
E v o l D i r

June 1, 2007

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.

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ChicagoBotanicGarden StudentPlantBio Jul6

GREAT OPPORTUNITY FOR STUDENTS TO PRESENT AND LEARN ABOUT PLANT BIOLOGY AND CONSERVATION RESEARCH IN A COLLEGIALLY LOW STRESS SETTING

WHAT: PLANT BIOLOGY AND CONSERVATION STUDENT RESEARCH SYMPOSIUM WHERE: CHICAGO BOTANIC GARDEN WHEN: JULY 6, 2007 (IMMEDIATELY BEFORE BOTANY 2007 MEETING IN CHICAGO)

The Chicago Botanic Garden is pleased to host the first ever Student Research in Plant Biology and Conservation Symposium especially for graduate and undergraduate students and postdocs. It will be held on Friday July 6, 2007 immediately before the Botany 2007 meeting in Chicago.

This will be a day-long event that is focused on providing students with an early opportunity to present their research to colleagues. It is a wonderful chance for students with related interests and concerns to learn about the research of others, make contacts, and present their

own work in a collegial and low stress environment. The event will close with our distinguished keynote speaker, Dr. Kent Holsinger, of the University of Connecticut.

For program updates and abstract submission guidelines, please visit:

<http://www.chicagobotanic.org/school/symposia> Or contact Beth Pinargote, Symposium Coordinator, at 847-835-8278.

The deadline for receipt of abstracts is MAY 15, 2007. Registration is \$29 and includes morning coffee, lunch, parking and all symposium handouts.

nzerega@chicagobotanic.org

ChicagoBotanicGarden StudentPlantBio Jul6 DeadlineExt

ABSTRACT SUBMISSION DEADLINE EXTENDED:

GREAT OPPORTUNITY FOR STUDENTS TO PRESENT AND LEARN ABOUT PLANT BIOLOGY AND CONSERVATION RESEARCH IN A COLLE-

GIAL LOW STRESS SETTING RIGHT BEFORE THE BOTANY 2007 MEETINGS

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For program updates and abstract submission guidelines, please visit:

<http://www.chicagobotanic.org/school/symposia> The deadline for receipt of abstracts is MAY 28, 2007.

nzerega@chicagobotanic.org

Halifax SMBE Jun24-28 AbstSubmission

2007 Annual meeting of the Society for Molecular Biology and Evolution

JUNE 24-28?Dalhousie University, Halifax, Nova Scotia, Canada

<http://www.smbe.org/> ABSTRACTS SUBMISSION DEADLINE?MAY 15 2007.

ACCOMMODATION?Halifax is a busy tourist destination in summertime. We strongly advise you to reserve your hotel or dorm rooms early via the conference website.

TRAVEL?As of January 2007, all United States citizens will be required to show United States passports in order to re-enter the US from Canada. This has resulted in delays in processing passport applications. If you need to renew or obtain a US passport in order to attend the conference, we recommend that you apply as soon as possible.

John Archibald <jmarchib@dal.ca>

Hangzhou QuantGenetics Aug19-24

Announcement The 3rd International Conference on Quantitative Genetics (ICQG3) will be held during August 19-24, 2007, in Hangzhou, China. As with the 1st ICQG in Ames, Iowa in 1976 and the 2nd ICQG in

Raleigh, North Carolina in 1987, the 3rd Conference will be a comprehensive survey of the current status of quantitative genetics. New technologies in areas ranging from genomics and molecular genetics to statistics are providing both opportunities and challenges for our understanding of the genetic basis of quantitative traits in natural populations, the evolution of characters, and use for plant and animal breeding. The Conference welcomes participants to submit contributed papers. Only an abstract is needed and is to be submitted at registration for the conference. A limited number of contributed papers will be selected for oral presentation in an appropriate session of the conference and all others will be presented in formal poster sessions. The deadline for the abstract submission for the selection of oral presentation has now been extended to June 1, 2007. The Conference will be held in an international hotel, the Yellow Dragon Hotel, in the downtown of Hangzhou. The program listing invited speakers is on the website. Please check out the conference website <http://www.icqg.org/> for more information about the conference and for registration and abstract submission. If you have questions and suggestions, please contact ICQG3@zju.edu.cn.

zeng@statgen.ncsu.edu

Hangzhou QuantGenetics Aug19-24 ICQG Deadlines

Third International Conference on Quantitative Genetics Hangzhou, China August 20-24, 2007

The deadlines for submitting an abstract and for US graduate students and junior faculty to submit travel grant applications have been extended to June 1, 2007.

The conference web site is <http://www.icqg.org/web/> Travel grant applications should be sent to bsweir@u.washington.edu <<mailto:bsweir@u.washington.edu>> Send CV, abstract of conference poster and letter from advisor or senior colleague as well as statement of purpose in attending conference and visiting China.

There will be three one-day short courses at Zhejiang University, Hangzhou on Sunday August 19 (Population Genetics: Amy Anderson and Bruce Weir; QTL Mapping: Rebecca Doerge and Zhao-Bang Zeng; Association Mapping: Lon Cardon and Dahlia Nielsen). Details on the conference web site.

Bruce Weir

Bruce Weir <bsweir@u.washington.edu>

London Linnaeus Jun1

In Linnaeus' Wake: 300 years of marine discovery

A meeting, to be hosted at the Linnean Society of London with an evening reception on the Swedish Ship Götheborg on the River Thames

June 1, 2007

The fundamental contribution of Linnaeus to the scientific world - a system of nomenclature and classification - was underpinned by his collections and those of his Apostles', made possible in the mid 18th Century by the maritime power of European nations. Ships, and shipping companies such as the Swedish East India Company (SOIC), were used by Linnaeus to expand his collections from all over the globe. To celebrate both the tercentenary of Linnaeus' birth, and the arrival of the Swedish Ship Götheborg in London (an exact replica of the 18th Century East Indiaman Götheborg used by the SOIC), a scientific meeting will be hosted this summer at the Linnean Society of London with an evening reception aboard the vessel moored on the River Thames.

The meeting will cover the historical importance of the SOIC and Linnaeus, life aboard an 18th century vessel, and scientifically will focus on marine systematic and taxonomic discoveries from the last three hundred years. It will show how in the age of DNA sequencing and deep-sea robotic submarines, much of marine science is still in the discovery phase', just as it was in Linnaeus' day. Our meeting, jointly sponsored by Göteborg University, Zoologica Scripta, the Hasselblad Foundation, the Linnean Society and The Natural History Museum will celebrate the life of Linnaeus and his legacy, and show what an 18th century square-rigged East Indiaman was like for the scientist and sailor.

Speakers will include: Dr Tony Rice, Prof Phil Rainbow, Dr Katrin Linse, Dr Ben Wigham, Dr Kenneth Nyberg, Dr Hans Nyman, Dr John Taylor, Dr Alex Rogers, Joakim Severinson

The full agenda is available here: <http://web.mac.com/adrianglover/iWeb/linnaeus/Agenda.html>

The registration form is avail-

able for download here: <http://web.mac.com/adrianglover/iWeb/linnaeus/Registration.html>

Please register soon as places are filling up!

Dr Adrian Glover Zoology Department The Natural History Museum Cromwell Rd., London SW7 5BD, U.K

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web: <http://web.mac.com/adrianglover>

Marseilles 11thEvolBiol Sep19-21 Abstracts

Dear all,

As you've been already informed about, the 11th Evolutionary Biology Meeting will take place in Marseilles on September 19,20,21.

The next deadline for submitting an abstract is June 31st.

You can find all the information about abstracts, registration, hotels (new compiled list) and program on our website:

<http://www.up.univ-mrs.fr/evol-cgr/> do not hesitate to contact me at eege@up.univ-mrs.fr

Best regards

- Julie Perrot Logistical Organisation Committee

EA 3781 Evolution Biologique Université d'Aix Marseille I - case 19 Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 <http://www.up.univ-mrs.fr/evol> We are organizing the 11th Evolutionary Biology Meeting at Marseilles - 19-21 September 2007 <http://www.evolutionary-biology.org> <http://www.up.univ-mrs.fr/evol-cgr/> eege@up.univ-mrs.fr

NHM London MolluscEvol Nov13

The Malacological Society of London

<http://www.Malacsoc.org.uk>

Molluscan Forum 2007

13th November 2007, 10.00 am - 6.30 pm Natural History Museum, London

CALL FOR REGISTRATIONS AND PAPERS This informal, annual meeting is designed to bring together people starting their research on molluscs, to give them the opportunity to present and discuss their work and to compare notes on methods and problems.

Attendance is open to all, but speakers and poster presenters should be research students, post-doctoral researchers, undergraduates starting molluscan projects or dissertations, and amateurs engaged in substantial projects, which have not yet been published. Any topic related to molluscs is acceptable: palaeontological, physiological, behavioural, ecological, systematic, morphological or molecular.

Short talks (15 min) or posters may be offered. They need not be polished accounts of completed work: descriptions of new methods, work in progress, appeals for assistance with unsolved problems are equally acceptable. Powerpoint presentations are the usual form, but should be discussed in advance (see registration form overleaf).

In addition to talks and posters there will be opportunities to acquire reprints contributed by members of the Society. The forum will end with a wine reception.

There is no registration fee; a limited amount of help with travel costs will be available for presenters who cannot claim them from elsewhere.

Enquiries and registrations to: Prof Georges B. Dussart, Canterbury Christ Church University, Canterbury CT1 1JK (tel: +0227 767700, email: gbd1@canterbury.ac.uk) or to Dr Manuel Malaquias, Department of Zoology, Natural History Museum, Cromwell Road, London SW7 5BD (email: m.malaquias@nhm.ac.uk). Non-presenters: please let us know you will be coming so that we may estimate numbers.

Deadline for registrations and abstracts submission: 22nd October 2007.

– Dr Manuel António E. Malaquias

Scientific Associate Department of Zoology Natural History Museum Cromwell Road, SW7 5BD London, United Kingdom

Email: m.malaquias@nhm.ac.uk Tel: +(0)2079425949 Fax: +(0)2079425054 Mobile phone: +(0)7742971138

m.malaquias@nhm.ac.uk

New York AGA Conservation Genetics Sep27-29 abstracts

POSTER ABSTRACT SUBMISSION IS OPEN -
Deadline July 1

REGISTRATION FEE: STUDENTS (US\$100),
POSTDOCS, RESEARCHERS, PROFESSORS
(US\$250)

ConGen3: The 3rd biannual International Symposium
on Conservation Genetics

sponsored by the American Genetic Association

Date: 27-29 September, 2007

Location: American Museum of Natural History, New
York, NY, USA

Website: <http://genomics.amnh.org/congen3> E-mail:
congen3@gmail.com

ConGen3 will be held at the AMNH Sackler Institute
for Comparative Genomics in New York City.

Session topics:

- Genetic research for biodiversity surveys, characterization of unique microbial communities, and barcoding initiatives.
- Conservation Genetics in Time: conservation phylogenetics and tree reconstruction for identification of hidden biodiversity and examination of hybrid zones.
- Ex Situ Conservation Genetics: intensive metapopulation management in theory and practice.
- Genetics of Invasive Species: patterns and control.

More information regarding registration will be made available soon at <http://genomics.amnh.org/congen3>.

Interested participants can exchange information on New York City related travel and housing options on the online forum <http://groups.google.com/group/-congen3> On behalf of the organizers: George Amato (American Museum of Natural History) Gisella Caccone (Yale University) Rob DeSalle (American Museum of Natural History)

— Sergios-Orestis Kolokotronis Sackler Institute for Comparative Genomics American Museum of Natural History Central Park West at 79th Street New York, NY 10024 -USA- tel +1 212 313 7648 koloko@amnh.org <http://koloko.net> koloko@amnh.org

RhodeIsland FuncGenomics Jul8-13

GORDON CONFERENCE: EVOLUTIONARY, ECOLOGICAL & FUNCTIONAL GENOMICS

We are pleased to announce this summer's Evolutionary, Ecological & Functional Genomics conference, which will take place July 8-13, 2007, at Salve Regina University in Newport, Rhode Island. This is a fairly new topic for a Gordon Conference, and we are hoping for a good turnout to encourage sustained meetings in this interdisciplinary field. We have a great group of speakers who will discuss a variety of emerging genomic approaches to speciation, adaptation, phenotypic plasticity, species interactions, and other processes; talks will cover a broad range of organisms from viruses to fishes to fungi to wild tomatoes.

Details about the program and registration information can be found at the Conference website at <http://www.grc.org/programs.aspx?year=2007&program=-evolecol>.

Poster presenters can apply for the opportunity to present short (20 min) talks at the conference. If interested, please send your poster title and abstract to Greg Wray (below).

Limited funds are available to assist graduate students and post-docs who are planning to present a poster at the conference (\$300 if traveling within North America and \$600 from outside North America). If you are interested in applying for these funds, send poster title and abstract along with CV to Greg Wray (email address below). US Citizens and Permanent Residents who are minorities can apply directly to the Gordon Research Conference for \$600 support at <http://www.grc.org/diversity.aspx?page=2> If you have any questions, please contact one of us (contact info below).

Regards,

Greg Wray & Scott Edwards

Greg can be reached at ggray@duke.edu, or 919-684-6696, and Scott at sedwards@fas.harvard.edu, or 617-684-8082

noon@duke.edu noon@duke.edu

Roscoff HostParasite Sep22-26

Jacques Monod Conference: Evolutionary genetics of host-parasite relationships

In Roscoff (Brittany), France, September 22-26, 2007

Deadline for application: May 15, 2007

More info under <http://www.cnrs.fr/sdv/cjm/-cjmebert.e.html> Organizers: Dieter EBERT, Universität Basel, Switzerland and Gabriele SORCI, Université de Bourgogne, Dijon, France

The Jacques Monod Conference "Evolutionary genetics of host-parasite relationships" aims to provide a state of the art assessment of what evolutionary thinking can contribute to an integrated understanding of the processes shaping host-parasite interactions. The conference is structured in three major topics, which are intimately linked with each other. Topic 1. Understanding the genetic interactions between hosts and parasites. Topic 2. Host and parasite evolution and the maintenance of sexual reproduction Topic 3. The evolutionary genetics of immune defence.

More info under <http://www.cnrs.fr/sdv/cjm/-cjmebert.e.html> -

Dieter Ebert [[Mailto:dieter.ebert@unibas.ch](mailto:dieter.ebert@unibas.ch)] <http://evolution.unibas.ch/> Universität Basel, Zoologisches Institut, Vesalgasse 1 4051 Basel, Switzerland Tel. +41-(0)61-267 03 60

RoyalSociety London EvolAnimals Jun18-19

Last Chance to Register. Last Chance to Register. Last Chance to Register.

Dear Colleague,

There are a few places left for registration for a meeting entitled:

The evolution of the animals: a Linnean tercentenary celebration

which takes place in the meeting rooms of the Royal Society, London, 18-19 June 2007. A full two days of

presentations by leading scientists in the field of animal evolution is planned.

The meeting is free to attend but pre-registration online is essential.

<http://www.royalsoc.ac.uk/event.asp?id=-3D4163&month=3D6,2006>

We expect the meeting to be of interest to all animal and evolutionary biologists, regardless of developmental stage or geological age. The Royal Society has assured us that a large audience can be accommodated, but early registration will guarantee admission to the main auditorium.

The list of speakers and session chairs can be found at the end of this email.

Please forward this announcement to anyone who might be interested.

With very kind regards and apologies for cross postings,

Yours sincerely,

Max Telford and Tim Littlewood

Chairs and Speakers:

Andrew Smith Simon Conway Morris Michael Akam Peter Holland Graham Budd, Kevin Peterson Jeff Boore Hervé Philippe Rudy Raff Nicole King Jaume Bagnuà Ronald Jenner Mark Martindale Gonzalo Gribet Detlev Arendt Max Telford Andrew Peel Billie Swalla Chris Lowe – Dr Max Telford Reader in Zoology Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 Fax: +44 (0)20 7679 7096 <http://www.ucl.ac.uk/biology/academic-staff/telford/telford.html> Zoonet: Marie Curie Research Training Network <http://www.zoonet.eu.com> ROYAL SOCIETY MEETING / LINNEAN SOCIETY MEETING : 18-19 JUNE 2007

The Evolution of the Animals - a Linnean Tercentenary Celebration

<http://www.royalsoc.ac.uk/event.asp?id=-3D4163&month=3D6,2006>

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

SarasotaFL InsectBioinformatics Jul15-18

Symposium Announcement:

As part of the Florida Entomological Society Annual Meeting a new symposium has been organized on the use of bioinformatic tools to study applied problems in insect research. The aim of this symposium is to highlight how to analyze genetic information using bioinformatic tools, what kinds of questions can be addressed with the available tools and how these tools are being applied to insect specific problems.

Invited Speakers:

Robert Shatters, Jr. (USDA)- Utility of population genetics software applied to *Bemisia tabaci*. Kim Van De Linde (FSU)- *Zaprionus indianus* an emerging pest in Florida. Rod Nagoshi (USDA)- Haplotyping of *Spodoptera frugiperda*. Laura Boykin (USDA)- Utility of phylogenetics software-*Diaphorina citri* and *B. tabaci*. Marjorie Hoy (UF)- Identifying parasitoids of *Toxoptera citricida* using DNA methods. Donna Devlin (FAU)- Microsatellites and the parasitic beetle (*Coccotrypes rhizophorae*).

When: July 15, 2007-July 18, 2007 (Symposium-July 16, 2007) Where: Ritz-Carlton, Sarasota, Florida

Deadline for abstract submission: June 1, 2007 Deadline for registration: June 22, 2007 Website for more information: <http://www.flaentsoc.org/annual.htm> Any questions: Laura Boykin laura.boykin@ars.usda.gov 772-462-5915

Laura Boykin, Ph.D. USDA, ARS, U. S. Horticultural Research Laboratory 2001 South Rock Rd. Fort Pierce, FL 34945

Phone: (772) 462-5915 FAX: (772) 462-5986

E-mail: laura.boykin@ars.usda.gov

Laura Boykin <laura.boykin@ARS.USDA.GOV>

Seattle StatGenetics Jun23

Registration is now open for the Seattle Showcase Symposium in Statistical Genetics at the University of Washington on Saturday June 23.

Speakers include Josh Akey, Lon Cardon, Mike Clegg, Michael Nachman, Margaret Pepe, Yun Song and Elizabeth Thompson. Mark Courtney will talk about funding opportunities at NSF.

Details at <http://www.biostat.washington.edu> Bruce Weir

Bruce Weir <bsweir@u.washington.edu>

St Andrews ArcticAlpineFlora Jun25-27

Dear All

The abstracts of oral presentations to be given at the international symposium on the

HISTORY, EVOLUTION AND FUTURE OF ARCTIC AND ALPINE FLORA

to be held in St Andrews, Scotland, June 25-27, 2007, can now be accessed at

<http://biology.st-andrews.ac.uk/aafcon/-programme.htm> Deadline for Registration and Submission of Poster Abstracts: 25 May 2007

Regards Richard Abbott (Symposium organizer)

– Richard Abbott School of Biology University of St Andrews St Andrews, Fife KY16 9TH UK Tel. 01334 463350 Fax. 01334 463366 Email. rja@st-and.ac.uk Website: <http://biology.st-and.ac.uk/-staff/abbott.html> rja@st-andrews.ac.uk rja@st-andrews.ac.uk

Taipei IntlDNABarcodingConf Sep16-21

The Consortium for the Barcode of Life will be holding the Second International Barcode of Life Conference at Academia Sinica in Taipei, Taiwan during the week of 16-21 September 2007. Feel free to contact me directly (not through TaxaCom, please!) at SchindelD@si.edu if you have comments or questions.

The conference website is at www.dnabarcodes2007.org <<http://www.dnabarcodes2007.org>> .

There is a 1 June deadline for submission of abstracts and applications for travel bursaries (for participants from developing countries only).

David E. Schindel, Executive Secretary

Consortium for the Barcode of Life 202/633-0812; fax 202/633-2938; portable 202/557-1149 Email: SchindelD@si.edu <<mailto:SchindelD@si.edu>> CBOL

WEBSITE: <http://www.barcoding.si.edu> <<http://www.barcoding.si.edu>> Office and overnight delivery address:

National Museum of Natural History Room CE-119
10th & Constitution Avenue, NW Washington, DC 20560

Postal mailing address:

National Museum of Natural History Smithsonian Institution P.O. Box 37012, MRC-105 Washington, DC 20013-7012

schindeld@si.edu schindeld@si.edu

Trento PopGenet Sep6-8

This is a reminder that all abstracts and applications for bursaries for the INTERNATIONAL WORKSHOP: "Population Genetics for Animal Conservation II" Monte Bondone, Trento, Italy. September 6-8, 2007 are due on 15 May 2007.

We would especially encourage applications for THREE FULL BURSARIES that are offered for attendance at the workshop to young doctoral or post-doctoral researchers from countries where animal conservation is particularly urgent, but severely underfunded.

ALL RELEVANT INFORMATION IS AVAILABLE AT the web site <http://www.cealp.it/PGAC/> (or send an e-mail to pgac2@cealp.it).

Invited speakers include: Karina Acevedo-Whitehouse (Institute of Zoology, UK) Eric Anderson (NOAA Fisheries Service, Santa Cruz, USA) Jon Ballou (Smithsonian's National Zoological Park, USA) Peter Beerli (Florida State University, USA) Giorgio Bertorelle (University of Ferrara, Italy) Luigi Boitani (University of Rome "La Sapienza", Italy) Mike Bruford (University of Cardiff, UK) Armando Caballero (University of Vigo, Spain) Rob DeSalle (American Museum of Natural History, NY, USA) Oscar Gaggiotti (Université J Fourier, Grenoble, France) Ilkka Hanski (University of Helsinki, Finland) Rus Hoelzel (University of Durham, UK) Michael Hofreiter (Max Planck Institute, Leipzig, Germany) Craig Moritz (University of California, Berkeley, USA) Rasmus Nielsen (University of Copenhagen, Denmark) Stephen Palumbi (Stanford University, USA) Josephine Pemberton (University of Edinburgh, UK) Craig Primmer (University of Turku, Finland) Pierre Taberlet (Université J Fourier, Grenoble, France)

Just to remind you: the aims of the workshop are to identify recent theoretical and methodological developments in population genetics suitable for understanding (and possibly solving) problems of animal conservation, to discuss recent solutions to past and present controversies in conservation genetics, and to allow theoretical and applied biologists to meet and discuss advanced methods of data analysis and software tools.

The scientific committee: Giorgio Bertorelle, University of Ferrara, Italy Mike Bruford, University of Cardiff, UK Claudio Chemini, CEA, Viote del Monte Bondone, Trento, Italy Heidi Hauffe, CEA, Viote del Monte Bondone, Trento, Italy Elena Pecchioli, CEA, Viote del Monte Bondone, Trento, Italy Cristiano Vernesi, CEA, Viote del Monte Bondone, Trento, Italy

Cristiano Vernesi Centro di Ecologia Alpina Viote del Monte Bondone - 38040 Trento - Italy tel +390461939529

vernesi@cealp.it vernessi@cealp.it

full and 2 half days will host 30 talks (15 invited) and 60 participants. Evenings will involve poster sessions and one social dinner, while after lunch hours will remain as an open slot to refresh the mind. There will be small walks in and around the medieval town of Trento for these times.

The conference call, a list of invited speakers, preliminary conference program, and venue details are available at:

<http://www.cosbi.eu/events/bwb07.php> Best Regards,

BwB Scientific Committee;

Orkun S. Soyer (CoSBI) Nicolas Buchler (Rockefeller University) Martin Ackermann (ETH)

– Orkun S. Soyer, PhD

CoSBI The Microsoft Research - University of Trento Centre for Computational and Systems Biology www.cosbi.eu Orkun Soyer <soyer@cosbi.eu>

Trento PopGenet Sep6-8 deadline

Dear Colleague,

We would like to remind you of the upcoming deadline (May 31st) for submission of oral and poster presentations to “Biology Without Borders”. The main aim of this event is to bring researchers that are using experimental and theoretical approaches to achieve a systems level understanding in biology, with an emphasis on evolutionary approaches. With the participation of leading scientists from the general field of systems biology and with a unique format that is a blend of conference and workshop this event is bound to be an excellent scientific meeting. The invited speakers are:

Sebastian Bonhoeffer, ETH Nicolas Buchler, Rockefeller University Wolfgang Marwan, MPI Michael Stumpf, Imperial College London Michael Laub, MIT Stas Shvartsman, Princeton Leah Cowen, University of Toronto Richard Lenski, Michigan State University Sarah Teichmann, MRC Francois Taddei, INSERM Uwe Sauer, ETH Doris Bachtrog, UCSD Dan Andersson, Uppsala University Andre Levchenko, John Hopkins University Andreas Wagner, Uni. Zurich

As mentioned previously, “Biology Without Borders” is organized by The Microsoft Research - University of Trento Centre for Computational and Systems Biology (CoSBI) on 2-5 October 2007 in Trento, Italy. The 2

UGuelph AppliedEvolution May15-16 4

REMINDER: Approximately 2 weeks left to register for the 2007 Peter Yodzis Colloquium in Fundamental Ecology

“Applied Evolution: Understanding the Past, Predicting the Future”

May 15th and 16th 2007 University of Guelph, Guelph, Ontario, Canada

The colloquium will focus on the mechanistic basis of adaptation and the potential to predict adaptive evolution in pure and practical applications. There will be a series of keynote lectures and an open poster session, all at a pace conducive to conversation and interaction.

Confirmed keynote lecturers include:

Graham Bell (McGill University)– “Adaptation of algae to elevated CO2” Michael Lynch (Indiana University)– “Evolutionary genetics/genomics of Daphnia” David Mindell (University of Michigan)– “Applied evolution in understanding disease, criminal justice and cultural change: what the public should know” Patricia Schulte (University of British Columbia)– “Mechanistic basis of adaptation to environmental change: lessons from a small fish” Ruth Shaw (University of Minnesota)– “Inferences about selection: a general solution to an

empirical challenge” John Willis (Duke University)–“Genetic analysis of adaptation and reproductive isolation in *Mimulus*”

For information, go to

<http://www.ecologycolloquia.uoguelph.ca/main.shtml>

For credit card registration (\$55 for students, \$130 for non-students, both including GST), go to

<http://www.peopleware.net/index.cfm?siteID=-323&eventDisp=07YODZIS>

Christina (Chris) Caruso Assistant Professor Department of Integrative Biology University of Guelph Axelrod Building 50 Stone Road East Guelph, Ontario N1G 2W1 CANADA 519-824-4120 ext. 52030 carusoc@uoguelph.ca

carusoc@uoguelph.ca carusoc@uoguelph.ca

UGuelph AppliedEvolution May15-16 5

REMINDER: Approximately ONE WEEK left to register for the 2007 Peter Yodzis Colloquium in Fundamental Ecology

“Applied Evolution: Understanding the Past, Predicting the Future”

May 15th and 16th 2007 University of Guelph, Guelph, Ontario, Canada sponsored by the University of Guelph and Blackwell Publishing

The colloquium will focus on the mechanistic basis of adaptation and the potential to predict adaptive evolution in pure and practical applications. There will be a series of keynote lectures and an open poster session, all at a pace conducive to conversation and interaction. In addition, Blackwell (publishers of the new journal *Evolutionary Applications*) is sponsoring prizes for the best posters (\$150 for first place, \$50 for second place). Consequently, we have extended the deadline for submitting a poster title until the end of the week (May 11th).

Confirmed keynote lecturers include:

Graham Bell (McGill University)–“Adaptation of algae to elevated CO₂” Michael Lynch (Indiana University)–“Origins of Genome Architecture” David Mindell (University of Michigan)–“Applied evolution in understanding disease, criminal justice and cultural change: what the public should know” Patricia Schulte (University

of British Columbia)–“Mechanistic basis of adaptation to environmental change: lessons from a small fish” Ruth Shaw (University of Minnesota)–“Inferences about selection: a general solution to an empirical challenge” John Willis (Duke University)–“Genetic analysis of adaptation and reproductive isolation in *Mimulus*”

For information, go to

<http://www.ecologycolloquia.uoguelph.ca/main.shtml>

For credit card registration (\$55 for students, \$130 for non-students, both including GST), go to

<http://www.peopleware.net/index.cfm?siteID=-323&eventDisp=07YODZIS>

To submit a poster title, go to

<http://www.ecologycolloquia.uoguelph.ca/postercall.shtml>

Christina (Chris) Caruso Assistant Professor Department of Integrative Biology University of Guelph Axelrod Building 50 Stone Road East Guelph, Ontario N1G 2W1 CANADA 519-824-4120 ext. 52030 carusoc@uoguelph.ca

UWarwick PopGenetics Dec17

Dear Colleagues,

The Population Genetics Group meeting (“the popgroup”) this year will be held on Monday 17th of December to Thursday 20th of December at the University of Warwick conference centre, Coventry, West Midlands, United Kingdom. Further details can be found on the website: <http://www.popgroup.org/> <<http://www.popgroup.org/>>

Best regards, Dmitry

Dr D.A.Filatov Senior Lecturer in Evolutionary Genetics School of Biosciences University of Birmingham Edgbaston, Birmingham B15 2TT United Kingdom

Dmitry Filatov <d.filatov@bham.ac.uk>

UZurich OriginEvolMediterraneanBiota Jul14-15 2

Dear Colleagues, please note the upcoming conference:

“Origin and Evolution of Biota in Mediterranean Climate Zones: An Integrative Vision”

14-15 July 2007, University of Zurich, Switzerland.

Registration deadline: May 30, 2007

Understanding the biotic and abiotic processes that contribute to high species numbers in biodiversity ‘hot spots’ is one of the major tasks of biology. The exceptional biological richness of the five mediterranean climate zones of the earth - the Mediterranean basin, South Africa, Australia, Chile and California - makes them an ideal case study to investigate the evolutionary and ecological dynamics that generate elevated species numbers. By focusing on the Mediterranean basin, the conference will synthesize the current state of knowledge on the origin of mediterranean biota, while charting a map for pushing the frontier of conceptual and methodological advances in biodiversity studies. The goal of the conference is to clarify the history of biotic assembly in mediterranean climate zones by integrating evidence across multiple disciplines, including evolutionary biology, systematics, ecology, paleontology, paleoclimatology, and paleogeology. Target audience The conference is aimed at scholars from various biodiversity disciplines at different stages of their careers, from beginning Ph.D. students to established scholars.

Speakers

Plenary Speakers: Michael Donoghue - Yale University, USA “Phylogenetic Biogeography: Past, Present, and Future”. John Thompson - CNRS, Montpellier, France “The dynamics of plant populations in the Mediterranean mosaic landscape: Ongoing adaptation and response to contemporary changes”. Invited Speakers: Ackerly, David - University of California, Berkeley, USA Case studies, Ecology “Climate and the California flora: Past, Present and Future”. Arroyo, Juan - University of Seville, Spain Case studies, Ecology “Sex polymorphism in Mediterranean plants: insights from heterostyly and floral biology”. Cheddadi, Rachid - Université Montpellier II, France Methods, Paleovegetation reconstruction “Past climate changes in the Mediterranean and potential impacts on some plant species”. Comes, Hans Peter - University of Salzburg, Austria Case studies, Microevolutionary patterns “Plant evolution in the Aegean region”. Conti, Elena - University of Zurich, Switzerland Case studies, Macroevolutionary patterns “Dating the origin of plants endemic to the Corso-Sardinian microplate: a window on the biogeography of the western Mediterranean Basin”. Cozzolino, Salvatore - University of Naples, Italy Case studies, Ecology “Pollination strategies, reproductive isolation and speciation processes in Mediterranean orchids”. Fady, Bruno - INRA,

Avignon, France Case studies, Microevolutionary patterns “Biodiversity at gene level in Mediterranean conifers”. Kadereit, Joachim - University of Mainz, Germany Case studies, Microevolutionary patterns “Determinants of phylogenetic structure in Mediterranean coastal plants”. Krijgsman, Wout - University of Utrecht, Netherlands Methods, Paleoclimate reconstruction “The Messinian Salinity Crisis in the Mediterranean”. Lamont, Byron - Curtin University, Perth, Australia Case studies, Ecology “Plant adaptations in mediterranean Australia”. Linder, Peter - University of Zurich, Switzerland Case studies, Macroevolutionary patterns “Evolution of the Cape flora of Southern Africa, and the influence of the mediterranean type climate”. Magallon, Susana - UNAM, Mexico Methods, Integration of fossils in molecular dating To be announced Medail, Frederic - University of Marseilles, France Case studies: Macroevolutionary patterns: “Importance of historical biogeography in shaping plant diversity in the Mediterranean basin”. Medel, Rodrigo - University of Chile, Santiago, Chile Case Studies, Ecology “Evolutionary ecology of mutualistic animal-plant relationships in mediterranean ecosystems”. Moore, Brian - Yale University, USA Methods, ancestral area reconstruction “A Maximum Likelihood framework for inferring biogeographic history”. Nieto Feliner, Gonzalo - Royal Botanic Garden, Madrid, Spain Case studies, Microevolutionary patterns: “Species distribution modeling matches phylogeographic patterns in the Atlantic-Mediterranean disjunct *Armeria pungens*”. Oberprieler, Christoph - University of Regensburg, Germany Case studies, Macroevolutionary patterns “The temporal, spatial, and ecological differentiation of Compositae-Anthemidae in the Circum-Mediterranean area”. Ree, Rick - Field Museum, Chicago, USA Methods, Ancestral area reconstruction “Stochastic models of geographic range evolution and likelihood-based inference of ancestral ranges”. Rosenbaum, Gideon - University of Queensland, Australia Methods, Paleogeological reconstruction “Geological history of the Mediterranean basin”: Rossello, Josep - University of Valencia, Spain

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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>

Vienna EuropeanDrosophila Sep12-14 correction

Contrary to my previous mail, the deadline is May, 31- sorry for the confusion!

20th European Drosophila Research Conference 12 - 14 September 2007, Reed Exhibitions & Congress Center Vienna

<http://www.imp.ac.at/EDRC2007/> DEADLINE FOR THE SUBMISSION OF ABSTRACTS: MAY, 31

Please note that this EDRC has a strong focus on Evolution and Population Genetics furthermore, the EDRC will be followed by an ESF sponsored workshop on Ecological Genetics <http://i122server.vu-wien.ac.at/-ESF.html> Plenary Speakers:

Michael Boutros, Heidelberg Maria Dominguez, Alicante Suzanne Eaton, Dresden Matt Freeman, Cambridge Peter Keightley, Edinburgh Mike Levine, Berkeley Gero Miesenboeck, Yale Linda Partridge, UCL Roland Strauss, Mainz Leslie Vosshall, Rockefeller

Session Chairs: Michael Ashburner, Cambridge, UK (Genomics, RNAi and Techniques) Mike Bate, Cambridge, UK (Neurobiology & Behaviour) Giacomo Cavalli, Montpellier (Chromatin & Gene Expression) Robert Farkas, Bratislava (Physiology) Greg Gibson, Raleigh, NC (Population Genetics) Nicolas Gompel, Marseille (Evolution) Jules Hoffmann, Strasbourg (Immunity & Apoptosis) Thomas Lecuit, Marseille (Cell Biology) Christian Lehner, Bayreuth (Growth Control & Cell Division) Benny Shilo, Weizman Institute (Development)

————— Christian Schlötterer Institut für Tierzucht und Genetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-250775603 fax: +43-1-250775693 <http://i122server.vu-wien.ac.at/> christian.schloetterer@vu-wien.ac.at christian.schloetterer@vu-wien.ac.at

Vienna EuropeanDrosophila Sep12-14 deadline

20th European Drosophila Research Conference 12 - 14 September 2007, Reed Exhibitions & Congress Center Vienna

<http://www.imp.ac.at/EDRC2007/> DEADLINE FOR THE SUBMISSION OF ABSTRACTS: MARCH, 31

Please note that this EDRC has a strong focus on Evolution and Population Genetics furthermore, the EDRC will be followed by an ESF sponsored workshop on Ecological Genetics <http://i122server.vu-wien.ac.at/-ESF.html> Plenary Speakers:

Michael Boutros, Heidelberg Maria Dominguez, Alicante Suzanne Eaton, Dresden Matt Freeman, Cambridge Peter Keightley, Edinburgh Mike Levine, Berkeley Gero Miesenboeck, Yale Linda Partridge, UCL Roland Strauss, Mainz Leslie Vosshall, Rockefeller

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————— Christian Schlötterer Institut für Tierzucht und Genetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-250775603 fax: +43-1-250775693 <http://i122server.vu-wien.ac.at/> christian.schloetterer@vu-wien.ac.at christian.schloetterer@vu-wien.ac.at

GradStudentPositions

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antonio.fontdevila@uab.es

AUBarcelona 2 EvolBiol

Graduate positions: Autonomous University of Barcelona (Spain) PhD studentship announcement

Two 4 year Graduate Student Positions in Evolutionary Biology at the Autonomous University of Barcelona, Department of Genetics and Microbiology, Spain

Two graduate PhD studentship positions are available for research in either of the following areas: a) evolutionary significance of transposable elements in processes of colonization of invasive species by molecular and chromosomal studies of insertion copy distribution b) speciation studies on the genetic architecture of reproductive isolation by molecular detection of genetic factors of male hybrid sterility

The work will be carried out in the Evolutionary Biology Group. Applicants must have completed their undergraduate studies in one of the following disciplines: Biology, Genetics, Biochemistry or Environmental Sciences. Salary: 11,460 per year during the first two years and 16,100 per year during the last two years.

Send grades of your undergraduate studies with a CV by e-mail to antonio.fontdevila@uab.es immediately specifying in which area (a, b) are you interested.

For further information contact: Antonio Fontdevila (<http://einstein.uab.es/afontdevila>) Principal Investigator Grup de Biologia Evolutiva Department de Genetica I Microbiologia Universitat Autònoma de Barcelona 08193 Bellaterra (Barcelona) Spain Phone: 34-93-581108 Fax: 34-93-5812726 e-mail: antonio.fontdevila@uab.es

AustralianNatIU 5 EvolBiol

The College of Science and the School of Botany and Zoology at The Australian National University will be offering up to FIVE PhD Scholarships. Please note that these are currently restricted to Australian and New Zealand citizens. For full details check out our web site <http://www.anu.edu.au/BoZo/-BoZoScholarships.html> The deadline for applications is May 31. If you miss this deadline, however, we still suggest that you contact potential supervisors to discuss forthcoming funding sources.

– Michael Jennions ARC Fellow/Senior Lecturer School of Botany & Zoology The Australian National University Canberra ACT 0200 Australia

T: +61 2 6125 3540 F: + 61 2 6125 5573 E: www.anu.edu.au/BoZo/jennions CRICOS # 00120C

michael.jennions@anu.edu.au
michael.jennions@anu.edu.au

ETH Zurich 3 PopGenet

Three funded PhD studentships in Population Ecology and Population Genetics at the Professorship of Ecosystem Management, ETH Zurich, Switzerland.

Title: Integrating genetic diversity and phenotypic plasticity into plant population responses to climate change in the Alps

Start Date: January 2008

The Professorship of Ecosystem Management is offering three PhD positions in Plant Ecology and Ecological Genetics to address the relative importance of intrinsic adaptive variation, local (pre-) adaptation and phenotypic plasticity to Alpine plant populations abilities to adapt to climate change.

All three projects will be supervised by Prof. Dr. Jaboury Ghazoul, Dr. Andrea R. Pluess and Dr. Chris Kettle, and will form part of the BIOCHANGE platform at ETH Zurich.

*Project: * Alpine plant populations are predicted to shift to higher elevations in response to climate change. Under such conditions core populations will move to higher elevations currently occupied by peripheral populations occupying the present species range limits. Should conservation efforts prioritize the current core populations which are predicted to contain greater genetic diversity or small isolated peripheral populations?

We will investigate the relative importance of intrinsic adaptive variation, local (pre-) adaptation and phenotypic plasticity to Alpine plant populations abilities to adapt to climate change. Key questions include: 1) Does local adaptation and phenotypic plasticity in high-altitude peripheral populations infer an advantage over core populations under predicted climate change scenarios? 2) Do small peripheral populations which are predicted to have lower genetic diversity than large central populations, have reduced adaptive potential? 3) Does gene flow via pollen between core and peripheral populations undermine local adaptation of peripheral populations and can this lead to outbreeding depression. These questions will be addressed using field-based reciprocal transplant experiments, experimental populations in climate-controlled chambers, artificial inter-population breeding experiments and direct and indirect measures of gene flow using molecular markers.

Requirements: We are seeking three highly motivated applicants, with a desire to work on the ecology and genetics of alpine plants in the context of climate change. Applicants should have a B.Sc and M.Sc degree, preferably with experience in experimental population biology, statistics, and ideally molecular work. Excellent spoken and written English is required, and German would be highly advantageous though not strictly necessary. Applicants should enjoy working both in the field (Swiss pre-alpine and alpine area) and in the labo-

ratory. The three PhD positions will be part of a team of researchers working on the general theme of plant responses to climate change in alpine systems, and will also be members of the Ecosystem Management group, led by Prof. Jaboury Ghazoul. Therefore, we place a strong emphasis on cooperation and team work. Requests for additional information on the three positions offered, or other informal enquiries, should be made to Dr. Pluess andrea.pluess@env.ethz.ch, tel: +41 (0)44 632 89 75. Information about the research group can be found at <http://www.ecology.ethz.ch/> *Conditions of Employment:* Three years appointment at ETH, Zurich. Starting Salary: minimum 37,600 Swiss Francs per year.

*Application: * Please send a letter of motivation, CV and names and addresses of two academic referees to Dr. Andrea Pluess, by e-Mail (andrea.pluess@env.ethz.ch).

Deadline: 10th July 2007

chris.kettle@env.ethz.ch chris.kettle@env.ethz.ch

Innsbruck HumanHistory

PhD-thesis: Phylogenetic reconstruction of human settlement in south-east Asia

Theme: The human settlement in south-east Asia is only known along general lines. The aim of this research project is to reconstruct migration routes and phylogenetic structures of selected south-east Asian populations by using modern yet established molecular DNA-typing technologies (DNA-high-throughput-sequencing; SNP-multiplex-typing) and appropriate phylogenetic algorithms.

Work conditions: We offer a full-time PhD-position in the frame work of the Austrian FWF Translational-Research project "EMPOP - an innovative mitochondrial DNA database" for a period of 3 years. The Institute of Legal Medicine at the Innsbruck Medical University, Austria, disposes a high-tech infrastructure for molecular DNA analytics. Through the establishment of the mitochondrial DNA database EMPOP (www.empop.org), the Institute of Legal Medicine in Innsbruck holds a worldwide key position in the field of forensic mtDNA analyses.

Job description: Generation of mtDNA control region sequences of selected south-east Asian populations; Determination of the mitochondrial haplogroup with

SNP-multiplexes; Phylogenetic reconstructions using PAUP*, MIGRATE, MrBAYES, NETWORK,...

Minimum requirements Candidates should hold a master's degree in the field of biological, chemical or life sciences. Practical experience of molecular biological lab work and computer literacy are essential, along with a high level of fluency in spoken and written English. Good communication and team-working skills are required and evidence of drive and self motivation. Experience and interest in mathematics/statistics would be desirable.

We offer: We offer a friendly and inspiring work atmosphere in an internationally renowned scientific team, access to brand-new scientific methods and IT-systems and efficient mentoring and support.

Please send your application to:

Prof. Walther Parson, PhD MSc Institute of Legal Medicine Innsbruck Medical University Muellerstrasse 44 A-6020 Innsbruck, Austria

T +43 (0)512 9003 70640 F +43 (0)512 9003 73640 E-Mail: walther.parson@i-med.ac.at

anita.brandstaetter@i-med.ac.at

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

<http://oldwebsite.laurentian.ca/biology/english/faculty/lesbarreres.htm> 935 Ramsey Lake Road, Sudbury, Ontario P3E 2C6, Canada phone: 705-675-1151 ext. 2275 Fax: 705-675-4859

Closing date for applications: July 01, 2007

dlesbarreres@laurentian.ca

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

Dr. David Lesbarrères Assistant Professor & Graduate Coordinator

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

<http://biology.laurentian.ca/faculty/lesbarreres.htm> 935 Ramsey Lake Road, Sudbury, Ontario P3E 2C6, Canada phone: 705-675-1151 ext. 2275 Fax: 705-675-4859

dlesbarreres@laurentian.ca

LaurentianU AmphibianDiseases

Amphibian Emerging Infectious Diseases

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

A minimum stipend (\$15.000 CAD) will be provided as well as opportunities for additional scholarships.

How to apply: Please send a letter of intent, CV, 2 references, and unofficial transcript to:

Dr. David Lesbarrères Assistant Professor & Graduate Coordinator

MasseyU EarlyEukaryotes

PhD Scholarship: Cell biology of early eukaryotes

Supervisors, Lesley J Collins and David Penny The Allan Wilson Center for Molecular Ecology and Evolution, Massey University, Palmerston North, New Zealand (<http://awcmee.massey.ac.nz/>) has a PhD Scholarship for an Integrated Bioinformatics approach to understanding the basic cell biological evolution of eukaryotes.

1. By combing bioinformatics and information on gene function and subcellular location we are beginning to build an excellent picture of the ancestral eukaryote cell. The project aims to help us understand both the ultimate origin of eukaryotes, and also the main features of the evolution of the cell biology within eukaryotes.

Preferred skills are a good background in molecular biology of eukaryotes with a strong interest in computers and bioinformatics. The necessary training in basic Perl or Python scripts can be learned as the project develops.

2. An alternative approach could come from a more computer science/physical science/ mathematics approach. This involves a more computer centered study that infers, for example, ancestral sequences and aims to reconstruct ancestral networks of related proteins in important aspect of cellular function. Necessary skills would require more computational skills with a good basic knowledge of molecular biology.

3. An excellent student may wish to propose their own approach to the topic.

Starting date: variable, depending on the academic year of Northern or Southern Hemisphere applicants.

For additional information, contact Dr Lesley Collins, L.J.Collins@massey.ac.nz Allan Wilson Center for Molecular Ecology and Evolution, see <http://awcmee.massey.ac.nz> Thank you Susan Adams

–

Susan Adams Executive Officer/Business Manager Allan Wilson Centre for Molecular Ecology and Evolution Massey University Private Bag 11-222 Palmerston North New Zealand

Tel: +64 6 350 5448 Fax: +64 6 350 5626 Mobile: 021 379 427

s.i.adams@massey.ac.nz

PurdueU Barcoding MHCevol

Two graduate positions (M.S. or Ph.D.) are available at Purdue University, one on DNA barcoding and another on the evolution of major histocompatibility complex (MHC) genes in wild vertebrates (salamanders, eagles, or kangaroo rats). Most of the research will be lab-oriented, but both projects have field components as well. Strong molecular and/or analytical skills are desired. For more information, contact Andrew DeWoody (dewoody@purdue.edu) or see <http://www.agriculture.purdue.edu/fnr/html/faculty/DeWoody/index.html>. Graduate assistantships are funded at ~\$19,000 per year (Ph.D.) plus a substantial waiver of tuition & fees. Motivated applicants should submit a short letter of interest, including cumulative GPA, GRE scores, and contact information for three references. Formal applications must be received by September 15, 2007 to be considered for spring 2008 admission, but informal inquiries are welcome beforehand.

dewoody@purdue.edu

Switzerland AlpineEvol

PH.D. POSITION IN ALPINE ECOLOGY IN SWITZERLAND

For a climate change project on plant growth at tree-line we are seeking a highly motivated PhD candidate (3 yrs, fully funded) in the field of alpine plant ecology. Research will be conducted at Davos in the Swiss Alps.

The successful candidate will investigate the impacts of warming and elevated CO₂ on plants, nutrient uptake and carbon cycling. Measurements include growth and phenology of trees and dwarf shrubs and analysis of above- and below-ground plant samples for stable isotopes. Results will be published in international peer-reviewed journals. We highly welcome development of independent ideas.

Your profile: graduate degree in natural sciences, preferably ecology or biology, experience in experimental field work and statistical analyses (particularly in R or SPlus), ability to move in steep alpine terrain under sometimes harsh conditions, experience in lab work, fluent in English. You are able to work independently, have good organization skills, are motivated and initiative, and in addition stand out as a good communicator and team player.

Our group is part of the Swiss Federal Institute for Forest, Snow and Landscape Research WSL and the Swiss Federal Institute for Snow and Avalanche Research in Davos.

The position needs to be filled soon. Please send your complete CV as soon as possible and latest by 31 May 2007 with photo using reference number 477 to Ms. Madeleine Oberhaensli, WSL-SLF, Fluelastrasse 11, CH-7260 Davos Dorf. For further information please contact Dr. Christian Rixen, Tel. +41 (0)81 4170214, email: rixen@slf.ch (additional electronic application welcome). Christian Rixen (PhD) Swiss Federal Research Institute WSL Research Unit Ecosystem Boundaries Team Alpine Ecosystems Flüelastrasse 11 CH- 7260 Davos tel ++41 81 417 02 14 fax ++41 81 417 01 10 e-mail: rixen@slf.ch http://www.wsl.ch/personal_homepages/rixen/ rixen@slf.ch

Sydney 2 EvolEcol

Two PhD Scholarships in Evolutionary Ecology (Sydney, Australia)

Both projects will be based in Macquarie University's Centre for the Integrative Study of Animal Behaviour (<http://galliform.bhs.mq.edu.au/~cisab/>) and are supported by MQRES Scholarships*.

Project 1. - Maintenance of polymorphism in the Gouldian finch

This project will investigate the persistence of the rare yellow morph of the endangered Gouldian finch in wild and captive populations. The general research theme is to understand why the genetically determined yellow morph naturally occurs at much lower levels (< 1%) than the red (30%) and black (70%) morphs of this species. Based on the genetic determination of the morphs we should expect to find a much higher frequency of the yellow morph in natural populations. However, previous work has shown that yellow individuals are behaviourally dominated by the other two morphs and also are generally avoided as mates. This project will investigate a variety of physiological and behavioural traits in an attempt to characterise both positive and negative selection on the yellow morph to understand its place in this classic balanced polymorphism. Although the research program into which this project fits is supported by ongoing ARC Discovery and Linkage grants, the student will have ample room for individual choice of specific topics and design of experiments. Applicants should have a background in some of the following areas: biology, animal behaviour, behavioural ecology, evolutionary ecology, genetics.

The project is based in the research group of A/Prof Simon Griffith, to whom enquiries should be directed (simon.griffith@mq.edu.au) before 31 May 2007. This project will be jointly supervised by Dr Sarah Pryke (also in CISAB).

Project 2. - Genetic structure of the chestnut-crowned babbler

We seek a student to investigate the genetic structure of the cooperatively breeding chestnut-crowned babbler: from family groups through local populations up to the broad-scale species range in arid, and semi-arid Australia. This research program, focusing on an avian equivalent of the meerkat, will include field-work, be-

havioural observation and a substantial molecular component (PCR-based microsatellite genotyping) with the main aim of understanding the breeding system of this species, and the way in which ecology interacts with dispersal and local adaptation to contribute to the evolution of cooperative breeding. This project will use an ongoing study population at the Fowlers Gap Arid Zone Research Station (far-west NSW) and a number of other wild populations throughout the range. Although the research program into which this project fits is supported by an ongoing ARC Discovery grant, the student will have ample room for individual choice of specific topics and design of research. Applicants should have a background in some of the following areas: biology, animal behaviour, behavioural ecology, evolutionary ecology, genetics.

The project is based in the research group of A/Prof Simon Griffith, to whom enquiries about the project should be directed (simon.griffith@mq.edu.au) before 31 May 2007. This project will be jointly supervised by Dr Andrew Russell (University of Sheffield, UK, <http://www.sheffield.ac.uk/aps/-contacts/acadstaff/russell.html>).

* MQRES scholarships are available year round for Australian and International students. MQRES scholarships include an APA-equivalent stipend (currently AU\$19,616 p.a. tax exempt), allowances for relocation and thesis costs, international tuition fees and overseas health cover for a maximum of 3.5 years tenure. Applicants should have completed equivalent research qualifications to a four-year Australian Bachelor degree with First Class Honours, such as a Bachelor degree plus a Masters degree with a substantial research component. AU\$6,000 p.a. is provided by CISAB to all PhD students to cover direct research expenses of their project, and several generous internal schemes are available to fund travel to visit overseas laboratories and to attend conferences.

Simon Griffith Centre for the Integrative Study of Animal Behaviour Macquarie University Sydney, NSW 2109, Australia. phone: +61 9385 8068 fax: +61 2 9850 9231 <http://galliform.bhs.mq.edu.au/~cisab/> simon.griffith@mq.edu.au

TrinityCollege MiscanthusGenomics

Genomics of the biomass crop *Miscanthus*: characterizing variation in the plastid genome and assessing nu-

clear polyploid variation

A three-year PhD fellowship funded under the Wash Fellowship Schema is available for a research project on the biomass crop plant *Miscanthus*. *Miscanthus* species are perennial, C4 grasses capable of tremendous biomass growth under a wide range of climatic conditions. Attention has focussed on biomass crops because of the need for alternative energy sources for sustainable living. Very few *Miscanthus* genotypes have been assessed for their biomass potential but work is underway to develop new genotypes. The overall aim of this project is to gather essential genomic information required for plant breeding in this poorly understood genus. The focus will be on the characterization of the nuclear and cytoplasmic gene pools. The entire chloroplast genome sequence will be sequenced, partial sequences of the mitochondrial genome will be generated and chromosome number and ploidy variation recorded for the nuclear genome.

We will use DNA sequencing and bioinformatics techniques to assess the sequence information of the *Miscanthus* organelles. We will study their features via annotated genome diagrams and via comparisons to other grasses especially sugarcane, sorghum and maize. Structural rearrangements will be recorded and assessments made of the molecular evolution of their genes. We will assess the cytoplasmic gene pools available for breeding by developing and applying molecular markers (including but not exclusively SSR variants) suitable for rapid screening of diversity. Furthermore we will use flow cytometry in conjunction with chromosome counts to assess polyploid complexes. We will determine crossability groups and gather essential information for future ploidy manipulation.

This is a collaborative project between Teagasc Crops Research Centre Oak Park in Carlow and the Botany Department of Trinity College Dublin (TCD). The researcher will be based in Oak Park but can spend some research time at TCD. The student will receive an annual tax free stipend of €21,000 for maintenance and to cover University fees (currently €4,708 pa for EU citizens, €12,067 pa for non-EU citizens). The PhD project is funded for three years and is expected to start on 1st October 2007.

Applicants must have or expect to gain a first or upper second class or Masters degree in an area of biological sciences. Informal enquires are welcomed and further information is available from the co-supervisors (below). Applications, including a covering letter detailing research interests and aspirations, a detailed CV including names and contact details of two referees should be made to Trevor Hodkinson (hodkinst@tcd.ie;

<http://www.tcd.ie/Botany/staff/THodkinson.html>) or Susanne Barth (susanne.barth@teagasc.ie; <http://www.teagasc.ie/oakpark/sbarth.htm>) as soon as possible; the position will be open until filled.

Dr. Trevor R. Hodkinson Botany Department School of Natural Sciences Trinity College Dublin Dublin 2, Ireland PHONE ++353 1 896 1128 FAX: +353 1 896 1147 hodkinst@tcd.ie

Dr. Susanne Barth Teagasc Crops Research Centre Oak Park Carlow, Ireland ++353 (0)599170290 ++353 (0)599142423 susanne.barth@teagasc.ie

Susanne Barth <Susanne.Barth@teagasc.ie>

UFribourg PlantPopEvol

PhD Position in Plant Population Ecology

Rationale: The European knapweed *Centaurea maculosa*, introduced from Central Europe (EU) into North America (NA) during the late 19th century, where it covers now an area larger than Switzerland, has become a model for research on the ecological and evolutionary causes and consequences of invasions. In recent studies based on field surveys covering well over 100 populations, we found both diploid (2x) and tetraploid (4x) plants in EU, but so far only 4x in NA. The NA plants are almost exclusively perennial and polycarpic, but the most widely distributed ones in EU are the 2x that are biennial and monocarpic. We presently explore the role of rapid evolutionary processes in the invasion success of *C. maculosa*, which involves both molecular marker studies to clarify the introduction history, and quantitative genetic experiments, and try to elucidate the complex taxonomic status of the various accessions.

Furthermore, we study preference, performance and impact of both generalist and specialist insect herbivores (some of which have been introduced as biological control agents 30 years ago) on various *C. maculosa* accessions in short-term greenhouse experiments using potted plants. For further information on the University and ongoing research on this topic visit <http://www.unifr.ch/biol/ecology/>. This is a project associated with the National Centre of Competence in Research (NCCR) Plant Survival (<http://www2.unine.ch/nccr>), funded by the Swiss National Science Foundation.

We now seek a highly motivated person to initiate and perform a three-year field demography study on the im-

pact of specialist insect herbivores on the *C. maculosa* biotypes differing in life cycle (monocarpic vs. polycarpic) and ploidy level. These studies are planned at various sites in Europe, possibly also in NA, in collaboration with colleagues from US (Ray Callaway and John Maron, Corvallis, MT using joint field sites and complementary experiments) and from Australia (Yvonne Buckley, Brisbane, for the modelling part) and will involve stays at these sites. New ideas and complementary studies are of course highly invited.

Requirements

- Master Thesis in Biology - knowledge of, and/or experience in one or several of the following areas of research is desirable: experimental field ecology, demography, plant populations ecology, modelling, insect-plant interactions.

Salary and conditions The position is planned to be filled in during summer/autumn 2007 and is available for 3-4 years. Salary according to the guidelines of the Swiss National Science Foundation (gross salary in the first year about CHF 34'200). The successful candidate will be enrolled in the NCCR doctoral school with a large offer of specific lectures and practicals.

Applications

Applicants should send their complete CV and the names of two professional referees to the address below (preferably by e-mail). We start evaluating the applications by end of June 2007.

For further information, please contact:

Prof. Dr. Heinz Müller-Schärer, Dép. de Biologie, Unité Ecologie & Evolution, Université de Fribourg, Chemin du Musée 10; CH-1700 Fribourg, SWITZERLAND; tel: + (41) (0) 26-300 88 35 direct, ++ 50 secr., e-mail: heinz.mueller@UNIFR.CH.

Gillianne Bowman <gilliann@uwinst.unizh.ch>

ULausanne HumanPopGenetics

PhD Position in statistical/computational human population genetics at the University of Lausanne, Switzerland in collaboration with Cambridge University, UK

We are seeking a highly motivated, creative and energetic person to work on the colonisation of the world by anatomically modern humans. Besides the obvious academic interest of an improved picture of the origin and

spread of our species, we expect the work to have direct relevance to our understanding of the current geographic distribution of disease resistance/susceptibility genes. The PhD project will take advantage of a newly developed geographically explicit modelling framework and is a direct extension of some of our previous work (see below for selected relevant papers). The successful candidate will be expected to run extensive computer simulations and analyse large genetic datasets. Applicants with expertise in mathematics, statistics or population genetics are particularly encouraged to apply.

The project will be supervised by Jérôme Goudet (Lausanne), François Balloux (Cambridge) and Andrea Manica (Cambridge). The candidate will be based in Lausanne, a town located in Switzerland at the shore of Lake Geneva, offering very high quality of life and beautiful surroundings (Alps, Jura mountains, Lake; see <http://www.lausanne-tourisme.ch/>). There is potential for extensive stays in Cambridge. Our research groups and departments make a lively and stimulating research environment (<http://www.unil.ch/dee>, <http://www.unil.ch/dee>, and <http://www.zoo.cam.ac.uk/zoostaff/manica/index.htm>).

The position entails some teaching at the undergraduate and graduate level in Lausanne, which needs not be in French. Salary ranges from 45000 to 55000 CHF per annum (30000 to 36700 Euros).

To apply, please send your CV, a brief statement of research interests and contact information for two references as a single file pdf e-mail attachment to Jérôme Goudet (jerome.goudet@unil.ch), François Balloux (fb255@cam.ac.uk) and Andrea Manica (am315@cam.ac.uk).

Deadline for applications: June the 10th, 2007

Informal enquiries can be obtained from Jerome.goudet@unil.ch

RECENT RELEVANT PAPERS

Linz L et al. (2007) An African origin for the intimate association between humans and *Helicobacter pylori*. *Nature* 445: 915-918

Liu H et al (2006) A geographically explicit genetic model of worldwide human settlement history. *American Journal of Human Genetics* 79: 230-237

Prugnolle F, A Manica and F Balloux (2005) Geography predicts neutral genetic diversity of human populations. *Current Biology* 15: R159-R160

Prugnolle F, et al (2005) Pathogen-driven selection and worldwide HLA class I diversity. *Current Biology* 15: 1022-1027

– Jérôme GOUDET Dep. Ecology & Evolution Biophore, UNIL-Sorge UNIL-CH-1015 Lausanne Switzerland <http://www.unil.ch/dee> <http://www.unil.ch/popgen> Tel: +41 21 692 42 42 Fax: +41 21 692 42 65 Secr:+41 21 692 42 60 jerome.goudet@unil.ch

ULiverpool MalariaComputerSimulation

PhD Studentship available

“Computer simulation of malaria transmission, drug resistance and its impact on human health” Liverpool School of Tropical Medicine, <http://www.liv.ac.uk/lstm/> Starting summer 2007.

Malaria kills an estimated 1 to 3 million people per year and its transmission depends on the interaction of three organisms: the malaria parasites, mosquitoes and humans. The Bill and Melinda Gates Foundation have commissioned the Swiss Tropical Institute (STI) to produce a comprehensive computer simulation of malaria transmission and its impact on human disease. The programme will be made publicly available and will enable researchers to gauge the likely impact of public-health strategies such as provision of bednets, spraying houses to kill mosquitoes, deployment of vaccines and so on. The programme uses distributed computing where volunteers run components as screen-savers. This has attracted considerable media interest from, among others, Nature, the BBC and the Economist, see the following URLs for more details: Malariacontrol.net and Africa-at-home.web.cern.ch

We are looking for someone to investigate how proposed interventions to control malaria may simultaneously affect the spread of drug resistant malaria; for example will periodically treating all children with antimalarial drugs pay a long-term penalty in driving drug resistance? This component will be based at the Liverpool School of Tropical Medicine and is offered as a PhD studentship.

Applicants need to have proven computing skills to extract and analyse the considerable amount of output produced during the STI simulations; these track factors such as the frequency of severe malaria attacks, number of infective bites per person, percentage of infections that are drug resistant, and so on. The applicant should also have an interest in the epidemiology of

infectious disease although this is a secondary requirement and may be learnt in-post.

Essential skills: * Good/excellent programming skills in C/C++ * Familiar with software development on Linux OS Additional useful skills: * Mysql * Scripting languages * XML

The applicant will probably have a background in quantitative biology, statistics or computer science. Unfortunately, due to the PhD fee structure they must be UK or EC citizens

Further details from: Ian Hastings, Liverpool School of Tropical Medicine. Email: hastings@liverpool.ac.uk

“Hastings, Ian” <hastings@liverpool.ac.uk>

UNamur EvolBiol

A six year Graduate position available at the Department of Biology at the University of Namur, Belgium (<<http://www.fundp.ac.be/>> <http://www.fundp.ac.be/>).

The graduate student has 6 years to accomplish his/her PhD since he/she is expected to teach practical courses too. The practical courses are in biology at the FUNDP, approximately 250h a year, and should be given in French.

The research project will investigate the population genetic structure of a bdelloid species and the host-parasite interactions within this unique group of organisms.

Bdelloid rotifers are abundant free-living multicellular animals, a few tenths of a millimetre long, characterized by apical bands of cilia. The entire Class Bdelloidea appears to be without males or hermaphrodites and is the highest-rank metazoan taxon to be obligately asexual. Bdelloids have been remarkably successful, speciating and adapting to many different types of freshwater and moist-terrestrial habitats like ponds, lakes, mosses, tree barks and soil all over the world. This success has come despite the fact that bdelloids inhabit microbial pathogen-filled environments and lack sexual recombination, a mechanism necessary to generate variation in response to rapidly evolving parasites. It is therefore timely to explore the response of bdelloids to their natural and less specific pathogens and to investigate the underlying genetic variation.

The specific aims of this project are:

- investigate the clonal diversity within and between bdelloid populations from the field, since few studies have been done on the population genetic structure of those organisms

- investigate the response of bdelloid individuals infected with the fungus *Rotiferophthora* and identify the natural parasites of bdelloid rotifers

The work will be carried out with Dr. Karine VAN DONINCK at the Department of Biology (URBO) at the University of Namur (Belgium). The research will be done in collaboration with Dr. Yannis Michalakis (GEMI, IRD Montpellier, France), the group of Dr. Timothy G. Barraclough (Imperial College London, UK) and Dr. Africa Gomez (University of Hull, UK).

Applicants must have completed their undergraduate studies, be motivated to do research in evolutionary biology and keen to teach.

Belgium is a very nice country to live in and the salaries for PhD students are generous.

If you are interested, please contact Dr. Karine VAN DONINCK at karine.vandoninck@mpl.ird.fr

To be eligible you have to submit the French application form before June 15 2007. The form is available online at <http://www.fundp.ac.be/universite/jobs/> - <http://www.fundp.ac.be/universite/jobs/> (click on 'personnel academique ou scientifique'). Send the completed word document to the rectorat of the University, to Dr. Karine VAN DONINCK and Prof. P. Kestemont patrick.kestemont@fundp.ac.be

The interviews for the job will be on June 25th 2007.

Karine VAN DONINCK
<karine.vandoninck@mpl.ird.fr>

UNewSouthWales EvolBiol

PhD scholarship in evolutionary biology

A full-stipend scholarship is available for PhD studies in the laboratory of Dr. Russell Bonduriansky in the School of Biological, Earth and Environmental Sciences at the University of New South Wales. Our lab pursues research on sexual selection and sexual dimorphism, evolutionary genetics, and the evolution of ageing through laboratory and field research on flies and other insects, as well as the development of new theory. The successful applicant will have the opportunity to choose from several interesting projects, or to develop

their own project within this broad area, in consultation with Dr. Bonduriansky.

The School includes one of Australia's most research-active clusters in the area of ecology and evolution, and the evolutionary biology group is currently expanding. The University of New South Wales is located in Sydney's eastern suburbs, about 5 km from the city centre.

For more information, visit: <http://www.bees.unsw.edu.au/research/research.html>
<http://www.bees.unsw.edu.au/school/researchstaff/-bonduriansky/bondurianskyrussell.html>

To apply, submit a CV, contact details for two academic referees, and a one-page statement of research interests to Dr. Russell Bonduriansky (r.bonduriansky@unsw.edu.au). Note that the successful applicant, if not an Australian citizen/resident, will also need to apply to the University for a fee-waiver scholarship.

r.bonduriansky@unsw.edu.au

r.bonduriansky@unsw.edu.au

UOklahoma EvolBiol

Graduate Research Assistantship/Studentship (GRA)

I am looking to fill a 12-month Graduate Research Assistantship/Studentship in my laboratory at The University of Oklahoma Biological Station (UOBS; <http://www.ou.edu/uobs>) with 2-year (24-month funding) secured, with additional funding pending. Applicants must apply and be accepted into either the M.S. or Ph.D. Graduate Program in Zoology at the Univ. of Oklahoma (OU; <http://www.ou.edu/cas/zoology>), as well as fill out the necessary forms for Graduate School Admission at OU (<http://gradweb.ou.edu> <<http://gradweb.ou.edu>>). The initial monthly stipend will be ~\$1,600 (~\$20,000 per year), plus tuition waiver and health insurance coverage included. This GRA/studentship is available beginning 1 January 2008, although a later start date is possible. For more information about my research interests, please visit <http://www.ou.edu/uobs/weider.html>.

Lawrence J. Weider, Ph.D. Director, The University of Oklahoma Biological Station HC-71, Box 205 Kingston, OK 73439 Phone: 1-405-325-7438 ljweider@ou.edu

and

Professor Department of Zoology University of Oklahoma Norman, OK 73019 Phone: 1-405-325-4766 FAX:

1-405-325-0835
ljweider@ou.edu

UReading EvolMedicinalPlants

PhD Opportunity: Evolutionary Origin of Medicinal Properties in Plants

DNA sequence data have provided new and reliable phylogenetic hypotheses for plants, but these new phylogenetic trees have yet to be related to the diversity of medicinal plants. A recent analysis of the evolutionary origin of economically important plants used a comprehensive phylogenetic tree for the flora of the Cape of South Africa and an inventory of useful plants, and showed that utility is not randomly distributed but instead clumped within particular lineages and locations¹. Using this study as a proof of concept, we propose a project that will investigate the power of phylogenetic hypotheses to explain the origin and diversity of medicinal plants at two levels of the taxonomic hierarchy (for the angiosperms and for a selected family), and with respect to floras for which databases of plants with medicinal properties have been compiled (Southern Africa, North America, and India). The student will test the hypothesis that medicinal properties are constrained by the phylogeny and shed light on the mechanisms underlying this pattern (including the role of human traditions and an evaluation of the constraints on chemical pathways for chemistries of interest). The student will also test the hypothesis that phylogeny-based conservation priorities are more efficient in preserving the diversity of medicinal plants in a given location, region or country.

1. Forest et al. (2007) Preserving the evolutionary potential of floras in biodiversity hotspots. *Nature* 445, 757-760.

The three year PhD studentship for a UK/EU student is funded by the John Spedan Lewis Foundation. The successful applicant will be co-supervised by Dr Julie Hawkins, Dr Elizabeth Williamson and Dr Vincent Savolainen. Drs Hawkins and Williamson are based at the University of Reading; it is expected that the student will be registered at the University of Reading but spend significant amounts of his/her time at Kew and/or Imperial College at Silwood Park (to be confirmed) with Dr Vincent Savolainen.

Informal enquiries to Dr Julie Hawkins on 0118 378

6546. To apply please submit a CV and covering letter to Miss Val Norris, School of Biological Sciences, AMS Building, University of Reading, Reading, Berkshire, RG6 6BX. Closing date for applications 29th May 2007.

“Julie A. Hawkins” <j.a.hawkins@reading.ac.uk>

UTurku LemmingPopEvol

PhD student position (alternatively Post Doc) available at Section of Ecology, Department of Biology, University of Turku; application deadline 25.5.2007

TITLE: TROPHIC CASCADES AND HERBIVORE IMPACTS ON TUNDRA: FEEDBACKS ON BIODIVERSITY AND CLIMATE; INSTRUCTOR: LAURI OKSANEN

Outlines of the project:

A lemming outbreak is coming on the mainland tundra of northernmost Norway, allowing us to study whether lemmings are dynamically in the role of predators of plants or in the role of prey of carnivorous mammals and birds. In this context, we will also study whether the lemmings respond to high population densities by “migrations” (long-range dispersal).

While the focus is ecological, the project has a clear evolutionary dimension. If lemmings were regulated by predationlike other microtine rodents, long range dispersal would be pointless and should not occur. If, however, lemmings are adapted to harsh environments where winter food is the limiting factor, emigration is the only chance to escape starvation. Our hypothesis is thus that those lemmings, which “jump the cliff” (leave crowded mountains) take their chance; suicide is committed by those which chicken. As for plants, there has been long standing argument that strong herbivory should select for low edibility. We doubt this. When winter food runs out, herbivores are not especially selective and can severely injure even maximally unpalatable plants, favoring resilience (e.g. graminoids). The outbreak will enable us to test this hypothesis, too. We know that woody plants are inedible for lemmings, while graminoids are their delicacy. We will test the inedibility hypothesis by studying the response of graminoids and ericaceous dwarf shrubs to the outbreak.

As typical, the lemmings come on short notice. Therefore, the current funding is improvised, sufficing for

8 months as a PhD project (PhD stipendium 1255 EUR/month) or for 6 months as a post doc project (stipendium 1600 EUR/ mo). Grant proposals for more sustained funding are pending, but lemmings do not wait. The project will thus be started already 1st July this summer. A detailed project description is found on my homepage (<http://users.utu.fi/lauoks/-2007-herbivoryproject.doc>)

The successful candidate is expected to start working in the project from 01.07.2007 and is expected to be prepared to do fieldwork on the tundra periodically in all seasons. We will indeed work on other rodents and their impacts, too, using e.g. experimental predator-free islands with introduced gray-sided voles.

applications with CV and list of publications should be mailed to: lauoks@utu.fi by 25.5. 2007. decision will be announced within a week.

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

phone: +358-2-333 55 57 cell phone +358-40-77 33 710

Lauri Oksanen <lauoks@utu.fi>

UVictoria 2 EvolEcol

Two Graduate Positions in Evolutionary Ecology

I seek 2 graduate students and to participate in either 1. The dynamic consequences of inducible defenses using the ciliate *Euplotes* as a model system. 2. The evolution and ecology of sex-ratio variation in the splash-zone copepod *Tigriopus*.

Successful candidates will have a strong quantitative approach with a flair for experimentation or theory. Basic molecular skills will be an asset but not essential.

The lab has a tradition of internal cooperation and ongoing international collaborations. Interested candidates should provide a cover letter, CV, and contact information for two referees by e-mail to banholt@uvic.ca.

I will be available to meet with potential students while attending the Yodzis Symposium in Guelph May 15, the Canadian Society of Ecology and evolution meetings in Toronto May 18-20, and the European Society of Evolutionary Biology meetings in Uppsala Aug 20-26.

Brad Anholt Dept. Biology University of Victoria ban-

holt@uvic.ca

banholt@uvic.ca

UZurich MolEvol

WAGNER Andreas, Prof. aw@bioc.uzh.ch six digit code: 010000

PhD thesis in molecular evolution/evolutionary bioinformatics

Mobile DNA is DNA that can change its position within a genome. It is an integral component of most bacterial genomes, and also implicated in the spreading of drug resistance genes among pathogenic bacteria. Why does mobile DNA persist in genomes? On one hand, mobile DNA may be a very effective parasite, replicating itself at the expense of its host. On the other hand, mobile DNA can also have beneficial effects, such as occasionally beneficial mutations. An ongoing project in our group aims at resolving the question why mobile DNA is maintained in bacterial genomes and in eukaryotic genomes. Despite thirty years of debate, the question still has no conclusive answer. The availability of many completely sequenced genomes provides a unique opportunity to remedy this situation. We are searching for a Ph.D. student with demonstrable experience and interest in evolutionary biology and a solid background in bioinformatics.

The Wagner lab at the University of Zurich studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. A sample of our research can be found at <http://www.biochem.unizh.ch/wagner/>. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and /or fundamental organizational principles of life.

The successful candidate will have a strong background in bioinformatics and computational biology. Fluency in a major scripting language such as perl, and experience in software development is a must. Also necessary is a strong background in biology. We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and independent, and has demonstrated interests in problems of molecular evolution. The working language in the laboratory is English. German skills are not essential.

Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many edu-

cational and recreational opportunities.

To be considered, please send a single (!) PDF file containing a CV including publication list (if available), a scanned academic transcript (list of grades in university courses), a statement of research interests not exceeding two pages, and three references to jobs_aw@bioc.unizh.ch <mailto:jobs_aw@bioc.unizh.ch>. Please include the word "MOBDNA" in the subject line. The application deadline is June 1, 2007.

With best regards Christiane

UtahStateU AvianConservation

From: David N. Koons, Ph.D. Max Planck Institute for Demographic Research Konrad-Zuse Str. 1 D-18057 ROSTOCK Germany

Tel. +49 (0)381 2081 226 Fax. +49 (0)381 2081 526 E-mail: koons@demogr.mpg.de Website: www.demogr.mpg.de Title: Lesser Scaup Population Biology Ph.D. Assistantship

School: Utah State University

Departments: The Ecology Center in connection with the Department of Wildland Resources <http://www.usu.edu/ecology/> <http://www.cnr.usu.edu/departments/departments/wild/wild> Location: Logan, UT 84322, USA

Description of research: The North American lesser scaup (*Aythya affinis*) population has been declining for over 20 years, which has raised concern amongst managers and the general public. Uncertainty about the effects of harvest-related mortality, recruitment, and population density on lesser scaup population dynamics make management extremely challenging. The current harvest-management strategy assumes a particular form of density-dependent population growth and additive effects of harvest on population abundance. One objective of this position will be to develop a set of alternative population models, such that management decisions can be based on the population model(s) that is(are) best supported by the data. The student will have freedom in the development and examination of relevant models. Factors that are of interest but have yet to be explored in scaup population models that explicitly include harvest are: age structure, additive vs. compensatory effects of harvest on mortality, alternative forms of density dependence in demographic vital

rates, effects of abiotic factors (e.g., climate) on demographic processes, etc.

In addition to the general Ph.D. education, the student will be expected to learn about waterfowl survey data, survival estimation, population models and Bayesian statistics. Using appropriate methods, the student will simultaneously incorporate multiple sources of data (e.g., abundance, harvest surveys and wing collections, capture-recovery data, etc.) into the estimation and development of alternative population models. A complementary objective of this project will be to conduct simulation analyses to identify information requirements to more objectively discriminate between alternative population models. The student will also be encouraged to develop papers related to this work that might be of broad interest to the population, conservation, statistics, and adaptive management communities.

Primary Funding Agency: Delta Waterfowl and Wetlands Research Station (DWWRs: <http://www.deltawaterfowl.org/research/graduate.php>)

Stipend: Up to \$21,000 per year (for 4 years) depending on experience and ability to compete for a DWWRs fellowship.

Qualifications: Applicants should have a background in Wildlife, Ecology, or Statistical disciplines. Preference will be given to applicants who have experience conducting population biology research, a strong quantitative background, good computing skills, and superior academic performance. A strong interest/experience in waterfowl biology is desired. Applicants must meet the entrance requirements of the Ecology Center (see web page listed above).

Application: Initial inquiries can be e-mailed to Dr. David N. Koons: koons@demogr.mpg.de. To apply before 31 July 2007 please send 1) a cover letter describing your research background and interest in the position, 2) your CV, 3) copies of transcripts and GRE scores, and 4) 3 letters of reference via e-mail to Dr. David N. Koons. Applications after 31 July 2007 can be done via e-mail or paper applications can be sent to Dr. David N. Koons, Department of Wildland Resources and the Ecology Center, Utah State University, 5230 Old Main Hill, Logan, UT 84322, USA.

Last Date to Apply: Until position is filled. Preferred starting date is 4 January 2008.

Koons@demogr.mpg.de Koons@demogr.mpg.de

Wageningen LivestockDiseaseEvol

PhD project on pathogen transmission and bio-security

Job description

This research project aims to obtain a better understanding of the disease transmission during outbreaks of highly transmissible diseases in livestock. Of particular interest is the transmission that occurs between (more or less nearby) farms and that is taking place despite the presence of animal movement restrictions and other intervention measures. Some of the characteristics of the dominant mechanisms are likely to be universal across different types of diseases, including highly transmissible diseases such as avian influenza, classical swine fever and foot-and-mouth disease, but also other infectious diseases such as *Campylobacter* in poultry and Influenza in pigs. The mechanisms will be studied through a combination of transmission experiments, parameter estimation and mathematical modelling.

This research project is funded by the Ministry of Agriculture, Nature and Food Quality. The relevance to the Ministry lies in its need to design well-founded intervention strategies for combating epidemic spread of highly transmissible diseases in livestock, including appropriate hygiene and bio-security approaches.

This research will be carried out in Lelystad, the Netherlands, at the Quantitative Veterinary Epidemiol-

ogy cluster of the Division of Infectious Diseases of the Animal Sciences Group (ASG), where experts both in mathematical modelling and in conducting transmission experiments will provide guidance. The project will be carried out under supervision of Prof. dr ir. M.C.M. de Jong, head of the Quantitative Veterinary Epidemiology group at Wageningen University, also part of ASG.

Requirements

University Graduate

An MSc degree in Biology, Animal Science or Veterinary Medicine, and an interest in quantitative approaches in infectious disease epidemiology.

Organization

Employed by Wageningen University and based with the Animal Sciences Group (ASG) in Lelystad, The Netherlands.

Additional information about the vacancy can be obtained from:

Prof.dr.ir. M.C.M. de Jong

Telephone number: +31 (0) 317 48 20 12

E-mail address: mart.dejong@wur.nl

Applications to this vacancy should mention the vacancy number AT DIE 2007-007 and be sent to: S.P. van Ee, Wageningen University, Department of Animal Sciences, P.O. Box 338, 6700 AH Wageningen, The Netherlands. E-mail:Sandra.vanee@wur.nl

Application deadline: 26 May 2007.

thomas.hagenaars@wur.nl thomas.hagenaars@wur.nl

Jobs

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BowlingGreenStateU FieldAssist EvolPlantDefense

RESEARCH FIELD ASSISTANT NEEDED TO WORK IN AN NSF-FUNDED PROJECT RELATED TO THE EVOLUTION OF PLANT DEFENSIVE METABOLITES AND TRI-TROPHIC INTERACTIONS. Responsibilities will include growing plants in growth chambers and transplanting them to the field, watering plants and applying insecticides to control plants, collecting data from the field such as measuring plant traits, monitoring plants for the presence of insects and their associated parasitoids and predators, determining insect damage on plants, rates of parasitism, etc. The field experiment will start in June and will end in August 2007, although there is funding available for a field/lab assistant for 6-7 months (June-Dec 2007). The field work will involve (at times) intense physical activity and exposure to hot weather. To apply, please send a CV and two references (by email) as soon as possible to: Gabriela Bidart-Bouzat, Assistant Professor Department of Biological Sciences Bowling Green State University 511 Life Sciences Building Corner of Merry and N College Bowling Green, OH 43403 E-mail: gbidart@bgsu.edu Phone: 419-372-4644 Fax: 419-372-2024

“M. Gabriela Bidart-Bouzat”
<gbidart@bgnet.bgsu.edu>

ETHZurich InsectEvolEcology

The ETH Applied Entomology Group investigates insect-plant relationships from the molecular to

the agroecosystem level, in particular as a basis for more sustainable pest and crop management (www.em.ipw.agrl.ethz.ch). A position with a several years perspective is open for a creative and cooperative scientist with strong Postdoc experience in multitrophic insect-plant interactions and chemical ecology.

Responsibilities include (1) research together with graduate and undergraduate students using state-of-the-art techniques, and (2) participation in teaching and administration.

Languages spoken in the group are mainly English and German.

The position will remain open until filled.

Please send curriculum vitae, a list of methods, and addresses with phone numbers of three references to:

Professor Dr. Silvia Dorn Subject: Position Chem.-Ecol. ETH Zurich Institute of Plant Sciences / Applied Entomology Schmelzbergstrasse 9 CH - 8092 Zurich, Switzerland silvia.dorn@ipw.agrl.ethz.ch

dominique.mazzi@ipw.agrl.ethz.ch

do-

minique.mazzi@ipw.agrl.ethz.ch

Fisheries MarineMammalGenet ResTech

Molecular Technician National Marine Fisheries Service Lafayette, LA

We seek a highly motivated technician to join an active lab investigating population genetics and evolutionary histories of marine mammal species. Applicants must have considerable experience with a variety of standard molecular techniques (DNA extraction, PCR, gel electrophoresis, DNA sequencing, microsatellites, etc.) so that he/she can work with minimal supervision. Re-

sponsibilities include DNA extraction, sequencing and genotyping as well as database entry and archiving, and general lab maintenance including ordering supplies.

Minimum Qualifications: Bachelor's Degree in an appropriate field of technology or science such as Biological Sciences, Molecular Biology, or Genetics, PLUS demonstrated research experience with DNA extractions, PCR, and sequencing; familiarity with genetic analyses of sequence and/or microsatellite data and facility with standard computer software programs. Experience with microsatellites and gene sequencing is required. Experience running a capillary sequencer is preferred. This is a full time contract position open immediately. Applicants should be US citizens. Qualified candidates should submit (via email) a letter of application describing qualifications for the position and reason for interest, CV, and names and email addresses of three references to Patricia.Rosel@noaa.gov.

Patricia.Rosel@noaa.gov

GroningenU ModellingTransgenes

PhD or Postdoc position "Modelling the spread of transgenes"

University of Groningen, Centre for Ecological and Evolutionary Studies

Context of the project: The introduction of transgenic crops raises some important environmental safety issues. One matter of concern is the question whether, and to what extent, gene flow involving transgenes significantly affects the population ecology of wild relatives. To assess the ecological implications of the genetic modification of crops the Dutch Science Foundation (NWO, www.nwo.nl) launched the new research initiative 'Ecology Regarding Gene-modified Organisms' (ERGO). In the context of ERGO, the research programme "Introgression of crop (trans-)genes into wild relatives: hybrid fitness, background selection and hitchhiking" is a joint effort of research groups at the University of Groningen, the University of Amsterdam and Wageningen University. This programme comprises four integrated projects that combine an experimental approach (focusing on the wild lettuce species *Lactuca serriola*) with a theoretical modelling approach. In addition to the theoretical project advertised here, there are two open PhD positions for the experimental projects.

Job description: In the project "Modelling the ecological implications of the spread from transgenic crops into wild relatives" simulation models will be developed for the spatial dispersal of transgenes (vegetatively or through pollen or seeds) in wild populations. The main objective is to predict the dispersal pattern and invasion prospects of a transgene on the basis of the life history of the plant species involved. The potential effect of transgenes on dispersal characteristics will receive special attention. In a long-term perspective, the project aims at the development of general-purpose predictive tools for scientists and decision-makers alike. To achieve this goal, it is crucial to first perform a detailed analysis for specific well-studied model organisms like *L. serriola*. This theoretical project will therefore strongly reflect progress in the three experimental projects. The models resulting from the project will be integrated and validated with existing data, including those generated for *L. serriola*.

Profile: For this challenging, multidisciplinary project we are looking for a highly motivated biologist (MSc or equivalent) with a strong background in modelling, population genetics and/or population biology. Experience with programming (preferably C++) is required. Proficiency in English (both oral and written) and excellent communication skills are indispensable for this integrative project. Although we are in the first place looking for a PhD student, qualified postdocs are also invited to apply.

Organization: The position will be embedded in the Centre for Ecological and Evolutionary Studies (CEES, www.rug.nl/biol/cees) a centre of excellence on ecology and evolution in the Netherlands. It will be carried out under the supervision of Prof. Kuke Bijlsma from the Evolutionary Biology Group (www.rug.nl/biol/evogen) and Prof. Franjo Weissing from the Theoretical Biology Group (www.rug.nl/biol/theobio). Both groups have excellent facilities, including a pc-cluster for running computer simulations. PhD students have the opportunity to participate in the national Research School Functional Ecology (www.rug.nl/biol/fe).

Conditions of employment: PhD students are first employed for a period of one year, with a possible extension of three more years. Salaries are according to the standard salary scale for PhD students with an estimated salary of E 1956,- per month in the first year, increasing to a monthly salary of E 2502,- in the fourth year. For postdocs, salary and project duration depend on personal details like qualifications and working experience.

Additional information: Prof. Dr. Kuke Bijlsma (r.bijlsma@rug.nl, Tel: +31 50 363 2117) or Prof. Dr.

Franjo Weissing (f.j.weissing@rug.nl, Tel: +31 50 363 2131)

Application: Applications (including a detailed letter of motivation, a CV, a complete list of courses followed and grades received, and the names and addresses of three potential referees) should be sent before 25 May 2007 to: Wageningen UR, Plant Sciences Group, Mrs. T. Schultz, P.O. Box 16, 6700 AA Wageningen, The Netherlands or by Email to: tanja.schultz@wur.nl. When applying always mention explicitly the vacancy number DPW07.17G.

joke.bakker@rug.nl joke.bakker@rug.nl

HopkinsMarineStation Tech MarinePopGenet

Research technician at Hopkins Marine Station

Part-time (75% FTE), benefits eligible position, at Stanford University's Hopkins Marine Station, in Pacific Grove, CA. Under the direction of the Principal Investigator the technician will assist with research related to genetic characterization of populations of marine vertebrates and invertebrates in the context of ongoing research into marine conservation and management. Duties include:

- Collecting larvae and adult specimens of marine species. This may involve some travel within California and into Oregon and possibly Washington.
- Extracting DNA and documenting genetic variation. This will include processing samples in the lab for DNA extraction and sequencing as well as entering, managing, and analyzing the resulting data. This will require the use (or development) of many research skills using a variety of molecular genetic tools. These include, but are not limited to DNA extraction, PCR, gel electrophoresis, and DNA sequencing.
- Field monitoring of multiple sites in central California.
- Animal care including aquarium maintenance and routine care and feeding of marine species (primarily invertebrates).
- Laboratory maintenance including maintaining the lab and taking responsibility for ordering some of the general supplies.

There is potential for extension of the technician position to other research projects as well as the possibility

of co-authorship of at least one resulting publication.

QUALIFICATIONS: The successful applicant will be highly organized, have attention to detail, be able to work as an independent part of a team, have a basic understanding of and facility with standard computer software programs, and have practical experience with a variety of standard molecular tools (for example, DNA extraction, PCR, gel electrophoresis, DNA sequencing, etc). In addition to these basic requirements, we desire an applicant with an interest in marine ecosystems and their ecological functioning.

To apply send CV and cover letter to:

Tim Knight Hopkins Marine Station
Stanford University phone: (831) 655-6210 email:
trknight@stanford.edu

trknight@stanford.edu

IndianaUBloomington ResAssociate Sunflower

Research Associate in Plant Evolutionary Genetics

The laboratory of Loren Rieseberg, Department of Biology, Indiana University, Bloomington has an opening for a full time Research Associate starting as early as June 2007. The Rieseberg lab conducts research in plant evolutionary genetics using the annual sunflower as a study system. The position will involve 1/4 time dedicated to lab management and 3/4 to research. General lab care is a priority on a daily basis. Lab management responsibilities include ordering supplies, maintaining equipment, supervising work-study students, and overseeing lab organization/functioning. Research responsibilities involve assisting graduate students and/or post-docs with molecular bench work such as DNA and RNA extraction, genotyping, qPCR, sequencing, and data scoring/analysis. Some minor greenhouse work may also be required. Initial projects will be closely supervised, with increased independence possible as experience and expertise are accumulated.

We seek an individual with a Bachelor's or Master's degree in Biology or related field. Some laboratory experience is strongly desired, although training will be provided. Attention to detail and an ability to work with others on a daily basis are both necessary. The base salary level will be \$26,500, with adjustment possible according to education and experience. Full benefits. Submit letter of interest, re-

sume and contact information for 3 references via email to Dee Verostko (dverostk@indiana.edu), using Rieseberg Research Associate' as the subject line. The position is available immediately and will remain open until suitable candidates are located. Direct inquires about the nature of the position to Ben Blackman (bkblackm@indiana.edu).

bkblackm@indiana.edu bkblackm@indiana.edu

K-StateU Bioinformatics ComputerSpecialist

Bioinformatics Specialist/Computer Specialist

The KSU Bioinformatics Center seeks to fill a new, service oriented, bioinformatics specialist position. The successful candidate will collaborate with faculty scientists on new bioinformatics research projects, apply existing bioinformatics tools to basic biological research, provide training and lead workshops in bioinformatics. Current projects at KSU include genomics, EST and gene expression analysis, lipidomic and genomic relational databases and data mining.

Required qualifications: M.S. in Computer Science or related field and demonstrated accomplishments in bioinformatics (e.g., developing Bioinformatics tools, data management, data mining, or database development and curation).

Preferred qualifications: Project management experience (e.g., supervising personnel, scheduling and monitoring projects to ensure accurate and timely completion, and effectively communicating with clients, colleagues and subordinates).

Applicants must be available to work in the United States by July 1, 2007. Excellent oral and written communication skills in English, and the ability to work both independently and in collaboration with other scientists and students are required. Review of applications will begin May 31, 2007, and continue until the position is filled. This full-time, 12-month, term position may be renewed annually contingent upon performance, need for services, and funding.

To apply: Send CV, statement of research interests, and names and contact information of three professional references by e-mail to dmerrill@ksu.edu or to:

Doris Merrill, Program Coordinator Division of Biology, 104 Ackert Hall Kansas State University Manhat-

tan, KS 66506-4901

Information about the Center and a complete position description may be found at www.Bioinformatics.K-State.edu <<http://www.bioinformatics.k-state.edu/>> .

The K-State Bioinformatics Center is supported by the Division of Biology and the Kansas Infrastructure Network for Biomedical Research Excellence (KINBRE, NIH-NCRR). The Center currently provides bioinformatics support to K-State researchers for EST sequence and microarray data analysis. GeneSpring software has been used for microarray data normalization, statistical inference and clustering analysis. With the anticipated accumulation of microarray data from insect genomics, a database system is needed for data management and integration. For spotted cDNA microarrays, the integrated database can provide information about the probe sequences and functional annotations, which may not be available in the public databases. On the other hand, the microarray data in the integrated database should provide valuable information about the expression patterns of insect genes.

For the Tribolium research community, the center has developed a comprehensive genome database (BeetleBase at <http://www.bioinformatics.K-State.edu/-BeetleBase/>). BeetleBase was built using the Chado generic data model designed by FlyBase and Berkeley Drosophila Genome Project (BDGP). BeetleBase has been populated with various types of data, ranging from genomic sequences to mutant phenotypes of Tribolium. A relatively large dataset of Tribolium ESTs is also stored in BeetleBase. A web interface has been developed to allow public access to the integrated data in BeetleBase. In particular, the generic genome browser (GBrowse) is used as one of the interactive visualization tools of BeetleBase.

KSU is an equal opportunity employer and actively seeks diversity among its employees.

Doris Merrill, Program Coordinator K-State Arthropod Genomics Center Division of Biology, Kansas State University 116 Ackert Hall, Manhattan, KS 66506-4901 (785) 532-3482, dmerrill@ksu.edu <<http://www.ksu.edu/agc>> www.ksu.edu/agc

dmerrill@ksu.edu

LausanneU GroupLeader EvolBiol

Junior Group leader in Ecology and/or Evolution at

the Department of Ecology and Evolution, University of Lausanne, Switzerland

The Department of Ecology and Evolution at Lausanne University, Switzerland, (<http://www.unil.ch/dee>) invites applications for a junior group leader position (Maitre assistant) in the field of Ecology and/or Evolution. We are seeking a highly motivated young scientist with a post doctoral experience, a strong publication record, and the will to develop an independent research group within the department. Scientists from any area of Ecology, Evolution or Genomics are encouraged to apply, be they field biologists, experimentalists, theoreticians or molecular biologists. The position is for a maximum of four years and annual salary ranges from 85'000 to 146'000 CHF (54'800 to 94'000 Euros).

Applicants will be expected to develop an externally funded and internationally recognized research program. Teaching duties include a 14 to 28 hours undergraduate course in experimental design, as well as taking part in the organisation of undergraduate practicals.

The department of Ecology and Evolution has a long track record of excellence in research. It is made of over 20 research groups in the field of ecology, evolutionary biology, behaviour, population genetics and genomics. The Department is currently home to 20+ post-docs and 40+ PhD students from many different countries and more than half of these are externally funded by Swiss and European research grants.

The University of Lausanne (<http://www.unil.ch>) provides excellent facilities, a lively intellectual and social environment and is beautifully located in Switzerland at the shore of Lake Geneva.

To apply for the position or for more information, please send a CV with a list of publications, a brief statement of research interests and the name of two referees in a single pdf file by email to:

Francoise Pham francoise.pham@unil.ch

DEE, Biophore UNIL-Sorge CH-1015 Lausanne Switzerland

For informal inquiries, please contact Jérôme Goudet (jerome.goudet@unil.ch) or Laurent Keller (laurent.keller@unil.ch).

– Jérôme GOUDET Dep. Ecology & Evolution Biophore, UNIL-Sorge UNIL-CH-1015 Lausanne Switzerland <http://www.unil.ch/dee> <http://www.unil.ch/popgen> Tel: +41 21 692 42 42 Fax: +41 21 692 42 65 Secr:+41 21 692 42 60 jerome.goudet@unil.ch

Jerome.Goudet@unil.ch Jerome.Goudet@unil.ch

Munich QuantGenetics

The FACULTY of BIOLOGY at the LUDWIG-MAXIMILIANS-UNIVERSITY of MUNICH

invites applications for an

ASSOCIATE PROFESSORSHIP (W2, tenure track) for Quantitative Genetics

The successful candidate is expected to have a strong research record in the areas of quantitative and/or statistical genetics with an emphasis on theory and the analysis of the genetic basis of adaptive traits. This may include, but is not limited to: QTL analysis, association mapping, or systems biology. The research should complement the current focus of the groups working in population genetics, evolutionary genomics, and evolutionary ecology.

The Faculty of Biology has strengths in both organismal and molecular/ cellular biology. It is located at the high-Tech-CampusLMU Martinsried, in close proximity to other life science departments and Max-Planck-Research Institutes. Close ties also exist with the Technical University of Munich and the Research Center for Environment and Health. The professorship will be integrated into the planned interdisciplinary "Center of Quantitative Methods" (run jointly by the Faculties of Biology, Medicine, Physics, Mathematics/ Informatics and Statistics).

The successful candidate must be able to establish international competitive research programs with extramural funding. Teaching obligations include courses for both undergraduate and graduate students in evolutionary biology and quantitative biology.

Prerequisites for the application are a doctoral degree, teaching skills and a record of research equivalent to the German "Habilitation". Scientific qualifications achieved in the private sector, outside Germany or as Junior professor will also be considered.

Applicants must be younger than 52 at the time of appointment. Exceptions to this rule may be considered if outstanding.

The University of Munich is interested in increasing the number of female faculty members and encourages women to apply. The University supports dual carrier couples.

The university is an equal opportunity employer

and handicapped candidates with equal qualifications will be given preference. Further information concerning the equal opportunity policy of the LMU can be obtained from Prof. K. Jung (kirsten.jung@lrz.uni-muenchen.de), concerning teaching from Prof. M. Starck (starck@uni-muenchen.de), concerning the structure of the Faculty from Prof. J. Soll (dekanat19@lmu.de), and concerning the scientific scope of the position from Prof. W. Stephan (stephan@zi.biologie.uni-muenchen.de).

Applications including CV, list of publications, a brief summary of present and future research interests, proof of teaching experience, five selected reprints and copies of relevant documents should be sent and a CD containing these documents before May 20, 2007 to Prof. Dr. Jürgen Soll, Dean of the Faculty of Biology, Ludwig-Maximilians-University of Munich, Großhaderner Str. 2, 82152 Planegg-Martinsried, Germany.

rose@zi.biologie.uni-muenchen.de rose@zi.biologie.uni-muenchen.de

QueenMaryU 4 EvolBiol

Queen Mary University of London School of Biological and Chemical Sciences

Four appointments of Lecturers (or Senior Lecturer or Reader, depending on experience)

The positions are in the following broad areas. The school is multidisciplinary with a strong commitment to evolutionary biology, so applications from evolutionary biologists working in these fields are strongly encouraged.

Marine Biology, Cognitive Biology, Structural Biology and Biochemistry.

The school has a tradition of recruiting the candidate considered to be the best scientist compatible with our research profile, rather than looking for the closest fit to a particular field of study.

Full details of the application procedure are at this site. <http://www.sbcs.qmul.ac.uk/vacancies/-index.shtml> Please note that, although the deadline for applications is Friday 1st June 2007, you are strongly encouraged to make enquiries at least one week before that date.

Contacts:

Chair of Research Strategy Group (and Evolutionary

Geneticist) Richard Nichols: r.a.nichols@qmul.ac.uk

Head of School, Peter Heathcote: p.heathcote@qmul.ac.uk

Candidates offered the posts will be required to take up the position by the 1st October 2007 at the latest.

r.a.nichols@qmul.ac.uk r.a.nichols@qmul.ac.uk

SouthamptonU ChairLifeSciences

Chair at the Life Sciences Interface School of Electronics and Computer Science Southampton University, U.K. Competitive Salary

Ref No. 1107-07-E

We wish to appoint a candidate to take a leading role in our developing research programme at the interface with the life sciences. The School is the largest of its kind in the UK and it was awarded the top grades (5*/5*) for its research in Electronics and Computer Science in the 2001 Research Assessment Exercise. In teaching the QAA ratings are also the highest possible. The school's continuing investment in new positions at the interface with the life sciences is part of a university wide initiative to enhance this activity. One example of this commitment is the founding of a new Institute for Life Sciences with a mandate to pursue collaborative cross-disciplinary research and facilitate communication between the disciplines associated with Medicine, Health Care, Life and Physical Sciences, Engineering and Mathematics.

The chair will join the Science and Engineering of Natural Systems (SENSe) Research Group which currently comprises five academic staff with research in: Adaptive Behaviour, Artificial Intelligence, Biological Computing Substrates, Evolutionary and Ecological Modelling, Microbial Ecosystems, and Theoretical Biology. Our research combines mathematical and simulation modelling with robotics and wet lab biology. Our collaborators span the social, biological, medical and physical sciences.

We are seeking an outstanding individual with research interests that enhance and complement our research profile in order to help drive forward our ambitious agenda. You will have demonstrated a record of internationally recognised research achievement at the life sciences interface, as well as the potential to sustain that record. Relevant research areas include both

those that take a computational approach to biological systems and those that draw inspiration from the life sciences for engineering purposes. As such, it is anticipated that the successful candidate will have a background in either, the life sciences, the natural sciences or computer science.

Information about the School can be found at <http://www.ecs.soton.ac.uk/> and on the SENSE website at <http://www.sense.ecs.soton.ac.uk/>.

Informal enquiries can be made in the first instance to Professor Wendy Hall wh@ecs.soton.ac.uk

Please visit www.jobs.soton.ac.uk and apply on-line, or call 023 8059 2750 <http://www.jobs.ac.uk/jobfiles/-RH722.html> – Dr Richard A. Watson Electronics and Computer Science Southampton University Rm. 1055 - Bld 16. <http://www.ecs.soton.ac.uk/people/raw> Tel: +44 (0) 2380 592690

raw@ecs.soton.ac.uk

TrinityCollege 2 EvolModelling

Potential opportunities in Earth System Science Modelling School of Natural Science, Trinity College, University of Dublin

The School of Natural Sciences in Trinity College, University of Dublin is seeking to appoint two ecosystem modellers, one at professorial level and the other at lecturer level. Candidates for the position should have experience in ecosystem modelling, preferably in the area of Ecosystem Responses to Climate Change or Biogeochemical Cycles. For further details visit http://www.naturalscience.tcd.ie/new_positions/-Earth_Systems_Science.php and contact either Professor David Taylor (taylor@tcd.ie) or Professor Mike Jones (mike.jones@tcd.ie).

Dr Andrew Jackson Research Fellow Trinity Centre For Bioengineering School of Engineering Parsons Building Trinity College Dublin 2 Ireland Tel. + 353 1 896 2396 Fax. + 353 1 679 5554 Email. a.jackson@tcd.ie <http://www.tcd.ie/bioengineering/researchers/jackson.htm> a.jackson@tcd.ie

UCDavis QuantGenetics

Assistant Professor- Quantitative Geneticist

The Department of Plant Sciences, University of California, Davis, CA invites applications for a faculty position. The position is one of seven positions in a campus-wide Computational Networks Initiative and thus the Geneticist would be expected to work collaboratively with other faculty hires under the initiative. Successful candidate's research will focus on using new theoretical approaches and computational biology methods to effectively mine the large multidimensional datasets generated by global genomic technologies to understand the basis of quantitative phenotypes and the consequences of natural variation in wild and domesticated plant populations. QUALIFICATIONS: Ph.D. or equivalent level of experience in genetics or related field. SALARY: Commensurate with qualifications and experience. For more information or to apply: Please visit <http://recruitments.plantsciences.ucdavis.edu>. The position will remain open until filled. The University of California is an Affirmative Action/Equal Opportunity Employer.

David Neale <dbneale@ucdavis.edu>

UCaliforniaLosAngeles 2Lectureships EvolBiol

INSTRUCTOR POSITIONS AVAILABLE

ECOLOGY AND EVOLUTIONARY BIOLOGY

Deadline: June 4, 2007

The Department of Ecology and Evolutionary Biology is seeking two full-time instructors starting Fall Quarter 2007 (nine-month appointment, with optional summer teaching). The normal teaching load is two courses per quarter. The successful candidate will teach a subset of the following courses, depending on expertise: (1) upper division major courses: introduction to ecology and evolution (EE Biol 100), evolution, vertebrate morphology, biology of vertebrates, marine biology laboratory, mammalogy, or plant biology; (2) lower divi-

sion: at least one course per year of Life Sciences 1 (LS 1, Evolution, Ecology and Biodiversity, majors); (3) lower division general education courses in marine biology, evolution, or genetics for non-majors. One of the positions will include course development of laboratory components in LS 1 or EE Biol 100 in lieu of one of the courses, and is intended to become an established position within our long-term teaching program.

The mission of the UCLA Department of Ecology and Evolutionary Biology is to provide new knowledge of the ecological and evolutionary processes that produce and sustain life on Earth and to educate the next generation of scholars, professionals, and citizens for the biological, environmental and biotechnological challenges of the future. For undergraduates, we offer three majors in biology that includes rigorous and stimulating classes, extensive individual research opportunities with professors, and exciting field courses in unique habitats..

Qualifications: Ph.D. degree in the biological sciences; demonstrated experience in undergraduate teaching at the university level; experience with laboratory instruction in the biological sciences. Salary range of \$42,780-\$74,328 commensurate with qualifications and experience.

Please submit curriculum vitae, written statement of teaching interests and background online to <http://www.eeb.ucla.edu/apply.php?idQ> and at least three letters of reference by June 4, 2007 to UCLA Ecology and Evolutionary Biology Instructor Search, ATTN: Ms. Grace Angus, 621 Charles E. Young Dr. South, Box 951606, Los Angeles, CA 90095-1606

UCLA is an Equal Opportunity/Affirmative Action Employer. Individuals with a commitment and record of working with under-represented minorities are encouraged to apply.

Posted by:

Victoria Sork Professor and Chair, Dept of Ecol & Evol Biology Professor, Institute of the Environment UCLA 310-825-7755 eebchair@lifesci.ucla.edu

V Sork <vsork@ucla.edu>

UCincinnati 2 EvolBiol

JOB 1

UNIVERSITY OF CINCINNATI

DEPARTMENT OF BIOLOGICAL SCIENCES

Research Associate (27UC1785)

Job Description: A Research Associate to acquire and maintain DNA sequence data for a federally-funded forensics research project in the field of forensic entomology. The applicant is expected to have experience in DNA extraction, DNA purification, PCR, gel electrophoresis and other laboratory procedures related to DNA manipulation. The applicant is expected to have excellent attention to detail, as well as excellent organizational and computer skills, particularly database maintenance. The applicant will assist in preparation of both technical reports and research publications, and is expected to be able to present results and findings in a clear and effective manner.

Minimum Qualifications: M.S. degree in Biology (or a closely related field), or equivalent experience, and work experience in PCR and other molecular biology techniques. Ability to work independently and to maintain accurate and careful records and notes is required.

Ideal Qualifications: Ability to work independently; extensive work experience in molecular biology.

In order to apply, go to: <http://www.jobsatuc.com>. The position number is 27UC1785.

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

JOB 2

UNIVERSITY OF CINCINNATI

DEPARTMENT OF BIOLOGICAL SCIENCES

Junior Research Associate/Research Associate (27UC1779)

A full-time position is available for a research technician to study the genetic basis and evolution of chemosensory behavior. The technician is expected to conduct molecular, genetic, and behavioral research on *Drosophila*. The successful candidate will also be asked to manage the day-to-day running of the laboratory and to maintain *Drosophila* stocks. In addition, the technician will interact closely with graduate students and help with the training and supervision of undergraduates.

Minimum Qualifications: B.S. degree in biology, or a related field, and a minimum of one to two years of experience in genetics or molecular biology. Familiarity with standard molecular techniques (e.g. DNA and RNA isolation, PCR, sequencing, gene expression assays, and cloning), good organizational skills, and the ability to work independently are essential.

Ideal Qualifications: M.S. degree in biology, or a related field, is preferred. Experience maintaining *Drosophila* stocks is desired.

In order to apply, go to: <http://www.jobsatuc.com>. The position number is 27UC1779.

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

Mary Elaine Wischer Program Manager Department of Biological Sciences University of Cincinnati Cincinnati, OH 45221-0006 (513) 556-6241 - Phone (513) 556-5299 - Fax

wischer@ucmail.uc.edu wischer@ucmail.uc.edu

UCincinnati ResAssoc DNA DrosophilaGenet

UNIVERSITY OF CINCINNATI

DEPARTMENT OF BIOLOGICAL SCIENCES

Research Associate (27UC1785)

Job Description: A Research Associate to acquire and maintain DNA sequence data for a federally-funded forensics research project in the field of forensic entomology. The applicant is expected to have experience in DNA extraction, DNA purification, PCR, gel electrophoresis and other laboratory procedures related to DNA manipulation. The applicant is expected to have excellent attention to detail, as well as excellent organizational and computer skills, particularly database maintenance. The applicant will assist in preparation of both technical reports and research publications, and is expected to be able to present results and findings in a clear and effective manner.

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UNIVERSITY OF CINCINNATI

DEPARTMENT OF BIOLOGICAL SCIENCES

Junior Research Associate/Research Associate (27UC1779)

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Minimum Qualifications: B.S. degree in biology, or a related field, and a minimum of one to two years of experience in genetics or molecular biology. Familiarity with standard molecular techniques (e.g. DNA and RNA isolation, PCR, sequencing, gene expression assays, and cloning), good organizational skills, and the ability to work independently are essential.

Ideal Qualifications: M.S. degree in biology, or a related field, is preferred. Experience maintaining *Drosophila* stocks is desired.

In order to apply, go to: <http://www.jobsatuc.com>. The position number is 27UC1779.

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

Mary Elaine Wischer Program Manager Department of Biological Sciences University of Cincinnati Cincinnati, OH 45221-0006 (513) 556-6241 - Phone (513) 556-5299 - Fax

wischer@ucmail.uc.edu wischer@ucmail.uc.edu

UGeorgia ResAssist PlantEvol

RESEARCH ASSISTANT POSITION: PLANT EVOLUTIONARY ECOLOGY UNIVERSITY OF GEORGIA

A research assistant position is available starting August 2007 for an NSF-funded project conducting an evolutionary and functional analysis of reproductive biology in flowering plants. Field and greenhouse experiments will be used to examine how plants vary in their male component of fitness. Responsibilities will include DNA extraction, PCR, allozymes and microsatellite DNA genotyping, and measuring morphological and

life history traits of plants. Other duties include: overseeing day-to-day management of the laboratory including the purchasing of supplies and equipment; insuring proper operation and maintenance of laboratory equipment; entering and managing electronic data files; working with undergraduate research assistants; maintaining greenhouse plants, and training of student workers. If interested, the individual hired is also welcome to participate in departmental seminars and discussion groups. The position is ideal for a student considering graduate school to gain paid research experience before committing to a program.

Requirements for the position are a bachelor's degree in biology, plant biology, ecology, evolution, or a related field as well as basic computer skills. Research experience in plants and an enthusiasm for field work will be advantageous. The RA must be able to do field- and greenhouse work in hot weather.

To apply, please send a curriculum vitae, a copy of current college transcripts and names and contact information of three references to: Shu-Mei Chang, chang@plantbio.uga.edu. Applications will be considered until position is filled.

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

UGeorgia ResTech

The Burke Lab at the University of Georgia in Athens, GA has an opening for a Research Technician. Broadly speaking, our lab studies plant evolutionary genetics. The successful applicant will be involved in various aspects of our research, including DNA/RNA extraction, PCR-based genotyping, sequencing, and data analysis. This individual will also be responsible for general lab management, including ordering supplies, maintaining equipment, supervising undergraduate researchers, and otherwise maintaining an organized lab. This position will also likely involve small amounts of greenhouse work.

Minimum qualifications are a Bachelor's degree in biology or a related field. Prior laboratory experience is desired, but not necessarily required. Training will be provided. While initial projects will be closely supervised, the ideal candidate will become more independent as they become more experienced. Perhaps important requirements are close attention to detail and good organizational skills.

To apply, please send a resume and contact information for three references to John Burke at: jmburke@uga.edu. Informal inquiries are also encouraged.

For details on our research, please visit <http://www.theburkelab.org/> -

====John M. Burke, Ph.D.

Tel: 706.583.5511 Fax: 706.542.1805 <http://www.theburkelab.org/>

====University of Georgia

Department of Plant Biology Miller Plant Sciences Athens, GA 30602

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UGloucestershire TeachingEvolBiol

Lecturer/Senior Lecturer Biology University of Gloucestershire, UK The main focus of this post will involve teaching within the undergraduate Biology Field. You will be expected to contribute to a variety of areas of biology and ecology but expertise in one or more of the following areas would be an advantage: parasitology, population ecology, invertebrate biology. You will also be expected to engage in other developments within the Department and participate in field course teaching. You will be expected to engage actively in research and knowledge transfer activity. In addition, research supervision is expected of staff with appropriate qualifications and experience. For further information, see <http://www.glos.ac.uk/jobs/-index.cfm?jobRef=A292> or contact Dr Adam Hart, ahart@glos.ac.uk

Adam Hart PhD, MA (Cantab), PGCHE

Senior Lecturer in Biological Sciences Field Chair in Environmental Science and Management, and Biology Associate Editor Ecological Entomology

Department of Natural & Social Sciences University of Gloucestershire Francis Close Hall, Swindon Road, Cheltenham GLOS GL50 4AZ, UK Email ahart@glos.ac.uk NOTE CHANGE IN NUMBER Tel +44 (0) 1242 714670

"HART, Adam" <ahart@glos.ac.uk>

UIdaho PlantSystematics

Assistant/Associate Professor of Plant Systematics

Department of Forest Resources College of Natural Resources University of Idaho

The Department of Forest Resources, College of Natural Resources, University of Idaho, invites applications for an academic-year, tenure-track faculty position in Plant Systematics at the rank of Assistant or Associate Professor.

RESPONSIBILITIES/DUTIES: The position is approximately 35% teaching, 50% research, 5% advising, and 10% service and outreach. We seek to appoint someone whose research makes use of molecular tools and approaches drawn from phylogenetics and systematics to address fundamental and applied questions in plant biology and forest field ecology. Applicants will be expected to develop an innovative, externally funded research program and contribute to teaching at the graduate and undergraduate levels. At the undergraduate level, Dendrology is a specific teaching requirement, and a field course in plant Community Ecology is highly desirable. A graduate course of your choice is also required. The successful applicant will serve key roles in the UI Laboratory of Ecological and Conservation Genetics, <<http://www.cnrhome.uidaho.edu/LECG>><http://www.cnrhome.uidaho.edu/LECG>, and in the Center for Research on Invasive Species and Small Populations (CRISSP) <<http://www.cnrhome.uidaho.edu/CRISSP>><http://www.cnrhome.uidaho.edu/CRISSP>.

QUALIFICATIONS:

Required: PhD in Plant Systematics or equivalent by time of hire. Proficient communication skills, both written and verbal. Demonstrated ability to publish research results in refereed journals. Evidence of ability in undergraduate and graduate education.

Desired: Demonstrated interest and ability in teaching Dendrology and plant Community Ecology. Experience in multidisciplinary collaboration addressing important questions in conservation and invasion biology. Postdoctoral experience with a successful record of extramural funding for research. Expertise in the woody plant flora of the Pacific Northwest.

APPLICATION PROCEDURE: Apply online at <http://www.hr.uidaho.edu>. The application consists of

a letter of application, curriculum vitae, statement of teaching philosophy, description of research focus, academic transcripts, contact information for three references, and copies of one or two of your refereed publications with a brief explanation of your role in preparing these publications if they are coauthored.

Review of applications will begin August 25th, 2007 and will continue until a successful candidate has been identified with a prospective starting date of January 2008.

Contact: George Newcombe, Chair Plant Systematics Search Committee Department of Forest Resources Moscow ID 83844-1133 OR georgen@uidaho.edu 208-885-5289

University of Idaho is an Affirmative Action/Equal Opportunity Employer.

cmerick@uidaho.edu

UKansas ResAssist DrosophilaEvol

Research Assistant, University of Kansas

Quantitative and Molecular Genetics in Drosophila

A research assistant position is available in a Drosophila quantitative genetics laboratory in the Division of Biological Sciences at the University of Kansas. The Macdonald lab explores the genetic basis of complex polygenic traits within and between species using Drosophila as a model system (www.people.ku.edu/~sj-mac). We seek an enthusiastic individual to participate in our large-scale quantitative genetics projects and to oversee various lab activities. The successful candidate should be motivated, organized and careful, with excellent oral and written communication skills, and be able to work largely independently. Salary will be commensurate with experience and will include benefits.

Job responsibilities will include performing basic molecular techniques (DNA extraction, PCR, sequencing, genotyping) in a high-throughput setting, maintaining and breeding Drosophila stocks, examining and dissecting out various Drosophila morphological structures (which will involve extensive microscope work), as well as general lab management (including some supervision of undergraduate researchers). Opportunities for independent research projects will also likely exist.

Required qualifications are a B.A./B.S. degree in biology (or a related field), and demonstrable experi-

ence conducting research in a (broadly-defined) genetics or molecular biology lab. Preference will be given to those candidates with significant laboratory experience that includes troubleshooting and optimizing molecular biology protocols, and/or those who have previously worked with *Drosophila* or other small invertebrates.

The University of Kansas (www.ku.edu) has an active academic community in the life sciences and the Macdonald lab is affiliated with both the Department of Ecology and Evolutionary Biology (www2.ku.edu/~eeb) and the Department of Molecular Biosciences (molecularbiosciences.ku.edu). The range and number of research groups presents many opportunities for fostering academic and social interactions. The University of Kansas is in the city of Lawrence (www.visitlawrence.com, www.visitlawrence.com, en.wikipedia.org/wiki/Lawrence,_Kansas) situated 45 minutes West of Kansas City.

Review of applications will begin June 1, 2007 and continue until the position is filled. Informal inquiries about the position are welcome and can be directed to Stuart Macdonald (sjmac@ku.edu). To apply, complete an online application at <http://jobs.ku.edu> (position number 00206322), and include a cover letter (describing your interest in the position and any relevant expertise), and a full CV. Also, arrange to have at least two professional letters of reference sent by email/fax/mail to:

Stuart Macdonald Division of Biological Sciences University of Kansas 1030 Haworth Hall 1200 Sunnyside Avenue Lawrence KS 66045 tel: 785-864-5362 fax: 785-864-5321 email: sjmac@ku.edu web: <http://www.people.ku.edu/~sjmac/> sjmac@ku.edu sjmac@ku.edu

ULiverpool EvoBiol

The University of Liverpool wishes to appoint a lecturer (=assistant professor equivalent) in evolutionary biology.

First class applicants with a desire to develop a research programme in any area of evolutionary biology are encouraged to apply, and we would particularly welcome those with interests in evolutionary and comparative genomics, molecular evolution, or host-parasite interactions. The post may also be offered as an Academic Fellowship and would suit someone with a recent fellowship award who wishes to develop their group in a

tenure track position.

Full details of the post, and how to apply can be found at http://www.liv.ac.uk/working/-job_vacancies/academic/B011.htm Application deadline: 4th June

The Department, rated 5 in the last UK RAE, has very active research groups in Evolutionary biology, Bioinformatics, Ecology, Host Parasite interactions, as well as other aspects of biological research, housed within the new Biosciences Building on the Main Campus, a purpose built £29M research centre. The School possesses a particularly wide range of research facilities for virtually all aspects of biological science, and has recently purchased the 454 GS-Flex pyrosequencing system, to complement the existing infrastructure in the Microarray facility. It also maintains a capacity to work with a wide range of organisms from exotic species through to models such as *Arabidopsis*, *Drosophila*, *C. elegans* and zebrafish. A profile of the department can be found at <http://www.liv.ac.uk/biolsci/> Liverpool is an interesting city, celebrating its 800th anniversary this year. It is European Capital of Culture 2008, located near fine countryside (lake district and North Wales), and is easily accessible for both Mainland Europe (via Liverpool airport, an Easyjet and Ryanair hub) and North America (via Manchester Airport).

g.hurst@ucl.ac.uk g.hurst@ucl.ac.uk

UReading LectureshipPlantCommunityEcol

The University of Reading is offering a full time post in Plant Community Ecology (<http://www.jobs.ac.uk/-jobfiles/RH450.html>) that might be of interest to some of the EvoDir readers.

Best wishes,

Alastair Culham

Dr Alastair Culham Centre for Plant Diversity and Systematics Plant Science Laboratories School of Biological Sciences University of Reading Whiteknights Reading, RG6 6AS U.K.

Alastair Culham <a.culham@reading.ac.uk>

UStAndrews ResTech FishGeneticDivergence

UK 1 YEAR RESEARCH TECHNICIAN POSITION

Genetic divergence in the Mexican Amarillo fish.

Mike Ritchie, Jeff Graves & Tino Macias have a position available for a 1 year research technician at the University of St Andrews, Scotland, starting 1st July 2007. Duties will involve basic techniques from molecular ecology (DNA extraction, PCR amplification of mtDNA loci and microsatellite loci, some data analysis).

This position is most suitable for a recent graduate in Biology or Genetics with an interest in evolution and population genetics, perhaps one who is considering subsequently doing a PhD in this area.

If you know someone suitable for this position, please bring this to their attention.

Enquiries and further details of the position are available from Mike Ritchie, mgr@st-and.ac.uk.

Mike Ritchie Phone 0 (44 outside UK) 1334 463495
Environmental & Evolutionary Biology Fax 0 (44 outside UK) 1334 463366
Dyers Brae House University of St Andrews
E-mail mgr@st-andrews.ac.uk St Andrews, Fife Scotland KY16 9TH

Website: <http://bio.st-andrews.ac.uk/staff/mgr.htm>
Research website via: <http://tiree.st-and.ac.uk/cegg/-research.html> mgr@st-andrews.ac.uk

UppsalaU EukaryoticEvolGenomics

LECTURESHIP IN EUKARYOTIC EVOLUTIONARY GENOMICS

With the aim of strengthen our research profile in evolutionary genomics and systematics, the Uppsala University Evolutionary Biology Centre (EBC) is recruiting 4 new Senior Lecturers / Associate Professors. Among them is one in

EUKARYOTIC EVOLUTIONARY GENOMICS

placed at the Department of Evolution, Genomics and Systematics.

In filling this position, special importance will be attached to research qualifications in evolutionary genetics, evolutionary genomics and molecular evolution. The position includes teaching in evolutionary genetics, evolutionary genomics and molecular evolution.

A person who is offered a position as Senior Lecturer / Associate Professor will be employed as Professor if she/he has requested this and is subsequently judged to be sufficiently competent.

The Department is situated in the recently-built Evolutionary Biology Centre of Uppsala University (<http://www.ebc.uu.se>). It is equipped with facilities for large-scale sequencing, genotyping and expression analysis, and houses a Centre of Excellence in Evolutionary Genomics funded by the Swedish Research Council, led by Siv Andersson and Hans Ellegren. The Evolutionary Biology Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 400 scientists and graduate students, with research programs in ecology, systematics, genetics, genomics, functional genomics and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated close to Stockholm.

For informal inquiries please contact Head of the Department, Professor Hans Ellegren (phone: +46-18-4716460, email: Hans.Ellegren@ebc.uu.se).

Further information about this position including details on how to apply is given at <http://www.personalavd.uu.se/ledigaplats/engindex.html>
Deadline is June 18, 2007.

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

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

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

UppsalaU MicrobialEvol

LECTURESHIP IN MICROBIAL EVOLUTIONARY GENOMICS

With the aim of strengthen our research profile in evolutionary genomics and systematics, the Uppsala University Evolutionary Biology Centre (EBC) is recruiting 4 new Senior Lecturers / Associate Professors. Among them is one in

MICROBIAL EVOLUTIONARY GENOMICS

placed at the Department of Evolution, Genomics and Systematics.

In filling this position, special importance will be attached to research qualifications in evolutionary genomics, molecular evolution and bioinformatics with focus on microbial systems. The position includes teaching in evolutionary genomics, bioinformatics and microbial genetics.

A person who is offered a position as Senior Lecturer / Associate Professor will be employed as Professor if she/he has requested this and is subsequently judged to be sufficiently competent.

The Department is situated in the recently-built Evolutionary Biology Centre of Uppsala University (<http://www.ebc.uu.se>). It is equipped with facilities for large-scale sequencing, genotyping and expression analysis, and houses a Centre of Excellence in Evolutionary Genomics funded by the Swedish Research Council, led by Siv Andersson and Hans Ellegren. The Evolutionary Biology Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 400 scientists and graduate students, with research programs in ecology, systematics, genetics, genomics, functional genomics and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated close to Stockholm.

For informal inquiries please contact Head of the Department, Professor Hans Ellegren (phone: +46-18-4716460, email: Hans.Ellegren@ebc.uu.se), or Professor Siv Andersson (email: Siv.Andersson@ebc.uu.se).

Further information about this position including details on how to apply is given at <http://www.personalavd.uu.se/ledigaplatser/engindex.html>. Deadline is August 31, 2007 (note this date is different from other lectureships currently announced at the EBC).

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

Phone: +46-18-4716460 Fax: +46-18-4716310 Email:

Hans.Ellegren@ebc.uu.se

Lab home page: <http://www.egs.uu.se/evbiol/-index.html> Personal home page: <http://www.egs.uu.se/evbiol/Persons/Hans.html>

Hans.Ellegren@ebc.uu.se Hans.Ellegren@ebc.uu.se

UppsalaU SystematicBotany**LECTURESHIP IN SYSTEMATIC BOTANY**

With the aim of strengthen our research profile in evolutionary genomics and systematics, the Uppsala University Evolutionary Biology Centre (EBC) is recruiting 4 new Senior Lecturers / Associate Professors. Among them is one in

SYSTEMATIC BOTANY

placed at the Department of Evolution, Genomics and Systematics.

In filling this position, special importance will be attached to qualifications in evolutionary oriented research in plant systematics. The position includes teaching in plant systematics and floristics.

A person who is offered a position as Senior Lecturer / Associate Professor will be employed as Professor if she/he has requested this and is subsequently judged to be sufficiently competent.

The Department is situated in the recently-built Evolutionary Biology Centre of Uppsala University (<http://www.ebc.uu.se>). Systematic Botany has a long and strong tradition in Uppsala, with a professorship dating back to Carl von Linneaus. The Evolutionary Biology Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 400 scientists and graduate students, with research programs in ecology, systematics, genetics, genomics, functional genomics and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated close to Stockholm.

For informal inquiries please contact Head of the Department, Professor Hans Ellegren (phone: +46-18-4716460, email: Hans.Ellegren@ebc.uu.se) or Professor Leif Tibell (email: Leif.Tibell@ebc.uu.se).

Further information about this position including details on how to apply is given at <http://www.egs.uu.se/evbiol/Persons/Hans.html>

/www.personalavd.uu.se/ledigaplatser/engindex.html
Deadline is June 18, 2007.

– Prof Hans Ellegren Dept of Evolutionary Biology
Evolutionary Biology Centre Uppsala University Nor-
byvägen 18D SE-752 36 Uppsala

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

Lab home page: <http://www.egs.uu.se/evbiol/-index.html> Personal home page: <http://www.egs.uu.se/evbiol/Persons/Hans.html>

Hans.Ellegren@ebc.uu.se Hans.Ellegren@ebc.uu.se

UppsalaU SystematicZool

LECTURESHIP IN SYSTEMATIC ZOOLOGY

With the aim of strengthen our research profile in evolutionary genomics and systematics, the Uppsala University Evolutionary Biology Centre (EBC) is recruiting 4 new Senior Lecturers / Associate Professors. Among them is one in

SYSTEMATIC ZOOLOGY

placed at the Department of Evolution, Genomics and Systematics.

In filling this position, special importance will be attached to qualifications in evolutionary oriented research in animal systematics. The position includes teaching primarily in systematics of evertebrates.

A person who is offered a position as Senior Lecturer / Associate Professor will be employed as Professor if she/he has requested this and is subsequently judged to be sufficiently competent.

The Department is situated in the recently-built Evolutionary Biology Centre of Uppsala University (<http://www.ebc.uu.se>). Systematics has a long and strong tradition in Uppsala, with a professorship in systematic botany dating back to Carl von Linneaus. The Evolutionary Biology Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 400 scientists and graduate students, with research programs in ecology, systematics, genetics, genomics, functional genomics and developmental biology. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated close to Stockholm.

For informal inquiries please contact Head of the Department, Professor Hans Ellegren (phone: +46-18-4716460, email: Hans.Ellegren@ebc.uu.se).

Further information about this position including details on how to apply is given at <http://www.personalavd.uu.se/ledigaplatser/engindex.html>
Deadline is June 18, 2007.

– Prof Hans Ellegren Dept of Evolutionary Biology
Evolutionary Biology Centre Uppsala University Nor-
byvägen 18D SE-752 36 Uppsala

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

Lab home page: <http://www.egs.uu.se/evbiol/-index.html> Personal home page: <http://www.egs.uu.se/evbiol/Persons/Hans.html>

Hans.Ellegren@ebc.uu.se Hans.Ellegren@ebc.uu.se

Valencia Bioinformatics ResContract

Research Contract, Bioinformatics Department CIPF, Valencia (Ref.: CI02/2007)

A research contract for a biostatistician is available in the Department of Bioinformatics, CIPF, Valencia.

Requirements:

- A degree in Mathematics, Statistics, or related fields.
- Experience in statistical analysis of large datasets in the field of biomedicine.
- Knowledge of programming languages such as R or C/C++.
- Good oral and written English level.
- Background in population genetics is highly desirable.

Job Description:

- Conducting statistical analysis and consulting, mostly involving DNA polymorphisms (mainly SNPs) and microarray data.
- Providing statistical support to the team.
- Developing bioinformatic/biostatistic software.
- Teaching short courses on biostatistics and data analysis.

We offer:

- The CIPF is dedicated to international excellence in biomedical research and to translating new knowledge into improved medical practice.
- The successful candidate will join a new, rapidly expanding team with access to cutting edge technology in an environment

of scientific excellence. - Work contract liked to the project GENOMA ESPAÑA for INB.

Please send your CV, cover letter and contact information of two referees to (Management(gerencia@cipf.es) and to HR (recursoshumanos@cipf.es). Please state the reference number as the subject of your e-mail.

Joaquin Dopazo <jdopazo@cipf.es>

WillametteU EvolBiol

Sabbatical Replacement Position in Ecology and Evolution at Willamette University

Willamette University announces a one-year opening for an A.B.D. or Ph.D. to teach a lecture and two laboratory courses in Evolution Ecology and Biodiversity (BIOL 125) and a Special Topic in Biology (BIOL 470) in Fall 2007. BIOL 470's small seminar format permits a timely focus on any newly emerging and/or significant area relevant to biology. The Spring 2008 course load would repeat the BIO 125 responsibilities and include Evolution (BIOL 376). This appointment is a full-time, sabbatical replacement position beginning late August

2007.

Willamette University, located in Salem, Oregon, is a liberal arts institution that values excellence in teaching and scholarship. Salem is the state capital of Oregon, and is located within about one hour of the Pacific coast, the Cascade mountains, and the metropolitan areas of Portland, Corvallis, and Eugene. The biology department is housed in a spacious new Olin science complex equipped with modern equipment and facilities for conducting effective programs in ecology and evolutionary biology at the molecular and organismal levels.

Applications should include curriculum vitae, brief description of scholarly interests, statement of teaching philosophy, and contact information for three references; evidence of teaching effectiveness is encouraged. Submit materials and any questions by email to Dr. David P. Craig (dpcraig@willamette.edu) preferably as pdf attachments. Applications materials may also be mailed to Dr. Craig at Willamette University, Department of Biology, 900 State Street SE, Salem, OR 97301. The search will be open until the position is filled.

Please excuse cross-listing repetition, but forward this to anyone who might be interested.

Susan Kephart <skephart@willamette.edu>

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AFLP run parameters 3730xl

Hi, I would be interested in finding out how other people are running AFLPs on a 3730 genetic analyzer. We are using the ROX size standard and are experiencing loss of resolution with the larger fragments and a “crunching” of the middle sized ladder fragments with either of the two following sets of electrophoresis parameters: Dense patterns: 12 sec injection time, 15 kV injection voltage, 30 min run time, 13 kV run voltage Simple patterns: 5 sec injection time, 13 kV injection voltage, 26 min run time, 15 kV run voltage

However, if we set the machine to the microsatellite parameters and run the plate a second time, the ladder looks beautiful but none of the AFLP fragments makes it through. Any advice would be much appreciated!
Amanda

Amanda M. Hale Dept. of Biology University of Miami
1301 Memorial Drive Coral Gables, FL 33124 305-284-5412 or 305-284-6566 <http://www.bio.miami.edu/hale>

ahale@bio.miami.edu ahale@bio.miami.edu

used them before) or comparison with Genotyper (the one I am most familiar with).

We have a large sample size (about 2000 samples and 9 primer combinations in 3 multiplexes) and are thus looking for a high throughput software with automatic processing, that would allow manual editing and would be versatile and easy to use. We are limited by cost, so not considering GeneMapper etc. I had previously also tried Genographer, but encountered some problems.

Many thanks,

Sarka

– Sarka Jahodova

Department of Ecology Charles University Vinicna 7
CZ-128 44 Prague 2 Czech Republic

Tel. +420 221951809 E-mail: jahodova@natur.cuni.cz

And

Department of Invasion Ecology Institute of Botany
Academy of Sciences of the Czech Republic CZ-252 43
Pruhonice Czech Republic

<http://www.ibot.cas.cz/invasions>

ja-

hodova@natur.cuni.cz

AFLP scoring software answers

AFLP scoring software

Dear EvolDir members,

We are planning to purchase GeneMarker (from Soft-Genetics) to score our AFLP profiles generated on ABI 3100 capillary system (using LIZ size standard). I would like to hear your experience with this software and possibly also comparison with other similar software. I would be particularly keen to hear about GelQuest, STRand and Peak Scanner (as I have not

Dear EvolDir members,

I've got several request for a summary of answers to my query regarding software for scoring AFLP. I received positive comments on GeneMarker, which is very encouraging, but I haven't heard much about most other programs apart from Genographer - that seemed to have mixed references. So please if you or your colleagues have experience with alternative AFLP scoring software, I'd still be interested in hearing from you!

Best wishes, Sarka

jahodova@natur.cuni.cz

RESPONSES I RECEIVED UP TO DATE (original post at the end):

Just to let you know that I own a copy of GeneMarker, and am very happy with it. I use it for data from an ABI 3730, and prefer it to GeneMapper, which I have also used, but refused to buy because of the cost. I've heard that there's a lite-version, free, of GeneMapper, and once I find the lead I'll send it to you. If you're familiar with using this kind of software then GeneMarker is great. The manual assumes you've already used something like GeneMapper. I like the flexibility in the software, and also the ability to create panels that don't require you to go through so many peaks each time, once you've identified the informative markers in a population, species, etc. I tried to use Genographer and STRand, and got fed up, realizing that for high-throughput work, they would really get on my nerves after a while.

Bob Marra

We have tried GeneMarker and found it an excellent program - it is very powerful and user-friendly. We routinely use GeneMapper and although GeneMarker is more user-friendly, these two programs give broad comparable results. Both GeneMarker and GeneMapper are fully automated (cf. Genographer). Also, I don't think Genographer supports the LIZ size standard.

SoftGenetics allow you to download either a limited-function version, or a full-functional 30-day trial version of GeneMarker (<http://www.softgenetics.com/downloads.html>).

We haven't had much experience with other programs, but you may find Table 1 in the attached paper helpful - it profiles most of the AFLP scoring software currently available. (Meudt, H.M. & Clarke, A.C. (2007) Almost Forgotten or Latest Practice? AFLP applications, analyses and advances. Trends in Plant Science, 12. p106-117.)

Andrew Clarke & Heidi Meudt

I have experience working with both GeneMarker and Genotyper for genotyping AFLP traces, and can report that GeneMarker is a much better program. In fact, I genotyped three primer combinations of about 300 samples with Genotyper and with GeneMarker. Genotyper is simply not set up for this kind of work, and was generally cumbersome and difficult to work with, although I've been pleased with it before for genotyping

microsatellite traces. GeneMarker is set up specifically for AFLPs (but works well to genotype microsatellites too), and the technical support is reasonably good. It allows you to correct for peak saturation and pullup between dyes, among other things, and does automatic genotyping of AFLP peaks in a way that makes a lot of sense to me, but is flexible as well. It does some things that are a little annoying, but may be corrected in the most recent update. For example, it re-sorts the marker table sometimes when you insert an allele (so you have to sort the table so the samples are arranged in order again, A1, A2, A3, etc.). It is also not possible to edit the marker table until you export into different software, such as Word or Excel.

Kevin

I've never used GeneMarker, but just a few things to mention.

1. Have you thought about using a 650 Rox ladder? When I did my AFLPs using a 3100 ABI I found that I had quite a few fragments as large as 450bp, so LIZ wasn't an adequate ladder for me.

2. If you're cost limited, why not try BinThere? <http://hcg.unh.edu/protocol/aflp/AFLPbinthere.html> It's free, downloadable software that I've heard is pretty good at auto-binning (particularly attractive for a large data set).

I ran my samples through Genotyper (to define the ladder) and then used Genographer - by far my favourite software for analyzing my AFLP data. What type of problems did you have with it?

Rachel

Genographer definitely will have size standard issues unless you analyze the data with GeneScan first - I'm not exactly sure what it does, but I think it might calibrate the ladder.... when you've analyzed the files with GeneScan the file itself is changed and then they should work fine in Genographer. I liked this software because it created a virtual gel - made looking at many samples at the same time possible (plus another group of neat features related to assessing peak height and exact size). If you decide to give it another try I'm happy to help you figure stuff out.

— / —

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>

AFLP training course

Dear All,

Does anyone know of any training courses/training tools for AFLP technique, preferably within Europe? In particular, I would like to learn how to analyse data following fragment analysis (e.g. how best to call peaks; how the AFLP markers you generate are stored/organised; how sets of markers are used to genotype individuals from wild populations).

I am a PhD student developing AFLP markers for an animal, with a view to genotype many individuals from different demes across at least 300 markers and use these markers to construct a preliminary linkage map. My samples are run on an ABI PRISM 3100 and visualised using GeneMapper (4.0).

Any information about any training course/tools would be most appreciated.

Many thanks,

Simit Patel

Simit Patel School of Biological Sciences Philip Lyle Building University of Reading Whiteknights, P O Box 68 Reading RG6 6BX, UK

Email: s.patel@rdg.ac.uk Telephone: +44(0) 118 378 5049 (internal: 5049)

sar06sp@reading.ac.uk sar06sp@reading.ac.uk

Coalescent software answers

Dear EvolDir members,

thanks to all who responded to my request about software for coalescence simulations. I have got many useful answers and post them to the list. Most of you suggested either using SimCoal / SimCoal2 or generating genealogies using MS and then and then using a sequence simulation program, like SeqGen, to generate sequences on those genealogies.

It seems that simulating selection together with complex demographies under the coalescence is not yet possible and/or feasible.

One comprehensive reply listed a number of software packages:

MS <http://home.uchicago.edu/~rhudson1/source/mksamples.html> SIMCOAL/SIMCOAL2 <http://cmpg.unibe.ch/software/simcoal2/> Serial SIMCOAL <http://www.stanford.edu/group/hadlylab/ssc.html> SPLATCHE <http://cmpg.unibe.ch/software/splatche/> Coasim <http://www.daimi.au.dk/~mailund/-CoeSim/> TREEEVOLVE <http://evolve.zoo.ox.ac.uk/software.html?name=Treevolve> SEQ-GEN <http://evolve.zoo.ox.ac.uk/software.html?id=seqgen> EASYPOP <http://www.unil.ch/izea/software/easypop.html> BOTTLESIM <http://chkuo.name/software/BottleSim.html> SIMUPOP <http://bp6.stat.rice.edu:8080/simuPOP/> FPG <http://lifesci.rutgers.edu/~heylib/HeylabSoftware.htm#FPG> Other replies and the original request are listed below.

thanks again, Asta

**

Can anybody suggest a software package for coalescence simulations under different population demographic models (subdivision, stable population size, bottlenecks) and different background mutation rates? Ideally there should also be a possibility to introduce selection, different mutation models, and I prefer the results (a random sample of sequences from the simulated populations) to be available in .nex or some other popular format.

Answers:

I do not now of any software that do all the stuff that you want would like to recommend Hudsons MS <http://home.uchicago.edu/~rhudson1/source/mksamples.html> and if you want to include selection try SelSim <http://www.stats.ox.ac.uk/~spencer/SelSim/Controlfile.html>. At least ms is used extensively and once you get started fairly easy to use.

** try SimCoal or SimCoal2 (<http://cmpg.unibe.ch/software/simcoal2/>)

** have a look at serialsimcoal

** Hi, you have a number of options. Probably the most efficient neutral simulator would be Richard Hudson's ms (<http://home.uchicago.edu/~rhudson1/source/mksamples.html>), the results of which can be piped into Andrew Rambaut's SeqGen (<http://evolve.zoo.ox.ac.uk/software.html?name=SeqGen>) to generate sequences under varying mutation models. For selection, have a look at Spencer & Coop's SelSim (<http://www.stats.ox.ac.uk/~spencer/SelSim/Controlfile.html>). All three are command line unix-type programs which are easy to incorporate into larger shell or perl scripts if necessary. Another option for selection simulations would be HYPHY (

www.hyphy.org/) which provides a framework for phylogenetic hypothesis testing. Selection can be simulated along phylogenetic trees from predefined roots under given models. Again unix-style batch processing is possible.

** The most popular program for coalescent simulation is ms (Hudson, Bioinformatics 2002). you can download at <http://home.uchicago.edu/~rhudson1/> Additionally, another programs have been constructed. I designed a program named mlcoalsim (Evolutionary Bioinformatics 2007) based on ms that construct sample sequences in fasta format and also calculates several neutrality tests. you can download at <http://www.ub.edu/softevol/mlcoalsim> ** I have a program which should allow you to do this (except for implementing selection) at ueg.ulb.ac.be/treesifter/

— / —

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>

Commercial Fragment analysis answers

Thank you to all for recommending commercial facilities for fragment analysis. Below is a compiled list of the facilities that were recommended. Some prices are noted, however, some of them are in-house and some are outside prices. The prices for fragment analysis are highly variable among facilities, and it is worth checking out each site individually.

Camille Barr

Fragment Analysis Facilities:

1. Cornell: <http://www.brc.cornell.edu/brcinfo/?f=3D1>
2. University of Guelph: <http://www.uoguelph.ca/ib/facilities/Genomics/GenomicsFacility.shtml>
3. Iowa State: www.dna.iastate.edu
4. Ohio State: http://www.oardc.ohio-state.edu/mcic/genomics/genotyping/gen_instructions.html#Instrucstionsforsamplesubmission \$144/plate
5. University of Arizona: <http://gatc.arl.arizona.edu/services/sequencing.php>

6. Yale: http://research.yale.edu/dna_analysis/
 7. Macrogen: http://www.macrogen.com/eng/-macrogen/macrogen_main.jsp
 8. East Malling Research registered office: New Road, East Malling, Kent
ME19 6BJ. Tel. 01732-843833. Registered in England No. 5019373. Charity registration No.1102243.
 9. GATC Biotech (Germany): <http://www.gatc.de/en/index.php>
 10. Ingentix (Austria): <http://www.ingenetix.com> <<http://www.ingenetix.com/>>
 11. Genetic Analysis & DNA Sequencing Facilities The Centre for Applied Genomics The Hospital for Sick Children TMDT-MaRS Building 14th floor, room 14-601 101 College Street Toronto, ON (\$1/sample)
 12. Georgetown: njp24@georgetown.edu \$10/sample
 13. Functional Genomics Bioinformatics Specialist W.M. Keck Center for Comparative and Functional Genomics Roy J. Carver Biotechnology Center University of Illinois, Urbana-Champaign:
<http://www.biotech.uiuc.edu/centers/Keck/fragment.htm>
 14. University of Utah DNA Sequencing and Genomics Core Facility
 15. University of Wisconsin-Madison: <http://www.biotech.wisc.edu/> \$141/plate
 16. Lakehead University: <http://www.ancientdna.com/>
 17. NGB Genetics s.r.l., spin off of the Ferrara University.
NGB is a company that develops and markets molecular tools for the genetic analysis in the human health, environmental, veterinary and food fields. Our customers are Universities, research institutes and private organisations that need custom-made solutions to develop and improve the efficiency of their research projects For more information about our company, the website is:
<http://www.ngbgenetics.com/>
- Camille M. Barr Division of Biological Sciences University of Montana 32 Campus Drive #4824 Missoula, MT 59812 (406) 243-5168
camille.barr@mso.umt.edu

Creation Research Journal

A creationism journal! Have you seen this? Is someone preparing an opposition to this?

International Journal for Creation Research The Institute for Creation Research is pleased to announce the inaugural Call for Papers for the International Journal of Creation Research (IJCR).

IJCR is a professional peer-reviewed journal of interdisciplinary scientific research that presents evidence for recent creation within a biblical framework.

Addressing the need to disseminate the vast field of research conducted by experts in geology, genetics, astronomy, and other disciplines of science, IJCR provides scientists and students hard data based on cutting-edge research that demonstrates the young earth model, the global Flood, the non-evolutionary origin of the species, and other evidences that correlate to the biblical accounts.

It is our hope that you will be encouraged in your study of creation science issues that remain at the forefront of education and research.

Andrew A. Snelling Editor-in-Chief

Voltolini

Prof. Dr. J. C. VOLTOLINI Grupo de Estudos em Ecologia de Mamíferos (ECOMAM) Universidade de Taubate - Departamento de Biologia Taubate, SP. 12030-010. E-Mail: jcvoltol@uol.com.br Website do ECOMAM: <http://jcvoltol.sites.uol.com.br/> Fotos de Cursos: <http://jcvoltol.fotoblog.uol.com.br/> Currículo Lattes: <http://lattes.cnpq.br/8137155809735635> Fotos Artísticas: <http://voltolini.fotos.net.br/texturas> “Siamo tutti angeli con un’ala e possiamo volare soltanto se ciabbracciamo”

jcvoltol@uol.com.br

about many topics pertinent to evolutionary biologists. (1) DATA DEPOSITORIES * we are limited (by journal policies) in showing all our data, which could help others doing similar projects or doing meta-analyses * PMR suggested having people in the same discipline brainstorm the best format for, for example, genotype data * a possible “role model” data depository is NIH’s DNA sequence depository, but our genotype depository would have to be maintained probably by a nongov agency (2) CREATIVE COMMONS LICENSE * the phrase “creative commons license” could appear after your email on the title page of your submitted MS: this phrase means you not the journal own the copyright; you could put your article as a pdf file on the web for anyone to access free * Springer, Elsevier etc make profits from the front and back end: this phrase would eliminate the back end (3) FOLLOW UPS if you want these changes * google PMR for details and implications * discuss on evoldir, with your colleagues, and journal editors

mouse <mouse@lamar.colostate.edu>

Drosophila proteome

Hello everyone, I am looking for a reference describing the average amino acid composition of Drosophila proteins.

Many thanks in advance!

– Markus Friedrich Associate Professor Department of Biological Sciences Wayne State University 5047 Gullen Mall Detroit, MI 48202

office: 313 577 9612 lab: 313 577 5120 fax: 801 305 6200 web: <http://bio.wayne.edu/mf/Markuslab.html> Markus Friedrich <mf@biology.biosci.wayne.edu>

Func ecology

Evolution on Ecological Time Scales. A special issue of Functional Ecology. Guest editors: Andrew Hendry, Scott Carroll, and David Reznick. All papers in this special issue are available free at <http://www.blackwell-synergy.com/toc/fec/21/3> CONTENTS:

Data depositories creativecommonslicense

Peter Murray Rust PhD (hereafter PMR; Chemistry Dept, Cambridge U, UK) talked before CSU librarians

Editorial: Evolution on ecological time-scales. S. P. Carroll, A. P. Hendry, D. N. Reznick, C. W. Fox ~mcmi-lab/ivceron@yahoo.com

Adaptive versus non-adaptive phenotypic plasticity and the potential for contemporary adaptation in new environments. C. K. Ghalambor, J. K. McKay, S. P. Carroll, D. N. Reznick

Maternal effects and evolution at ecological time-scales. K. Rasanen, L. E. B. Kruuk

Contemporary evolution of secondary sexual traits in the wild. E. I. Svensson, T. P. Gosden

The multifarious effects of dispersal and gene flow on contemporary adaptation. D. Garant, S. E. Forde, A. P. Hendry

Eco-evolutionary conservation biology: contemporary evolution and the dynamics of persistence. M. T. Kinison, N. G. Hairston Jr

The speed of ecological speciation. A. P. Hendry, P. Nosil, L. H. Rieseberg

Eco-evolutionary dynamics of communities and ecosystems. G. F. Fussmann, M. Loreau, P. A. Abrams

Andrew Hendry, Assistant Professor Redpath Museum & Dept. of Biology McGill University 859 Sherbrooke St. W. Montreal, QC H3A 2K6 Canada Phone: 514-398-4086 ext. 00880# FAX: 514-398-3185 Email: andrew.hendry@mcgill.ca Website: <http://www.biology.mcgill.ca/faculty/hendry/>

GeneMarker scoring

Dear EVOLDIR members Recently we read favorable comments in the Evoldir list about using GeneMarker software to score AFLPs. We would like to know your experience with GeneMarker software to score microsatellites. We are considering shifting from GeneMapper to GeneMarker because we are having some problems with GeneMapper. We would appreciate any comments on the pros and cons of GeneMarker. Would you recommend GeneMarker? Or do you know about any other software compatible with ABI machines and able to score microsatellites and AFLPs? Thank you!

Ivania

Ivania Cerón Souza University of Puerto Rico Biology Department JGD 208 P.O. BOX 23360 San Juan, Puerto Rico 00931-3360 Tel: 1-787-764 0000 ext 2853, 2908 Fax: 1-787-764 3875 <http://zephyr.hpcf.upr.edu/>

HRAS mutation list

Dear all

Would anyone know of a full list of HRAS21 mutations (locations and nature of substitution, indels, etc.) besides the one in sanger?

Thank you,

Johnathan

whitmanjohnathan@yahoo.com

HostParasite textbook

Dear EvolDir members,

I'm starting a PhD project on a host-parasite interaction assessed by population genetic means. I have no experience in the field of host-parasite interaction and would like to read an introducing textbook about that topic. Does anyone of you know of a nice introducing textbook? All I find are collections of articles like "Genetics of Host and Parasite: Implications for Immunity, Epidemiology and Evolution (Parasitology), Paperback by D. Walliker, D. Wakelin."

Please send your recommendations to:

robert.kraus@wur.nl

Cheers, Robert H. Kraus

HostParasite textbook answers

Dear Evoldir members,

thanks a lot for your replies concerning an introducing textbook about host-parasite interaction. Many people asked me to post the results. I summarize them below without any special order. Details for the different books can be found easily at amazon, a short description is available there for each of these books.

Cheers, Robert Kraus

Robert Poulin "Evolutionary Ecology of Parasites", 2nd Ed. 2007, Princeton Univ. Press

Steven A. Frank, "Immunology and Evolution of Infectious Disease", Princeton University Press, 2002

Claude Combes - "Parasitism: The Ecology and Evolution of Intimate Interactions (Interspecific Interactions)", University of Chicago Press, 2001

Combes, Claude. 2005. "The Art of Being a Parasite." University of Chicago Press.

Hassell. 2000. "The SPATIAL & TEMPORAL DYNAMICS OF HOST-PARASITOID INTERACTIONS". Oxford.

Hochberg & Ives. 2000. "Parasitoid Population Biology". Princeton.

Hawkins. 1994. "Pattern & process in host-parasitoid interactions." Cambridge.

Brooks, D. R. and D. A. McLennan. 1993. "Parascript: Parasites and the Language of Evolution."

Moore, Janice. 2002. "Parasites and the Behavior of Animals." Oxford Series in Ecology and Evolution. Oxford University Press.

Page, R. D. M., ed. 2003. "Tangled Trees: Phylogeny, Cospeciation, and Coevolution." University of Chicago Press

Thompson, J. N. 2005. "The Geographic Mosaic of Coevolution." University of Chicago Press

Zimmer, Carl. 2003. Parasite Rex: Inside the Bizarre World of Nature's Most Dangerous Creatures. Arrow Books (Random House), London.

Frederic THOMAS, Francois RENAUD and Jean-Francois GUEGAN "Parasitism and Ecosystems", Oxford University Press, 2005

Thompson, "Interaction and Coevolution"

Dale H. Clayton and Janice Moore, "Host-Parasite Evolution: General Principles and Avian Models"

Hudson et al. "The Ecology of Wildlife Diseases", Oxford University Press (2002)

Stearns "Evolution in Health & Disease", Oxford University Press (2002)

Collinge "Disease Ecology. Community Structure and Pathogen Dynamics" Oxford University Press (2006)

robert.kraus@wur.nl robert.kraus@wur.nl

INRA PopGenet CallForProposals

For the second time, the National Institute for Agricultural Research (INRA, French Institute) is launching a call for proposals of research projects for scientists who work in the areas of food, environment and agriculture. The projects will be selected in December 2007 and the selected scientists will have considerable means at their disposal for 4 years, particularly in terms of wages .

The deadline for submitting applications is November 15th, 2007.

All information on Web site : http://www.international.inra.fr/join_us/-call_for_proposals.2008.scientific_package

For any question concerning this call for proposals, please send a message to package@paris.inra.fr

Fabienne Giroux

INRA DRH Service recrutement et mobilité 147, rue de l'Université 75338 PARIS cedex 07

Tel : 01-42-75-90-77 Fax : 01-42-75-90-39

Fabienne Giroux <Fabienne.Giroux@paris.inra.fr>

LargeScale DNA extraction

Dear all,

I would like to know whether any of you has ever used (genomic) DNA extraction kits (for tissue) in 96 well plates format - that is, for DNA extraction of many samples.

If so, it would be of great help if you could let me know which kit(s) did you use and if you obtained satisfactory results.

Thank you!

Sara Carvalho Evolutionary Genetics Group Instituto Gulbenkian de Ciencia Portugal saracarvalho@igc.gulbenkian.pt

Sara Carvalho <saranlcarvalho@gmail.com>

LargeScale DNA extraction answers

Dear all,

Thank you very much for all the input and recommendations. They were all extremely helpful.

Below are all the answers I got for those of you interested in them (I included the ones already posted in evoldir for the most distracted).

Once again, thank you.

Sara Carvalho Evolutionary Genetics Group Instituto Gulbenkian de Ciencia Portugal saracarvalho@igc.gulbenkian.pt

Sara,

You might be interested in this paper: IVANOVA, NATALIAV, DEWAARD, JEREMYR, HEBERT, PAULDN (2006). An inexpensive, automation-friendly protocol for recovering high-quality DNA. *Molec. Ecol. Notes* 6: 998-1002.

best,

Kathryn

Kathryn Elmer, Ph.D. Postdoctoral Researcher

LS Evolutionary Biology Dept. of Biology University of Konstanz D-78457 Konstanz Germany

phone: +49 (0) 75 31 88 37 10 (from abroad, no (0)) fax: +49 (0) 75 31 88 30 18 e-mail: elmerk@biology.queensu.ca website: <http://www.walled.net/~kelmer/> <<https://webmail.igc.gulbenkian.pt/horde2/util/go.php?url=http%3A%2F%2Fwww.walled.net%2F%7Ekelmer%2F&Horde2=d5fd48f904ed3a132015a413435ccf81>>

Hi Sarah, I used the Qiagen kit for two 96-well plates in a time. It works nice and it is very easy to follow the instruction. The DNA was relatively clean. The only down-side is that the yield is relatively low - I got around 20-50 nano-gram/micro-liter in the final solution. Cheers, Yuval

Hi Sara,

Yes, I have used 96-wells plates from Qiagen (DNA easy 96 Tissue kit) to extract genomic DNA. It has worked fine for me. Two remarks however: 1) you need to buy a powerful and expensive centrifuge to use the kit. 2) I find the collection tubes (those in which you elute the

extracted DNA at the end of the procedure) pretty bad. They come in strips of 8 tubes, with the associated caps attached to each other. This means that when you open these tubes, it is easy to contaminate the samples with one another.

Hope this helps.

Patrick Marduly Unit of Evolutionary Genetics (UEG) Institute of Molecular Biology and Medicine (IBMM) Free University of Brussels (ULB) rue Jeener et Brachet, 12 6041 Gosselies Belgium

Phone: (32)(71)378-954 Fax: (32)(71)378-950 e-mail: pmarduly@ulb.ac.be <http://homepages.ulb.ac.be/~pmarduly/> <<https://webmail.igc.gulbenkian.pt/horde2/util/go.php?url=http%3A%2F%2Fhomepages.ulb.ac.be%2F%7Epmarduly%2F&Horde2=d5fd48f904ed3a132015a413435ccf81>>

Hi Sara I have used the promega sv96 wizard kit - it has always given great results, even when all other extraction methods have failed! You also need a vacuum pump though.

Cheers

Amber Teacher Wildlife Epidemiology Institute of Zoology Regent's Park London NW1 4RY tel: 020 7449 6696 fax: 020 7483 2237 www.zsl.org email: amber.teacher@ioz.ac.uk

hei,

i have used a kit for the 96 well DNA extraction for plant materials 2-3 years ago. it worked very well provided that you take great care to avoid of retro-contamination among samples. This kit could be got from QIAGEN, which is very likely called DNeasy Kit. it is for 6x96well preparation. but it costs a lot.

good luck!

jinyong

We perform chelex extractions in 96 well plates. It is cheap, easy and fast and gives perfectly good DNA for microsat amplification.

Our protocol is below.

All the best, Andrew Pemberton

Making up the chelex suspension:

6% (w/v) ?solution? (really a suspension) in ddwater (Lukas? lab).1.5gchelex beads in 23.5ml ddwater. Make up in autoclavable glass jar with lid and add (clean) magnetic stirring flea. Autoclave before first use and at intervals after that. Make up 2 or 3 bottles at a time so have spares (perhaps of x1.5 the above volumes). Use 150ul chelex for Scathophaga heads.

Protocol:

1. Aliquoting out the chelex suspension: Whilst stirring on magnetic stirrer, pipette 150 ul chelex solution into each well using a wide-ended P200 tip (either then special white 'cell-saver' tips we have got or just cut the end off a regular tip with scissors or a knife). This is an inexact science as the number of beads you get will vary. Try to get roughly the same by looking at the pipette tip before dispensing.

2. Add the fly head and crush on side of well or against beads. Clean tweezers with bleach then deionised water then 70% ethanol between flies and have at least 3 sets of tweezers so the get a few minutes in the bleach.

3. Seal the plate with a clean ABI rubber sealing mat. Spin down with salad spinner. Using a PCR machine with hot lid on (105C) incubate at 55C for 1hr

— / —

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>

Leaf Preservation

Dear all,

I would like to ask for advice/suggestions about the long-term preservation of leaf material in silica gel (for molecular studies). We have quite abundant collections from worldwide field trips and wish to optimize their storage conditions for long-term preservation while simultaneously keeping this material available (easy to sample) for current research projects.

To our knowledge, no real data are available yet on this topic, and we would like to know what the experience of Evoldir members might suggest about: - Temperature of conservation: -20C, 4C, or room temperature? -20C (or even -80C?) could appear the best solution, but what about the condensation that will form on the samples when taking them out of the freezer to remove a piece of leaf? Are summer high temperatures (30-35C) detrimental to DNA preservation? - Is light to be strictly avoided for DNA preservation? - Bags, tubes, boxes? Although tubes with screw-caps may be optimal for DNA preservation, they are very space-consuming. Therefore, we are rather thinking of using hermetically-sealed bags (e.g. Minigrip). These bags should then probably be placed in airtight plastic containers such

as Tupperware boxes.?? - Some people put the leaf material into an individual bag only after the leaf is dry. In this case, should we add silica gel in the bag? Or would a small amount of silica gel in the box containing several bags be enough?

In short, any suggestions on the long-term preservation of dry leaf material for DNA studies would be greatly appreciated! Thanks to all who could supply ideas.

Best regards,

Myriam Gaudeul Department of Systematics & Evolution Muséum National d'Histoire Naturelle, Paris (France)

gaudeul@mnhn.fr

ML DNA partitioning answers

Hello Evoldir.

Here are the replies to my request for programs that could do ML phylogenetic reconstruction with DNA data partitioning, such as when one has multiple genes and wants to run by codon position by gene partitions (as one can do in MrBayes).

exact response listed below.

My summary:

TREEFINDER (www.treefinder.de) or RAxML (<http://icwww.epfl.ch/~stamatak/index-Dateien/Page443.htm>) or HyPhy www.hyphy.org thanks for all the feedback and help,

chris

1) Hi, Chris. I've created such a program as part of my PhD dissertation, which I'll be completing this summer. The manuscript is in prep; I won't distribute the program until its approach has been peer-reviewed and the paper is at least in press. Preliminary comparisons, running the same non-partitioned models in PAUP and in the new program, suggest that it can be up to 20 times faster than PAUP at finding the ML topology, plus the program can run partitioned models, too (but I haven't evaluated its speed for that, yet).

One thing you could try in the interim (and assuming that you don't find other programs which can already do partitioned ML quickly) is to do site-specific rate models in PAUP. It won't take into account different base frequencies or transition matrices across partitions, but will let you allow different partitions to at

least have different average rates. Also, five years ago, it was announced that there would be a “bleeding-edge” version of PAUP which would have new goodies such as partitioned models: I haven’t heard anything about this since then, but you could check with the developers.

2) To my knowledge, the only program (other than codeml) that can do this currently is RAxML. You can download it at: <http://icwww.epfl.ch/~stamatak/index-Dateien/Page443.htm> I believe that Derrick Zwickl is also working on implementing partitioned models in Garli, although I don’t think it’s ready to go yet. You can check for Garli updates at: <http://www.zo.utexas.edu/faculty/antisense/garli/Garli.html> 3) TREEFINDER (www.treefinder.de) is a ML program that will accept multiple gene partitions along with different rate heterogeneity models. It will assume that branch lengths are proportional between gene partitions. RAxML (<http://icwww.epfl.ch/~stamatak/index-Dateien/Page443.htm>) is a very fast and efficient ML program that will allow for the existence of different GTR(Gamma or CAT) models in a multipartition analysis. It estimates a single branch length across partitions. By the way, codeml is not designed for phylogenetic reconstruction.

4) Our open-source phylogenetic software package, called HyPhy, is particularly well-suited for your problem. Please feel free to check it out at www.hyphy.org
5) If you are working with RNA genes, then try PHASE.

Christopher W. Wheat, PhD

Postdoctoral Researcher

Pennsylvania State University University of Helsinki
University of Miami

<http://www.helsinki.fi/science/metapop/english/People/Chris.htm> Christopher West Wheat
<cww10@psu.edu>

Male gonad RNA

Dear All members I am studing gene expression in Sturgeon and I need to extract RNA from Gonads, I use High pure RNA isolation Kit for this purpose but I just could extract total RNA from female Gonads (ovary) but I couldnt extract from testis tissue. Would you please recommend me how can I do it. Thank you.

Best regards Mahtab yarmohammadi

Mahtab yarmohammadi International Sturgeon Research Institute P.O.Box 41635-3464 Rasht-Iran

mahtab yarmohammadi
<mahtab_yarmohammadi@yahoo.com>

Multigenotype infections

Dear evoldirists

I am reviewing the literature for reports of multiple-genotype infections (i.e. genotypes of the same parasite/pathogen species) in the field. If you are aware of any published cases in species not listed below I would greatly appreciate any relevant citations (only direct, conclusive evidence). I’m interested in human and non-human parasites/pathogens. Thanks a lot!

Oliver oliver.balmer@unibas.ch

African horsesickness virus Chlamydia trachomatis Crithidia bombi Cryptococcus neoformans Cryptosporidium parvum Dengue virus Epstein-Barr virus Escherichia coli Helicobacter pylori Hepatitis C virus HIV Human TT virus Mycobacterium bovis Mycobacterium tuberculosis Pasteuria ramosa Plasmodium chabaudi Plasmodium falciparum Schistosoma haematobium Schistosoma mansoni Staphylococcus aureus Streptococcus pneumoniae Theileria annulata Theileria parva Toxoplasma gondii Trypanosoma brucei Trypanosoma congolense Wolbachia spp. Yersinia enterocolitica

– Oliver Balmer Zoologisches Institut der Universität Basel Vesalgasse 1 CH-4051 Basel Switzerland <http://www.evolution.unibas.ch/people/oliver/index.htm>
oliver.balmer@unibas.ch oliver.balmer@unibas.ch

NESCent Newsletter

NESCent (The National Evolutionary Synthesis Center) has released its first Newsletter. To review the Newsletter, visit the NESCent web site at <http://www.nescent.org/news/newsletterhome.php>. To learn more about activities and initiatives at NESCent, you can get the Newsletter at <http://www.nescent.org/>

about/contact.php . khenry@nescent.org

NeiLi GenetDistance software

Dear all,

I am looking for a software program available to calculate Nei and Li's (1979) genetic distance among populations for AFLP data. I do know that programs such as PAUP and Phylip can calculate Nei and Li's distance among individual samples, but I can't find any tools to calculate it among populations. AFLPsurv and GenAlEx are great programs for calculating population distance based on Nei's D, but they are not available for Nei and Li's.

I am wondering if anyone knows how to calculate population based Nei and Li's distance. I appreciate it. Thank you.

Young Jin Chun Ph. D. Candidate Department of Ecology, Evolution, and Organismal Biology Interdepartmental Program in Ecology and Evolutionary Biology 253 Bessey Hall Iowa State University Ames, IA 50011 USA

Phone : 515-450-4270 (cellular) Email : yjchun@iastate.edu

yjchun@iastate.edu

Nematode systematics

To those of you who have conducted biodiversity surveys or ecological studies, particularly in terrestrial biomes:

Could you please let me know if you have encountered nematodes (esp. rhabditids) that you could not (easily) identify, but which may have been an important part of the ecological community you were studying. Would your study have benefitted by the availability of a good, online, interactive key and database for rhabditid nematodes?

(Rhabditids are tiny (0.5-4mm) roundworms that are commonly found in many types of terrestrial (esp. saprobic) environments and often associated phoretically or otherwise with other animals.)

From our phylogenetic work, it is clear that there is a need for the classification system of these nematodes to be completely revised, but we would also like to get a general sense of the need/ demand for resources and tools for identification. Ideally, we would love to hear about specific cases where such resources and tools would have been useful.

Please send your replies directly to: david.fitch@nyu.edu

Many thanks! David Fitch

David H. A. Fitch Associate Professor Department of Biology New York University Main Building, Room 1009 100 Washington Square East New York, NY 10003 U S A Tel.: (212) 998-8254 Fax: (212) 995-4015 e-mail: david.fitch@nyu.edu

<http://www.nyu.edu/projects/fitch/>

NonMicro genetic markers

Dear All,

I am a PhD student working on population/ecological genetics of mosquitoes *Anopheles gambiae* I am interested in knowing which other markers beside microsatellites are most appropriate in analyzing population structure. I wish also to know which genetic markers I can use to test genetic differences in mosquitoes from different ecological settings, thus which genetic markers are applied in ecological genetics.

Thank you all.

Godwil.

"Otsyula, Godwil" <GOtsyula@kisian.mimcom.net>

Primer pairs cost

We seek info about delegating to companies/academics the cost of developing microsatellite primers: - cost per pair - pricebreak if buy several primers - any type of assurance that the primer pairs will be polymorphic for N populations with >> Y alleles per locus - reliability of company - turn-around time from when we place an order until we get primer pairs

Thanks in advance to all who respond: all responses with email addresses will be summarized and sent to all evoldir readers.

AEM Baker

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

Promoter alignments

I am looking for example sets for a research project I am carrying out. What I need are multiple sequence alignment(s) of gene regulatory regions (preferably eukaryotic) which include both regulatory and non-regulatory sequence and in which at least some of the regulatory elements are defined. If anyone could point me either to a web resource or help me out with an appropriate alignment(s) I would be very grateful.

Thanks,

John Hancock

Dr John M. Hancock Head of Bioinformatics, MRC Mammalian Genetics Unit, Harwell, Oxfordshire OX11 0RD, U.K.

E-mail: J.Hancock@har.mrc.ac.uk Telephone: +44 (0)1235 84 1014 Fax: +44 (0) 1235 84 1200
WWW: <http://informatics.har.mrc.ac.uk/> Personal Page: <http://informatics.har.mrc.ac.uk/jmhwww/>
j.hancock@har.mrc.ac.uk j.hancock@har.mrc.ac.uk

Restriction enzymes

Dear all

Could anyone answer the following:

- Do any restriction enzymes or endonucleases of organisms other than humans exist naturally, in vivo, in cells of humans?
- Of the endonucleases that do exist naturally in humans, such as those involved in mismatch repair, are there any specific recognition sites/sequences that they identify?

Thank you in advance,

Johnathan

johnathan whitman <whitmanjohnathan@yahoo.com>

River Bacterial Quantification

Hello, I would like to quantify the amount of bacterial genetic diversity in stream habitats using TRFLP or DGGE analysis of 16S rDNA. I am considering filtering (0.22um pore) stream water for bacteria. I would then want to halt any bacterial enzymatic action in the filter and begin the extraction at a later time in the laboratory.

I would appreciate any advice on a simple, reliable extraction method/kit. Any procedure that can be used in the field or with basic laboratory equipment is preferred.

Kind regards

Mark

M.Mc-Mullan@biosci.hull.ac.uk

SREL closing

The Savannah River Ecology Laboratory's funding from the U.S. Department of Energy (DOE) will be exhausted at the end of May 2007 and the lab will be forced to close. The DOE or its equivalent has supported SREL for ecological research and environmental education for 56 years.

During the past year, SREL has worked with Savannah River Site (SRS) representatives to implement a new 5-year cooperative agreement with task-based funding, similar to what has been used for the past 20+ years. According to written and verbal communications from DOE, the funds have been budgeted for SREL tasks that have been underway since September 2006 and the funds are actually at the SRS to complete these tasks, however, the funds have not been released to SREL. The decision to hold back funding from SREL is solely due to officials at DOE Headquarters in Washington DC who seem determined to cut off all DOE funding for SREL regardless of the nature of the tasks proposed and agreed upon with SRS managers.

SREL programs are more important than ever. Independent environmental evaluation is critical for SRS programs that will process new nuclear materials brought to the SRS and current SRS processes that will leave residual high-level waste in place forever. SREL researchers are funded by many other agencies, but the core mission of SREL remains independent environmental evaluation of SRS activities and long-term stewardship of the SRS. DOE Officials in Washington DC are forcing the local SRS managers to discontinue funding for an environmental program that has benefited the SRS, people of the Aiken-Augusta area, and the entire country for more than half a century.

If DOE funding is not restored immediately, SREL will be forced to close. All SREL animals will need to be transferred or euthanized by the end of May. All tasks that SRS managers have identified as important to long-term environmental stewardship of the site will not be completed. About 100 people will lose their jobs, hundreds affiliated with or dependent upon SREL research will be affected significantly, and tens of thousands of teachers, students, and members of the public who are touched by SREL education and outreach programs will lose out. SREL employees and programs funded by non-DOE grants will also be forced to move due to lack of funding to meet DOE mandated safety and security requirements. Presentations to regional schools, libraries, civic groups, and other organizations will end in May, as will all funding for SREL student programs on the SRS. The independent, oversight studies SREL conducts and publishes on radiation effects, chemical releases, and environmental health will also be terminated at the end of May.

All citizens, including researchers, parents, teachers, and children, who want to urge DOE to release the funding for SREL to continue tasks agreed upon with SRS managers should contact individuals who could make this happen. The more people who express their concern, the more likely it is that action will be taken. You may contact the individuals listed below, write letters to newspapers, or inform anyone else you think should know. One suggestion is to write a short letter that you can email, surface mail, and fax. Then make a telephone call.

Jeffrey M. Allison Manager, Savannah River Operations Office Savannah River Site Aiken, SC 29801 Phone: (803) 952-6337 Fax: (803) 952-8144 e-mail: jef-frey.allison@srs.gov

Samuel W. Bodman Secretary of Energy Forrestal Building, U.S. Department of Energy 1000 Independence Avenue, SW Washington, DC 20585 Phone: (202) 586-6210 or (1-800-342-5363) Fax: (202) 586-4403

e-mail: The.Secretary@hq.doe.gov

Representative Gresham Barrett Aiken Office 233 Pendleton Street, NW Aiken, SC 29801 Phone: 803-649-5571 Fax: 803-648-9038 For email go to <http://www.barrett.house.gov/> and click Contact Gresham

Senator Lindsey Graham Midlands Regional Office 508 Hampton Street, Suite 202 Columbia, South Carolina 29201 phone: (803) 933-0112 For email go to <http://lgraham.senate.gov/index.cfm?mode=contact> and click on e-mail

Representative John Barrow 699 Broad Street, Suite 1200 Augusta, GA 30901 Phone: 706 722-4494 Toll free: 800 890-6236 Fax: 706 722-4496 For email go to <http://barrow.house.gov/> and click Contact John

In general, to find a congressman/woman: <http://www.house.gov/> To find a senator: <http://www.senate.gov/index.htm> South Carolina Senators: <http://lgraham.senate.gov/> <http://demint.senate.gov/> Georgia Senators: <http://chambliss.senate.gov/public/index.cfm>

— / —

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>

Sequence how many clones

Dear All

When cloning and identifying individual alleles of mixed PCR products, a key question is how many clones do I have to sequence to ensure that I have approached a good probability (eg 95%) that I have identified all different copies. In the past when I have been isolating two heterozygotic copies of a nuclear marker, simply sequencing five colonies always identified the two variants. But how many colonies would I have to sequence if there were 3, 4, 5, 20 etc...?

Does anyone out there know of a formula, or publication, that covers the above issue please?

With best wishes and thanks

Si Creer

– Si Creer Post Doctoral Research Fellow Molecular Ecology and Fisheries Genetics Group School of

Biological Sciences University Wales, Bangor Bangor
Gwynedd LL57 2UW UK

e-mail: s.creer@bangor.ac.uk Tel: +1248 382302
Fax: +1248 371644 Home Page: <http://biology.bangor.ac.uk/~bssa0d/> Si Creer
<s.creer@bangor.ac.uk>

results (a random sample of sequences from the simulated populations) to be available in .nex or some other popular format.

Thanks Asta

*** Asta Audzijonyte Finnish Museum of Natural History POB 26 (Teollisuuskatu 23) FI-00014 University of Helsinki

asta.audzijonyte@helsinki.fi

Silene nutans samples

Dear all,

I am working on a research project concerning the study of the phylogeography of *Silene nutans* (Caryophyllaceae) in Europe, in collaboration with Pascal Touzet and Solenn Le Cadre of the Lab. of Genetics and Evolution of Plant Populations (University of Lille1, France). During the last 15 years, I have been collecting leaf material or seeds in more than 100 populations from Belgium, France, Sweden (and northern Finland), which can now be used for DNA analysis. This year we plan to collect (or we will receive material) from British populations. *Silene nutans* has a quite wide continental distribution in Europe, so we would like to extend your sampling area, especially to the east (and to complete the northern distribution). Anyone who could help us by collecting seeds and capsules (for 5-10 maternal plants) in wild populations of *Silene nutans* is welcome and can contact me for more information.

Best regards,

Fabienne Van Rossum

Department of Vascular Plants National Botanic Garden of Belgium Domein van Bouchout, BE-1860 Meise, Belgium e-mail: fabienne.vanrossum@br.fgov.be

fabienne@br.fgov.be

Software Coalescent simulations

Can anybody suggest a software package for coalescence simulations under different population demographic models (subdivision, stable population size, bottlenecks) and different background mutation rates? Ideally there should also be a possibility to introduce selection, different mutation models, and I prefer the

Software Coalescent GUI

For all users interested in using the coalescent but consider that most programs are hard to use, we have developed a easy to use GUI for coalescent simulations (currently using simcoal2) called modeler4simcoal2 (m4s2)

For anyone interested in an easy way to use the coalescent, you can visit:

<http://popgen.eu/soft/m4s2/> or:

<http://bioinformatics.oxfordjournals.org/cgi/content/abstract/btm243v1> Many thanks

tiagoantao@gmail.com

Software LAMARC 2.1

Announcing the release of LAMARC v2.1

We have just released a new version of the LAMARC program, available at <http://evolution.gs.washington.edu/lamarc/> for free download.

LAMARC is a program which estimates population parameters such as effective population size, population growth rate, migration rates among subpopulations, and recombination rate. It performs Markov chain Monte Carlo to search among possible genealogies which can explain the observed data, and constructs an estimate from these genealogies using either a Bayesian or a maximum likelihood approach. It can use full DNA or RNA sequence data, SNPs, microsatellites, or electrophoretic data.

LAMARC is available as pre-compiled executables for

Windows, Mac OSX (PowerPC or Intel), and Linux, and as source code which can be compiled on most systems.

Changes for version 2.1

Trait mapping. LAMARC can now be used to map a phenotypic trait to a position in the sequence, if a model of the relationship between trait phenotype and genotype is available. This is a form of fine-scale linkage disequilibrium mapping. It may be useful in narrowing down the position of an already-mapped genetic trait.

Multiple data types. Linked regions containing diverse data (for example, a group of SNPs and an adjacent microsatellite) can now be analyzed.

Linked data with different mutation rates: Linked data with known differences in mutation rate (for example, introns and exons of the same gene) can now be analyzed more correctly.

Gamma-distributed rates among genomic regions. If mutation rates are believed to vary among regions of the genome, but the rate for each region is not known, LAMARC can now model this as a collection of unknown rates drawn from a gamma distribution. Doing so both provides an estimate of the gamma shape parameter and provides more realistic confidence intervals for the the population size parameter. We expect this to be particularly useful for large collections of unlinked microsatellites.

GUI interface for file conversion. This release of LAMARC features a greatly enhanced GUI interface for converting files into LAMARC-readable input. For users whose computers do not support windowing, we also provide a batch version usable from the command line.

TRACER compatibility. LAMARC now writes files that can be read by the TRACER utility of Drummond and Rambaut, which provides graphical and statistical feedback on whether the parameter estimates have converged.

If you have any questions about LAMARC or encounter difficulties in downloading it, please contact us at lamarc@gs.washington.edu. We do not require registration to download LAMARC, but encourage you to register so that you can receive updates and bug fixes, and so that we can document use of the program to our granting agencies.

Mary Kuhner LAMARC development group Dept. of Genome Sciences, University of Washington lamarc@gs.washington.edu

mkkuhner@u.washington.edu
mkkuhner@u.washington.edu

mkkuh-

Software NewTreefinder

A new TREEFINDER version is online at:

www.treefinder.de New features are:

- more paired-sites tests: ELW, BP, KH, SH, WSH, AU
- LRS edge support replaced by LR-ELW (based on expected-likelihood weights) - output of sitewise likelihoods - information criteria: AIC, AICc, BIC - protein models with optimized and empirical amino acid frequencies (+F) - utilities to concatenate alignments, reports and sample files - utilities to change tree topology and arrange hypotheses - parallel bootstrapping - Intel and G5 binaries for the Mac

Please note that I am still not being paid for my work and that I had no income for years.

Gangolf Jobb

Gangolf Jobb <gangolf@treefinder.de>

Software SciRoKo

Dear EvolDir members,

I am pleased to announce a new tool for whole genome comparative genetics: SciRoKo 3.1 SciRoKo allows a fast whole genome microsatellite search (*H. sapiens* in 600 sec on a common PC) and comparison of all identified microsatellites in fully sequenced species. Since a total of 1.2 Mio SSRs (e.g.: *H. sapiens*) is somewhat difficult to evaluate, SciRoKo provides statistical analysis of the SSR-search results. For this similar microsatellite motifs are grouped into the same category according to several considerations (eg.: trinucleotide SSRs->trinucleotide category; AG, GA, TC, CT-> into AG category etc etc). For each category SciRoKo calculates the average length, the average number of mismatches, average density (SSRs/Mbp) and average standard deviation of the length. As a novelty SciRoKo allows determining which microsatellite motifs can be most frequently found in close proximity! SciRoKo is platform independent and ships with a convenient GUI (graphical user interface) SciRoKo is compatible with many already existing SSR-search tools (Sputnik-family), which SSR-search reports are accepted as input

files.

obtain your copy of SciRoKo for free at: www.kofler.or.at/bioinformatics please cite: SciRoKo: A new tool for whole genome microsatellite search and investigation Robert Kofler; Christian Schlotterer; Tamas Lelley Bioinformatics 2007; doi: 10.1093/bioinformatics/btm157

Best regards, Robert Kofler

GoingSouth@web.de

Which Mycena mtDNA loci

Hello ,

I would like to ask for a suggestion about

I am doing a phylogenetic study of the *Mycena* (*Prunulus*) *pura*-complex. I have a relatively large sample of mostly European, but also North and South American taxa fra the *Calodontes* group. I am mostly interested in seeing 1) whether the *Mycena pura*-complex can be properly subdivided with molecular methods, and 2) if the *Calodontes* group (or rather, our subsample thereof) is likely to be monophyletical. I presently have about 600 ITS-sequences as well as 100 EFsequences (with, hopefully, some RPB1-sequences yet to come), but I would like to supply with some sequences of a mitochondrial locus. I have been thinking of sSU or MIP, but I have found little encouraging literature to support these thoughts. Does anybody have a good suggestion?

Best regards,

Christoffer Bugge Harder Dep. of microbiology University of Copenhagen

CBH-DRONTE@stud.ku.dk

Which loci

Dear all,

Thanks for the comments on my question posted last week. In short I'm searching for low copy nuclear genes to get a better resolution for my constructed topology. One can find the original question and some of the an-

swers to this question below. Thanks to all that supplied the cited suggestions bellow. If some of you still have other options or things to try, please feel free to let me know,

Best regards,

Philippe.

Original post:

Dear all,

I'm studying *Opuntia* (prickly pear) cacti in weakly divergent species complex. I already sequenced some Trn (chloroplast level) - and ITS - loci to construct a phylogeny. But because of the small amount of parsimony informative sites I'm now thinking about adding one or a few extra nuclear loci to get a better resolution. Do some of you have some experience with this, or have a nice idea about which nuclear loci to use, or have other suggestions. Ideally these loci should have some described conservative primers (for Cactaceae or Caryophyllales).

Best regards and thanks in advance,

Philippe.

Answer from Bernard Pfeil:

Just a thought - check out the *Silene* (Caryophyllaceae) work by Popp and Oxelman. They used introns from rna polymerases and had nested primers, if I recall correctly (some conservative, others less so). But I'm not sure I would agree that adding loci necessarily gives you better resolution - that makes assumptions about common signal among loci, lack of hybridisation, lineages sorting, etc.

Suggestion from Mark Chapman:

Dear Philippe,

Is there an EST database for a closely related species? We used the lettuce and sunflower EST libraries to design a suite of markers usable across the Asteraceae (paper in submission) and then used them to identify the progenitor of safflower.

All the best

Suggestion by Taina M. Price

Philippe,

I saw your posting on evoldir, and I am working with a very similar problem in *Phemeranthus* (Portulacaceae sens. lat. or Montiaceae). I am doing phylogeny and phylogeography but the species are weakly divergent and there is very little informative variation in chloroplast regions, so I am looking for nuclear regions. One region that I am having some success with, though the

data is very preliminary at this point, is the fourth PepC intron, developed for *Tamarix* (Tamaricaceae, Caryophyllales). The primers I'm using are PepC 4F and 5R which you can find in Lohmann 2006, *Am. J. Bot.* 93: 304-318.

Thank you,

Taina M. Price

Philippe Cuénoud sent me one of his publications with primers used and the variation he found when using them.

Cuenoud P, Savolainen V, Chatrou LW, Powell M, Grayer RJ, Chase MW 2002 Molecular phylogenetics of Caryophyllales based on nuclear 18S rDNA and plastid *rbcL*, *atpB*, and *matK* DNA sequences *AMERICAN JOURNAL OF BOTANY* 89 (1): 132-144

Suggestion by Brian Foley:

LOCUS AB219582 928 bp DNA linear PLN 27-APR-2007 DEFINITION *Minuartia arctica* chloroplast *trnL*(UAA), *trnF*(GAA) genes for tRNA-Leu, tRNA-Phe, partial sequence, *trnL-trnF* spacer region, specimen_voucher:N. Fujii F01657 (MAK). ACCESSION AB219582 VERSION AB219582.1 GI:83758437 KEYWORDS . SOURCE chloroplast *Minuartia arctica* ORGANISM *Minuartia arctica* Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Caryophyllales; Caryophyllaceae; *Minuartia*. REFERENCE 1 AUTHORS Senni,K., Fujii,N., Takahashi,H., Sugawara,T. and Wakabayashi,M. TITLE Intraspecific chloroplast DNA variation of the alpine plants in central Honshu, Japan *JOURNAL* Unpublished ...

Then BLAST that, to see 1) how many other plants have been sequenced there, so you have outgroups and diversity within other species to compare to. 2) How much diversity is found within species or between related species.

For example:

```
>gb|DQ907861.1| Schiedea hookerii tRNA-Leu (trnL)
gene, intron; >gb|chloroplast LengthY2
```

Sort alignments for this subject sequence by: E value
Score Percent identity Query start position Subject
start position

Score = 385 bits (426), Expect = 2e-103 Identities = 263/293 (89%), Gaps = 5/293 (1%) Strand=Plus/Plus

```
Query 226 TTTTTTATTTATTTCTAAAATTGA-
GAAATATTTAGATATAGAAATCTATATTAATC-
TATA 285 || ||||| || | ||| ||||| |||||
||||| || Sbjct 303 TTCTTTATTTT---
```

```
AGAATTTGCGAAATATTTATATATAGAAATCCATATTAATCAAT-
360
```

```
Query 286 TTTTTGTTTAGAATATGGAATGAAAAATA-
ATAATTGTTATGAATCGATTACGCGTTGA 343
```

— / —

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>

Whole mitochondrial genomes

Dear EvolDir members, I have just started a project about the whole mitochondrial genome of the decapod *Munidopsis polymorpha*. I amplified a fragment for the genes 12S, *cytb*, *COI* and *ND5*, and after I designed species-specific primers for LONG PCR.

The problem is that I don't get amplifications with those primers for the LONG PCR. I have high quality DNA, but I don't know which is the order of the genes.

Thank you very much in advance.

Cabezas, Patricia pcabezas@mncn.csic.es
mcnpc774@mncn.csic.es

mtDNA hypervariable regions

Dear all, I am currently trying to design primers to amplify the hypervariable region I (and possibly II) of human mtDNA. This is a small scale educational project with a tight deadline, so thought I would ask if anybody has primer sequences designed already that they would be prepared to share with me. Ideally, I need primers designed to conserved regions (i.e. so that they will amplify the HVR of mtDNA from most/all human samples) and that avoid the problem of amplification from gDNA.

Thank you in advance for your help, with best wishes,
Becky

RL Poole, School Biological Sciences
R.L.Poole@bristol.ac.uk

mtDNA mutation rates

Dear Evoldir members

I am looking for any references that have compared the mutation rates in different mtDNA genes within the

same group of species. I am specifically interested in comparing the rates for COI, 12S and 16S. The majority of references I have found just seem to give an overall mutation rate.

Any help would be appreciated greatly

Cheers

Andy

sbiak1@groupwise.cf.ac.uk

PostDocs

CSIRO Canberra PlantBiodiversity	59	UBristol SoilNematodeEvol	66
CollegeWilliamMary EvolutionaryPhysiology	60	UCaliforniaIrvine ButterflyVision	66
Cologne PlantGeneRegulationEvol	61	UCambridge StatHumanPopGenet	67
DukeU EvolGenomics	61	UFribourg PlantTaxonomy	67
ESF ThermalAdaptation	62	UGeorgia 2 HostParasitoid	68
HopkinsMarineStation WhalePopulations	62	Uillinois BeeConsGenetics	68
INRA 41 EvolBiol	63	UIowa Bioinformatics	69
MaxPlanck Weewisen GenomeAnalysis	63	ULisbon FishGenomeDynamics	69
MichiganTechU HybridMetabolism	63	ULiverpool Bioinformatics	70
NewZealand PlantConsGenet	64	UMunich SexEvol	70
NorthCarolinaStateU PlantPopConsGenetics	64	UQueensland EvolViralGenetics	71
PurdueU SturgeonMolEvol	65	YaleU ButterflyEvoDevo	72
SUNYBuffalo EvolutionaryBiology	65		
SUNY Buffalo BioinformaticsPhylogenetics	65		

CSIRO Canberra PlantBiodiversity

Post Doctoral Fellow - Several Positions CSIRO Canberra and LaTrobe University Albury, Australia

These postdoctoral fellowships form part of the CERF National Taxonomy Research hub. The positions will contribute to the goals of the hub, particularly addressing recognised taxonomic gaps in knowledge and enhancing the nation's capacity to manage the environment effectively. These research projects will be

expected to create, collect, manage and deliver data in systems and formats compatible with emerging new biodiversity data management systems delivering web-based information on Australian plants and animals, moving towards the creation of a 'one stop shop' for accessing key information on Australia's biodiversity. The National Taxonomy Research hub is supported by the Australian Government's Commonwealth Environment Research Facilities (CERF) programme.

Environmental Weeds Centre for Plant Biodiversity Research, CSIRO Plant Industry, Canberra

We require a highly motivated Postdoctoral Fellow to assist a research team to conduct research on systematics and diversity of Australia's Weeds of National Sig-

nificance (WONS), with specific emphasis on Lantana. The research will involve the establishment of the identity, diversity and origins of Australian introduced environmental weeds - including determining identification of progenitors and the existence of one or many distinct genetic races of lantana. The project will use the collection resources of the Australian National Herbarium and its partner agencies together with those of weed management agencies.

Aquatic Macroinvertebrates LaTrobe University Albury

We require a highly motivated Postdoctoral Fellow to assist a research team to conduct research on systematics and diversity of Australia's Aquatic Insects, with specific emphasis on the Ephemeroptera (Mayflies). The research will involve the establishment of the identity, diversity and phylogenetic relationships of the Ephemeroptera and other aquatic groups with the aims to establish a sound taxonomic basis for identification of these important water quality indicators. The research will be based at the Albury-Wodonga campus of La Trobe University.

Insect Systematics CSIRO Entomology Canberra

We require a highly motivated Postdoctoral Fellow to assist a research team to conduct research on systematics and diversity of Australia's Ants, with specific emphasis on the ecologically important genus *Iridomyrmex*. The research will involve a species-level revision of the genus using modern taxonomic methods including morphological and molecular techniques. Field work within Australia will be required and extensive use will be made of electronic data management, imaging and publishing methodologies. The research will be based at the Australian National Insect Collection and will use the combined collection resources of Australian and overseas museums.

Vertebrate Taxonomy and Biogeography CSIRO Sustainable Ecosystems Canberra

We require a highly motivated Postdoctoral Fellow to assist a research team to conduct research on systematics and diversity of Australia's Small Terrestrial Vertebrates, with specific emphasis on cryptic diversity in reptiles and small mammals of western and northern Australia, and the 'lost' diversity of eastern Australian small mammals. Both components will involve integration of morphological and molecular datasets to resolve difficult taxonomic problems. The latter component will involve the collection of skeletal remains from surface cave deposits and detailed studies of early historical collections. The research will be based at the Australian National Wildlife Collection and will use the

combined collection resources of Australian and overseas museums.

For details of these positions please see <http://recruitment.csiro.au/asp/job_details.asp?RefNo=-3D2007%2F313>

Steve Shattuck CSIRO Entomology
steve.shattuck@csiro.au

College William Mary Evolutionary Physiology

EVOLUTIONARY PHYSIOLOGY Postdoctoral Position, College of William and Mary. A postdoctoral position will be available beginning August of 2007, renewable through May 2009, to investigate the evolution of complex neuroendocrine pathways. Applicants should have a PhD prior to August 2007 and experience in one or more of these areas: physiological ecology, neuroendocrinology, behavior, evolutionary biology, physiology, or cell and molecular biology. The research focus is on the contribution of genetic variation and phenotypic plasticity to the evolution of the photoneuroendocrine pathway in mammals. This pathway integrates photoperiod and other environmental information to regulate reproductive, physiological and behavioral responses to seasons. The model system is a wild-derived laboratory colony of white-footed mice (*Peromyscus leucopus*). The successful candidate will conduct collaborative research, help supervise students in the research laboratory, and teach a one semester course in animal physiology during the spring. More details on the research are available at: <http://faculty.wm.edu/pdheid>. The College of William and Mary is a ³Public Ivy² with 5500 undergraduate enrollment, an excellent undergraduate program, and a strong research tradition. Starting salary is \$39,000 plus benefits. Contact information is available for the previous postdoctoral fellows (both in or about to begin permanent positions). Please send curriculum vita, a brief description of research interests/experience, and the names and contact information of three references to: Dr. Paul Heideman, Chair, Department of Biology, P.O. Box 8795, College of William and Mary, Williamsburg, VA 23187-8795; e-mail: pdheid@wm.edu. Review of applications begins immediately and continues until the position is filled. The College of William and Mary is an Affirmative Action/Equal Opportunity Employer.

Paul D. Heideman, Professor and Chair Department of

Biology email: pdheid@wm.edu College of William and Mary P.O. Box 8795 FAX: 757-221-6483 Williamsburg, VA 23187-8795 Ph: 757-221-2239

<http://pdheid.people.wm.edu/> Paul Heideman
<pdheid@wm.edu>

Cologne PlantGeneRegulationEvol

Postdoc: Evolution of plant gene regulation in Cologne, Germany

A Postdoc position is available at the Max Planck Institute for Plant Breeding Research in Cologne, Germany; to join Juliette de Meaux's lab, in the department of Genetics and Plant Breeding.

Our research group is interested in evaluating the role played by cis-regulatory DNA in adaptive evolution. For this, we are studying the evolutionary dynamics of functional non-coding regions within and among closely related species of the Arabidopsis genus. Simultaneously, to relate this diversity to its ecological role in natural environments, we are investigating the molecular basis of adaptation in traits of great ecological importance (seed dormancy, plant innate immunity). The successful applicant will be encouraged to develop his/her own research project within this framework. We especially encourage evolutionary geneticists (including evolutionary bioinformaticians) interested in transcriptomics or population genetics of non-coding DNA to apply. We are also very interested by molecular or evolutionary biologists interested in characterizing molecular functional variation of ecological relevance.

The Max Planck Institute offers an outstanding environment for carrying out ambitious and innovative research. Our research group exists since September 2005. It belongs to the Department of Genetics and Plant Breeding, which brings together plant molecular biologists, quantitative geneticists and evolutionary biologists to investigate the causes and consequences of plant natural variation. The Institute benefits from a superb interdisciplinary scientific community, with world class molecular biology being performed and active contacts with outstanding evolutionary geneticists located in the nearby University of Cologne.

Cologne, the metropolis on the Rhine, has just over one million inhabitants and is the fourth-largest city in Germany. It offers plenty of cultural and recreational activities. The city further benefits from its central

location in the European travel network. Trains go directly from downtown Cologne to Frankfurt International Airport. Low cost air companies operate at the local airport (Köln-Bonn) and can take you anywhere in Europe in a couple of hours.

Applicants are encouraged to consult the Institute/Departmental websites at <http://www.mpiz-koeln.mpg.de/english/research/koornneefGroup/-demeaux/index.html>. Review of applications will begin on June 15th and continue until the position is filled. Please provide a cover letter (detailing your research achievements, goals and motivation for joining our group) as well as a curriculum vitae and contact information for three referees and submit to: Juliette de Meaux <demeaux@mpiz-koeln.mpg.de>. We will not review applications containing superficial cover letters. The position is funded by a fellowship of the Max Planck Society for up to three years. Starting date is October 1st 2007 or later. Don't hesitate to contact J. de Meaux if you have specific questions about this announcement.

demeaux@mpiz-koeln.mpg.de

demeaux@mpiz-koeln.mpg.de

DukeU EvolGenomics

Postdoctoral Fellowship in Evolutionary Genomics and Molecular Evolution

The Center for Evolutionary Genomics at the Duke Institute for Genome Sciences & Policy is pleased to announce the continuation of its Postdoctoral Fellowships in Evolutionary Genomics and Molecular Evolution. This Fellowship provides an annual salary of \$37,500 plus benefits and \$11,000 in research funds per year for a two-year period. The program allows Fellows to pursue research in the laboratory of a sponsoring faculty member affiliated with the Institute for Genome Sciences and Policy. One Fellowship will be awarded this year (2007).

We invite innovative proposals from scientists of any nationality to carry out research at Duke University for a two-year appointment beginning in the fall of 2007. We are particularly interested in proposals that address mechanisms of molecular evolution, comparative genomics, and the evolution of development. Proposals focused exclusively on building phylogenies will not be considered, although the application of phylogenetic approaches to analyzing the evolution of genes

and genomes is certainly appropriate. Faculty sponsors can be located within any department or school at Duke University; the only stipulation is that the project fall within the areas of research listed above.

Please submit curriculum vitae, a three-page research proposal (not counting literature cited), and a one-page summary of past research, and arrange for two letters of recommendation to be sent to: Evolutionary Genomics, c/o Jennifer Foreman, Department of Biology, Box 90338, Duke University, Durham, NC 27708-0338, USA, or emailed to Jennifer.Foreman@duke.edu. Electronic submissions are preferred, although not required. Applications received by 1 June 2007 will be guaranteed full consideration.

Questions can be directed to Greg Wray by email (gwrays@duke.edu). For information about the Institute for Genome Sciences & Policy and the Center for Evolutionary Genomics at Duke University, visit <http://www.genome.duke.edu/> Duke University is an Equal Opportunity/Affirmative Action Employer. Female and minority candidates are encouraged to apply. noor@duke.edu noor@duke.edu

ESF ThermalAdaptation

***** 3rd CALL *****

The Objective of the ESF Programme “Thermal adaptation in ectotherms: Linking life history, physiology, behaviour and genetics” (ThermAdapt; <http://www.esf.org/thermadapt>) is to foster a multidisciplinary European network of scientists working on thermal adaptation. We particularly aim to integrate research at multiple levels of investigation, including genetics, physiology, ecology, behaviour or theory. Interested persons or groups are encouraged to join our activities. These include advertising their expertise via our web site, and participation in various activities to be announced separately and regularly over the next 5 years such as workshops, training courses, short and long exchange grants, exchange of specimens and expertise, sharing of facilities, and scientific collaboration of any kind.

We here Call for Applications for a number of

Short Visit Exchange Grants (< 15 days)

broadly related to the scientific objectives of the Programme (deadline 30 September 2007). Short Visits

may serve for planning collaborative research projects, brief data gathering or data analysis (see <http://www.esf.org/thermadapt> under Grants for application guidelines and forms).

Similar calls are planned to occur repeatedly over the next 5 years. We advise applicants to contact potential labs of interest early to jointly prepare the application. Grant applications will be chosen by the Steering Committee based on scientific quality, and priority will be given to applicants who come from or intend to visit countries supporting the programme (Austria, Belgium, Czech Republic, Denmark, Estonia, Finland, Germany, Hungary, Netherlands, Portugal, Slovenia, Spain, Switzerland), but other European nations can be involved.

If you wish to be included in the ThermAdapt e-mail list to receive regular updates on Programme activities, please send an email to edegott@esf.org.

For further inquiries contact:

Ellen Degott (ESF office liaison; Email: edegott@esf.org) Wolf Blanckenhorn (chair; Email: wolf.blanckenhorn@zm.uzh.ch) Mauro Santos (co-chair; Email: mauro.santos@uab.es)

APPLICATIONS ARE SUBMITTED ONLINE UNDER <http://www.esf.org/thermadapt> Dr. Wolf Blanckenhorn Zoological Museum, University of Zurich-Irchel Winterthurerstrasse 190 CH-8057 Zurich Phone: +41 44 635.47.55 Fax: +41 44 635.47.80 e-mail: wolf.blanckenhorn@zm.uzh.ch http://www.unizh.ch/zoolmus/zmneu/englisch/forschung_e/blanckenhorn_wolf_e.html <http://www.esf.org/thermadapt> wolfman@zm.uzh.ch

HopkinsMarineStation WhalePopulations

Molecular genetics of whales: POSITION AS DOCTORAL RESEARCH FELLOW in biology (molecular ecology) is available in Steve Palumbi's lab at Stanford University's Hopkins Marine Station.

The position is affiliated with a Pew Charitable Trusts-funded project exploring historical and molecular estimates of historical population size in baleen whales. The candidate should have a Ph.D. in biology, molecular biology or related fields. Experience in molecular genetics and/or population dynamic modeling is required. Applications should include a statement summarizing

the applicant's scientific work and interest, curriculum vitae and three letters of recommendation. The position is available as of Feb 1, 2007, and applications will be accepted until the position is filled.

Contact Tim Knight at trknight@stanford.edu.

For more information on the program, see <http://palumbi.stanford.edu/historical.htm>

trknight@stanford.edu

INRA 41 EvoBiol

INRA is organizing a campaign to recruit 41 post-doctoral fellows

These young researchers are selected, irrespective of nationality, on the basis of a coherent scientific and professional project to work as part of INRA's research teams.

The recipients are recruited on a two-year contract with a gross monthly salary of 2150???

These post-doctoral positions are proposed in the following fields of research:

- Environment and rural space - Food and human nutrition - Agricultural products and process engineering
- Generic research - Innovative and sustainable agricultural systems - Strategy and organisation of actors, public policies

Opening date for applications and announcement of projects: 1st of June 2007
Deadline for submitting applications: 31st of July 2007

All information on INRA's web site:

<http://www.international.inra.fr/join_us/positions/post_doctoral_positions/annual_campaign> http://www.international.inra.fr/join_us/positions/post_doctoral_positions/annual_campaign For any question concerning post-doctoral positions, you can send an email to the following address: post-doctorant@paris.inra.fr

Fabienne Giroux INRA ??? DRH Service recrutement et mobilité 147, rue de l'Université 75338 PARIS cedex 07 Tel : 01-42-75-90-77 Fax : 01-42-75-94-86

Fabienne Giroux <Fabienne.Giroux@paris.inra.fr>

MaxPlanck Weewisen GenomeAnalysis

Open Post-Doc Position in Genome Analysis 10. May 2007

A Post-Doc position (1 year plus possible extension; BAT IIa) is available for computational analyses of conserved non-genic DNA sequences (CNGs). Of particular interest are content-based relationships between CNGs and genic regions, which will be modelled by methods coming from communication engineering and information theory. Alternatively, a phylogenetic profiling approach together with a novel conservation score will be used to test for functional relationships between CNGs and genic regions. Candidates should have a strong background in genome analysis, (i.e. database queries, genome annotation, etc.), in genetics and potentially in biological modelling and should be highly motivated to broaden their methodological spectrum by the interdisciplinary approach. If you are interested please contact:

Dr. Jakob C. Mueller Max Planck Institute for Ornithology Dept. Behavioural Ecology & Evolutionary Genetics D-82305 Starnberg (Seewiesen), Germany phone: ++49-8157-932-312 e-mail: comingen@orn.mpg.de homepage: <http://www.orn.mpg.de/staffall.html> DFG project in collaboration with Prof. Joachim Hagenauer at the Institute of Communications Engineering at the Technical University Munich, Germany <http://www.lnt.ei.tum.de/comingen> Date of posting: 10. May 2007

mueller@orn.mpg.de mueller@orn.mpg.de

MichiganTechU HybridMetabolism

A bioinformatics postdoctoral position is available at the Biotechnology Research Center (<<http://www.biotech.mtu.edu/>>www.biotech.mtu.edu) of Michigan Technological University to join a team investigating variation and regulation of secondary metabolism among *Populus* hybrids originating from an ecological gradient. Primary job respon-

sibilities include management and integration of relational databases (<<http://www.aspendb.mtu.edu/->www.aspenDB.mtu.edu>), including a custom EST database, a microarray database on the BASE platform, and a custom metabolite profiling database. Strong quantitative background required, and familiar with Unix/Linux, Java, Perl, Shell, MySQL, R, and PHP.

Send curriculum vitae including a publication list, and names of three references to Dr. Chung-Jui Tsai, Biotechnology Research Center, School of Forest Resources and Environmental Science, Michigan Technological University; e-mail: chtsai@mtu.edu. The School of Forest Resources and Environmental Sciences at Michigan Tech currently ranked 4th among all academic forestry programs in the US. The campus is located in the heart of Upper Michigan's scenic Keweenaw Peninsula, just a few miles from Lake Superior. Houghton is rated the safest college town in Michigan and the eighth safest in the nation. It also has been named one of the nation's top-ten summer sports areas and one of the top-ten best places in the country to live. Michigan Technological University is an equal opportunity/affirmative action employer.

Chung-Jui Tsai <chtsai@mtu.edu>

NewZealand PlantConsGenet

Post Doctoral Researcher - Plant Population Genetics
Fixed term for 2 years with Landcare Research

This post doctoral position will be working with the Ecological Genetics group in Auckland who are part of the Biodiversity & Conservation science team. The team consists of about 50 scientists and science technicians based in Auckland, Hamilton, Nelson, Lincoln and Dunedin. Its mission is to undertake world class scientific research to underpin the protection of New Zealand's biodiversity, and to minimise the impacts of invasive weeds and invertebrates.

<http://www.landcareresearch.co.nz/research/biocons>

The position is located in Auckland and you will be applying genetic analysis to specific projects in plant conservation genetics and provide evolutionary ecology expertise for our program in environmental biosafety. In particular, the position is aimed at determining the relationship between genetic diversity and population/species viability in threatened plant taxa. This research programme you will be working in, aims to

develop a framework for identifying and conserving genetic diversity in threatened indigenous plants in order to reduce further allelic losses and decrease the risk of species extinction. This will be achieved by: * Examining the relationship between genetic diversity and key demographic and life-history factors that influence population persistence * Determining the level of relevant genetic variation necessary to maintain population viability * Generating management guidelines that maximise the probability of population viability and long-term evolutionary potential in plant species with varied ecological attributes.

This project is part of a larger research programme on sustaining and restoring biodiversity in New Zealand <http://www.landcareresearch.co.nz/research> and involves close collaboration with New Zealand's key conservation agency, the Department of Conservation.

The position will suit someone who is able to relate to people in all circumstances, who works well in a team and is versatile using their initiative to solve problems. Accompanying these attributes is the ability to work effectively under pressure, be self motivated and well organised. A PhD in plant genetics and/or evolutionary ecology is required along with at least some experience in the analysis and interpretation of molecular markers such as AFLP's and chloroplast DNA sequence data.

Applications are made through the Landcare Research NZ Ltd website - www.landcareresearch.co.nz/-jobs . or contact Dianne Gleeson gleesond@landcareresearch.co.nz. Please include the names and contact details of at least two referees.

The closing date is Friday, 1 June 2007.

Dianne M. Gleeson Research Scientist Ecological Genetics Laboratory Landcare Research PB 92170, Auckland, New Zealand ph +64-9-5744121 (DD)

GleesonD@landcareresearch.co.nz

NorthCarolinaStateU PlantPopConsGenetics

A postdoc position will be available in January 2008 in Plant Biology Department at North Carolina State University to conduct population genetic and phylogeographic analyses of some pendant lily species in the eastern US. Please send applications to jenny_xiang@ncsu.edu

(Jenny) Qiuyun Xiang, Ph.D. Associate Professor Department of Plant Biology North Carolina State University Raleigh, NC 27695-7612 Phone: 919-515-2728 Fax: 919-515-3436 Homepage: <http://www4.ncsu.edu/~qyxiang> Jenny Xiang <jenny_xiang@ncsu.edu>

PurdueU SturgeonMolEvol

Postdoc opportunity at Purdue University

A postdoc position in sturgeon genomics and molecular evolution is available at Purdue University. Strong molecular and/or bioinformatic skills are essential. For more information, contact Andrew DeWoody at Purdue University or see <http://www.agriculture.purdue.edu/fnr/html/faculty/DeWoody/index.html>. The cost of living in West Lafayette is low, and we are only an hour from Indianapolis and two hours from Chicago. Motivated applicants should submit (as PDFs) a short letter of interest, a curriculum vitae, relevant reprints, and contact information for three references. Anticipated start date is 1 September 2007 but is somewhat flexible.

dewoody@purdue.edu

SUNYBuffalo EvolutionaryBiology

University at Buffalo, NY College of Arts and Sciences Department of Biological Sciences Postdoc (Evolutionary Biology)

A postdoctoral fellow position is available in the laboratory of Katharina Dittmar De La Cruz at the Department of Biological Sciences, SUNY Buffalo, NY (<http://www.wyomingbioinformatics.org/~kdittmar/>). The post-doc should have a keen INTEREST IN EVOLUTIONARY BIOLOGY, and some experience in molecular biology (e.g., in situ hybridization, RT-PCR, protein expression). Previous exposure to phylogenetics and/or genomics is advantageous. The candidate will work on protein coding sequences that appear to be undergoing adaptive evolution/ changes of function in specific parasitic groups (e.g. Siphonaptera, Streblidae, Nycteribiidae) and study them from a computational and

experimental perspective (see my website for details). The post-doc IS ABSOLUTELY ENCOURAGED to pursue own ideas and projects.

Available Lab Resources include: 1. A PCR wet lab combined with molecular biology facilities. 2. Ample computational resources (e.g., Individual Lab Cluster)

Additional Facilities that are available include: 1. The CCR (Center for Computational Research); 2. A computer visualization lab; 3. The LMVA (Laboratory for Molecular Visualization and Analysis).

The desired starting date is November 1, 2007 (negotiable). The position is for two years with possible extension. Salary will start at \$36,000 - \$38,000 plus benefits, depending on experience. Participation in international field work (e.g., India, Europe, Puerto Rico, Brazil) is possible if desired. Qualified women are especially encouraged to apply. Non-US based applicants are also encouraged to apply, and will receive assistance with VISUM requirements. However, English communication skills are a MUST! Qualified applicants should submit a CV and contact information of three references to Katharina Dittmar De La Cruz @ katharinad@gmail.com.

Katharina Dittmar de la Cruz
<katharinad@gmail.com>

SUNY Buffalo BioinformaticsPhylogenetics

University at Buffalo, NY College of Arts and Sciences Department of Biological Sciences Postdoctoral Research Fellow (Bioinformatics, Phylogenetics, Comparative Genomics)

A postdoctoral fellow position is available in the laboratory of Katharina Dittmar De La Cruz at the Department of Biological Sciences, SUNY Buffalo, NY (<http://www.wyomingbioinformatics.org/~kdittmar/>). The post-doc should have a keen INTEREST IN EVOLUTIONARY BIOLOGY, and a training in computational biology or related fields. Some previous exposure to phylogenetics and/or genome sequence analysis is desired. Excellent programming skills in Python, Perl or C++ , and familiarity with LINUX systems are ESSENTIAL. The post-doc IS ABSOLUTELY ENCOURAGED to pursue own ideas and projects while in my lab.

Computational Resources include: 1. A 12 node lab

Linux cluster for smaller tasks (individual administration), 2. The CCR (Center for Computational Research); 2000 processor DELL P4 (64-bit) Linux Cluster, 64 processor shared memory SGI Altix, 25 TByte EMC SAN [total = 13 Tflops of peak performance), 3. A computer visualization lab with tiled display wall, VisDuo passive stereo system, and SGI Onyx3 Infinite Reality4 graphics computer, 4. The LMVA (Laboratory for Molecular Visualization and Analysis) visualization and computational tools for structural and functional analysis of proteins and nucleic acids, and for the design of synthetic ligands and drugs.

The desired starting date is November 1, 2007. The position is for two years with possible extension. Salary will start at \$35,000 plus benefits (1 year), and \$37,000 - 38,000 plus benefits (2nd year)[the pay rise is dependent on the productivity of the candidate]. Participation in international field work (e.g., India, Europe, Puerto Rico, Brazil) is possible if desired. Qualified women are especially encouraged to apply. Non-US based applicants are also encouraged to apply, and will receive assistance with VISUM requirements. However, English speaking at communication levels are a requirement. Qualified applicants should submit a CV and contact information of three references to Katharina Dittmar De La Cruz @ katharinad@gmail.com.

– Dr. Katharina Dittmar de la Cruz, DVM, Ph.D. University of Wyoming College of Agriculture Department of Molecular Biology DEPT. 3944 1000 E. University Avenue Laramie, Wyoming 82071 Tel.: 307- 766 5223

katharinad@gmail.com <http://www.wyomingbioinformatics.org/~kdittmar> <http://fleasoftheworld.byu.edu> <http://nabn.info> Katharina Dittmar de la Cruz <katharinad@gmail.com>

UBristol SoilNematodeEvol

A postdoctoral research fellow is required to initiate an 18 month 'Proof of Concept' study to investigate the interactions between pathogenic bacteria and nematode worms, both commonly found co-occurring in the soil. The research fellow will join a multidisciplinary team of microbiologists, disease ecologists and molecular biologists at UWE Bristol (UK), The Center for Infectious Disease Dynamics (CIDD), Penn State University USA and The School of Veterinary Science, University of Bristol (UK). For further details and to apply for this job please follow this link <http://info.uwe.ac.uk/>-

vacancies/job_details.asp?ref=R/11237RWS Closing date: June 15th 2007

Informal enquires can be made to Sarah Perkins, via email: sep18@psu.edu

Sarah Perkins Center for Infectious Disease Dynamics 208 Mueller Laboratory Penn State University University Park Pennsylvania 16802 Tel: (814) 863-2099 http://www.cidd.psu.edu/people/bio_perkins.html sep18@psu.edu

UCaliforniaIrvine ButterflyVision

POSTDOCTORAL RESEARCHER/SCHOLAR POSITION

The Department of Ecology and Evolutionary Biology in the School of Biological Sciences at the University of California, Irvine seeks a Postdoctoral Scholar to join an NSF-funded international research team focusing on the physiological, anatomical and genetic basis of visual pigment spectral tuning in butterflies. Butterfly visual pigments have evolved under positive selection (See Frentiu et al. 2007, PNAS U.S.A. 104: 8634-8640) and undergone extensive spectral diversification following gene duplication (See Sison-Mangus et al. 2006, JEB 209: 3079-3090). The spectral and eye pattern variations are adaptations that reflect the diversity of butterfly host plant usage and wing color evolution. The successful candidate will have opportunities to engage in physiological (electroretinogram recordings), transgenic (*Drosophila*), cell culture and candidate gene approaches including mRNA and protein in situ studies to study the genetic basis of this extraordinary evolutionary radiation.

Postdoctoral positions start at a salary of \$37,548 per annum, plus benefits. The successful candidate will have a strong background in molecular and cellular biology (e.g. PCR, cloning, sequencing, protein biochemistry), neuroanatomical, and/or physiological techniques (electroretinograms, microspectrophotometry). Excellent oral and verbal communication skills are also required.

To apply, send a letter of application, curriculum vitae, two reprints/preprints and the names and e-mail and postal addresses of three references to:

Dr. Adriana D. Briscoe University of California-Irvine Department of Ecology and Evolutionary Biology 321 Steinhaus Hall Irvine, CA 92697-2525

abriscoe@uci.edu <mailto:abriscoe@uci.edu>

<http://ecoevo.bio.uci.edu/Faculty/Briscoe/-Briscoe.html>

The University of California, Irvine is an equal opportunity employer committed to excellence through diversity.

abriscoe@uci.edu abriscoe@uci.edu

UCambridge StatHumanPopGenet

Postdoctoral position in statistical/computational human population genetics in Cambridge, UK

Simon Tavaré, Manolis Dermitzakis, Carlos Bustamante, Rasmus Nielsen and Andy Clark seek a creative and energetic postdoctoral fellow to engage in NIH-funded research on the analysis of genome-wide SNP genotype data for purposes of identifying associations with measured phenotypes. This is a wonderful opportunity for a highly motivated post-doctoral fellow to benefit from the intellectually stimulating environment of the University of Cambridge and the Wellcome Trust Sanger Institute.

We are pursuing a series of investigations that include the development of Bayesian methods for identifying genomic regions most likely to harbor variation associated with phenotypic differences. A particular focus is the identification of regulatory element variation. We have full genome expression microarray data for the 270 human HapMap samples to serve as a test bed for statistical methods, and further studies involving thousands of individuals genotyped and screened for gene expression are underway.

Our research groups make a lively and stimulating research environment. Facilities include large-scale compute farms. Applicants with expertise in statistics and population genetics are particularly encouraged to apply. Please email your resumé, statement of research interests and contact information for three references as an attachment to Simon Tavaré (S.Tavare@damtp.cam.ac.uk) and Manolis Dermitzakis (md4@sanger.ac.uk). The position comes with competitive salary and fringe benefits and is available immediately. Application deadline is May 25 2007.

st321@hermes.cam.ac.uk st321@hermes.cam.ac.uk

UFribourg PlantTaxonomy

Postdoctoral Position in Modern Plant Taxonomy

Rationale: The European knapweed *Centaurea maculosa*, introduced from Central Europe (EU) into North America (NA) during the late 19th century, where it covers now an area larger than Switzerland, has become a model for research on the ecological and evolutionary causes and consequences of invasions. We presently explore the role of rapid evolutionary processes in the invasion success of *C. maculosa*, which involves both molecular marker studies to clarify the introduction history, and quantitative genetic experiments. Over the past three years, we have collected seed material from well over 100 populations from both the native EU and introduced NA range and are presently growing most of them in a common garden.

We seek a highly motivated person to help clarifying the complex taxonomy, phylogeny and history of introduction of *C. maculosa*, which may involve various subspecies and hybrids, differing in ploidy level. Part of the task will be to link our molecular data, life-history data and results from modelling and field experiments with the morphological characters yet to be collected from our plant material. Finally, these findings need to be confronted with published data and herbarium specimen to come up with a more consolidated picture of this taxon, its phylogeny and history of introduction (e.g. single versus multiple events).

Requirements - doctoral degree in modern plant taxonomy or related disciplines; - knowledge of, and experience in one or several of the following areas of research is highly desirable: complex multi-variate statistics, nomenclature, phylogeny, biogeography, population genetics, experimental ecology and evolutionary biology

Salary and conditions Salary dependent on age and status (gross salary in the first year about CHF 70'000). Start date: preferentially summer 07, autumn 07 the latest. The position will also include support of research activities of our group. The candidate will be located at the University of Fribourg, but regular travel to the University of Lausanne is expected. The position is for 1.5 years.

Applications Applicants should send their CV, including the publication list, a short summary of research

experience and interests, and the names of two professional referees jointly to heinz.mueller@UNIFR.CH and Antoine.guisan@unil.ch. We start evaluating the applications by end of June 2007.

For further information, please contact: Prof. Dr. Heinz Müller-Schärer, Département de Biologie, Unité Ecologie et Evolution, Université de Fribourg, Chemin du Musée 10; CH-1700 Fribourg, SWITZERLAND; tel: + (41) (0) 26-300 88 35 direct, ++ 50 secr., e-mail: heinz.mueller@UNIFR.CH; cf. <http://www.unifr.ch/biol/ecology/> for further information and recent publications on this subject.

This is a joint position between Antoine Guisan (Uni Lausanne), Urs Schaffner (CABI Bioscience, Delémont) and Heinz Müller-Schärer, (Uni Fribourg) within the National Centre of Competence in Research (NCCR) Plant Survival (<http://www2.unine.ch/nccr>), funded by the Swiss National Science Foundation.

Gillianne Bowman <gilliann@uwinst.unizh.ch>

UGeorgia 2 HostParasitoid

POSTDOCTORAL RESEARCH ASSOCIATES Institute of Ecology, University of Georgia, USA

Applications are invited for two postdoctoral research fellowships in Mathematical Ecology and Epidemiology. One position will focus on the development of mathematical models applied to an experimental host-parasitoid-pathogen system. Within this project, there will be a strong emphasis on understanding and predicting long-term population and evolutionary dynamics, within the context of climate change. The second position will involve developing theory relating to the persistence, transmission dynamics and evolution of Avian Influenza Viruses within North American wild bird populations. This project is funded by the Centers for Disease Control and Prevention and is in collaboration with Dr David Stallknecht at the Southeastern Cooperative Wildlife Disease Study.

A PhD in statistics, applied mathematics or a highly quantitative field is essential. Previous experience in the analysis of ecological or epidemiological systems would be desirable.

The positions are for 18 months in the first instance, with a salary in the range of \$32-37,000 per year (depending on experience), plus fringe benefits.

For further information about these projects, contact Pej Rohani +1 706 542 9249, e-mail: rohani@uga.edu <<mailto:rohani@uga.edu>>.

Applicants should send a detailed CV, together with a brief statement of research interests and three references to Pej Rohani, Institute of Ecology, University of Georgia, Athens GA 30602. Electronic applications are encouraged.

Review of applications will start on June 15 and will continue until the posts have been filled.

Pejman Rohani <rohani@uga.edu>

Ullinois BeeConsGenetics

Postdoctoral Research in Conservation Genetics– 2-yr term

This postdoctoral research position is part of a multi-team effort to investigate causes of decline in several species of North American bumble bees, among the Nation's most important wild and managed pollinators. Reports of decline in range and abundance of several species of North American bumble bees is cause for concern as effective pollination is critical for the health of most terrestrial ecosystems and for agriculture.

The position is based at the University of Illinois and will include extensive fieldwork in both the midwestern and western U.S. The research team comprises scientists from UIUC, the USDA Bee Biology and Systematics Laboratory (Logan, UT) and the Natural History Museum, London. The principal goal of the research is to determine whether population fragmentation, among other potential causes, is leading to serious reduction in genetic diversity in wild bumble bee populations. Genetic diversity in declining species will be compared to that of presumed healthy species to understand the role that diversity may be playing in species population dynamics.

This research is part of a larger effort to determine the current status and causes of decline in bumble bees, which includes surveys of current and past abundance and distributions of targeted species as well as studies of invasive pathogens.

We expect to hire someone with a PhD who has experience in the theory and methodology of population genetics and phylogeography. The postdoc will be expected to contribute evolutionary/conservation ge-

netics expertise to the project, in collaboration with other team members. Required expertise includes DNA technology (extraction, amplification, multiplex high throughput sequencing and fragment-size analysis), development of molecular markers (microsatellites, SNPs, RFLPs), sibship analysis and population genetic estimation, including effective population size, genetic diversity, hierarchical genetic structure, evidence for inbreeding and linkage disequilibrium. Expertise is expected in the use of relevant statistical software.

A background in molecular phylogenetics and statistics along with experience in computer programming is also highly desirable. Experience with nested clade analysis of phylogeographic data is also important.

Additional interests should include an active interest in invertebrate biodiversity and conservation, with relevant publications in international journals.

The position is best suited to a person who has independent initiative for problem-solving, is well organized and works well with a team, and can work effectively under pressure. –

Interested applicants may contact Sydney Cameron (scameron@life.uiuc.edu) for further information, or e-mail directly the following required materials as a single attachment:

1) CV, 2) statement of research interests and explanation of why this postdoc is suitable to your experience and skills, and 3) names and contact information for at least three referees with whom you have worked.

Application deadline is 15 July 2007 or until a suitable candidate is selected.

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

Ph: 217-333-2340 Fax:217-244-3499 e-mail: scameron@life.uiuc.edu <http://www.life.uiuc.edu/~scameron> – Sydney A. Cameron Department of Entomology and Program in Ecology and Evolutionary Biology 320 Morrill Hall 505 S. Goodwin Ave. University of Illinois Urbana, IL 61801

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

UIowa Bioinformatics

University of Iowa Department of Internal Medicine, Carver College of Medicine Postdoctoral Research Fellow in Bioinformatics

A postdoctoral fellow position in bioinformatics and comparative genomics is available in the laboratory of Dr. Yi Xing (<http://www.int-med.uiowa.edu/Divisions/Bioinformatics/Directory/YiXing.html>) at the Department of Internal Medicine, University of Iowa. The postdoc will study mammalian transcriptome diversity and evolution (see Nature Reviews Genetics 2006, 7:499-509; Genome Biology 2007, 8:R82). Applicants must have a PhD with training in computational biology or related fields. Excellent programming skills (e.g. R, Python or Perl) are essential. A strong background in microarray data analysis or genome sequence analysis is desired.

The desired start date is Nov 1, 2007. Salary will be provided at the NIH/NRSA recommended level. Qualified applicants should submit a CV and contact information of three referees to Dr. Yi Xing at yi-xing@uiowa.edu.

yi-xing@uiowa.edu yi-xing@uiowa.edu

ULisbon FishGenomeDynamics

POST-DOC POSITION in the Cytogenetic Unit of the Freshwater Fish Group of the University of Lisbon

Project: Genome dynamics in diploid and polyploid cyprinid fishes of hybrid origin: a molecular cytogenetic approach

We are seeking a highly motivated and enthusiastic candidate to pursue studies on the evolutionary consequences of hybridization and polyploidy in cyprinid fishes. In particular, the hybridogenetic minnow *Squalius alburnoides* has been studied by our team for several years and may be used as a model system to study the earliest stages of genome evolution in polyploids (for detailed information about the research team visit <http://ffishgul.fc.ul.pt> <<http://ffishgul.fc.ul.pt>>).

We are looking for someone whose research interests focus on fish cytogenetics, molecular biology and reproductive genetics under an evolutionary perspective. The successful applicant will be responsible, with under- and post-graduate students, for maintaining experimental crosses and for conducting molecular cytogenetic work (FISH and GISH in the frame of a specific international collaboration) and test, among others, the

hypothesis that hybridization may trigger undermethylation of the genome, resulting in high activity of TEs and subsequent chromosomal rearrangements.

A specific proposal will be discussed and prepared for the candidate who must have obtained his/her PhD after 2004-2005. The application is for a maximum of 6 years, being renewed each annual period, and will be submitted to the Portuguese Funding Agency (FCT - <http://www.fct.mctes.pt/bolsas/concurso2007/>) until the 20th June or the 17th September (to start by October 2007 or by January 2008, respectively).

Applicants should send a complete CV and names of three references via email to Prof. MJ Collares-Pereira (mjpereira@fc.ul.pt), Department of Animal Biology, Faculty of Sciences, University of Lisbon.

Hoping to hearing from you, many thanks and best regards

Maria

Maria Joao Collares-Pereira Centro de Biologia Ambiental Departamento de Biologia Animal Faculdade de Ciências 1749-016 Lisboa, Portugal Phone: # 351 21 7500000 (ext. 24309) Fax: # 351 21 7500028 Research Group Webpage: <http://ffishgul.fc.ul.pt> Webpage of the European Ichthyological Society: <http://artedi.nrm.se/eis/>

Maria João Pereira <mjpereira@fc.ul.pt>

grade dependent on level of experience and/or qualifications. The post is available for three years. Quote Ref: B/003. Informal enquiries to Dr Neil Hall (neil.hall@liverpool.ac.uk).

Post 2: To work on a BBSRC-funded project which aims to develop improved phylogenetic methods for gene content data and to investigate the process of gene loss in parasitic prokaryotes. You should have a PhD in statistics, phylogenetics, bioinformatics or a related discipline and excellent statistical and programming skills. The post is available for one year. Quote Ref: B/004. Informal enquiries to Dr Matthew Spencer (m.spencer@liverpool.ac.uk). The background to the project is described in Spencer, M., Bryant, D. and Susko, E. (2007) Conditioned genome reconstruction: how to avoid choosing the conditioning genome. *Systematic Biology* 56, 25-43. Some of the work will be in collaboration with Dr David Bryant (Department of Mathematics, University of Auckland) and Dr Brian Golding (Department of Biology, McMaster University).

Closing date for both posts: 1 June 2007

For full details, or to request an application pack, visit www.liv.ac.uk/university/jobs.html or e-mail jobs@liv.ac.uk Tel 0151 794 2210 (24 hr answerphone). Please quote the reference number in all enquiries

M.Spencer@liverpool.ac.uk M.Spencer@liverpool.ac.uk

ULiverpool Bioinformatics

THE UNIVERSITY OF LIVERPOOL
SCHOOL OF BIOLOGICAL SCIENCES

TWO POSTDOCTORAL RESEARCHERS (BIOINFORMATICS)

£27,465 - £31,840 pa / £27,465 pa (For Post 1, a higher salary may be available for an exceptional candidate)

Post 1: Based in the Advanced Genomics Facility, the project involves the development of software and database tools and protocols for genomic analysis using massively parallel pyrosequencing technology currently being installed. In addition to tool and database development you will also undertake comparative analysis of microbial genomes to study genome evolution and host adaptation. You should have a PhD or equivalent experience in bioinformatics or computer science. Under exceptional circumstances we may appoint at a higher

UMunich SexEvol

Marie Curie Research training network (MRTN) SEX-ASEX - Experienced Researcher position Cytogenetics

Researchers interested in the paradox of sex in evolutionary biology are invited to apply for an Experienced Researcher position within the framework of the European Union Marie Curie Research Training Network SEXASEX, which comprises nine institutions across as many countries. The network's theoretical and empirical research applies 13 major approaches, including genetic, genomic and cytogenetic approaches, phylogeography, ecology and behavioural studies. With this multidisciplinary approach, SEXASEX investigates why sex exists at all, given its evolutionary costs, using the model organism *Eucypris virens*, a non-marine ostracod species with both sexual and asexual reproduction (<http://evirens.group.shef.ac.uk> for detailed information).

Job title: Marie Curie Research training network (MRTN) experienced researcher position at Ludwig-Maximilians-University Munich, Germany. Starting date: 1st November 2007 or as soon as possible thereafter Duration: 4 months Salary: The gross salary is up to 60.000/year Place of work: Ludwig-Maximilians-University Munich, Department Biology II, Section Anthropology and Human Genetics (<http://www.zi.biologie.uni-muenchen.de>) Job description: Investigation of chromosomal sex determination mechanisms in freshwater ostracods with focus on *Eucypris virens*. Correlations between chromosomal architecture and/or other cytological factors and reproductive mode will be examined, using molecular cytogenetic (fluorescence in situ hybridization) techniques. Candidate profile: PhD or equivalent in Genetics, Molecular Biology or Evolutionary Biology and less than 10 years research experience after obtaining the degree that gives access to a PhD programme (e.g. BSc, MS, Diploma, Honours); experience in cytogenetic and molecular genetic techniques. A background in invertebrate biology is desirable but not essential. Preference will be given to applicants who are citizens or residents of the European Union and associated countries. Only non-German persons are eligible. The application of female candidates is especially encouraged. How to apply: Send full applications, comprising letter of motivation, CV and coordinates of at least two potential referees before the 1st of August 2007 to PD Dr. Stefan Mueller Ludwig-Maximilians-University Munich Department Biology II - Anthropology und Human Genetics Grosshaderner Strasse 2 82152 Planegg-Martinsried Phone: +49-89-218074325 Fax: +49-89-218074331 E-mail: s.mueller@lrz.uni-muenchen.de Correspondence by email is preferred.

Stefan Mueller, PD Dr.rer.nat. Ludwig Maximilians Universitaet Muenchen Department Biologie II - Anthropologie und Humangenetik Raum B 03.052 Grosshaderner Strasse 2 82152 Planegg-Martinsried

Phone: +49-89-218074325 Fax: +49-89-218074331 E-mail: s.mueller@lrz.uni-muenchen.de AIM/iChat/Skype: [cystofef](#) URL: <http://www.zi.biologie.uni-muenchen.de> Stefan Mueller <S.Mueller@lrz.uni-muenchen.de>

UQueensland EvolViralGenetics

Post doctoral Research Fellow

An opportunity exists to work, as a Postdoctoral Research Fellow, on a project funded by an Australian Research Council Discovery grant. A motivated PhD graduate is required to undertake original research modelling the stochastic dynamics and evolutionary genetics of virus populations.

The research will take place at the School of Physical Sciences of The University of Queensland, which undertakes a broad program of theoretical research, ranging from astrophysics to bio-informatics research, in conjunction with a strong biological sciences precinct. This project will extend the School's research scope to include theoretical population genetics and population dynamics. The project has a computational and quantitative focus, aided by close cooperation with biologists and experts in computational bio-informatics.

Genetic complexity is at the heart of many problems in theoretical biology. This type of exponential complexity - which is found in many areas of science - often leads to intractable computational issues. However, recently developed stochastic gauge techniques for phase-space representations provide powerful approaches to solving these problems. These have greatly extended the work of 2005 Nobel laureate Roy Glauber, into fields well beyond the original applications to quantum optics. They are potentially relevant to the grand challenge problems of evolution, adaptation and speciation. This project is an interdisciplinary application of these novel techniques to genetics.

Specifically the successful candidate will focus on the highly relevant case of modeling viral evolution in a single infected host using recent computational techniques developed for quantum physics. Familiarity with high-level computer languages would be useful, as would a knowledge of modern population genetics or the use of stochastic differential equations for modeling physical systems.

You should possess a PhD in an area of theoretical population genetics, mathematics, quantum statistical physics or bioinformatics/computational biology, and should have authored articles in international peer-reviewed journals.

This is a fixed term (one year with possible on year extension), full-time appointment at Academic Level A.

Applications close on July 1st, 2007.

Contact:

Professor P. D. Drummond,

School of Physical Sciences University of Queensland
Brisbane, Queensland 4072, Australia.

Email: drummond@physics.uq.edu.au

adru001@cs.auckland.ac.nz

YaleU ButterflyEvoDevo

Postdoctoral Position in Butterfly or Moth Evo-Devo at Yale

I am looking for a postdoctoral candidate that has interest in pursuing functional genetic work on *Bicyclus anynana* butterflies and/ or in other butterfly or moth species.

We have developed a new set of plasmid constructs that once inserted into the germ-line can either ectopically express candidate genes or knock them down using transgenic RNAi approaches. We have been obtaining significant effects on the *B. anynana* adult wing pattern by ectopically expressing *B. anynana* *Distal-less* or *Drosophila spalt* either throughout the whole body (via a whole body heat-shock) or via a laser-mediated local heat-shock applied to the pupal wing. The genes that still need to be tested, and for which we have made both ectopic expression and RNAi constructs, include *decapentaplegic*, *wingless*, *engrailed*, and *spalt* (RNAi).

This project will provide someone with an opportunity to learn about transgenic techniques in Lepidoptera, as well as wing color pattern evo-devo and functional genetics.

The position is funded for two years (\$37,000/year) with the possibility of renewal contingent on additional external funding. If candidates are interested in pursuing functional genetic techniques in butterfly/moth species of their choice then the candidate will be sup-

ported for a year but will be asked to apply for own external funding during that year. In this case, additional funding after the first year may be contingent on promising successful germ-line transformation of the novel species.

Experience with molecular biology techniques such as PCR, real-time PCR, Southern-blotting is desired. Experience with Immunohistochemistry is desired but not essential.

For references about this type of work I recommend reading the following:

Marcus, JM, DM Ramos, and A Monteiro (2004) Germ line transformation of the butterfly *Bicyclus anynana*. *Proc R. Soc. Lond. B* 271: S263-S265

Ramos, DM, F Kamal, EA Wimmer, A Cartwright, A Monteiro (2006) Temporal and spatial control of transgene expression using laser induction of the *hsp70* promoter. *BMC Developmental Biology* 6: 55

Monteiro A, G Glaser, S Stockslagger, N Glansdorp, and DM Ramos (2006) Comparative insights into questions of lepidopteran wing pattern homology. *BMC Developmental Biology* 6:52

Applications will be considered in the order in which they are received. An ideal starting date would be August 2007.

If interested please contact:

Antónia Monteiro Ecology and Evolutionary Biology
Yale University P.O. Box 208106 New Haven, CT
06520-8106

e-mail: antonia.monteiro@yale.edu tel: + 1 203
4323109

Antónia Monteiro <antonia.monteiro@yale.edu>

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Europe ConsGenetics proposals

The ConGen program, funded by the European Science Foundation (www.esf.org) is calling for applications for the organization of Winter- or Summer-Schools to be held in late 2007 or in 2008. The School's aim is to provide the opportunity for younger researchers to meet for discussions on the most recent developments in their fields of research within conservation genetics. The School, which usually last 5 days, should have a wide participation from across Europe and involve young, independent researchers and scholars with leadership potential. The relatively small scale (in terms of people involved which should be around 25 to 30 persons) provides an ideal platform for focus on the topic and for all participants to contribute to discussions and plan follow-up collaborative work. The ConGen programme invites applications for Winter/Summer Schools within the field of Conservation Genetics with special emphasis on the use of the application of genetic tools and genetic softwares; interdisciplinary topics are greatly encouraged. More specific guidelines on the main aims of the Summer-(Winter-) School and of the suggested structure of the course are given below: The effects of environmental stressors on ecosystems are complex, and tools that improve our understanding are necessary. Until now, efforts have been mainly ecologically based with little practice of incorporating genetic diversity measurements into risk assessment. However, with the use of genetic approaches the information level returned is potentially much higher. The precise genetic consequences of population perturbations result from a complex balance among effects on population substructure, size, and founding events. Hence, there is a need for tools that will support the interpretation of genetic erosion effects and selective effects in investigations aimed to detect such events.

The course should provide an introductory overview of the most essential methods commonly used in Conservation Genetics and of the most essential genetic methods commonly used for the detection of environmental perturbations, focusing on the joint application of neutral and non-neutral genetic markers and demographic techniques. The course should be structured with morning lectures and afternoon exercises in which

the researcher will be given datasets to analyse and will have an opportunity to analyse (their own) data. Rather than provide comprehensive coverage of any single technique, the course aims to teach young researcher how to identify the most appropriate technique(s) for specific types of data sets, and for specific questions. Guidance should be provided to assist researchers in finding references and software to address specific problems.

For further details and the address where to send applications, please read the web page: www.congen.biz or www.congen. For further information please contact: Prof. Kuke Bijlsma: r.bijlsma@rug.nl or Celine Seewald: cseewald@esf.org

Cino Pertoldi Associate Professor Dpt. Ecology and Genetics University of Aarhus

biocp@nf.au.dk

IowaStateU PopGenet Jun29-30

Dear All,

Rod Peakall and I (John Nason) are organizing a 1.5 day population genetics training workshop using Rod's software package GenAlEx. Cross-platform and free, it is both an excellent research and teaching tool.

Workshop dates, location, sessions, and registration instructions are described below.

Please forward this announcement along to students, staff, or faculty you think may be interested.

We look forward to seeing you at the workshop.

Cheers, John (contact info at bottom of page)

Population Genetics Training Using GenAlEx When: Friday June 29 and Saturday June 30, 2007 Where: Scheman Building, Iowa State University Class size: Limited to 25 participants

Instructor: Dr. Rod Peakall, The Australian National University, Canberra, Australia

Overview This summer, ISU is pleased to host a hands-on workshop to enhance population genetic training of faculty, staff, and students. This training will be cen-

tered around the use of GenAIEx, a free, user-friendly, cross-platform package for population genetic analysis that runs within Microsoft Excel (on Macs and PCs). GenAIEx enables population genetic data analysis of codominant, haploid, and binary genetic data providing analytical tools applicable to plants, animals, and microorganisms. Workshop instructor Dr. Rod Peakall is the lead author of GenAIEx and with the release of GenAIEx 6 introduces many new features for both teachers and researchers, including:

Features for research - Tools for importing, editing and manipulating raw genotype and sequence data from automated sequencing or genotyping software. - A diverse range of tools for data exploration. - AMOVA. - Mantel tests. - Calculation of genetic distance and diversity statistics. - Tests of Hardy-Weinberg equilibrium. - Principal Coordinates Analysis of multivariate genetic data. - Spatial autocorrelation procedures. - 2D local spatial analysis. - Estimation of pairwise relatedness among individuals. - Population assignment. - Tools for genetic tagging applications, including location of matching genotypes and calculation of probabilities of identity. - Tools to assist users keep track of data analysis. - Data export options to other population genetic software packages.

Special features for teaching - More than 20 different kinds of graphs to summarize data analysis. - An intuitive and consistent user interface with context-dependent dialog boxes to guide students. - Several tools designed specifically for teaching students. - A free, user-friendly software package that runs on both Mac and PC computer platforms.

Overview of Workshop The workshop is limited to 25 people so as to provide hands-on experience analyzing population genetic data. A brief overview of the workshop follows below:

Session 1. "An Introduction to GenAIEx" - Friday, June 29, 8am - 12pm - For people with little or no experience using GenAIEx; participants should have a basic understanding of population genetic principles.

Session 2. "Advanced Features of GenAIEx" - Friday, June 29, 1pm - 5pm - For people with using GenAIEx; participants should have a sound understanding of population genetic principles. The Introduction to GenAIEx training session is suitable preparation for this more advanced session.

Session 3. "Getting the Most Out of GenAIEx for Teachers" - 8am - 12pm on Saturday, June 30 - Designed to help instructors use GenAIEx as an effective teaching tool in the classroom and homework assignments. Depending on prior experience with GenAIEx,

participants in this session may benefit from attending one or both the Friday sessions.

Registration The GenAIEx Training Workshop is being offered as a stand-alone, post-conference activity associated with the 9th International Pollination Symposium being held at ISU June 24-28, 2007. Registration for GenAIEx training is organized through the Pollination Symposium website but does not require registering for the Symposium itself. Attendees can register for individual workshop sessions, or for all sessions (at a reduced rate). To register for GenAIEx training see: <https://www.ucs.iastate.edu/mnet/plantbee/quickregister.html> To learn more about GenAIEx GenAIEx software comes with extensive documentation. Both can be downloaded for free from: <http://www.anu.edu.au/BoZo/GenAIEx/> Contact information For additional information concerning any aspect of the population genetics workshop with GenAIEx please contact John Nason (jnason@iastate.edu) or Rod Peakall (Rod.Peakall@anu.edu.au).

Dr. John Nason Associate Professor Dept. of Ecology, Evolution, and Organismal Biology Iowa State University Ames, IA 50011

Phone: 515-294-2268 email: jnason@iastate.edu Web page: jnason.eeob.iastate.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/evoldir.html>

Lisbon ConGen Sep19-21

Dear evoldir members, A ESF ConGen (<http://www.esf.org/congen/>) funded workshop entitled "Population genetics modelling and habitat fragmentation: separating recent and ancient events for efficient conservation" will be held at the Instituto Gulbenkian de Ciências in Oeiras (<http://www.igc.gulbenkian.pt/>) from the 19 to 21 Sept 2007.

The aim of the workshop is to bring together specialists from different areas related either to conservation biology and population genetics, including statistical modelling. We shall discuss the current needs of conservation biologists in connection with the achievements and limitations of current population genetics methods. Discussions will revolve around case studies, and ongo-

ing theoretical work to unravel the past demography of species. One aim is to show conservation biologists the existence of tools that can be applied to infer the past of endangered species and that this knowledge can be used to improve conservation strategies. Another aim is to show theoreticians that interesting inference problems still need to be addressed in conservation biology. Case studies, theoretical work and software related presentations will all be represented during the workshop. Current invited speakers are (in alphabetical order):

D. Balding, M. Beaumont C. Bessa-Gomes, B. Crouau-Roy M. Currat, L. Excoffier P. Garnier-Géré, B. Goossens D. Hudson, C. Lavigne R. Nielsen, U. Radespiel I. Togan, L. Vigilant

The Workshop aims at favouring discussion between participants and is thus open to up to 25 participants in addition to the invitees mentioned above. Local costs (meals and lodging close to the Instituto Gulbenkian de Ciências) will be taken care of for *all 25* participants. Moreover, a limited number of grants will be given to participants to reimburse partly flight tickets.

The selection of participants will be based on scientific criteria and on the need to maintain a balance between theoretical and case studies. Participants coming from ConGen contributing countries will be favoured in the selection process (Austria, Belgium, Croatia, Czech Republic, Denmark, Finland, France, Hungary, Netherlands, Norway, Spain, Sweden, Turkey). A couple of self funded participants may also be accepted depending on the number of applications.

Applications should be submitted online through the following website: <http://www.igc.gulbenkian.pt/-node/view/23> Note that there is more than one workshop/course on this page and that you should click on the right "Application" link. A preliminary program will soon be available on the same site (clicking on the Workshop name).

The DEADLINE for registration is 15/06/2007. BEFORE APPLYING: please remember to name any file you upload with your name.

If you have any problem with the application, please do not hesitate to contact me, best wishes, Lounès Chikhi

Organizer: Lounès Chikhi (chikhi@cict.fr – chikhi@igc.gulbenkian.pt) CNRS, Université Paul Sabatier, Toulouse, France Instituto Gulbenkian de Ciências, Oeiras, Lisboa, Portugal

Workshop location: <http://www.igc.gulbenkian.pt/> chikhi@cict.fr chikhi@cict.fr

Lisbon Darwin Sep10

Call for submissions/participation:

EXTENDING THE DARWINIAN FRAMEWORK, LISBON, SEPTEMBER 10, 2007

<http://www.uea.ac.uk/~e197/darwinWorkshop.html>
Associated with ECAL 2007.

UPDATE: 8th May 2007

* New Speakers Announced * Submission Deadline Extended *

We are pleased to announce that additional speakers are now confirmed for the workshop, and that the submission deadline for papers and abstracts has been extended until July 2nd 2007. This workshop offers an opportunity to be bold and creative, and to discuss exciting new questions in evolutionary theory in a stimulating environment.

This workshop will explore the formation of new levels of selection and inheritance, the origin of the first evolutionary units and novel modes of natural selection. Recent work in a variety of fields has presented a challenge to standard gene-centric evolutionary theory. Higher-level and non-genetic sources of heredity have been discovered. Artificial selection experiments have demonstrated a response to selection of whole microbial ecosystems, with concomitant implications for the formation of new evolutionary units. These results bear important relation to long-standing questions regarding the formation of new levels of biological organisation. The debate over levels of selection has an extended history. However, given recent empirical results and outstanding unresolved issues, it again seems pertinent to ask: What can selection act on? What sources of heritable variation exist? How can selection bring about new units of selection? And how can artificial life models help to answer such questions?

Areas of interest:

Major transitions in evolution, formation of new units of selection and/or levels of inheritance, non-genetic heredity/epigenetics, evolution of co-operation, ecosystem selection, multi-level selection theory, niche construction and extended heredity, origins of life, homeostasis and heredity/levels of homeostasis, self-organisation and formation of new levels of selection and heredity, development and selection, disam-

biguating co-evolution and higher-level selection, co-evolutionary transitions in life and the environment,...

More information at the workshop website:

<http://www.uea.ac.uk/~e197/darwinWorkshop.html>

Please contact Hywel Williams (h.williams@uea.ac.uk) if you have any enquiries. Hope to see you in Lisbon!

h.williams@uea.ac.uk h.williams@uea.ac.uk

LundU AnimalMigration Oct17-26

Dear All,

we would like to announce that we are again giving an international PhD student course in Ecology of Animal Migration at the Department of Animal Ecology at Lund University. The course will be held 17-26 October 2007, and you will find more information (program, registration etc) on our web page:

<http://orn-lab.ekol.lu.se/birdmigration/> During the course lectures will be given by invited experts in their field, there will be seminars, own projects with practice of field equipment as well as an excursion. There will be ample time for interactions between students and lecturers and we invite PhD students from any country to participate in the course.

Please, contact Håkan Karlsson (Hakan.Karlsson@zooekol.lu.se) for registration.

Very Welcome to a very stimulating and exciting course!

Susanne Åkesson and Thomas Alerstam Professor, PhD Susanne Åkesson FRIN Department of Animal Ecology, Ecology Building, 223 62 LUND, Sweden Tel. +46 46 2223705, Fax. +46 46 2224716, <<http://orn-lab.ekol.lu.se/birdmigration/>> <http://orn-lab.ekol.lu.se/birdmigration/>

Susanne Åkesson <susanne.akesson@zooekol.lu.se>

Montana ConservationGeneticDataAnalysis Sep11-16 2

Second Announcement

2nd Conservation Genetics Data Analysis Course

Recent Approaches for Estimation of Population Size, Structure, Gene flow, Landscape Genetics, Selection Detection & Bioinformatics

11 - 16 September, 2007, Flathead Lake Biological Station, Montana

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genetics of natural and managed populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 28 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students at the end of their degree program). Deadline for application is 15 June, 2007

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

Instructors:

Oscar Gaggiotti, University Joseph Fourier in Grenoble, France Gordon Luikart, CIBIO-University of Porto, Portugal & University of Montana Bruce Rannala, University of California at Davis, USA Albano Beja-Pereira, CIBIO, University of Porto, Portugal David Lynn, Simon Fraser University, Burnaby (Vancouver), Canada Mark Miller, Utah State University, Logan, USA Jonathan Pritchard, University of Chicago, Logan, USA Mike Schwartz, US Forest Service, Missoula, USA David Tallmon, University of Alaska, Juneau,

USA Robin Waples, Northwest Fisheries Science Center of the National Marine Fisheries Service, Seattle, USA

Location: The course will be held at the beautiful Flathead Lake Biological Station near Glacier National Park (see ?Location? at <http://popgen.eu/congen2007/>, click ?Site Map? then ?Location Map?). The International airport is 40 miles drive north of the Biological Station (see <http://www.iflyglacier.com/>).

Application and cost: For detailed information see <http://popgen.eu/congen2007/>. Accommodations and meals are included in the registration fee. Cost: \$US 1,100 per person (plus \$200 if payment arrives after June 15) will cover all meals, lodging, transportation to and from the airport, and a visit to Glacier National Park. Up to two reduced-cost scholarships could be available for candidates with no funding.

congen@popgen.eu

conservation genetics course
<congen@mail.icav.up.pt>

Munich EES Sept9-14

The Munich Graduate Program for Evolution, Ecology and Systematics (EES) invites applications for an International EES Summer School on 'Evolutionary and Ecological Consequences of Global Change' held at Frauenchiemsee (80 km east of Munich) from 9 - 14 September 2007.

The 5-day Summer School will consist of lectures, discussions and exercises provided by the invited teachers as well as oral and/or poster contributions by the more advanced student participants. Arrival of participants is scheduled for Sunday 9 September evening, departure for Friday 14 September early afternoon.

Invited teachers and preliminary topics:

Christiaan Both, University of Groningen, The Netherlands: Evolutionary and ecological responses to climate change in bird populations

Arndt Hampe, INRA, UMR Biodiversity, Genes & Ecosystems, Cestas, France: Conserving diversity of species and genotypes under climate change: the rear edge of the species range matters

Nils Christian Stenseth and Dag Hjermand, University of Oslo, Norway: Trophic interactions under cli-

mate fluctuations:and Environmental change and mammalian evolution

Håkan Wallander, Lund University, Sweden: Global change as seen from a below-ground perspective

Local organizers: Reinhard Agerer, Sebastian Diehl, Bart Kempnaers, Pleuni Pennings (Ludwig-Maximilians-University Munich and Max Planck Institute for Ornithology Seewiesen)

The summer school is open to students at the PhD and Master/advanced Diploma levels. The course language will be English. Students who are involved in global change related research are encouraged to prepare short oral contributions or posters highlighting their research interests and/or achievements.

Thanks to support from the Volkswagen Foundation, the University of Munich's EES program will cover costs for housing and meals during the Summer School. Participants will have to cover their travel expenses and must pay a 50 registration fee. A limited amount of funding is available to partly subsidize travel expenses for students from the most distant localities.

Applicants should provide a full CV, a statement about your research interests/current projects (max. half page), a statement about why you want to attend the Summer School, explicitly addressing how you expect to benefit and what you can contribute (max. half page). Application deadline is 11 June.

Questions can be addressed to Ms Pleuni Pennings (pennings@lmu.de). Please send your application by e-mail, preferably as a single pdf file, to Ms Katrin Kümpfbeck Program Secretary of the Munich Graduate School for Evolution, Ecology, and Systematics (k.k@lmu.de). Further information is available at http://www.eeslmu.de/eeswiki/-index.php?title=3DSummer_school.2007.

diehl@zi.biologie.uni-muenchen.de

diehl@zi.biologie.uni-muenchen.de

Seattle StatGenetics Jun11-29

The deadline for early registration at the 2007 Summer Institute in Statistical Genetics, June 11-29 in Seattle, WA, is May 21.

Some of the more popular modules are nearly filled.

Scholarships are available for European students to attend the European Institute in Statistical Genetics,

September 3-12 in Liege, Belgium.

Details for both events are available at <http://www.biostat.washington.edu> Bruce Weir

Bruce Weir <bsweir@u.washington.edu>

Switzerland CompBiol Aug5-11

!!! Application deadline: May 25 2007 !!!

COMPUTATIONAL BIOLOGY

AN INTENSIVE TRAINING COURSE IN A RAPIDLY EVOLVING FIELD

5-11 August 2007 - Alpine Lyceum Disentis, Switzerland

See: <http://www.biosym.unizh.ch/index.php> Offered by the BioSym and SIMOLIFE Teams of the Universities of Zürich and Winterthur and the ETH Zürich

Participants:

Students and researchers at the graduate, postgraduate and professional level - maximum 25 and minimum 15 participants.

Stipends:

The course is supported by a grant from the Swiss Virtual Campus, and a number of stipends are thus available for students who would not otherwise be able to pay the course fee. The awards will partially cover tuition, room and board, but not travel.

COURSE OBJECTIVES

The purpose of the course is to provide an overview of the many facets of the exciting field of computational biology by bringing together various aspects of a number of biological and mathematical sciences. It is primarily a skills course. Participants will develop mathematical models to solve biological questions. Since a major goal of the course is to initiate contacts between workers in scientific fields which are not usually combined, it encourages a rapprochement between various areas of biology, biochemistry, biophysics and mathematics and treats them with an interdisciplinary outlook.

COURSE DESCRIPTION

Over a period of six days the participants will be exposed to an in-depth treatment of how biological processes can be described in mathematical terms and how

biological concepts can be translated into mathematical models. We will employ Matlab-Simulink and other software tools.

This year's course will focus on eighth main themes which are most central to the discipline of computational biology:

* Growth * Biofilm formation * Epidemics * Virulence and pathogenicity * Ecology and evolution * Human physiological processes * Pharmacokinetics * Antibiotic resistance

COURSE ORGANIZERS

Advisory committee

- Barbour, Andrew D. - Bonhoeffer, Sebastian

Coordinator

- Kurt Hanselmann

Teaching team

- Christoph Fuchs - Kurt Hanselmann - Dominik Heinzmann - Barbara Hellriegel - Roman Kälin - Hansueli Schwarzenbach - Jakob Zinsstag

Web scripts, Matlab and Simulink models

- Stefan Schafroth

Information

Kurt Hanselmann, University of Zürich, Institute of Plant Biology / Microbiology, Zollikerstr. 107, CH-8008 Zürich, Switzerland,

tel: +41-44-63 48284, fax: +41-44-63 48204, hanselma@botinst.uzh.ch

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Trento Italy AnimalPopGenet Sep6-8 2

This is the FINAL reminder that all abstracts and applications for bursaries for the International Workshop: "Population Genetics for Animal Conservation II" Monte Bondone, Trento, Italy. September 6-8, 2007 are due on 15 May 2007.

Please look at the web site <http://www.cealp.it> (or send an e-mail to pgac2@cealp.it) for further information.

The scientific committee: Giorgio Bertorelle, University of Ferrara, Italy Mike Bruford, University of Cardiff, UK Claudio Chemini, CEA, Viote del Monte Bondone,

Trento, Italy Heidi Hauffe, CEA, Viote del Monte Bondone, Trento, Italy Elena Pecchioli, CEA, Viote del Monte Bondone, Trento, Italy Cristiano Vernesi, CEA, Viote del Monte Bondone, Trento, Italy

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Vienna EvolEcolGenetics Sep15-16

ESF sponsored exploratory workshop on

Ecological genetics: understanding the functional consequences of natural variation in adaptation

Vienna 15.-16.9. 2007 Note: this is immediately after the European Drosophila Research Conference (<http://www.imp.ac.at/EDRC2007/>)

Synopsis

It is well established that natural populations harbor huge amounts of molecular variation. The neutral theory of molecular evolution suggested that the effect of most of mutations is so small that they can be considered as neutral. Recent evidence, however, demonstrated that a large proportion of natural variation seems to be involved in adaptation to the environment. Population genetics has developed powerful tools to identify genes under selection, but the functional validation of such ecologically important variants requires new functional approaches suitable to measure effects that are important in the wild, but difficult to score in

the laboratory. Conversely, there is increasing evidence that natural variation in structural or regulatory genes have major effects, which were only recognized through the comparison of different naturally occurring variants.

This workshop provides a platform for both functional biologists and population geneticists with the aim to develop concepts and new tools to study the functional consequences of natural variation, in particular in the context of ecology.

The invited speakers cover a broad range of topics and approaches, ranging from theoretical population genetics and quantitative genetics to developmental biology. The impact of environmental and genetic variation on phenotypic traits will be covered. It will be discussed how the knowledge of well-studied model organisms, such as *D. melanogaster*, yeast and *A. thaliana*, can be extended to less studied organisms.

Speakers

Patricia Beldade Jean David Jean-Michel Gibert Greg Gibson Joachim Hermisson Martin Jaekel Volker Loeschcke Artyom Kopp Sergey Nuzhdin Leonie Ringrose Christian Schlötterer Karl Schmid Lars Steinmetz

The workshop will be open to a limited number of additional participants, in particular functional biologists are encouraged to participate. Applications including CV and motivation statement should be sent to jmg@i122server.vu-wien.ac.at until June, 19th.

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Instructions

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

once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

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

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be 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 \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.