENCES

Microsatellites are abundant, highly variable, repeated DNA sequences that are regarded as the most versatile genetic markers yet discovered. They are a cornerstone of the current biological revolution and are used in gene mapping, in DNA forensic work, and as population markers. Conclusions drawn from such studies in many cases depend critically on assumptions about how microsatellites evolve. Despite its importance, our understanding of microsatellite evolution remains surprisingly sketchy. Current models of microsatellite evolution are overly simplistic and almost certainly incorrect, potentially leading to widespread data misinterpretation. In particular, genetic recombination, whilst known to be the major generator of genomic variability, is widely regarded as a minor contributor to microsatellite evolution, if indeed it contributes at all. Here we seek to quantify the extent and nature of microsatellite mutation, and, for the first time, explicitly examine the role of sexual recombination in generating microsatellite variability, using near identical yeast strains that variously do and do not engage in sex, and thus recombination. If, as we suspect, recombination is an important force in microsatellite evolution, evolutionary models will need to be modified, potentially with far-reaching consequences for how we analyse and interpret microsatellite data and for our understanding of trinucleotide repeat disorders, such as Fragile X and Huntington's disease.

Applications are invited from postdoctoral candidates

who have experience in molecular and population genetics. The Department offers opportunity to work in studies using leading edge DNA technologies. The successful candidate will have skills in molecular genetic techniques, particularly genotyping and sequencing, be highly skilled in analysis of genetic data and statistics, and be self-motivated and able to work alongside a wide variety of people.

Specific enquiries may be directed to Professor Neil Gemmell, Department of Anatomy and Structural Biology, Tel 03 479 6824, Fax 03 479 7254, Email neil.gemmell@otago.ac.nz.

Applications quoting reference number A08/150 close on Monday 1 December 2008.

APPLICATION INFORMATION

With each application you must include an application form, an EEO Information Statement, a covering letter, contact details for three referees and one copy of your full curriculum vitae. For an application form, EEO Information Statement and a full job description go to: www.otago.ac.nz/jobs <<http://www.otago.ac.nz/jobs>> Alternatively, contact the Human Resources Division, Tel 03 479 8269, Fax 03 479 8279, Email job.applications@otago.ac.nz <<mailto:ling.chong@stonebow.otago.ac.nz>>

Equal opportunity in employment is University policy.

E tautoko ana Te Whare Wananga o Otago i te kaupapa whakaorite whiwhinga mahi.

Neil J. Gemmell Professor and Director Centre for Reproduction and Genomics Department of Anatomy & Structural Biology University of Otago, PO Box 913 Dunedin 9054 New Zealand

Phone: +64 3 479 6824 Fax: +64 3 479 7254 e-mail: neil.gemmell@otago.ac.nz

UOulu Arabidopsis Speciation

Post doctoral position in genomics of speciation in *Arabidopsis lyrata*, in the plant genetics group, Department of Biology, University of Oulu, Finland,.

Arabidopsis lyrata is an outcrossing relative of the *A. thaliana*. The genome sequence of *A. lyrata* has just been completed. The project examines the genetics of incipient reproductive isolation between subspecies of *A. lyrata* and its ecological consequences (e.g. Kuittinen et al. 2004 Genetics, Leppälä et al. 2008 Heredity), exploiting the methods applicable in a fully sequenced species.

The post doc will have considerable independence in shaping the details of the project. The post doc will interact with doctoral students already working on related issues, and with partners of an ERANET Plant genomics project Arelatives <http://www.erapg.org/everyone/9587/18624/18614/18626>.

The duration of the project is two years, possibly extended for a third year. The project is funded by the Biosciences and Environment Research Council of Finland.

The salary is based on the Finnish Universities scales for teaching and research personnel, which include a component based on personal work performance.

The application should include a CV, a publication list, a statement of research interests and a short description of the motivation for applying for this position, and the names of two references.

The applications should be sent to Outi.Savolainen@oulu.fi, preferably by e-mail, before December 15, (or until position is filled). For further information, please contact Outi.Savolainen@oulu.fi (phone +358-8-5531782).

Outi Savolainen <outi.savolainen@oulu.fi>

UOxford Plant Chromosome Evolution

I'm looking for a motivated postdoctoral researcher to work on a 12 month project to study sex chromosome evolution in the plant *Silene latifolia* using the latest high-throughput sequencing technology. The successful candidate will ideally have strong interest in evolutionary genetics, some programming experience that will be essential for analysis of large amounts of DNA sequence data and experience in molecular genetics work. Experience with 454 sequencing technology will be a significant advantage. The funding is available to start as soon as possible. For informal enquiries please contact Dmitry Filatov on Dmitry.Filatov@plants.ox.ac.uk.

Dmitry A. Filatov, PhD Department of Plant Sciences, University of Oxford, South Parks Road, Oxford, OX1 3RB, United Kingdom

Dmitry Filatov <Dmitry.Filatov@plants.ox.ac.uk>

Uppsala Salix Adaptive Traits

A new Post doctoral position in genetics of adaptive traits and molecular breeding of Salix is now announced at the Dept. of Plant Biology and Forest Genetics (Faculty of Natural Resources and Agricultural Sciences at SLU in Uppsala). The position will be within a faculty project integrating different disciplines as molecular genetics, ecophysiology and plant breeding with focus on adaptive traits important for sustainable growth of Salix. Attached the announcement of the position. The announcement is also available at: <http://personal.slu.se/jobb> .

Best regards,

Ann Christin Rönnerberg-Wästljung

Ann Christin Rönnerberg-Wästljung, Assoc. Prof. (Docent) Department of Plant Biology and Forest Genetics, Uppsala BioCenter, SLU, Box 7080, S-750 07 UPPSALA, SWEDEN

Phone: +46-18 67 33 16 Fax: +46-18 67 33 89 E-mail: anki.wastljung@vbsg.slu.se

Ann Christin Rönnerberg-Wästljung
<Anki.Wastljung@vbsg.slu.se>

UQueensland Mosquito CoEvolution

Postdoctoral Fellow Positions Available

The School of Integrative Biology, The University of Queensland, Australia Laboratories of Professor Scott O'Neill and Dr Elizabeth McGraw

We have been funded by the NH&MRC and the Bill & Melinda Gates Foundation Grand Challenges in Global Health Initiative to develop new methodologies for the management of emerging vector-borne disease threats. The research program involves infection of mosquito vectors with an endosymbiotic bacterium, *Wolbachia pipiensis*, that is capable of reducing insect lifespan to reduce vectorial capacity. The project has successfully transinfected *Ae. aegypti* with the life shortening bacterium and is currently moving toward contained field

cage trials and developing a more comprehensive understanding of the host: pathogen interaction.

We are seeking Postdoctoral Fellows to work on projects in three areas: (1) Transcriptional age grading of mosquitoes (2) Physiological effects of *Wolbachia* infection on mosquitoes (3) Co-evolution of *Wolbachia*, mosquitoes, and Dengue virus

Salaries range from AUD\$62,500 - 72,000 + superannuation. The appointments are for 2 years initially and we are seeking to fill the positions as soon as possible.

The School of Integrative Biology (SIB) is a vibrant unit with a strong commitment to research excellence. Brisbane offers a beautiful climate and outdoor lifestyle.

Please contact Scott O'Neill (scott.oneill@uq.edu.au) for further information.

Elizabeth McGraw <e.mcgraw@uq.edu.au>

UTexas Population Genetics

Postdoc in population genetics:

We are searching for a postdoc to join us in a study of chromosome evolution using computation genomics. The project is a collaboration between Mark Kirkpatrick (University of Texas), Laurent Excoffier (Berne University), and Ary Hoffmann (Melbourne University).

We are investigating chromosome inversions by analyzing sequence data from *D. melanogaster* using large-scale genetic simulations and recently-developed statistical methods (Approximate Bayesian Computation). The goal is to develop quantitative tests of alternative hypotheses for how inversions evolve. The larger goals are to understand evolutionary forces shaping the genome's architecture and rates of recombination.

The postdoc will be responsible for developing simulation and statistics software. Experience with C/C++ programming, population genetics, and/or bioinformatics are desirable. There will be opportunities to work in all three of the participating laboratories.

The position will likely begin in the summer of 2009. Interested individuals are asked to email a CV and brief statement of qualifications to Mark Kirkpatrick (kirkp@mail.utexas.edu). Please also have three letters of recommendation emailed to that address.

kirkp@mail.utexas.edu kirkp@mail.utexas.edu

UTuebingen EvolutionaryMarineBiology

Eberhard-Karls-University Tuebingen, Germany

Research associate (PostDoc) *M a r i n e B i o l o g y*
(2x3 Years)

The group of Animal Evolutionary Ecology at the Faculty of Biology of the University of Tuebingen, Germany, has a position available for a research associate (appointment level TVL 13) für 3 years, with prolongation option for another 3 years.

The successful candidate is expected to develop an independent research and teaching program in experimental marine ecology. This includes the successful acquisition of external funding. Integration in a new project on the function of red fluorescence on coral reefs is desirable (Michiels et al, BMC Ecology 2008, 8:16). Crucial requirements are a Ph.D. in a relevant field by the time of employment, as well as a competitive publication record (corrected for vita). The teaching load represents 4 h/week during term. Most teaching is in English. International experience, fluency in English and a higher qualification in SCUBA diving are essential. Fluency in German is initially not required, but is an advantage.

Disabled candidates will be given preference when qualifications are equivalent. The University of Tuebingen would like to increase the proportion of women in academic science and teaching and therefore strongly encourages qualified female scientists to apply.

Send your application (c.v., publication list, references, short summary of research interests and teaching experience) in one pdf by Email to Nico Michiels (nico.michiels@uni-tuebingen.de). Screening will start from 15 December 2008 onwards. An appointment is possible from 1 January 2009. More information can be obtained from www.evoeco.uni-tuebingen.de or Nico Michiels.

The appointment is made by the central administration of the university.

Nico K. Michiels (Prof.) Animal Evolutionary Ecology Zoological Institute, Faculty of Biology University Tuebingen Auf der Morgenstelle 28 E 72076 Tuebingen Germany

Tel. +49 7071 29 74649 Mobile +49 170 4758003 Fax +49 7071 29 5634

nico.michiels@uni-tuebingen.de <http://www.evoeco.uni-tuebingen.de>
<http://www.eve.uni-tuebingen.de>

Nico Michiels <nico.michiels@uni-tuebingen.de>

UUtah Genomics

Post Doctoral Research Associate

Genomics, Ecological Immunology, Behavioral Ecology,

The overarching goal of this project is to examine the pathogenesis of Sin Nombre virus (SNV) infection in wild populations of deer mice. In particular, we are investigating behavioral and immune responses of deer mice to infection with SNV. One segment of this project involves require adapting existing genomic techniques used in model systems to deer mice as well as developing reagents for deer mice (e.g., custom microarrays). Another area of this project is focused on the behavioral response of deer mice to SNV infection. The successful candidate can choose the area in which they wish to concentrate.

Qualifications: Applicant must have a Ph.D. with background in one of the following: small mammal ecology, disease ecology, immunology, or related area. Prior experience in general laboratory techniques needed and preferred in the areas of immunological and molecular approaches (e.g., immune challenge assays, ELISA, RNA extraction, PCR, cloning, sequencing, microarrays). Prior experience needed trapping and handling small mammals or other vertebrates. Applicant must be willing to commit a minimum of four weeks per year in the field and able to lead a small field crew (3-4). Strong writing skills as evidenced through a publication record are essential.

To apply, send a cover letter detailing your interest in this project and suitability as well as career goals, CV, research statement, representative reprints, names and email addresses of at least three references to Dr. Denise Dearing <denise.dearing@utah.edu>. Start date February 1, 2009. Salary commensurate with experience. Funding guaranteed for 1 year; future funding possible. Publications from our lab in this area are available @ <http://www.biology.utah.edu/dearing/-index.html> .

Denise Dearing <dearing@biology.utah.edu>

UWashington PlantEvolution**Postdoctoral Position in Evolution of Plant Development**

Position available for NSF funded project to study the genetic and developmental basis of flower diversity in the laboratory of Dr. Verónica Di Stilio at the University of Washington in Seattle. Research is on the basal Eudicot genus *Thalictrum* (Ranunculaceae), using an evolution of development approach towards understanding morphological diversification of flowers. Current focus is on transcription factors as key regulators of development, in particular belonging to the MYB and MADS box families, that regulate organ identity and tissue differentiation in the flower.

Requirements: PhD in Plant Biology, Molecular, cellular, developmental biology or related field. Basic molecular biology and microscopy skills. Ability to perform in situ hybridizations, transgenic techniques, molecular evolution and phylogenetic analyses desired.

Funding is available for 2 years beginning January of 2009 (negotiable). Review of applications will begin immediately and continue until the position has been filled. Please send CV, research statement and 3 reference contacts to: Verónica Di Stilio, Department of Biology, University of Washington, Hitchcock Hall 506, Box 351800, Seattle WA 98195-1800. E-mail: distilio@u.washington.edu.

Verónica S. Di Stilio, PhD Assistant Professor Department of Biology University of Washington Hitchcock Hall 506 Box 351800 Seattle WA 98195-1800 (206) 616-5567 off (206) 685-4755 lab FAX (206) 616-2011

Veronica S Di Stilio <distilio@u.washington.edu>

Vienna ComputationalBiol**Research Position**

Research Biologist (2000€/month) 1-3 months contract

The Institute of Wildlife Biology and Game Management at the University of Natural Resources and Applied Life Sciences in Vienna is seeking an enthusiastic and innovative computational biologist to further enhance its biodiversity research in Austria.

Candidates should have a PhD in biodiversity biology with computational and data base expertise with a proven track record of research development and most preferably with scientific publication in that field.

Applications from researchers with experience of applied issues in spatial modelling and GIS-based analyses of distribution and diversity patterns of animal communities (birds, mammals) and environmental parameters (habitat structure and climate) are particularly welcome.

Closing date for receipt of applications is 30.11.2008

Further details on the post are available from:

Dr. Sabine Marlene Hille Institute of Wildlife Biology and Game Management University of Natural Resources and Applied Life Sciences

Gregor Mendel-Stra©33 1180 Vienna Austria Tel.: +431 47654 4463 Fax.: +431 47654 4459

sabine.hille@boku.ac.at

Dr. Sabine Marlene Hille

Institute of Wildlife Biology and Game Management

University of Natural Resources and Applied Life Sciences

Gregor Mendel-Stra©33 1180 Vienna Austria

Tel.: +431 47654 4463 Fax.: +431 47654 4459 skype: sabinehille

Sabine Hille <sabine.hille@boku.ac.at>

WorkshopsCourses

HinxtonUK MolEvol Mar29-Apr9	84	UCopenhagen PlantGenetics Jan12-23 NewDate ...	86
Portal Arizona AntSystematics Aug6-16	84	UFlorida MolecularMarkers Dec8-12	87
UCopenhagen PlantGenetics Jan12-23	85		

HinxtonUK MolEvol Mar29-Apr9

There are still places available at the following course. Please feel free to draw this to the attention of anyone who may be interested:

Molecular Evolution

29 March-9 April 2009 Wellcome Trust Genome Campus, Hinxton, Cambridge, UK

Deadline for applications: 21 November 2008

Course summary This joint Wellcome Trust-EMBL-EBI advanced course aims to provide researchers with the theoretical knowledge and practical skills required to carry out molecular evolutionary analysis on their own data, as well as on data drawn from sequence databases. The course will combine basic assumptions and ideas fundamental to the field with discussion of cutting-edge methodologies, and is therefore relevant to researchers with a range of different experience levels.

Programme * interpretation of molecular phylogenetic trees and sequence alignments * genomics resources and sequence alignments * phylogeny reconstruction models * hypothesis testing in phylogenetics * coalescent model and inference from population data.

Course organisers * Nick Goldman (European Bioinformatics Institute, Hinxton, UK) * Ziheng Yang (University College London) * Aidan Budd (European Molecular Biology Laboratory, Heidelberg)

Guest instructors * Ewan Birney (European Bioinformatics Institute), * Martin Embley (University of Newcastle) * Adrian Friday (University of Cambridge) * Olivier Gascuel (LIRMM, Montpellier, France) * Arndt von Haesler (Center for Integrative Bioinformatics, Vienna, Austria) * Rasmus Nielsen (University of California, Berkeley) * Bill Pearson (University of Virginia) * Alexandros Stamatakis (Ludwig-Maximilians University, Munich) * Jeff Thorne (North Carolina State University) * Ken Wolfe (Trinity College Dublin)

For full details, see <http://www.wellcome.ac.uk/>-

Professional-resources/Courses-and-conferences/-Advanced-Courses/Courses/WTX049272.htm or <http://tinyurl.com/5xgkww> Nick Goldman tel: +44-(0)1223-492530 EMBL - European Bioinformatics Institute fax: +44-(0)1223-494468 Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK goldman@ebi.ac.uk goldman@ebi.ac.uk

Portal Arizona AntSystematics Aug6-16

ANT COURSE 2009 <http://www.antweb.org> Southwestern Research Station (SWRS), Portal, AZ, USA August 6-16, 2009

DEADLINE FOR APPLICATION: April 1, 2009 Application form: http://spreadsheets.google.com/viewform?key=pJ5tAoQvdvQ-GA_IFRxxdZA

COURSE OBJECTIVES. - ANT COURSE is designed for systematists, ecologists, behaviorists, conservation biologists, and other biologists whose research responsibilities require a greater understanding of ant taxonomy and field research techniques. Emphasis is on the identification of the ant genera and species occurring in North America. Lectures will include background information on the ecology, life histories and evolution of ants. Field trips are structured to teach collecting and sampling techniques, and associated lab work provides instruction on specimen preparation, sorting and labeling. Information on equipment/supply vendors, literature, and myrmecological contacts are also presented.

COURSE SIGNIFICANCE. - Ant Course is a unique opportunity to acquire training that is unavailable elsewhere. This course will provide students with 1) the confidence and skills to identify the ant genera of North America; 2) an understanding of modern specimen processing and curation techniques; 3) an appreciation for the biological diversity of ants, and 4) experience keying to the species level.

SPONSORS. -California Academy of Sciences and Museum of Comparative Zoology, with funding in part from National Science Foundation.

BACKGROUND INFORMATION. - ANT COURSE will be taught from August 6 - 16, 2009 at the Southwestern Research Station (SWRS) in Portal Arizona (<http://research.amnh.org/swrs/>). The Station is centered amid the richest ant fauna in North America. This is an ongoing course, offered annually.

PARTICIPANT ACCEPTANCE CRITERIA. - ANT COURSE is open to all interested individuals. Priority will be given to those students for whom the course will have a significant impact on their research with ants. An entomological background is not required. We aim to include students with a diverse interest in biology, including ant systematics, ecology, behavioral biology, genetics, and conservation. The high instructor to student ratio will allow students to receive individual attention. ANT COURSE is presented in English and limited to 30 participants

COSTS. - Tuition for the 10-day COURSE is \$475 for current students and \$675 for non-students. In addition, the Southwestern Research Station (SWRS) fee for this period, covering dormitory room and board, is \$600. Transportation costs between home and Tucson (air) or SWRS (auto) are to be borne by all participants.

FELLOWSHIPS. - Four fellowships are available for 2009. Two fellowships cover tuition fees and two fellowships cover station fees. Foreign students may apply for additional fellowships to assist in travel. Those interested in attending the course should seek all possible avenues to secure funding for the course. You should only apply for the Ant Course fellowship if you can not find other support and it is essential for your participation in the course. Beware that if you apply for an ant course fellowship it implies that fellowship funding is essential to your participation in the course. Thus, if you are not selected for a fellowship, you might not be accepted into the course. Please notify the course if your funding request status changes before the application due date.

COURSE APPLICATION. - Application and course information at <http://www.antweb.org> . The first step is to fill out a form at: http://spreadsheets.google.com/viewform?key=pJ5tAoQvdvQ-GA_IFRxxdZA In addition, you must also submit a CV, personal statement, and letter of reference to 2009AntCourse@gmail.com.

2009 Possible **INSTRUCTORS:** Brian Fisher (Coordinator), Dept. of Entomology, California Academy of Sciences, San Francisco, CA, bfisher@calacademy.org

Stefan Cover (Coordinator), Museum of Comparative Zoology, Harvard University, Cambridge, MA, cover@oeb.harvard.edu Lloyd Davis, Gainesville, FL, ants@gru.net Mark Deyrup, Archbold Biological Station, P.O. Box 2057, Lake Placid, Florida 33862 USA, mdeyrup@archbold-station.org Bob Johnson, Dept. of Biology, Arizona State University, Tempe, Arizona, atraj@imap1.asu.edu Mike Kaspari, Dept. of Zoology, University of Oklahoma, Norman OK, mkaspari@ou.edu Joshua King, Department of Biological Science, Unit 1, Chieftain Way, Florida State University, Tallahassee, FL 32306-4370, jking@bio.fsu.edu Jack Longino, Lab I, The Evergreen State College, Olympia WA, longinoj@evergreen.edu

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

UCopenhagen PlantGenetics Jan12-23

COURSE ANNOUNCEMENT:

“Molecular Markers in Plant Genetics 2009”

Again, in January 2009, we are offering a Ph.D. course on the topic

“Molecular Markers in Plant Genetics” (course credit: 20%, 6 ECTS points).

TIME AND PLACE:

This course will be conducted from 12-01 to 23-01-2009, at the University of Copenhagen, Faculty of Life Sciences (former Royal Veterinary & Agricultural Univ., KVL),

Department of Agriculture and Ecology, Plant and Soil Sciences Laboratory, Copenhagen.

TARGET GROUP:

Even though the course mainly aims to PhD students, senior scientific staff, technical lab staff and other professionals interested in the area are encouraged to consult the course responsible in order to arrange a possible attendance. The number of participants is limited due to optimal lab working conditions.

CONTENT:

- * DNA isolation from plant tissues
- * SSR (single sequence repeats or microsatellites) detection
- * AFLP (Amplified fragment length polymorphism) detection
- * Tilling/Eco-tilling (high-throughput method to detect mutations and allelic variations)
- * Semi-automated fragment analysis on AB (capillaries) and LI-COR (gel) systems.
- * Sequencing of PCR fragments (AB capillary system) and primer design
- * SNP (single nucleotide polymorphism) detection
- * Principles of different marker applications (Diversity, Mapping, QTL detection)

TEACHING ARRANGEMENTS:

The participants will have two weeks (two times 5 days) of a full-day mixture of theoretical introductions and laboratory work. The main emphasis is on practical experience, the theoretical background targets towards the understanding of the basis of the techniques to enable troubleshooting and the application in the participant's projects. During the course, informal oral presentation and discussion of those projects will take place.

The course language will be English.

EVALUATION:

At the end of the course the participating PhD-students will be asked to give an oral examination

on selected papers that are related to the course content.

PREREQUISITES:

Basic knowledge of genetic/molecular genetics and basic experience in a molecular lab is highly recommended.

COURSE FEE:

The course fee to cover the lab cost for PhD student is 3.840 DKK

and for participants from the private sector 7.680 DKK.

CONTACT AND REGISTRATION:

Participants should register latest 19-12-2008 to

Gunter Backes (Assoc. Professor)

University of Copenhagen

Faculty of Life Sciences

Department of Agriculture and Ecology

Thorvaldsensvej 40

DK-1871 Frederiksberg C

Denmark

eMail: guba@life.ku.dk Phone: +45 35 33 34 34

Gunter Backes <guba@life.ku.dk>

UCopenhagen PlantGenetics

Jan12-23 NewDate

COURSE ANNOUNCEMENT:

“Molecular Markers in Plant Genetics 2009”

Again, in January 2009, we are offering a Ph.D. course on the topic “Molecular Markers in Plant Genetics” (course credit: 20%, 6 ECTS points).

TIME AND PLACE:

This course will be conducted from 19-01 to 30-01-2009, at the University of Copenhagen, Faculty of Life Sciences (former Royal Veterinary & Agricultural Univ., KVL), Department of Agriculture and Ecology, Plant and Soil Sciences Laboratory, Copenhagen.

TARGET GROUP:

Even though the course mainly aims to PhD students, senior scientific staff, technical lab staff and other professionals interested in the area are encouraged to consult the course responsible in order to arrange a possible attendance. The number of participants is limited due to optimal lab working conditions.

CONTENT:

* DNA isolation from plant tissues * SSR (single sequence repeats or microsatellites) detection * AFLP (Amplified fragment length polymorphism) detection * Tilling/Eco-tilling (high-throughput method to detect mutations and allelic variations) * Semi-automated fragment analysis on AB (capillaries) and LI-COR (gel) systems. * Sequencing of PCR fragments (AB capillary system) and primer design * SNP (single nucleotide polymorphism) detection * Principles of different marker applications (Diversity, Mapping, QTL detection)

TEACHING ARRANGEMENTS:

The participants will have two weeks (two times 5 days) of a full-day mixture of theoretical introductions and

laboratory work. The main emphasis is on practical experience, the theoretical background targets towards the understanding of the basis of the techniques to enable troubleshooting and the application in the participant's projects. During the course, informal oral presentation and discussion of those projects will take place.

The course language will be English.

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Basic knowledge of genetic/molecular genetics and basic experience in a molecular lab is highly recommended.

COURSE FEE:

The course fee to cover the lab cost for PhD student is 3.840 DKK and for participants from the private sector 7.680 DKK.

CONTACT AND REGISTRATION:

Participants should register latest 19-12-2008 to

Gunter Backes (Assoc. Professor) University of Copenhagen Faculty of Life Sciences Department of Agriculture and Ecology Thorvaldsensvej 40 DK-1871 Frederiksberg C Denmark eMail: guba@life.ku.dk Phone: +45 35 33 34 34

Gunter Backes <guba@life.ku.dk>

Molecular Markers Workshop

ICBR's Genetic Analysis Laboratory and Education Core at the University of Florida are offering its Molecular Markers: Tools for Developing Enriched Microsatellite Libraries workshop on December 8-12, 2008. This popular workshop will take participants through the steps of a tried and true enrichment protocol which includes restriction enzymes, size selection, PCR, fragment selection with probes, and other techniques commonly used in a molecular laboratory using DNA they bring. Participants will learn about newer technology being used to develop microsatellite libraries, such as FLX 454 sequencing, gain some experience designing primers, analyzing data, and will have the potential of leaving with an enriched library.

The cost of this workshop is: \$500.00 for all registered UF students, faculty and staff. \$900.00 for all others.

Register on-line: <http://www.biotech.ufl.edu/-educationtraining/registration.html> For further information contact:

Ginger Clark, Genetic Analysis Laboratory: 352-273-8044 or ginger@biotech.ufl.edu

Thank you, Sharon Norton

Sharon E. Norton Scientific Education Coordinator University of Florida ICBR Education and Training Core Laboratory PO Box 103622 Gainesville, FL 32610 office:(352) 273-8048 lab: (352) 273-8047 fax: (352) 273-8069 <<http://www.biotech.ufl.edu>> www.biotech.ufl.edu

ICBR Announcement <norton@biotech.ufl.edu>

UFlorida MolecularMarkers Dec8-12

Instructions

Instructions: To be added to the EvoDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it

originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

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

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

Afterward

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