
E v o l D i r

March 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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Basel PopulationBiologyCall May17-19

****Call for abstracts** **registration open****

Dear colleague

The 20th Annual Conference of the Plant Population Biology Section of the Ecological Society of Germany, Switzerland and Austria, GfOe will be held from 17-19 May in Basel, Switzerland.

Perspectives of Plant Population Biology for the next 20 years

Registration is open now. We invite you to submit abstracts for oral and poster contributions. We especially encourage presentations by students.

For further information, visit the Popbio 2007 conference website: <http://pages.unibas.ch/botschoen/-popbio2007> To register reply to this eMail that contains a registration form. Please, fill in your personal information into the empty lines provided.

We urge you to independently book your accomodation as soon as possible. For hotel suggestions visit conference website.

Kind regards Sylvia Martinez

Name:

First name:

Complete Address (use comma as separator):

eMail:

Member GfOe, yes/no:

Student yes*/no:

1 Lunch on Thursday (8) yes/no:

1 Lunch on Friday (8) yes/no:

1 Conference dinner Fri, 18 May (18) yes/no:

Excursion participation incl. bag lunch on Sat, 19 May (10) yes / no:

Title of presentation:

Presentation type oral/poster:

Main-author:

Co-authors:

Abstract (max 2200 characters, no graphs):

– abwesend/away from work 16 Feb - 10 Mar 2007

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Brno GregorMendelNetwork
May31-Jun2

Dear colleague!

The Gregor-Mendel-Network, an association aimed at promoting computational biology in infrastructure, science and education in the Vienna-Brno area, organizes its first meeting (31st May - 2nd June 2007). It will take place in Brno in the premises of the abbey where Gregor Mendel has carried out his famous experiments.

The selected topics for this year are the fields of biomolecular sequence analysis (gene function prediction), comparative genomics (evolutionary studies based on completely sequenced genomes) and 3D structural analysis (biomolecules in context with drugs).

The event involves advanced tutorials (including lectures and practical exercises) and scientific lectures. The latter are thought to extend the tutorial part and to present front edges of research that can be reached with the theoretical approaches in the respective fields. More detail is available at the conference WWW site (<http://gmn.imp.ac.at/conference2007.shtml>)

The expected audience will involve qualified young scientists (from various biological labs) that wish to complement their skills in computational biology in addition to scientists from the region.

We would be happy to have you with us in Brno at the conference. With kind regards (also in the name of Arndt von Haeseler and Jaroslav Koca),

Frank Eisenhaber

–

Dr. Frank Eisenhaber Bioinformatics Group Institute of Molecular Pathology

Mail : Dr. Bohr-Gasse 7, A-1030 Vienna, Austria E-mail: Frank.Eisenhaber@imp.univie.ac.at Tel. : +43-1-7973 03370 FAX : +43-1-7987 153

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Can you please post the following announcement.

Conference:, Evolution 2007 - Notice of meetings and call for papers

The annual meetings of The American Society of Naturalists (ASN) <http://www.amnat.org/>, Society of Systematic Biologists (SSB) <http://systbiol.org/>, and the Society for the Study of Evolution (SSE) <http://www.evolutionsociety.org> are to be held June 16-20, 2007 at the Christchurch Convention Centre, Christchurch, New Zealand.

Saturday June 16 is the arrival day (pre conference tours, council meetings, opening reception), Sunday June 17 through Wednesday June 20 (scientific sessions) with the closing awards banquet scheduled for the evening of Wednesday June 20. Thursday June 21 is departure day.

Full details on this combined meeting are available at the Evolution 2007 website, www.evolution2007.com On line registration and talk/poster registration now available at this site.

PLEASE NOTE THE FOLLOWING DEADLINES

For submission of talk/poster titles - April 15, 2007

For early bird discounted registration rates - March 31, 2007

Delegates can register early and submit presentation details no later than the above deadline.

Information on travel to New Zealand and accommodation options for the conference can be found on the conference website.

Direct general enquiries on Evolution 2007 to:

Dr Ian Anderson Conference Secretary Evolution 2007 Phone: 64 6 3566520 Email: I.L.Anderson@massey.ac.nz

Thank you in anticipation.

Kind regards

Ian Anderson

I.L.Anderson@massey.ac.nz

I.L.Anderson@massey.ac.nz

ChristchurchNZ ASNSSBSSE2007 4

ChristchurchNZ ASNSSBSSE2007 3

EVOLUTION 2007

Notice of meeting and call for papers

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Full details on this combined meeting are available at the Evolution 2007 web site, www.evolution2007.com

On line conference registration and talk/poster registration is now available at this site. Delegates intending to present a talk or display a poster at Evolution 2007, must first register through the on line registration process.

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Information on travel to New Zealand and accommodation options for the conference can be found on the conference web site.

Chris Simon Professor, Ecology & Evolutionary Biology 75 North Eagleville Road, University of Connecticut Storrs, CT 06269-3043

chris.simon@uconn.edu (Please note that my old uconnvm address no longer works) Office (860) 486-4640; Lab (860) 486-3947; Fax (860) 486-6364, Biopharm 305D, 323,325

June-August: Victoria University of Wellington, School of Biological Sciences, Wellington, New Zealand Office: Kirk 611; Office phone: +64-4-463-5026; Fax: +64 4 463 5331; email: as above Home phone 64-4-970-0265

Home page: <http://hydrodictyon.eeb.uconn.edu/people/simon/Simon.htm> Reprints: <<http://hydrodictyon.eeb.uconn.edu/projects/cicada/Resources/reprints.html>> Chris Simon <chris.simon@uconn.edu>

Croatia FishHybridization Sep9-13

ECI XII

XII EUROPEAN CONGRESS OF ICHTHYOLOGY

Cavtat (Dubrovnik), Croatia

9-13 September 2007

e-mail: ecixii@biol.pmf.hr <<mailto:ecixii@biol.pmf.hr>>

SYMPOSIUM ON Fish Hybridization and Introgression - Evolutionary and Conservation Approaches

The role of hybridisation in evolution throughout extensive gene flow and the establishment of new evolutionary lineages is now becoming increasingly clear by the new insights of molecular genetics and ecology of hybrids (from both genetically divergent populations and species). Moreover, hybridization also has important implications for management and conservation, once it is well known that human activities such as stock transfer and exploitation, habitat changes and interaction with alien species all act to increase the incidence of hybridization among populations and species and affect the survival of indigenous populations.

In this symposium, we plan to bring together experts from a variety of disciplines including genetics, morphology, behavior and ecology, management and conservation, to review recent knowledge about the impacts of hybridization on fishes. Topics for discussion will include:

- i) detection of hybridization using molecular and morphological tools;
- ii) hybrid (tension) zones;
- iii) case-studies linking the genetics of hybridization and introgression with the fitness performance of hybrids and parentals;
- iv) role of hybridization in speciation (in both homoploid and polyploid conditions);
- v) evolutionary aspects of sexual versus non-sexual modes of reproduction;
- vi) strategies for preserving the genetic integrity of native species;
- vii) impact of hybridization on endangered species, management decisions and legislation.

INVITED SPEAKERS: Louis Bernatchez - Université

Laval, Québec, Canada; Patrick Berrebi - University of Montpellier II, France; Karel Janko - Institute of Animal Physiology and Genetics, Czech Republic

The organizers plan to compile and edit a book in 2008 with the invited lectures and selected contributions.

SYMPOSIUM ORGANIZERS: M.J. Collares-Pereira, M.M. Coelho & P. Rab

CONTACT: mjpereira@fc.ul.pt

Maria Manuela Coelho

Maria Manuela Coelho <mmcoelho@fc.ul.pt>

Edinburgh Systematics Aug28-31

Systematics Association Biennial Conference

Royal Botanic Garden Edinburgh, 28-31 August 2007

Registration now open! Please visit: <http://www.systass.org/biennial2007/>

The Biennial conferences of the Systematics Association provide a forum for systematists from different disciplines to present and discuss their research. The Sixth Biennial Conference will be held at Royal Botanic Garden Edinburgh from 28th to 31st August 2007 (registration opens on the 27th). The format will be a mixture of both open sessions and focused thematic symposia.

Speciation symposium confirmed speakers: Jim Mallet (UC London), Alfred Vogler (Natural History Museum), Nick Barton (Edinburgh), Christophe Thebaud (Toulouse), Christian Lexer (Kew), Peter Comes (Salzburg), John Willis (Duke), Roger Butlin (Sheffield), Mike Ritchie (St Andrews), Salvatore Cozzolino (Naples), Simon Hiscock (Bristol), Chris Jiggins (Edinburgh), Peter Linder (Zurich)

UK Research Councils Systematics Symposium confirmed speakers:

Sandie Baldauf (York), Mark Wilkinson (Natural History Museum), Roger Thorpe (Bangor), Tim Littlewood (Natural History Museum), Lee Hastie (Aberdeen)

Programme Overview

Monday 27 August Registration

Tuesday 28 August

Morning Registration, Open session

Afternoon Concurrent Sessions: (1) Open and (2) Flo-

ras & Faunas

Evening Poster session and drinks reception

Wednesday 29 August

Morning Concurrent Sessions: (1) Open and (2) Floras & Faunas

Afternoon UK Research Council systematics symposium

Thursday 30 August

All day Concurrent Sessions: (1) Open and (2) Speciation symposium

Evening Conference Banquet and Ceilidh, Our Dynamic Earth

Friday 31 August

All day Open sessions

Rebecca Yahr <R.Yahr@rbge.ac.uk>

Gatersleben Germany Apomixis

Dear Colleagues,

The official program of the International Apomixis Congress 2007, including invited speakers and titles, is now online:

<http://meetings.ipk-gatersleben.de/apomixis2007/-index.php> PLEASE REMEMBER THAT THE REGISTRATION AND ABSTRACT SUBMISSION DEADLINE IS 31 MARCH!!!

Very best wishes, Tim and Emidio

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

Apomixis Group Webpage <http://www.ipk-gatersleben.de/en/02/04/01/05/> International Max Planck Research School (IMPRS) http://-imprs.ice.mpg.de/people/Faculty_Members.htm?mp=-3D12

IPK Webpage www.ipk-gatersleben.de tel: +049 (0)39482 5608 fax: +049 (0)39482 5137

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

Halifax SMBE Jun24-28

SMBE 2007

You are invited to attend the 2007 annual meeting of the Society for Molecular Biology and Evolution (SMBE) at Dalhousie University in Halifax, Nova Scotia, Canada. The meeting is being co-hosted by the Canadian Institute for Advanced Research and will run from June 24-28.

Conference registration and abstract submission is now available online at the SMBE website (<http://www.smbe.org/>) or directly via Dalhousie University (<http://smbe2007.dal.ca/>). The site also contains additional information on accommodation and travel, confirmed speakers, as well as the Walter M. Fitch Prize competition for young investigators, graduate student travel awards, and the Undergraduate Diversity Mentoring Program awards.

The conference will open with registration between 3:00-7:00 PM on Sunday, June 24, a reception between 5:00-7:00 PM, and an opening keynote address at 7:30 PM. The meeting will close at 12:30 PM on Thursday, June 28.

Sponsors

Society for Molecular Biology and Evolution (<http://www.smbe.org/>) Canadian Institute for Advanced Research (<http://www.ciar.ca/>) Oxford University Press (<http://www.oxfordjournals.org/>) NASA Astrobiology Institute (http://nai.arc.nasa.gov/institute/-focus_groups_detail.cfm?ID=4) Atlantic Association for Research in the Mathematical Sciences (<http://www.aarms.math.ca/>)

Plenary Speakers

May Berenbaum, Department of Entomology, University of Illinois at Urbana-Champaign Deborah Charlesworth, School of Biological Sciences, University of Edinburgh Marcus Feldman, Department of Biological Sciences, Stanford University Brian Spratt, Molecular Microbiology, Imperial College London Trudy Mackay, Genetics, NC State University

Public Lecture

Nick Lane, University College London, author of ?Oxygen: The Molecule that made the World? and ?Power, Sex, Suicide: Mitochondria and the Meaning of Life?

Symposium Topics

-Bayesian phylogenetic inference -Towards more realistic models of protein evolution -Eukaryotic and prokaryotic genome beginnings -Evolutionary genomics of domestication -Evolution and function of non-protein-coding sequences in complex organisms - Extreme genomes -Gene / genome duplication - Genomics of speciation -Introns early, introns late: the sequel -Lateral gene transfer, the tree, ring, web or network of Life -Molecular and developmental approaches to speciation -Plant population genomics - Recombination (emphasis on molecular mechanisms) - Resolution and dating of the eukaryotic tree

Conference Organizers

John Archibald (organizing committee chair) Ford Doolittle Wanda Danilchuk (conference secretary) Joseph Bielawski Christian Blouin Mark Johnston Robert Lee Andrew Roger Alastair Simpson Edward Susko

Honorary co-chairs

Michael Gray Brian Hall

External Scientific Program Committee

Laura Katz, Smith College John Logsdon, University of Iowa Julio Rozas, Universitat de Barcelona Carmen Segarra, Universitat de Barcelona

John Archibald <jmarchib@dal.ca>

Halifax SMBE Jun24-28 UndergradAwards

SMBE Undergraduate Diversity Mentoring Program Awards

2007 Annual meeting of the society for molecular biology and evolution?

June 24-28, Halifax, Nova Scotia, CANADA

CONFERENCE WEBSITE

<https://smbe2007.dal.ca/> Program outline

The Society for Molecular Biology and Evolution (SMBE) is pleased to make available 10 awards for undergraduate students from underrepresented groups to participate in a Diversity Mentoring Program. The goals of this program are: (1) to promote diversity at the SMBE annual meeting, (2) to provide students with the opportunity to experience the excitement of attend-

ing and presenting at an international scientific conference, and (3) to foster enthusiasm for molecular biology and evolution as well as a possible career in this field.

To achieve these goals, each recipient of an SMBE Undergraduate Diversity Mentoring Program Award will be paired with two mentors, one a senior graduate student and the other a postdoctoral fellow or faculty member (who may or may not be the student's current advisor). Specific mentoring activities will include:

? Attending conference sessions with the student, answering questions about the basic concepts being presented, and, more generally, explaining the "goings-on" at a multi-day scientific conference.

? Interacting with the student during some mealtimes, coffee breaks and other social gatherings.

? Introducing the student to other undergraduates, graduate students, postdoctoral fellows and faculty members as a way of facilitating connections with potential future graduate supervisors and colleagues.

? Attending the poster session and SBME Undergraduate Diversity Program Award reception with the student in order to minimize/overcome the anxiety often felt by first-time conference attendees.

? Serving as a contact point for the student to help resolve any issues surrounding conference registration, travel and accommodation.

Eligibility

Candidates must currently be enrolled as undergraduate students (Bachelor's level degree) or have graduated within the last 6 months at the time of application and be from groups underrepresented in our scientific discipline (e.g., minority groups and/or women).

Selection

Ten individuals will be chosen to receive the award and participate in the program on the basis of their submitted abstracts (below).

Conference participation

Recipients of an SMBE Undergraduate Diversity Mentoring Program Award will be invited to present their research at a special poster session on the evening of Monday, June 25. Awardees will also attend a reception to be held in their honor, along with their mentors and other interested conference attendees.

Award

Award recipients will receive US \$1,000 to be used to help cover the cost of airfare, accommodations, and meeting registration. Each participant will also receive an online student membership to the Society journal,

Molecular Biology and Evolution, for the year of 2008.

Application

Faculty members will be responsible for nominating undergraduates. A brief letter/email of recommendation outlining the student's eligibility for the award and confirming their current academic status should be sent to Laura Katz (Lkatz[at]email.smith.edu) and John Archibald (jmarchib[at]dal.ca).

John Archibald <jmarchib@dal.ca>

IndianaU

MechanismsofGenomeEvolution Jul

Conference organized by Michael Lynch and Eva Allen.

The availability of genome-sequence data has forever transformed our ability to understand the molecular basis of the evolutionary process, but it also remains true that the mechanisms of evolutionary change ultimately reside at the population-genetic level. Thus, the goal of this conference is to help bring about a synthesis of our understanding of genomic evolution from the standpoint of both population genetics and molecular biology, and to outline the major challenges to the transformation of the descriptive field of comparative genomics into an explanatory field of evolutionary genomics. The meeting will consist talks, and poster and discussion sessions to encourage broad participation. Funds will be made available, on a competitive basis, to defray the costs of student registration.

Featured Speakers

Wilhelmine Key Lecturer: Sally Otto: The Causes of Evolution...in the Era of Genomics.

John Archibald: Genome reduction in eukaryotes: nucleomorph genomes as a case study.

Chris Burge: Determinants of microRNA targeting.

Francesco Catania, X. Gao, & D. Scofield: Origins and evolution of spliceosomal introns.

Brian Charlesworth: Mutation, selection and genome evolution.

Andrew Clark: 12 Drosophila genomes: Some lessons in evolutionary genomics.

Adam Eyre-Walker: The relationship between gene expression evolution and sequence evolution - exploring the hidden content of the genome.

Matthew Hahn: Natural selection on gene duplication and loss.

Eugene Koonin: Origins and evolution of eukaryotic gene structure.

Harmit Malik: Causes and consequences of centromere complexity in plants and animals.

Eric Meyer: Recognition of intervening sequences with weak consensus signals: RNA and DNA splicing in the ciliate *Paramecium*.

Jeffrey Palmer: Horizontal gene transfer gone wild in plant mitochondrial genomes.

David Penny: The RNA infrastructure of the ancestral eukaryote.

Victoria Prince: The role of gene and genome duplications in evolution: insights from the ray-finned fishes.

Ellen Pritham: Transposable elements and the dynamic genome.

Scott Roy: Unraveling the mysteries of transcript splicing in eukaryotes.

Arlin Stoltzfus: Mutation as a cause of non-randomness in evolution.

Soojin Yi: Molecular mechanisms of mutations and genome evolution.

For more information, visit the symposium website: <http://www.theaga.org/agasymposium/index.html>

Michael Lynch milynch@indiana.edu

Distinguished Professor Dept. of Biology Phone: 812-855-7384 Indiana University FAX: 812-855-6705 Bloomington, IN 47405

Lab: www.bio.indiana.edu/facultyresearch/faculty/Lynch.html <<http://www.bio.indiana.edu/facultyresearch/faculty/Lynch.html>>

2007 AGA Genome Evolution Symposium:

www.theaga.org/agasymposium/index.html <<http://www.theaga.org/agasymposium/index.html>>

IU Biology: www.bio.indiana.edu <<http://www.bio.indiana.edu>> Daphnia Genomics Consortium: daphnia.cgb.indiana.edu <<http://daphnia.cgb.indiana.edu>> NSF Training Grant: Evolution, Development, & Genomics: evodevo.uoregon.edu

milynch@indiana.edu

KansasCity EcolGenomics Nov9-11

Plan now to attend the 5th Annual “Genes in Ecology, Ecology in Genes” Symposium on November 9, 10, & 11, 2007, in Kansas City. We will convene in the Intercontinental Hotel on the beautiful Country Club Plaza on Friday at 6:00 p.m. and conclude on Sunday at noon. Information will be posted on our website, www.K-State.edu/ecogen, as details are finalized.

Ecological Genomics is a field at the interface of ecology, evolution and genomics that seeks to place the functional significance of genes and genomics into an ecological and evolutionary context. Please refer to our website for future announcements of our exciting line-up of renowned speakers.

Participants are invited to share their own research with the group through a poster session on Friday night and Saturday. Poster topics should be related to the field of Ecological Genomics. A limited number of submitted poster abstracts will be selected for oral presentations.

Please share this announcement with colleagues and students who are interested in learning more about the field of Ecological Genomics. If you have questions, please contact us at (785) 532-3482 or ecogen@ksu.edu. Additional information about this interdisciplinary research initiative is available at www.K-State.edu/ecogen.

Funding for this symposium is provided by Targeted Excellence at Kansas State University.

Ecological Genomics Institute Directors: Dr. Loretta Johnson Dr. Michael Herman Kansas State University, Division of Biology Ackert Hall, Manhattan, KS 66506-4901 (785) 532-3482, www.ksu.edu/ecogen dmerrill@ksu.edu

Mytilene Greece QuantitativeMethodsPopDynamics Jun11-15

Upcoming beginner level workshop on Quantitative Methods in Population Dynamics at University of the

Aegean, Mytilene, Greece, 11-15 June 2007 (see attached file).

You are hereby cordially invited to take part in the following workshop:

Quantitative Methods in Population Dynamics <http://www.aegean.gr/environment/popdyn2007/> <http://www.cefe.cnrs.fr/biom/Workshop/QMPD2007.htm>

This workshop will deal with the analysis and modelling of population dynamics. The content is aimed at providing the participants with a solid background in the philosophy, theory and practice for the analysis of data. We will cover population projection matrix models, the estimation of demographic parameters (survival, recruitment, dispersal and growth rate) using capture-recapture models and the estimation of population densities and abundance using capture-recapture and distance sampling models. Finally, we will review recent advances in the combination of those different sources of information (Integrated Population Modelling). The format of the workshop will be a combination of lectures and computer sessions with programs ULM, M-SURGE & U-CARE, DISTANCE and MARK. It is our hope that participants will bring their own data to work on during the workshop. All lectures and course material will be in English.

Teachers: Olivier Gimenez, Jean-Dominique Lebreton, Roger Pradel (CNRS/CEFE, FRANCE) and Panagiotis Besbeas.

The registration fee for the workshop is 360 euros (180 euros for students). Check the websites for details on how to apply.

Thank you for disseminating this message to colleagues and students who may not have received it. Apologies for cross postings

Olivier Gimenez (olivier.gimenez@cefe.cnrs.fr <<mailto:olivier.gimenez@cefe.cnrs.fr>>)
and Kostas Theodorou (ktheo@aegean.gr <<mailto:ktheo@aegean.gr>>) Workshop organizers
ktheo@aegean.gr

Paris DNASampling Mar15-16

Dear Evoldir members,

The programme of the international conference DNA SAMPLING STRATEGIES & DESIGN (Paris, 15-16

March 2007) is finally available. Registrations are now OPEN. We very much look forward to see you in Paris !!!

Franz Manni and Evelyne Heyer (convenors)

Conference website: http://www.mnhn.fr/mnhn/ecoanthropologie/DNAsampling_2007/ Speakers are (in order of appearance): Marc FELDMAN (University of Stanford - USA), Brigitte PAKENDORF (Max Planck Institute - Germany), J. Stephen LANSING (University of Arizona USA), Karla SANDOVAL (University Pompeu Fabra Spain), Vincent DUBUT (CNRS France), Ivan NASIDZE (Max Planck Institute - Germany), Hafid LAAYOUNI (University Pompeu Fabra Spain), Chris TYLER-SMITH (Sanger Centre UK), Ville PIMENOFF (University of Helsinki Finland), Rasmus NIELSEN (Cornell University USA), M. ASHRAFIAN-BONAB (University of Cambridge UK), Pablo MATEOS (University College London UK), Alessio BOATTINI (University of Bologna Italy), Manfred KAISER (University Medical Centre Rotterdam - the Netherlands), Pierre ZALLOUA (American University of Beirut Lebanon), Benjamin BRAUDE (Boston College USA), Olivier FRANCOIS (University of Grenoble France), Stuart BAIRD (Montpellier, FRANCE), Murray COX (University of Arizona USA), Noah ROSENBERG (University of Michigan USA), Christina SAMPOGNA (OCDE France).

Dr. Franz Manni Maître de conférences / Lecturer UMR 5145 - Eco-Anthropology Group National Museum of Natural History MNHN - Musée de l'Homme 17, Place du Trocadéro 75016 Paris - France Tel. 0033 1 44 05 72 84 Fax. 0033 1 44 05 72 41 Telex Musethno

Franz Manni <manni@mnhn.fr>

Philadelphia Drosophila Mar9 12Genomes

Dear Drosophila Researcher,

For those of you attending the 47th Annual Drosophila Research Conference in Philadelphia, we want to call your attention to a workshop entitled "A Dozen Fly Genomes: What Have We Learned and What's Next?", which will take place on Friday, March 9, from 1:45pm-3:45pm. The goal of this workshop is to reflect on what we have learned thus far as a way of determining future genome scale resource needs to advance our understanding of genome organization and evolution in

the genus *Drosophila*.

For example, some of the resource questions we will ask are:

”What are our needs in terms of:

- Assembly improvements/fixes on the dozen flies?
- Sequencing multiple strains of a single species?
- Sequencing additional species?
- Expression resources such as transcriptome and genome tiling arrays, SAGE, proteomics surveys, comparative in situ studies.
- Forward and reverse genetic tools;

We encourage you to contact us if you are interested in making a short presentation or if there are specific topics that you would like to see discussed. We hope that much of the time of this workshop will be reserved for an open forum amongst the participants.

For those of you who will be unable to attend, we would be pleased to hear your thoughts about discussion topics as well as future resource needs.

We look forward to seeing you in Philadelphia.

Sincerely,

Bill Gelbart (gelbart@morgan.harvard.edu)

Thom Kaufman (kaufman@indiana.edu)

Workshop Co-Organizers

FlyBase Project Members
<FlybaseP@rail.bio.indiana.edu>

Sydney AustralasianEvolSoc Jun12-15

Call for Registration and Papers

The next meeting of the Australasian Evolution Society will be held at the University of New South Wales in Sydney from the evening of Tuesday 12 June to the night of Friday 15 June 2007.

<http://aes.eriophora.com.au/events/-2ndannouncement.htm> Our plenary speakers will be: Lindell Bromham (Australian National University) Scott V. Edwards (Harvard University) Paul B. Rainey (The University of Auckland) Michael Ruse

(Florida State University)

ACCOMMODATION UNSW is situated in the eastern suburbs of Sydney, near to Coogee, Clovelly and Maroubra beaches. We have compiled a list of [local](http://aes.eriophora.com.au/events/-accommodation.htm) hotels and their contact details as a starting point for delegates wishing to book accommodation. There are many excellent restaurants in nearby Randwick, Coogee and Kensington.

COST We have made every effort to keep the costs of the conference low to ensure accessibility for students and early-career researchers. To ensure that everyone has a chance to attend the major social events, the cost includes registration, morning teas, the welcome reception at the Royal Hotel on Tuesday and the Conference Dinner on Friday night. There are many excellent local restaurants and watering holes for the other nights.

Early-bird registration (until April 30) = AUD 230 for paid-up members, AUD 270 for non-members, AUD 140 for student members, AUD160 for student non-members . After 30 April these prices rise to AUD 290/ 330 / 180 / 200

The conference immediately precedes “<http://www.evolution2007.com/>Evolution 2007”, the joint annual meeting of the <http://www.evolutionsociety.org/>Society for the Study of Evolution (SSE), the <http://systbiol.org/>Society of Systematic Biologists (SSB), and the <http://www.amnat.org/>American Society of Naturalists (ASN). These meetings are being held in Christchurch, New Zealand from 16-20 June 2007. Several major airlines fly daily from Sydney to Christchurch directly or via connections in Auckland.

<http://aes.eriophora.com.au/events/-2ndannouncement.htm> – Dr Alistair G. B. Poore Secretary, Australasian Evolution Society School of Biological, Earth and Environmental Sciences University of New South Wales Sydney, 2052 Australia

Phone: 61 2 9385 2154 Fax: 61 2 9385 1558 E-mail: a.poore@unsw.edu.au Web: www.bees.unsw.edu.au/school/staff/poore/poorealistair.html CRICOS Provider Code: 00098G

School of Biological, Earth and Environmental Sciences The University of New South Wales Kensington, Sydney 2052 NSW, Australia PH: +61-2-9385-2587 FAX: +61-2-9385-1558 <http://www.bees.unsw.edu.au/school/staff/brooks/brooksrob.html> Australasian Evolution Society: <http://www.evolutionau.org>

Toronto CanSocEcolEvol May17-20

Meeting reminder: The deadline for registration at a reduced fee for the 2007 CSEE meeting in Toronto is next week (March 1). If you plan to attend, please register at: <http://www.eeb.utoronto.ca/CSEE/> Logo contest: Students and post-doctoral fellows can win a \$500 research prize that can be used to attend the meetings (deadline March 1). See <http://www.ecoevo.ca/en/findlogo.htm> Membership renewal: If you haven't already done so, please renew your membership at <http://www.ecoevo.ca/en/index.htm> (or you can renew when you pay for the meeting).

Many thanks, Sally Otto (Secretary, CSEE)

Rappel: la date limite pour obtenir le tarif réduit pour l'inscription à conférence de la SCEE est le 1 mars. Si vous souhaitez assister à la conférence, veuillez SVP vous inscrire à <http://www.eeb.utoronto.ca/CSEE/fr/index.htm>. Concours de logo: Les étudiants et les stagiaires postdoctoraux peuvent gagner une bourse de recherche d'une valeur de 500\$, qui peut être utilisée pour défrayer les frais de voyage pour assister à la conférence (date limite : 1 mars). Consultez: <http://www.ecoevo.ca/fr/trouvezlogo.htm>. Renouvellement de votre l'adhésion: Si vous ne l'avez pas encore fait, veuillez renouveler votre adhésion à <http://www.ecoevo.ca/fr/index.htm> (ou bien faites votre renouvellement au moment de vous inscrire à la conférence).

Merci beaucoup, Sally Otto (Secrétaire, SCEE)

"Sarah P. Otto" <otto@zoology.ubc.ca>

TrentoItaly Biology Oct2-5

?BIOLOGY WITHOUT BORDERS? 2-5 October 2007, CoSbi, Trento, ITALY <http://www.cosbi.eu/events/bwb07.php> As we try to increase our understanding of biology, the focus of research is shifting from parts to systems. This shift brings with itself a blending of tools, scientific fields, expertise, and people in order to properly address the new challenges that arise.

?Biology without Borders? recognizes such shift and

aims to embrace it with a unique open format. Its focus will be theoretical and experimental approaches which are allowing a more complete and system level understanding of biology and which recognize the importance of evolution for achieving such understanding. Expected attendees are scientists with such a research agenda, irrespective of the tools they use or their background. The scientific exchange in this highly interdisciplinary setting will be catalyzed by the following invited speakers:

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 Michael Elowitz*, Cal. Inst. of Technology Andreas Wagner*, Uni. Zurich *to be confirmed.

A blend of conference and workshop, ?Biology without Borders? is intended to provide the right stage to interact and discuss. Organized by the Microsoft Research ? University of Trento Centre for Computational and Systems Biology (CoSbi), the meeting found the perfect setting for such stage in the beautiful medieval town of Trento, Italy. Over two full and two half days, participants will attend 30 talks in 6 sessions. Afternoons will be open, featuring small walks in and around Trento to refresh the mind. To enhance the quality of discussion and interaction, attendance will be limited to 60, including selected and invited speakers.

Interested participants should apply with the abstract of the intended presentation or a short description of research interests. Deadline for applications is 31 May 2007. Conference details and application forms can be found online at: <http://www.cosbi.eu/events/-bwb07.php> – 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>

UGuelph AppliedEvolution May15-16 2

Please note the updated list of confirmed keynote speakers. Also, the conference registration page should

become available in the next few weeks.

Announcing 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) Michael Lynch (Indiana University) David Mindell (University of Michigan) Patricia Schulte (University of British Columbia) Ruth Shaw (University of Minnesota) John Willis (Duke University)

For information, go to

<<https://webmail.uoguelph.ca/services/go.php?url=http://www.ecologycolloquia.uoguelph.ca/main.shtml>>

or e-mail the organizers (Brian Husband and Chris Caruso) at <<https://webmail.uoguelph.ca/mail//mail/compose.php?to=pycolloq%40uoguelph.ca&thismailbox=INBOX.sent-mail>> 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

UGuelph InvasiveSpecies Mar12-16

Workshop postponed until further notice

.....

“Managing the effects of the spatiotemporal spread of harmful species in ecosystems: The Integration of Theoretical and Empirical Approaches”

March 12-16, 2007 University of Guelph Arboretum

Workshop details:

As part of the Environmental Science Research Initiative funded by the Faculty of Environmental Science, a weeklong interdisciplinary workshop will present current progress in theoretical and empirical-based ap-

proaches aimed at determining, predicting, and managing the effects of the spatiotemporal spread of potentially harmful species in ecosystems that have become susceptible to invasion because of external stresses (hereafter, at-risk ecosystems). The appeal of the broad scope of the workshop theme is evident by the wide range of research that will be presented during the workshop. A group of esteemed scientists led by keynote speaker Dr. Mark Lewis, from the University of Alberta, Dr. Marie-Josée Fortin, from the University of Toronto, Dr. Frédéric Guichard, from McGill University, and Dr. Brian Maurer, from Michigan State University, will present research based within the framework of the workshop theme. In addition, a number of scientists from a wide-range of disciplines will attend and give seminars throughout the weeklong workshop, which will add insight into strengthening previous theoretical and empirical work aimed at managing at-risk ecosystems.

Workshop goals:

To provide a forum that generates collaborations among on-campus and off-campus scientists from the life sciences, physical sciences, and social sciences interested in determining, predicting, and managing the effects of the spatiotemporal spread of potentially harmful species in at-risk ecosystems

To use current and future research presented at the workshop to develop sound management strategies aimed at protecting at-risk ecosystems whose conservation may impact the economic needs of societies

To use the workshop as a springboard for future development of theoretical and empirical research projects in Canada and abroad

To provide an environment where students at the University of Guelph, and students from surrounding universities are exposed to scientific research that they would not normally encounter in their coursework.

Call for contributed talks:

For those of you who wish to contribute a talk during the workshop proceedings, please specify a date and time based on the tentative agenda outlined in the workshop advertisement (time slots contributed talks). Instructions for those interested in contributing a talk can be found on the pre-registration form (a link to the form is embedded within the workshop description pdf).

For more information contact Michael Golinski (golinski@uoguelph.ca)

Dr. Michael Golinski Postdoctoral Fellow Departments of Mathematics & Statistics and Environmental Bi-

ology 50 Stone Road East Room 437 MacNaughton Building University of Guelph Guelph ON Canada N1G 2W1 Tel: 519-824-4120 ext 53836 Fax: 519-837-0221 Email: golinski@uoguelph.ca

UZurich
OriginEvolMediterraneanBiota
Jul14-15

Dear Colleagues,

Please, find below and attached the first circular of an upcoming conference at the University of Zurich. I would be grateful if you could circulate it broadly among your colleagues and students.

Thank you.

Elena Conti

International Conference Announcement:

'Origin And Evolution Of Biota In Mediterranean Climate Zones: An Integrative Vision'

Webpage for registration and additional information <http://www.systbot.unizh.ch/mediterranean/-index.htm> July 14-15, 2007, University of Zurich, Switzerland

Conference language: English

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.

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 Plate: 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"

Feliner, Gonzalo Nieto - Royal Botanic Garden, Madrid, Spain Case studies, Microevolutionary patterns: "Species distribution modeling matches phylogeographic patterns in the Atlantic-Mediterranean disjunct *Armeria pungens*"

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

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"

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"

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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>

UnivCentralFlorida SEEC Mar16-18 RegistrationExtended

REGISTER FOR SEEC! Deadline extended

The 4th annual Southeastern Ecology and Evolution Conference will be hosted by the University of Central Florida, Orlando from 16-18 March 2007. All graduate students, undergrads, and post-docs are cordially invited and encouraged to participate in talks and poster presentations. Sessions include but are not limited to topics in community, ecosystem, population and behavioral ecology; evolution: phylogenetics and behavior; conservation: genetics, biodiversity and climate change. For more information and to register visit us at <http://biology.ucf.edu/seec/>. Early registration and abstract deadlines were February 16, but we have extended registration to Feb. 22.

All attendees will receive a conference t-shirt and green bag (shopping tote with conference logo), as well as a full buffet dinner, continental breakfasts and snacks. We will also be giving out awards for the best posters and talks.

BGSA Officer SEEC Co-Coordinator Email: seec2007@mail.ucf.edu Website: biology.ucf.edu/seec
SEEC 2007 <SEEC2007@mail.ucf.edu>

Vienna EuropeanDrosophila Sep12-14

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

<http://www.imp.ac.at/EDRC2007/> Please note that this EDRC has a strong focus on Evolution and Population Genetics

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

YorkU EGLME 2007 May5 2

Eastern Great Lakes Molecular Evolution XI
ANNOUNCEMENT AND CALL FOR ABSTRACTS
Saturday, May 5, 2007 York University, Toronto, Ontario

The 2007 Eastern Great Lakes Molecular Evolution Meeting will be held on Saturday, May 5, 2007, at York University in Toronto. Registration, coffee, and poster setup will begin at 8:30 A.M. and the talks will end around 5 PM. Posters will be displayed all day, with a mid-day poster session set aside. The following is a tentative list of invited speakers:

Chip Aquadro (Cornell) Patricia Wittkopp (Michigan)
Asher Cutter (Toronto) Ben Evans (McMaster)

Further information, including information about traveling to Toronto and maps of the York campus, is available at <http://www.barnard.edu/biology/-eglme.html>. If you wish to register, please follow the directions below.

In addition to the invited speakers, there will be shorter contributed talks that will be selected from submitted abstracts, and will be of 12 - 15 minutes duration. Selections will be made by the organizing committee based on the submitted abstract, with an effort to have as many labs represented as possible. Abstracts must be submitted by March 9, 2007. Individuals submitting abstracts will be informed by March 30, 2007

as to whether they have been selected to give a talk. Those not chosen for talks will be strongly encouraged to present a poster on their work.

Please feel free to duplicate and distribute copies of this notice to anyone who might be interested in attending the meeting, particularly students and faculty who are new to these meetings or to the field of molecular evolution. A schedule will be posted at <http://www.barnard.edu/biology/-eglme.html> when it becomes available and will also be distributed by email no later than April 6, 2007 to all those who pre-register.

To register, submit an abstract, or if you have any questions, please contact:

Stephen Wright Department of Biololgy York University e-mail: [stephenw \(at\) yorku.ca](mailto:stephenw@yorku.ca) phone: 416- 736-2100 ext 20213

or

Brian Morton Department of Biological Sciences Barnard College, Columbia University e-mail: [bmorton \(at\) barnard.edu](mailto:bmorton@barnard.edu) phone: 212-854-5454

Format:

Registration: Please provide your name, institution, mailing address, email address and telephone number (please remember that this information will be made available to other registrants).

Abstract: Along with the information requested of registrants, please submit a Title and an Abstract of 250 words or less, along with the name of the lab PI to help us maintain an equitable distribution amongst labs.

Organizing Committee: Stephen Wright, Brian Morton bmorton@barnard.edu

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Adelaide Australia 2 AncientDNA

Two PhD opportunities currently exist at the Australian Centre for Ancient DNA, in Adelaide, Australia: Research in permafrost areas of northern Canada, and the 'hobbit' site of Liang Bua, Flores.

Ancient DNA studies of permafrost-preserved ecosystems across a complete glacial cycle.

The Yukon Territory (northwestern Canada) preserves a unique frozen record of plants, animals and microbes dating from more than 130 kyr to the modern day. This time span covers the last glacial cycle from the Last Interglacial warm period 130 kyr, through to the last glacial maximum around 20kyr, and onto the Holocene. The frozen biotic remains record the migrations, extinctions and evolution of various organisms during this period in the arctic refugium of Beringia, and allow a detailed real-time investigation of ecosystem responses to climate change. Ancient DNA will be used to record the changes in genetic diversity, heterozygosity and speciation events that have taken place as a result of these events, allowing many evolutionary models and processes to be examined. The research will concentrate on plant records, including the large numbers of frozen seeds, fruits and leaves (plant macrofossils) recovered from sub-fossil ground squirrel burrows throughout the area. Other exceptional remains recovered from frozen contexts include buried, in situ sub-fossil vegetation, mammalian coprolites (faeces) and paleosols. The project will be performed with leading Quaternary scientists from Canada (Dr G. Zazula and Prof. D. Froese) and members of ACAD, and will involve fieldwork in remote areas, and challenging laboratory work. This research will be integrated with ongoing Quaternary geological and multi-proxy paleoenvironmental research in the region. This project is available to international graduate students with strong research and/or publication records.

Contact: Prof. Alan Cooper, Australian Centre for Ancient DNA; alan.cooper-at-Adelaide.edu.au www.adelaide.edu.au/acad Dr. Grant Zazula, Yukon Paleontology Program; grant.zazula-at-gov.yk.ca www.yukonheritage.com Genetic analyses of the paleoecology of the Homo floresiensis site of Liang Bua, Flores

The cave site of Liang Bua, western Flores records the only known specimens of Homo floresiensis, informally known as 'hobbits'. This project will use ancient DNA to examine the paleoecology of the site through plant and animal DNA preserved in sediments (cave, terrace and lake), skeletal remains, on stone tools, and in other records such as speleothems. The ancient DNA records offer a new approach to studying the diversity and composition of local Flores plant communities through time and, hence, the prevailing climatic and environmental conditions. These will be directly compared to established rainfall records inferred from stable isotope analysis of speleothems, and used to reconstruct the climates and environments of western Flores. These reconstructions will identify periods of extreme or abrupt environmental change or major environmental turning points, such as rainforest expansion and contraction and changes in floral composition and diversity, which may have influenced the course of faunal (and human) evolution, dispersals and extinctions. The project is part of a largescale Quaternary dating and landscape evolution analysis performed by Dr Kira Westaway and Prof. Mike Morwood at the University of Wollongong, in collaboration with archaeological investigations performed by Indonesian archaeologists from ARKENAS, Jakarta. The ancient DNA research will involve both fieldwork at the site, and challenging laboratory research at ACAD. This project is available to international graduate students with strong research and/or publication records.

Contact: Prof. Alan Cooper, Australian Centre for Ancient DNA; alan.cooper@Adelaide.edu.au www.adelaide.edu.au/acad Dr Kira Westaway, University of Wollongong; kira@uow.edu.au www.uow.edu.au/science/eesc/student/Postgr/-

westa/profile.html –

Prof. Alan Cooper, Federation Fellow

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

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

<http://www.ees.adelaide.edu.au/acad/>
alan.cooper@adelaide.edu.au

CarletonU EvolTheoryEvolSex

Graduate Position in evolutionary theory & evolution
of sex at Carleton University

Root Gorelick is seeking new graduate students (PhD
and MSc) to develop evolutionary theory. My primary
focus is on the evolutionary origin and maintenance of
eukaryotic sex. I also work on other areas of evolution-
ary theory, such as quantifying and explaining patterns
of biodiversity (details at www.carleton.ca/~rgorelic).
It would be desirable, but not necessary, for prospective
graduate students to have some knowledge of popula-
tion genetics, epigenetics, mathematics, computer al-
gorithm development, phylogenetic comparative meth-
ods, or a wide variety of organisms. If interested, please
electronically send me an initial inquiry, including re-
search interests (Root_Gorelick@carleton.ca). More in-
formation about the graduate program can be obtained
from the Ottawa-Carleton Institute of Biology website
(www.carleton.ca/biology/ocib/)

Root Gorelick, PhD Assistant Professor Department of
Biology Carleton University 1125 Colonel By Drive Ot-
tawa, Ontario K1S 5B6 Canada

Voice 613-520-2600 ext. 1586 URL
www.carleton.ca/~rgorelic <<http://www.carleton.ca/~rgorelic>>
E-mail Root_Gorelick@carleton.ca

Root_Gorelick@carleton.ca

ETH Zurich PlantSexChromEvol

ETH Zurich, Switzerland Institute of Integrative Bio-
logy (IBZ)

PhD position in Plant Sex Chromosome Evolution

A three year PhD position is available in the Plant Eco-
logical Genetics group at ETH Zurich to work on the
evolution of a plant sex chromosome. The project will
focus on the X chromosome in the dioecious white cam-
pion, *Silene latifolia*. The aim of the project is to map
new genes on the *S. latifolia* sex chromosomes and to in-
vestigate gene traffic between the sex chromosomes and
autosomes. Our group is using *Silene* as a model system
for ecological genetics. Current research topics include
hybridisation and introgression, habitat adaptation, re-
productive isolation and speciation, and genome evolu-
tion.

I seek a highly motivated candidate with a strong in-
terest in sex chromosome evolution. Experience with
molecular techniques and methods for analyzing DNA
sequences in the context of molecular evolution are re-
quired. Candidates must have completed their Master's
degree or equivalent (Diplom) in a relevant field and be
fluent in English.

Our group offers a supportive and stimulating environ-
ment, a state-of-the-art molecular lab, as well as climate
chambers, greenhouses and common garden facilities.

Zurich is an international city of about 350,000 people
in the heart of Europe and has been recently rated as
the city with the highest quality of life in Europe. Ex-
cellent public transportation exists within the city, to
the nearby mountains, and to the rest of Europe.

The position can start as early as March 2007, however,
later starting dates can be negotiated. To apply, please
send to the address given below: 1) a letter describing
your research motivation and experience 2) a CV in-
cluding publication list, and 3) full contact details of
two persons who are willing to write a letter of rec-
ommendation. Applications by email are encouraged.
Application deadline is 9 March 2007.

Further information and address for applica-
tion: Prof. Dr. Alex Widmer ETH Zurich
Plant Ecological Genetics Institute of Integra-
tive Biology (IBZ) 8092 Zurich, Switzerland e-
mail: alex.widmer@env.ethz.ch www.peg.ethz.ch
alex.widmer@env.ethz.ch alex.widmer@env.ethz.ch

Groningen GreatTitDemography

The Research Group Animal Ecology of the research
institute Centre for Ecological and Evolutionary Stud-

ies (CEES), Groningen, has a vacancy for a full-time PhD position:

PhD Project title: Influence of sex-specific competition and density on demography in the great tit

We are looking for a PhD student to study how competition explains the distribution, survival and reproductive rates in great tits. The PhD position is part of a unique large-scale project where we manipulate different aspects of competition (fledgling density and fledgling sex ratio) to study fitness consequences of competition and avian sex allocation.

Parents should invest equally in the two offspring sexes and hence adjust the sex ratio of their offspring to both the fitness costs and benefits of producing them. In this project we started to measure whether fitness benefits of producing a particular sex ratio dependent on the sex ratio in the population and whether parents adjust their reproductive decision to that. Two current projects (to be continued for one year) focus on the experimental effects of 1) fledgling density on the costs and benefits of brood size and 2) fledgling sex ratio on the fitness of the sexes.

We find promising results in the first experimental years: some plots have consistent low or high natural breeding densities, and reproductive investment and sex ratio are correlated with this breeding density. So far, experimental changes in fledging sex ratio did not affect reproductive investment and sex allocation decisions of the parents. Sex-specific and density dependent dispersal neutralized the effect of our experimental sex ratio skew and density manipulation in the next breeding season. Therefore, the aim of the new projects is to experimentally alter sex specific competition and density just before breeding by selective removal of breeders.

The questions are:

- 1) Do breeders adjust sex ratio of their offspring to skewed breeder sex ratio?
- 2) Do breeders adjust clutch size of their offspring to manipulated breeder density?
- 3) Are these changes adaptive?
- 4) How is settlement of the new generation affected by (sex specific) breeder removal?

To judge how optimal brood size and sex ratio depend on breeder density we will manipulate offspring brood size and sex ratio. The work of the PhD will concentrate on the offspring side (starting manipulations in 2008) while the joint project will concentrate on parental decisions (starting manipulation in spring 2009). We offer a stimulating working atmosphere, with ample opportunity for discussion and with top-quality

science.

Requirements

Candidates must have a degree in biology, with specialisation in ecology, and a driver's license. We are looking for an enthusiast researcher with ample experience in field research on birds. Theoretical interest in evolutionary ecological research is a prerequisite; knowledge of database management in Access is an advantage.

Conditions

The University of Groningen offers an appointment for a period of four years that should be completed with the defence of a PhD-dissertation. During the first year the stipend is ??? 1905,- for a Dutch student and ??? 1422,- per month for a foreign student (stipend lower than that for a Dutch student because of tax exemption) and will be adjusted to general price movements once a year. After one year, the performance of the candidate will be evaluated to decide whether there is sufficient progress to expect a successful completion of the PhD thesis within the remaining three years. A training programme is part of the agreement. You and your supervisor will make up a plan for the additional education and supervising that you specifically need.

Background

This PhD project is part of a large research grant on Sex-specific reproductive tactics: fitness consequences of avian sex allocation and dispersal strategies granted to Prof. dr. ir. J. Komdeur by the Dutch Organisation of Scientific research. The research will take place in the ???Animal Ecology??? research group. You will be supervised by Prof. dr. J.M. Tinbergen and Prof. dr. ir. J. Komdeur. The group participates in the Centre for Ecological and Evolutionary Studies (CEES) and the Graduate School Functional Ecology.

Information

Information about the position can be obtained from Prof. dr. Joost M. Tinbergen (phone ++31)-50-3632065 or -3632040), J.M.Tinbergen@rug.nl <mailto:J.M.Tinbergen@biol.rug.nl> and Prof. dr. ir. Jan Komdeur (phone ++31)-50-3632056), J.Komdeur@rug.nl

Additional information

On the project and research group Animal Ecology:

<http://www.rug.nl/biologie/animalecol>

On CEES <http://www.rug.nl/cees>

On the Faculty of Mathematics and Natural Sciences <http://www.rug.nl/fwn>

Applications



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To read the entire message look it up at <http://life.biology.mcmaster.ca/~brian/evoldir.html>

IdahoStateU WoodratHybrids

PhD GRADUATE RESEARCH ASSISTANTSHIPS

Two Ph.D. Graduate Research Assistantships are available to study the ecological, behavioral and genetic dynamics of contact zones between two species of woodrats in California. Successful applicants will play a large role in the design of several projects that will integrate data from intensive fieldwork focused on small mammal trapping and resource use, laboratory behavioral trials and molecular genetic analyses. Candidates will also have an opportunity to help develop and deliver a series of molecular genetic lab activities for local high school students. Candidates should be creative and highly motivated with strong writing and communication skills. Candidates must have a B.S. and preferably an M.S. in biology, or a closely related discipline, field experience, ability to work under rigorous field conditions and interest in evolutionary ecology, genetics, and science education.

Positions are available August 2007 and funded for 5 years. Review of applications will begin February 12 and continue until the positions are filled. Submit (preferably by email) a letter of interest that includes a description of work experience and career goals including both research and education, curriculum vitae, copies of transcripts, GRE scores, and the names and contact information (phone and e-mail address) of 3 academic references to:

Marjorie Matocq, PhD Assistant Professor Director, Molecular Research Core Facility Department of Biological Sciences Idaho State University Campus Box 8007 Pocatello, Idaho 83209 Tel: 208-282-3914 FAX: 208-282-4570 <http://www.isu.edu/bios/MatocqLab/Marjorie1.shtml> matomarj@isu.edu matomarj@isu.edu

ImperialCollegeLondon EvolOfAmphibianDisease

NERC 3 1/2 year Studentship available from October 2007

Supervisor: Dr Matthew Fisher and Dr Nick Grassly, Dpt. Infectious Disease Epidemiology, Faculty of Medicine, Imperial College London, UK. W2 1PG

Modelling the environmental and ecological drivers of disease emergence in amphibian chytridiomycosis.

Amphibian chytridiomycosis, caused by the fungus *Batrachochytrium dendrobatidis* (Bd), is now known to be one of the most potent threats to biodiversity yet discovered. This project will work with a NERC-funded team at Imperial College and the Zoological Society of London to analyse the dynamics of disease transmission within Europe by developing epidemiological models of the chytrid and its amphibian hosts.

The disease dynamics that we observe from our models will allow us to determine the likely effect of different biotic and abiotic reservoirs, the influence of individual-level heterogeneity in transmission and the likelihood of survival of different host species with differing susceptibility and life history. While these models will be developed to describe single-site situations, we will subsequently investigate whether there are any spatial components to the disease dynamics by establishing sub-population connectivities between sites and utilising metapopulation models.

The student will further refine statistical models that we are developing in order to determine factors that are associated with prevalence of infection and mortality across several spatial scales. Ecological regression models will be used to derive predictions of geographic sites that are most at risk of disease emergence due to the presence of a Bd - favourable ecology. Environmental forcing of Bd transmission dynamics will then be incorporated into our mathematical models to examine the impact on patterns of mortality across the amphibian communities in different locations. Ultimately, we will use existing climate models for Europe to assess the likely implications of future trends of climate-change on the evolutionary dynamics of infection within areas where our surveillance has identified endemic infection.

All students will belong to the Graduate School of Life Sciences and Medicine which provides a full programme

of training in research and transferable skills. Students will be based in the Department of Infectious Disease in the Division of Epidemiology, Public Health and Primary Care. Further details of the Department can be found at <http://www1.imperial.ac.uk/-medicine/about/divisions/ephpc/ide/>

Applicants should send two hard copies of a full CV, including two original references, and a letter stating why you wish to pursue postgraduate study in the Dpt. of Infectious Disease Epidemiology to Matthew Fisher, Dpt Infectious Disease Epidemiology, Imperial College London, Norfolk Place, London, W2 1PG. Email: matthew.fisher@imperial.ac.uk. Unfortunately, this application is only open to UK applicants.

Please note that candidates must fulfil College admissions criteria. For an informal discussion please contact Dr Matthew Fisher, tel: +44 (0) 207 594 3787, email: matthew.fisher@imperial.ac.uk.

Closing Date: 1st April 2007

matthew.fisher@imperial.ac.uk

matthew.fisher@imperial.ac.uk

ImperialCollegeLondon HumanFungalEvol

BBSRC 4-year Studentship (1 year MSc + 3 years PhD stipend) available from October 2007

Supervisor: Dr Matthew Fisher, Dpt. Infectious Disease Epidemiology, Faculty of Medicine, Imperial College London, UK. W2 1PG

The molecular epidemiology and evolution of emerging human pathogenic fungi

Cryptococcus neoformans var. *grubii* causes a common and often fatal infection in AIDS patients, despite antifungal therapy. In northeast Thailand, cryptococcal disease is second only to tuberculosis as an AIDS-defining illness, while in many areas of Sub-Saharan Africa *C. neoformans* is now the commonest cause of adult meningitis. Heterogeneity occurs in the response of patients to infection by *C. neoformans* and recent studies have shown that the genotype of the infecting strain is predictive of its virulence. The key goal of this project is to apply a newly developed genetic tool to analyse the molecular epidemiology and evolution of natural populations of *C. neoformans*, Multilocus Sequence typing (MLST). We will use this tool to

perform an in-depth analysis of *C. neoformans* strains that cause disease within AIDS patients in southeast Asia and Africa. This analysis will have four aims: (1) we will statistically test whether there is an association between Sequence Type (ST) and disease progression/outcome in patients suffering from AIDS; (2) we will assess the relative frequencies of STs between clinical and environmental strains in order to identify stains that are differentially associated with infection, and are therefore candidate isolates with high virulence; (3) we will use quantitative genetics to test whether ST is correlated with clinically-relevant phenotypes in the laboratory, by measuring natural variation in genetically determined traits using morphometric and microarray analyses and (4) we will investigate whether there is an association between ST and virulence using cell-culture and mouse models. Identifying the genetic basis of virulence in *Cryptococcus* will allow us to better describe host-level infection parameters, thus enabling us to develop a predictive biology for human cryptococcal infection. Further, the development of MLST as a tool will allow us to ascertain whether there is variation between geographical regions in the severity of infection, to what extent genotype accounts for regional variation, and what evolutionary mechanisms are likely to be governing virulence in this widespread and important pathogen.

All students will belong to the Graduate School of Life Sciences and Medicine which provides a full programme of training in research and transferable skills. Students will be based in the Department of Infectious Disease in the Division of Epidemiology, Public Health and Primary Care. Fieldwork will be in South Africa and Zambia. Further details of the Department can be found at <http://www1.imperial.ac.uk/-medicine/about/divisions/ephpc/ide/>

Applicants should send five hard copies of a full CV, including two original references, and a letter stating why you wish to pursue postgraduate study in the Dpt. of Infectious Disease Epidemiology to Nicky Henson, EPHPC, Imperial College London, Norfolk Place, London, W2 1PG. Email: n.henson@imperial.ac.uk. Please mark this application 'Emerging Human pathogenic Fungi'. This application is open to UK/EU applicants.

Please note that candidates must fulfil College admissions criteria. For an informal discussion please contact Dr Matthew Fisher, tel: +44 (0) 207 594 3787, email: matthew.fisher@imperial.ac.uk.

It is anticipated that the interviews will be held between 19th - 30th March 2007.

Closing Date: 14th March 2007

matthew.fisher@imperial.ac.uk
matthew.fisher@imperial.ac.uk

LavalU SalmonidConservGenetics

We are currently looking for a Ph.D. candidate starting in May 2007 that would be involved in our ongoing research program aiming at evaluating the evolutionary consequences of stocking practices in the salmonid *Salvelinus fontinalis* (Brook charr). The main objective is to evaluate the level of genetic contamination (introgressive hybridization) in wild populations by means of both molecular genetics, functional genomics (microarrays) and phenotypic analyses. These patterns of variation will be put in relation with the history of stocking and the heterogeneity of environmental variables that may potentially influence the impact of stocking. This research will lead to develop a unique method for documenting and predicting the biological and economical impacts of stocking salmonids. This multidisciplinary project is a collaboration between Louis Bernatchez (Universite Laval) and Dany Garant (Universite de Sherbrooke) and is funded by NSERC Canada.

We are primarily looking for a student with strong laboratory skills and expertise in DNA analyses, a solid background in population and conservation genetics, as well as experience in field work.

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

To learn more about Quebec city : <http://www.quebecweb.com/tourisme/quebec/villequebec/introang.html>
Laval University : <http://www.ulaval.ca/>
The Canadian Research Chair in Genomics and Conservation of Aquatic Resources : <http://www2.bio.ulaval.ca/louisbernatchez/>
Louis Bernatchez, Titulaire de la Chaire de recherche du Canada en Genomique et Conservation des Ressources Aquatiques Departement de biologie, Pavillon C-H Marchand Universite Laval, Québec, QC G1K 7P4 Canada Phone: 1 418 656-3402 E-mail : Couriel: Louis.Bernatchez@bio.ulaval.ca

Nous recherchons un(e) candidat(e) intéressé(e) A poursuivre un Ph. D. et pret a debuter des l'ete 2007. Le sujet de doctorat s'insere dans le cadre d'un projet multidisciplinaire finance par le CRSNG et realise en collaboration avec

Dany Garant (Universite de Sherbrooke) L'objectif general de ce projet est d'évaluer les consequences evolutives des pratiques d'ensemencements chez l'omble de fontaine (*Salvelinus fontinalis*). Plus specifiquement, le projet vise à évaluer le niveau de contamination genetique (hybridation introgressive) de populations d'omble de fontaine par la quantification de la variation genetique moléculaire, de niveau d'expression de genes (microarrays) et phenotypique. Cette variation sera mise en relation avec l'historique des ensemencements et l'heterogeneite de facteurs environnementaux pouvant en moduler l'impact.

Nous recherchons un(e) candidat(e) avec une excellente connaissance de la genetique des populations, et possedant a la fois une solide expertise pour le travail en laboratoire et sur le terrain.

Si le projet vous interesse, veuillez faire parvenir une courte lettre indiquant le pourquoi de votre interet, votre CV ainsi que le nom et adresse electronique de trois personnes susceptibles de fournir des references e votre sujet e l'adresse suivante:

Louis.Bernatchez@bio.ulaval.ca

Pour en connaitre plus sur Québec : <http://www.quebecweb.com/index.html>
L'Universite Laval : <http://www.ulaval.ca/>
La Chaire de Recherche du Canada en Genomique et Conservation des Ressources Aquatiques: <http://www2.bio.ulaval.ca/louisbernatchez/>
Louis Bernatchez, Titulaire de la Chaire de recherche du Canada en Genomique et Conservation des Ressources Aquatiques Departement de biologie, Pavillon C-H Marchand Université Laval, Quebec, QC G1K 7P4 Canada Phone: 1 418 656-3402 E-mail : Couriel: Louis.Bernatchez@bio.ulaval.ca Louis Bernatchez

Titulaire de la Chaire de recherche du Canada

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MississippiStateU PlantSystematics

Opportunities for Graduate Study Mississippi State University

Graduate student positions (M.S. or Ph.D.) in plant systematics, population genetics, or conservation biology are available in the lab of Dr. Lisa Wallace at Mississippi State University. Current projects include phylogenetic and population genetic studies in the orchid genus *Platanthera*, phylogenetic and phylogeographic patterns in the Hawaiian genus *Schiedea*, and conservation genetics of endemic plants from the California Channel Islands. Related expertise in the biological sciences department (<http://www.msstate.edu/dept/-biosciences/bio.html>) includes plant ecology, evolutionary biology, landscape ecology, and community ecology. Additional expertise in GIS technology through the GeoResources Institute, computational biology through the Center for Computational Sciences, proteomic and genomic applications through the Life Science and Biotechnology Institute, and biological microscopy through the Electron Microscopy Center is available across campus. Students should have an interest in one of the focal research areas and prior experience in molecular methods and/or field biology, and must meet the minimum eligibility requirements for acceptance into the graduate program. Accepted students will be supported on assistantships. For more information contact Dr. Lisa Wallace (LisaWallace@biology.msstate.edu).

LisaWallace@biology.msstate.edu

QueenMaryULondon Evolution of Bat echolocation

NERC funded PhD studentship, School of Biological & Chemical Sciences, Queen Mary, University of London. Three years starting Oct 2007. Deadline for applications - 30 March 2007. Funding is available to students from the UK ONLY.

'Genetic basis of bat echolocation'

Supervisor: Dr Stephen Rossiter

Echolocation in bats is a striking example of evolutionary innovation, yet the evolution and genetic basis of echolocation are poorly understood. Echolocation in bats has either evolved twice or has been lost by fruit bats. The main aim of this studentship will be to identify genes involved in echolocation and to screen bats with divergent sonar signals. Episodes of convergence provide a means of elucidating functional genetic changes associated with different modes of echolocation.

The student will receive training in a range of molecular genetics techniques including DNA and RNA isolation, PCR, RT-PCR and sequencing. A period of training will be spent in Dr Emma Teeling's lab in Dublin. The opportunity to undertake fieldwork in the tropics is also possible though not essential.

Applicants must hold or be expected to achieve at least a BSc 2i (or equivalent) in a relevant subject. A strong background in genetics and an interest in evolutionary processes are essential. Laboratory experience of genetic analysis and knowledge of bioinformatics approaches are desirable. Applicants should send a CV to s.j.rossiter@qmul.ac.uk, and include a covering letter explaining their motivation for the project and the names of two academic referees. Short-listed applicants will be interviewed.

Stephen Rossiter <s.j.rossiter@qmul.ac.uk>

RoslinInst Edinburgh GeneticDiversity

A Ph.D. studentship is available to study genetic diversity and conservation of livestock species at the Roslin Institute (Edinburgh) starting in September 2007.

Using a variety of computer-based statistical and population genetics approaches, the student will analyze existing genetic diversity data for both pigs and chickens to improve understanding of breed origins, relationships and structure and to guide future conservation decisions. Researchers at Roslin are currently taking advantage of advances in molecular techniques to generate large-scale genetic data from cattle, pigs, sheep and poultry. The ultimate aim is to exploit these data for a better understanding of the history of domestication and to characterize the diversity both within and between breeds to inform their future use. One specific issue that will be addressed in this project is the detection of introgression into breeds that will facilitate conservation of historical genomes. This project will look specifically at genetic diversity in a group of Chinese and European pig breeds and in British chicken breeds.

The student will be registered at the Institute of Evolutionary Biology, University of Edinburgh. He or she will be based at Roslin and will also spend time working at the Rare Breeds Survival Trust (RBST) in Warwickshire to become familiar with RBST objectives and to

disseminate the results of the research to the Trust. Interested candidates must be British citizens or residents, should hold a first or upper second class honours degree and have some familiarity with evolutionary biology, population/quantitative genetics or conservation biology.

For further information, contact Pam Wiener (pam.wiener@bbsrc.ac.uk) or see the full ad on the Roslin web site (<http://www.roslin.ac.uk/jobsStudentships/studentships/geneticDiversityConservationLivestockSpecies.php>).

Applications including a full CV with names and addresses (including email addresses) of two academic referees, indicating the project of interest, should be sent to: Human Resources, Roslin Institute (Edinburgh), Roslin, Midlothian, EH25 9PS (tel 0131 527 4481) by 1 March, 2007.

Pam.Wiener@bbsrc.ac.uk

UAmsterdam EvolEcol

PhD student in Evolutionary Ecology (f/m)

The department of Animal Ecology, Vrije Universiteit Amsterdam, The Netherlands has a PhD position available for the project:

“Parasitism and the evolutionary loss of lipogenesis”

In contrast to other organisms parasitoid wasps lack the ability to store excess energy in the form of lipid reserves. This project studies if this remarkable lack of lipogenesis is associated with the parasitic lifestyle of these insects and how they can avoid detrimental effects of their strategy. The two most important questions are what are the physiological and genetic mechanisms underlying lack of lipogenesis and how common is lack of lipogenesis in other parasitoid taxa. Experimental work will include sequence and expression analysis of candidate genes involved in lipid metabolism, physiological manipulation and phylogenetic analysis. The project may start very shortly.

Tasks -Executing scientific research as detailed in the project description. -Publication of results of the research in scientific journals as well as in a thesis. -Assisting in undergraduate courses given within the Institute of Ecological Science. -Following the PhD educational programme as prescribed by the institute. Required skills and education -MSc degree in Biology, preferably with advanced courses in animal ecol-

ogy, evolutionary biology, molecular biology, and animal physiology, or equivalent. -Proficiency in both written and spoken English. -Excellent social skills, ability to work independently and high motivation will be assets.

Details The appointment will initially be for 12 months. After a successful evaluation the contract will be prolonged with 36 months. The employment will have to result in a written thesis. Our fringe benefits of employment can be found at www.vu.nl/vacatures. Salary Gross monthly salary, based on experience, amounts to 1.933,- Euro during the first year up to 2.472,- Euro during the last year.

Information and applications Upon request, applicants can obtain the complete project description from Désirée Hoonhout (tel. +31 20 5987004; desiree.hoonhout@falw.vu.nl). Further information can be obtained from Prof. Dr. J. Ellers (tel. +31 20 5987076; jacintha.ellers@falw.vu.nl). Please, send your application with Vacancy number: 1.2007.00017, including your expression of interest (with a brief statement of your personal research aims and interests), a detailed resume, and two reference names before February 16th, 2007 addressed to Dr. J.M.R.M. Neutelings, managing director Faculty of Earth & Life Sciences, Vrije Universiteit. You may also send your application by e-mail at: falw-vacatures@falw.vu.nl.

jacintha.ellers@falw.vu.nl jacintha.ellers@falw.vu.nl

UBasel 2 HostParasite

University of Basel, Switzerland Institute of Zoology

PhD positions in host-parasite interactions and coevolution

2 PhD-positions in host-parasite interactions and coevolution are available in the group of Dieter Ebert in the division of Evolutionary Biology, Institute of Zoology at Basel University. I am looking for highly motivated candidates with interests in the fields of evolutionary biology, host-parasite interactions and microbiology. The two PhD projects are concerned with host-parasite interactions and coevolution. The research group covers the entire range from epidemiological and ecological aspects of host-parasite interactions, to studies on the population genetics and genomics of the antagonists. Work is carried out in the field and in the lab. The details of each PhD project will be worked

out with the candidates, to accommodate interests and strength. The positions are supported by the Swiss National Science Foundation and the University of Basel.

Starting date is negotiable (any time from March 2007 onwards). German is helpful in every day life, but the working language in the group is English. A Diploma or Master degree (or equivalent) in biology or related subject is necessary for admission.

Please send your application by email (all material in one file please) to Dieter Ebert. Applications should include a CV, a list of publications (if any) and a statement about research interests. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 30th March 2007 will be given full consideration.

Further information and address for application: Prof. Dr. Dieter Ebert, University of Basel, Institute of Zoology, 4051 Basel, Switzerland, Email: dieter.ebert@unibas.ch Tel. +41-(0)61-267 03 60, Fax +41-(0)61-267 03 61. Web: <http://evolution.unibas.ch>

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

dieter.ebert@unibas.ch dieter.ebert@unibas.ch

UBristol AdaptationToClimate

NERC PhD Studentship available from Oct 2007

Supervisor: Dr Jon Bridle Department of Biological Sciences, University of Bristol, BS8 1UD, UK

Tests for adaptation at expanding and contracting species' margins

At least 10% of all species are predicted to become committed to extinction this century due to climate change. However, these estimates assume that the ecological tolerances of species' will not evolve to accommodate some of this environmental change. This is because we lack the empirical data to predict how quickly, and under what conditions, populations can adapt when faced with rapid ecological change.

In Europe, recent climate change has generated range expansions in the north of butterfly species' distributions, and corresponding range contractions in the south. However, the ranges of some species have ei-

ther not contracted, or have involved shifts in habitat or behaviour associated with range expansion. These exceptions may reflect adaptation at the range edge, allowing populations to persist in previously unsuitable conditions.

This project will explore such cases in detail to test for recent evolution at range margins, and to provide insight into what conditions prevent or favour local adaptation in natural populations. It will also address the more general question of why all species are restricted in their distributions, given that adaptation at the range edge is possible in certain circumstances, even over short timescales. The studentship is likely to involve a combination of genetic and ecological analyses in the UK and/or southern Europe, and could focus on the Brown Argus butterfly *Aricia agestis* or the Comma, *Polygonia p-album*, for which extensive data are already available. Alternatively, a number of other butterfly species could also be feasible as model organisms.

Interested students should contact me (jon.bridle@ioz.ac.uk <<mailto:jon.bridle@ioz.ac.uk>>) in the first instance with a CV and details of two academic referees. They will then need to submit a formal application by March 15th 2007. Unfortunately, this studentship is only open to UK residents.

For detailed eligibility requirements see <<http://www.nerc.ac.uk/funding/available/postgrad/-eligibility.asp>> <http://www.nerc.ac.uk/funding/available/postgrad/eligibility.asp> <<http://www.nerc.ac.uk/funding/available/postgrad/-eligibility.asp>> For further information on Biological Sciences at Bristol, see <http://www.bio.bris.ac.uk/-admiss/pgrad/studentships.htm> <<http://www.bio.bris.ac.uk/admiss/pgrad/studentships.htm>>

Jon Bridle <Jon.Bridle@ioz.ac.uk>

UCambridge HorseEvol

PhD Studentship in The Archaeogenetics of Horse Domestication (UK/EU)

Dr Mim Bower, McDonald Institute for Archaeological Research, University of Cambridge Prof Chris Howe, Department of Biochemistry, University of Cambridge Dr Ellen Nisbet, Department of Biochemistry, University of Cambridge

We invite applications for a fully funded PhD studentship in archaeogenetics. The project detailed below is a candidate for a studentship, and applicants will be in open competition with others applying both for this project and other candidate projects within the Graduate School of Biological Sciences. In the event of a successful application, the project will be supervised jointly by Prof. Christopher Howe, Department of Biochemistry and Dr Mim Bower, McDonald Institute for Archaeological Research.

A good first degree in Biology, Genetics, Zoology or Archaeology (1st class or 2:1 or equivalent) is essential and a Masters degree in a relevant scientific or archaeological discipline will be an advantage. Experience in the standard range of molecular biology techniques is essential; experience with low-copy number methods (ancient DNA) is desirable, but not essential.

Applicants should send a CV and a covering letter detailing their suitability for the project and evidencing relevant experience, along with two academic references, to Dr Mim Bower, McDonald Institute for Archaeological Research, University of Cambridge, Downing Street, Cambridge, CB2 3ER or by email to: mab1004@cam.ac.uk.

Applicants must be UK or EU citizens.

Informal enquiries can be made to Dr Mim Bower at mab1004@cam.ac.uk

The closing date for applications is: Wednesday 7th March 2007 Shortlisted candidates will be invited for interview on Wednesday 21st March 2007.

The location and timing of the domestication of the horse is still a contentious question in archaeology. The direct evidence for the use of horses before the development of the chariot in the 2nd millennium BC, i.e., for riding, is scarce and few archaeologists agree on its interpretation, yet it is clear from the recurrent use of the horse in imagery and ritual that the horse has been of great importance to humans for a long time. But if archaeological evidence cannot be used to understand the human-horse relationship through time, how are we to investigate this question?

Archaeogenetics, the use of modern population genetics coupled with the analysis of ancient DNA from the archaeological specimens themselves has proved a highly useful tool for understanding the domestication of many of our other economically important plant and animal species (pigs, cattle, goats, chickens, maize, wheat, barely etc..). In the case of horses, a large amount of mitochondrial data from living horse populations is now available, but it is proving to be difficult to resolve a clear phylogeny with biogeographic structure

using this data. A more robust phylogeny will be possible if a number of informative nuclear loci are used. This project proposes to screen an extensive sample set of living horse populations from central and east Asia for nuclear markers (microsatellites and SNiPs) and develop methods for the analysis of these same nuclear markers from archaeological horse skeletons from across central and east Asia in order to resolve the biogeography of horse domestication.

The successful applicant would be part of a growing team working on the archaeogenetics of horse husbandry and adjunct to a new project on the spread of the chariot across central Asia. There will be opportunities for fieldwork, attending conferences and training both here at Cambridge, and also in collaborating labs. The studentship is BBSRC funded, covering both fees and subsistence, and for up to four years.

rern2@mole.bio.cam.ac.uk rern2@mole.bio.cam.ac.uk

UDusseldorf EvolSystemsBiol

The Bioinformatics Institute (Prof. Martin Lercher) of the Heinrich Heine University of Düsseldorf, Germany, invites applications for

2 Ph.D. studentships (EGr.13 TV-L 50%)

(fixed-term) to be filled as soon as possible.

Research area: Applied bioinformatics: evolutionary genomics and systems biology. Topics of interest include the evolution of biological networks (metabolism, protein interaction, regulation), and the function of non-coding RNA.

Qualifications: We invite applications from individuals with a PhD in biology, computer science, or physics/mathematics.

The Heinrich Heine University of Düsseldorf is an equal opportunity employer and is attempting to increase the percentage of women in research and teaching, and therefore explicitly invites applications by women. These will be given preference when qualifications are equal between candidates. Disabled candidates with the necessary qualifications are also strongly urged to apply for the position.

Applications, including CV and list of publications, should be sent (preferably via email) to the following address:

Lehrstuhl Bioinformatik, Prof. M. Lercher Heinrich-

Heine-Universität Düsseldorf Universitätsstr.1 40225
Düsseldorf, Germany lercher@cs.uni-duesseldorf.de

lercher@cs.uni-duesseldorf.de lercher@cs.uni-
duesseldorf.de

AUSTIN,JAMES D
austinj@ufl.edu

UFloridaGainesville FreshwaterMussels

A PhD graduate assistanceship is available to study the conservation genetics of native freshwater mussels of Florida and the SE United States in the laboratory of Jim Austin at the University of Florida, Gainesville. This position will begin in August 2007.

I am looking for an exceptional, self-motivated graduate student who is broadly interested in biogeography, evolutionary biology and the conservation of freshwater mollusks. This position will be part of a larger project to detail the diversity, status, and distribution of Unionidae in Florida. A large number of species endemic to the state and adjacent portions of southern Alabama and Georgia characterize the Florida Unionidae, although their taxonomic status and distributions are poorly known.

The successful applicant will be involved in phylogenetic and biogeographic analysis of selected species groups, and will be expected to develop an independent research project related to the conservation of freshwater mussels in Florida. Potential examples include: comparative mussel-host fish evolution, community level comparative genetics, developing models to predict the impacts of water use and climate change on mussel distributions.

Prerequisites for this position include a MS in biological sciences, with preference for students with experience with population/phylogenetic tools, and an interest in, and knowledge of, freshwater mussel biology. Additional skills with modeling, GIS, and field experience are desirable. Full support (12 month stipend, plus tuition) is available for three years, although students will be expected to be competitive for internal and external fellowships.

Interested students should contact me at austinj@ufl.edu to discuss their interests further. Please provide a statement of interest, CV, transcripts, at contact information for three faculty willing to write letters of reference. Visit <http://plaza.ufl.edu/austinj/> for more information on the Austin lab.

UGlasgow AvianSexRatio

NERC PhD Studentship, Division of Environmental and Evolutionary Biology, University of Glasgow (3 years, starting October 2007)

Sex ratio adjustment in birds

Supervisors: Dr Kathryn Arnold (DEEB) and Professor Neil Evans (Vet School)

Avian mothers seem to be able to adjust the sex ratio of their clutches, however, results from different populations of the same species have produced contradictory results. A vital missing step in the study of sex ratio adjustment is identifying an underlying physiological mechanism. This NERC-funded (British Natural Environment Research Council) studentship is concerned with why and how birds 'decide' to adjust the sex ratio of their offspring. The project will involve fieldwork on a nestbox population of blue tits *Parus caeruleus*, in Scotland as well as the development and use of biochemical and endocrinological assays. The student would be fully trained in field and lab techniques, and would benefit from the extensive transferable skills training offered by IBLS Grad School.

Eligibility: The PhD position is restricted to UK residents. EU nationals are eligible for full funding only if they have worked or studied in the UK for a period of 3 years or more prior to the studentship. EU nationals who have not been resident in the UK are eligible for "fee only" awards that do not include a personal stipend.

To Further Information: Please contact Dr. Kathryn Arnold (K.Arnold@bio.gla.ac.uk or DEEB, Graham Kerr Building, University of Glasgow, Glasgow G12 8QQ, UK). Further information about the research environment can be found at: Dr Arnold's website: <http://www.gla.ac.uk:443/ibls/staff/staff.php?who=PGe~Pn>

Closing date: 1st March 2007. Interviews will be held shortly after this.

Dr. Kathryn Arnold

Royal Society University Research Fellow

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

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

UIdaho Stochastic cellular automata

A Research Assistantship is available for a Ph.D. student to work on stochastic cellular automata (CA) models/simulations of the spread and persistence of antibiotic resistance plasmids in bacterial biofilms. The student will work under the direction of Professor Steve Krone (Mathematics; Bioinformatics and Computational Biology) and in close collaboration with Professor Eva Top (Biological Sciences; Bioinformatics and Computational Biology) on this NIH-funded interdisciplinary project.

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

The student will have the option of pursuing his/her Ph.D. in Bioinformatics and Computational Biology (<http://www.bcb.uidaho.edu/default.aspx?pid454>) or in Mathematics (<http://www.uidaho.edu/math/>).

The stipend pays US\$20,600 per year and tuition, fees, and health insurance are covered. In addition, funds are available to attend conferences. Moscow, the home of the University of Idaho, is a city of 22,000 people, nestled between Moscow Mountain and the beautiful rolling hills of the Palouse. With a small town friendliness and safety, Moscow is referred to as the "Heart of the Arts"—with an annual international Jazz Festival, live music on the town and summer theatre. Moscow is also a great place for those who love the outdoors, with beautiful rivers, lakes, and diverse mountains within short driving distance. The University of Idaho and Washington State University, just eight miles apart, share a large number of cross-listed courses and many collaborative programs and research activities.

HOW TO APPLY: For preliminary screening, email a

statement of background and interests, TOEFL scores (for foreign applicants), GRE scores (if you have them), and a copy of transcripts of academic courses taken. Starting date is flexible.

Contact: Steve Krone (krone@uidaho.edu) to apply and for further information. Web sites: Steve Krone (<http://www.webpages.uidaho.edu/~krone/>); Eva Top (<http://www.sci.uidaho.edu/biosci/labs/top/>)

krone@uidaho.edu krone@uidaho.edu

UNeuchatel EvolEntomology

TWO PhD POSITIONS IN ENTOMOLOGY AT THE UNIVERSITY OF NEUCHÂTEL, SWITZERLAND

Tasks: (in addition to research) contribution to the setting up of the practicals in Entomology (2nd year) for the students following the Bachelor of Science in Biology and/or lecturing for Master students in Plant Ecology and Physiology (PEP).

Candidates will be given the opportunity to undertake a PhD in the framework of the research interests of the laboratory of Evolutionary Entomology: Chemical Ecology, Tri-trophic Interactions and Applied Entomology.

For more details on the laboratory of Evolutionary Entomology of the University of Neuchâtel please refer to <http://www2.unine.ch/leae> <<http://www2.unine.ch/leae>> or contact Prof. Martine Rahier (tel. +41 32 718 3137, e-mail: martine.rahier@unine.ch) or Prof. Ted Turlings (tel. +41 32 718 3158, e-mail: ted.turlings@unine.ch)

These positions are open from 1 April 2007 for students with a Master in the field of Evolutionary Ecology, Agro-ecology or similar fields. A solid knowledge of French is expected.

Applications (including CV, cover letter, one reference letter, and the name and address of one additional referee) can be sent until 20 February 2007 to the following address:

- Prof. Martine Rahier Institut de biologie Case Postale 158 2009 Neuchâtel fax 032/718 30 01 e-mail: martine.rahier@unine.ch

and/or

- Prof. Ted Turlings same address e-mail: ted.turlings@unine.ch

Nicolas.Margraf@unine.ch Nicolas.Margraf@unine.ch

UNottingham InvasiveMoths

A PhD studentship is available to study the traits of potentially invasive moth species in the United Kingdom. The project will be supervised by Dr Tom Reader at the University of Nottingham and Dr Jason Chapman at Rothamsted research centre, and would start in October 2007. Funding (stipend plus tuition) is available to UK/EU students for three years. A project description follows:

Natural and human-induced biological invasions are an increasingly significant problem, both for natural ecosystems and human activities. Invasive species often have catastrophic impacts on the structure and function of native animal and plant communities, on human health, and on agricultural crops. An important finding arising from both theoretical and empirical studies of the invasion process is that the rate of arrival of propagules in a new habitat (“propagule pressure”) is a key determinant of the probability of successful invasion. It is surprising, therefore, that very few attempts have been made to quantify or explain the natural variance which exists within and among species in the propagule pressure applied to potential new habitats.

The aim of this project is to improve our understanding of the early stages of the invasion process by exploring natural variance in propagule pressure within and among potentially invasive moth species in the UK. The successful candidate will develop their project independently, using data describing the abundance, life history, phenology and voltinism of potentially invasive species to answer questions such as: a) which biological factors influence the probability of propagule arrival? b) what is the likelihood that anthropogenic climate change will modify the rate of invasion through impacts on propagule pressure? and c) is the general prediction that species exerting strong propagule pressure are large, fecund and vagile correct?

The project offers research experience in a range of modern techniques in ecological analysis (e.g. time-series analysis, phylogenetically-controlled comparative analysis) and bioclimatic modelling, and will also provide opportunities for field and laboratory studies of moth life history. We are seeking an independent-minded candidate with good data handling and analytical skills, undergraduate experience in ecology and

evolutionary biology, and preferably some knowledge of entomology.

Informal enquiries and applications (CV plus covering letter and the names of two academic referees) should be sent to: tom.reader@nottingham.ac.uk.

The deadline for applications is 1st March 2007.

Dr Tom Reader School of Biology University of Nottingham Nottingham NG7 2RD +44 (0)115 9513213 tom.reader@nottingham.ac.uk

Tom.Reader@nottingham.ac.uk

Tom.Reader@nottingham.ac.uk

UStAndrews Bioinformatics CompBiol

Dear EvolDir Members,

I would be grateful if you would share the below PhD studentship advertisement with any interested parties.

Thank you, Anne Smith

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

A pdf of the below PhD advertisement is downloadable from: <http://biology.st-andrews.ac.uk/-vannesmithlab/genenetsPhD.pdf> PhD studentship in Bioinformatics and Computational Biology

Revealing gene regulatory networks

Existence of a gene in the genome is not the whole story-whether or not, how much, and when a gene is expressed (i.e., transcribed into mRNA which is then translated into protein) governs how that gene affects an organism. Recent advances in biological techniques, such as gene expression microarrays, has enabled the development of computational algorithms for revealing the networks controlling gene expression. Such systems level understanding of gene regulation impacts research in areas such as development, evolution, and medicine.

In this studentship, you will explore the development of algorithms for revealing gene regulatory networks from multiple sources of genomic data. You will build off previous research in the group on Bayesian network inference algorithms for revealing gene regulatory

networks from gene expression data, developing algorithms capable of integrating other types of information, such as prior biological knowledge, sequence motifs, protein-protein interactions, etc., into this task. The opportunity exists for performing biological experiments to directly test your computational predictions, using our laboratory facilities, which maintain yeast (*Saccharomyces cerevisiae*) to perform genetic manipulation studies. Particulars of the project's ultimate direction will be modified to fit student interest. Potential directions include: creating a generic framework for integrating multiple sources of genomic information into Bayesian networks; combining Bayesian networks with other algorithms to increase recovery accuracy; combining text-mining for prior information with a Bayesian network; or further developing biological verification techniques.

The studentship will be based at the School of Biology at the University of St Andrews, supervised by Dr. V. Anne Smith. Applicants should have a background in Statistics, Mathematics or Computer Science; or in Biology with strong computational interests. For more details, please contact anne.smith@st-andrews.ac.uk and/ or visit: <http://biology.st-andrews.ac.uk/vannesmithlab/> BB-SRC funded: Fees plus stipend (UK residents) or fees only (other EU)

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

anne.smith@st-andrews.ac.uk anne.smith@st-andrews.ac.uk

UStAndrews PlantEvol

Dear All

Applications are invited for the following PhD studentship in my lab:

Plant Evolution: Origins and evolution of invasive weeds

Two highly invasive weeds to have come out of South Africa in recent years are Narrow-leaved ragwort (*Senecio inaequidens*) and Fireweed (*Senecio madagascariensis*). By accident these two species were introduced to Europe and to various parts of the South-

ern Hemisphere, respectively, where they have become highly invasive during the last 50 years. The two weeds form part of a complex of closely related taxa native to South Africa in which species boundaries are difficult to distinguish, polyploid relationships are confused, and mating system variation requires detailed examination. It is proposed to analyse the pattern of genetic divergence within this complex to obtain an improved understanding of species' relationships and evolution. A range of recently developed molecular tools for *Senecio* will be used to analyse material sampled from throughout the native (South Africa) and introduced ranges of species comprising the complex. The research will help clarify the origins and evolution of two highly invasive weeds within the context of the evolution of the group from which they are derived.

For informal enquiries contact Richard Abbott (rja@st-and.ac.uk; Tel: 01334 463350; <http://bio.st-andrews.ac.uk/staff/rja.htm>)

Eligibility: UK* and other EU citizens. The studentship covers subsistence for UK residents* and fees at home/EU rate. Applicants should have or expect to have a first or upper second class honours degree, or equivalent, in Biology, Plant Biology, Evolution, Genetics or another relevant subject.

University Application Form and Reference Form please contact Postgraduate Secretary (pgbiology@st-and.ac.uk).

Regards

Richard Abbott – Professor Richard Abbott Mitchell Building, 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://bio.st-andrews.ac.uk/staff/rja.htm> BSS Symposium: History, Evolution & Future of Arctic and Alpine Flora, St Andrews, June 25-27 2007 <http://biology.st-andrews.ac.uk/aafcon/> rja@st-andrews.ac.uk

UZurich EvolBiol

Doctoral position available in Evolutionary Biology and Biodiversity in the Zoological Museum at the University of Zurich in Switzerland

The research group in Evolutionary Biology and Biodiversity led by Professor Tony Wilson in the Zoological Museum (www.unizh.ch/zoolumus) is seeking a well-qualified and highly motivated doctoral candidate for

a position at the University of Zurich. This position is for three years, beginning in May 2007, with a yearly salary of 36,000 Swiss Francs (\$30,000US). A later start date is possible for exceptional candidates. A Masters degree or equivalent is a prerequisite for acceptance into the Ph.D. program at the University of Zurich.

Our group concentrates on the role of sexual selection in the speciation process. Integrating molecular phylogenetic, population genetic and functional genomic approaches, our work spans a broad temporal scale in an effort to derive testable hypotheses on the evolution of taxonomic diversity. Over the past several years, our research has concentrated on syngnathid fishes (seahorses and pipefish), a group of particular interest due to specialized morphological adaptations for male parental care and female-dominated competition for access to mates. Our work involves ongoing collaborations with researchers in America, Europe and Australia.

Major histocompatibility (MH) genes are part of the adaptive immune system and are believed to play an important role in vertebrate mate choice. The PhD candidate will investigate the evolution and diversification of MH genes in syngnathid fishes and the role of these molecules in mate choice decisions of *Hippocampus* seahorses. Genome size estimates suggest a large scale gene and/or genome duplication event occurred early in the evolution of syngnathid fishes, an event which likely influenced the subsequent diversification of MH genes in this group. Recent research in our lab has identified a large number of unlinked MH loci in the compact genome of *Hippocampus abdominalis*. The candidate will construct a genetic linkage map for a laboratory population of this species using a suite of 300 microsatellite loci and characterize the distribution and variance of MH genes in the genome. Following the characterization of MH diversity in *Hippocampus*, a comparative approach will be used to study rates and patterns of genetic change of these loci in related species. At the same time, candidate MH loci will be used in a series of mate choice trials.

Our lab is equipped with three 5000L climate-controlled aquarium facilities for the culture of marine fishes under controlled conditions. Our laboratory facilities include a MJ Tetrad PCR machine and an ABI 3100 sequencer, with access to a high-throughput ABI 3730 48-capillary machine. In addition, our Functional Genomics center (www.fgc.unizh.ch) offers extensive facilities for proteomics and bioinformatics. The core bioinformatics facility of the University consists of two 4 processor Opteron Servers and an 8 TB file system capable of running all Unix-based bioinformatics and phylogenetics software packages.

The University is one of the top comprehensive institutions in Europe and the Zoological Museum is a center of excellence in behavioural ecology, population genetics and evolution. With a critical mass of researchers in Ecology and Evolutionary Biology at the University and the neighbouring Swiss Federal Institute of Technology (ETH Zurich), Zurich offers an exceptional academic environment for research and study.

Zurich is an international city of 350,000 located at the heart of Europe, with world-class facilities for sport, music and theatre. With its location at the head of Lake Zurich and its proximity to the Swiss Alps, there are incredible opportunities for sailing, skiing, hiking and mountaineering in the region. For all of these reasons, Zurich has been ranked the top city in the world for quality of living.

Interested candidates should submit a Curriculum vitae and statement of research interests, along with a list of two references, by email or post to Rosemarie Keller, Institute Secretary (kellerro@zoolmus.unizh.ch) by March 15, 2007. Any questions on the position should be directed to Prof. Wilson (tony.wilson@zoolmus.unizh.ch).

Tony Wilson Assistant Professor, Evolution and Biodiversity Zoological Museum University of Zurich Winterthurerstrasse 190 CH 8057 Zurich Switzerland Tel: 41 44 635 4790 Fax: 41 44 635 4780

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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>

UppsalaU 3 EvolGenomics

Evolutionary Biology Centre, Uppsala University, Sweden

3 PhD positions in evolutionary genomics/evolutionary biology

Three PhD positions are available at the Swedish Research Council Centre of Excellence in Evolutionary Genomics at the Evolutionary Biology Centre (EBC) in Uppsala, under the supervision of Prof. Hans Ellegren. The overall profile of the group is the general analysis of how mutation, selection, recombination and gene expression relate to molecular mutation, and the

study of the genetic architecture behind phenotypic diversity and fitness related traits.

There are several possibilities for research projects and the precise line of research will be discussed and decided together with the successful applicants, depending on their background and interest. Together with colleagues in Los Angeles, Illinois and St Louis, our group has a coordinating role in the zebra finch genome project. Much of our research the coming years will therefore be devoted to whole-genome analysis of avian genomes, with comparison to mammalian and outgroup genomes, including large-scale data on polymorphism and gene expression. Example of questions that will be addressed include the analysis of selection and function of conserved non-coding DNA, the role of positive selection in driving the evolution of genes behind certain phenotypes, the genetic background to avian-specific adaptations, sexual antagonism and sex-biased gene expression, and evolution of the transcriptome and of protein networks. Another approach will involve QTL-mapping in pedigrees of different bird species, with the aim of identifying genes governing behavioural, morphological and other traits.

Swedish PhD positions are for 4 years and are paid throughout the studies. The new students will be part of a group consisting of 5 post-docs, 3 PhD students and 1 technician. The Evolutionary Biology Centre (<http://www.ebc.uu.se>) is situated in recently-built localities in central Uppsala and is equipped with facilities for large-scale sequencing, genotyping and ex-

pression analysis. The working atmosphere is international with English as working language. The Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 400 scientists and graduate students, with research programs including 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.

The positions are open to everyone with a BSc or (preferably) MSc with experience from and interest in one or several of the following areas: bioinformatics including own programming, population genetics, genomics, evolutionary biology, or related subjects. Interested parties should send a statement of interest, and a detailed CV including contact information for two references to Hans Ellegren (Hans.Ellegren@ebc.uu.se), to whom informal inquires also can be made. The search will continue until the positions are filled - starting date is open to discussion.

Further information is given at <http://www.egs.uu.se/-evbiol/Persons/Hans.html> Prof Hans Ellegren Dept of Evolutionary Biology Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

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

Hans Ellegren <Hans.Ellegren@ebc.uu.se>

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AgResearchNZ Bioinformatics

AgResearch is a new Zealand based crown research institute. The CRI Act defines AgResearch's purpose as "undertaking research". Within this purpose we must adhere to six principles; to benefit New Zealand, pursue excellence, be ethical, transfer technology, be a good employer and exhibit a sense of social responsibility. However, none of this must occur at the expense of our financial viability, defined by the Act as operating as a going concern and earning an adequate rate of return on shareholders' funds.

As part of AgResearch's company strategy we are continuing to grow our business in the area of bioinformatics. This capability is essential for our science discovery.

In this position you will be part of a national team of 26 bioinformaticians, mathematical biologists and statisticians and be based at our Grasslands campus at Palmerston North. This is a permanent position.

You will be an advocate for bioinformatics within AgResearch; you will work collaboratively on projects and will provide bioinformatics training and advice to science staff working in the biotechnology area.

We are seeking a person who has: * An excellent tertiary qualification in molecular biology or genetics * Experience with the use of bioinformatics applications * Knowledge of life sciences databases and the internet * Well developed IT technical skills and web based technologies * Experience in a training environment * Excellent writing, speaking and interpersonal skills * Familiarity with Perl, Java or Unix Scripting

If you possess the above skills, we would like to hear from you.

To find out more about this position please contact Peter Johnstone by email pe-

ter.johnstone@agresearch.co.nz or alternatively phone +64 3 489 9081.

For a job description and to apply on line please go to <http://www.agresearch.co.nz/recruitment>. Vacancy No AGR494. Please provide contact details for 2 referees with your application.

For general information on AgResearch please visit our website at www.agresearch.co.nz Applications close 9th March 2007.

Linda Murray Science Administrator AgResearch Limited Invermay Agricultural Centre Private Bag 50034 Mosgiel, New Zealand Phone: +64 3 489 9011 Email: linda.murray@agresearch.co.nz

S. Anette Becher D.Phil. Senior Computational Biologist Tel. +64 3 489 9028

anette.becher@agresearch.co.nz

ClarksonU TeachingBiol

Dear Brian,

Here is an ad that should be posted in Science now but would be of interest to evolutionary biologists as it requires quite a breadth of knowledge for the position:

Biology Faculty Position - 2007

The Biology Department at Clarkson University invites applications for Director of First Year Biology at the level of Assistant Professor. This non-tenure track, full-time, renewable position is appropriate for doctoral-level professionals in the life sciences committed to excellence in teaching introductory college biology in both lecture and laboratory format. Experience and demonstrated success in teaching a broad array of topics in contemporary biology to both biology ma-

jors and non-science majors is required. The position includes responsibility for designing and implementing lab exercises, training and supervising teaching assistants, and conducting an annual departmental teaching assessment. Candidates with research experience who are interested in collaborating on externally funded pedagogical or laboratory-based projects are especially encouraged to apply. Clarkson is a small private university with a mission focused on technology serving humanity. Potsdam is an educational and cultural center of northern New York located in proximity to the Adirondack Park and within two hours of Ottawa, Montreal, and Lake Placid. Applicants should submit a cover letter with CV, a statement of teaching philosophy, and contact information for 3 or more references in one PDF file to biologysearch@clarkson.edu or by mail to Biology Search Committee, Box 5805, Clarkson University, Potsdam, NY 13699. Applications received before February 28, 2007 will receive full consideration. Clarkson University is an Equal Opportunity / Affirmative Action Employer. POS#77-06

Thanks, Jim

—

James A. Schulte, II Department of Biology 177 Clarkson Science Center, MRC 5805 8 Clarkson Avenue Clarkson University Potsdam, NY 13699-5805 Phone: 315-268-4401 Fax: 315-268-7118

“James A Schulte, II” <jschulte@clarkson.edu>

CornellU ResAssist PlantEvol

RESEARCH ASSISTANT POSITION: PLANT EVOLUTIONARY ECOLOGY CORNELL UNIVERSITY

A two-year research assistant position is available immediately for an NSF project on the ecology and evolution of geographic ranges in plants. Responsibilities include organizing greenhouse and field studies, assisting with and supervising data collection, performing moderately complex statistical analysis, conducting library research, and managing lab. Fieldwork involves three trips to California for a total of 3.5 months per year. Travel and room expenses are provided. Bachelor's degree in ecology, evolution, or related field, prior research experience and a driver's license required. Preference is for candidates with experience in fieldwork and plant biology. RA must be able to do fieldwork on steep slopes and in hot weather.

To apply, please send a CV and names of three references to: Monica Geber, Associate Professor, Department of Ecology & Evolutionary Biology, Cornell University, Ithaca, NY 14853; E-mail: mag9@cornell.edu; Phone: (607) 254-4208. Formal application must also be made on line at <http://www.ohr.cornell.edu/jobs/-index.html>, follow link to “Staff (non-academic) and Librarian Positions”, enter job search number 06527. Applications considered until position filled.

Monica A. Geber Associate Professor Department of Ecology and Evolutionary Biology Corson Hall Cornell University Ithaca, NY 14853

tel: 607-254-4208 fax: 607-255-8088

Monica Geber <mag9@cornell.edu>

CostaRica FieldAssist BatEvolution

“Jobs”

Field assistants for a project on the influence of diet on metabolism in bats in Costa Rica wanted.

Scientific assistant for Costa Rica

We are searching for a scientific assistant for a project on the feeding ecology and metabolic physiology of bats in Costa Rica from mid April to the end of May.

The assistant will help to coordinate a telemetric study on nectar-feeding bats in the lowland rainforest of Costa Rica. We are looking for a person who is experienced with telemetry, preferably with bats. The candidate should be able to coordinate a telemetry team under tropical field conditions (rain, mosquitos, etc.). The study will take place in a lowland rainforest at the La Selva Biological Station in Costa Rica (www.ots.ac.cr). Candidates should be fluent in English or German, Spanish is advantageous. Knowledge of ArcView and telemetry data processing is required. All expenses will be paid by the project. A recent rabies vaccination is a prerequisite (Note: no rabies has ever been found in bats in the research area).

Applications should enclose: Cover letter and motivation statement, description of qualifications, CV. Deadline for applications is February 25th 2007

Send applications to: Dr. Detlev Kelm; Leibniz-Institute for Zoo- and Wildlife Research, Berlin, Germany (kelm@izw-berlin.de).

Field assistants for Costa Rica

We are searching field assistants for a project on the feeding ecology and metabolic physiology of nectar-feeding bats in Costa Rica for between mid-April and June 2007. Participants are to help with mist-netting and radio-tracking bats in the rainforest at night and with identifying the food plants of the bats.

We are looking for candidates who are willing to work in a team, and help with field work, even under tough conditions (night work, rain, mosquitos etc.). The project will take place at the La Selva Biological Station in the Atlantic lowland forest of Costa Rica (www.ots.ac.cr). English or German is a prerequisite, knowledge of Spanish is advantageous. Participants must pay their own travel to the field site. However, food, lodgings and station fees will be paid by the project. Participants must have a recent rabies vaccination (Note: no rabies has ever been found in bats from the field site).

Applications should enclose: Cover letter and motivation description, characterisation of qualifications, CV.

Deadline is March 5th 2007 Please send applications to: Dr. Detlev Kelm; Leibniz-Institute für Zoo- and Wildlife Research, Berlin, Germany (kelm@izw-berlin.de).

Dr. Detlev Kelm Institute for Zoo and Wildlife Research Evolutionary Ecology Research Group Alfred-Kowalke Str. 17 10315 Berlin Germany

“Kelm, Detlev” <kelm@izw-berlin.de>

DexterNewMexico ConservationGenetics

Salary Range: 43,731.00 - 52,912.00 USD per year Open Period: Wednesday, February 14, 2007 to Wednesday, February 28, 2007 Series & Grade: GS-0482-09/11 Position Information: Full Time Term NTE 13 months (4 Years potential) Promotion Potential: 11 Duty Locations: 1 vacancy - Dexter, NM <http://www.fws.gov/southwest/fishery/dexter/index.html> to apply: http://jobsearch.usajobs.opm.gov/series_search.asp, and search for the series 0482.

The incumbent performs a variety of duties and investigations integral to the Center's Applied Research Program in Genetics. Major duties include preparing laboratory solutions, extracting DNA from fish tissues or blood samples; conducting polymerase chain reaction (PCR) of extracted DNA, and generating DNA sequence or genotypic data; designing specific primers

for mitochondrial and nuclear DNA markers using genbank and other sources, and microsatellites for conservation and ecological genetic applications; identifying and isolating data collection or evaluation problems; collecting, filing and storing data to assist in broader studies; monitoring genetic studies in a laboratory setting, analyzing and interpreting data; design sampling protocols and implementing genetics sample and data collection on fish from the Colorado River systems and other species in the Southwest; conducting study planning, data collection, entry, analysis and interpretation; operating, configuring and maintaining specialized molecular population genetics laboratory equipment such a thermocyclers, 3700 Avant DNA sequencer, electrophoresis cells and centrifuges.

Connie Keeler-Foster, Ph.D. Research Leader Dexter National Fish Hatchery and Technology Center 7116 Hatchery Road, P. O. Box 219 Dexter, NM 88230 Phone 505.734.5910 ext 16, Fax 505.734.6130

“I've lost all patience with the search for peace of mind”
Alice in Chains

Connie_KeelerFoster@fws.gov

EAWAG Switzerland FishGeneticsConservation

Tenure Track Research Group Leader in Ecology/Genetics/Conservation of Fish Location: Eawag Center for Ecology, Evolution & Biogeochemistry in Kastanienbaum (near Lucerne)

We are inviting applications for a tenure track research group leader position in the broad field of ecology/genetics/conservation of fish at the department of Fish Ecology and Evolution of the Swiss Institute for Aquatic Science and Technology (Eawag), located in Kastanienbaum (Center for Ecology, Evolution & Biogeochemistry) near Lucerne.

We are seeking a dynamic and innovative scientist with an excellent track record in science, and proven ability to attract extramural funding. S/he should be well versed in ecological and evolutionary theories and have strong aspiration for understanding how environmental changes interact with ecological and evolutionary processes to generate and maintain biodiversity at any levels of biological organization from genes to communities. The successful candidate is expected to attract extramural funding from Science Founda-

tion and/or other sources to build a research group in any aspect of ecology, genetics and conservation, seeking to build bridges between theory and conservation/management of fish. We welcome applications both from theoreticians who work closely with empiricists to develop testable theories, and from empirical scientists who conduct theory-driven research. The successful candidate is expected to actively engage in collaborations with other scientists at Eawag. A small contribution to teaching (e.g. one course) at the University of Bern is envisaged, as is the supervision of graduate students. Scientific language of the lab is English, and teaching is in English too. The advertised position is a tenure-track senior researcher with review for tenure after four years. A formal affiliation (lectureship) with a university is possible and strongly encouraged.

The department of Fish Ecology and Evolution is one of three Eawag science departments in Kastanienbaum and is closely affiliated with the Division of Aquatic Ecology and Macroevolution of the Institute of Zoology, University of Bern. The core research of our department involves building and testing general ecological and evolutionary theories with fish as a model system, and applying such theories to aid the conservation and management of fish populations and communities. The excellent departmental research facilities are located in Kastanienbaum, on the shores of Lake Lucerne, about 20 minutes from Lucerne town and 1.5 hours from Bern University by public transport. Facilities include a fully equipped molecular genetics laboratory with two 8 capillary DNA sequencers, two large outdoor glass troughs with lake water through-flow suitable for population level experimental work with large and small fish, a modern indoor lake water through-flow aquarium system, a large state of the art tropical fish aquarium facility, a fleet of several stationary and portable research vessels and cars for fieldwork. The Center further has fully equipped laboratories for stable isotopes, sedimentology and analytical chemistry. Other recently started research groups at the ecology/evolution interface are theoretical ecology (Akiko Satake), evolutionary ecology of algae and experimental evolution (Bas Ibelings), molecular microbial ecology (Helmut Bürgmann), evolutionary ecology (Jukka Jokela), evolution of species diversity (Ole Seehausen).

Applicants should send their applications, including CV, publication list, a short (less than two pages) summary of future research interests, and the names and email addresses of five referees to Sandra Isenring, Human Resources, Eawag, Ueberlandstrasse 133, CH-8600 Duebendorf or per e-mail to sandra.isenring@eawag.ch.

For questions please contact Prof. Dr. Ole Seehausen (ole.seehausen@eawag.ch). For information on Eawag mission and research please consult http://www.eawag.ch/index_EN, for information on our department please consult www.fishecology.ch Application deadline: March 11, 2007, but later applications will be considered until the post is filled.

Eawag is the Swiss Federal Institute of Aquatic Science and Technology, a Swiss-based and internationally active research institute within the ETH domain, committed to an ecological, economical and socially responsible management of water.

Prof Ole Seehausen Aquatic Ecology & Evolution

EAWAG Center for Ecology, Evolution and Biogeochemistry (CEEB) Seestrasse 79 CH-6047 Kastanienbaum Phone +41 41 349 21 21 Fax +41 41 349 21 68 and Institute of Zoology University of Bern Baltzerstr. 6, CH-3012 Bern Phone +41 31 631 31 31 FAX +41 31 631 30 08 and

<http://www.fishecology.ch/> Ole.Seehausen@eawag.ch
Ole.Seehausen@eawag.ch

FreieUBerlin SystematicBotany

Freie Universität Berlin

Full Professorship in Systematic Botany and Plant Geography

Department of Biology, Chemistry, Pharmacy (Institute of Biology) and Botanic Garden and Botanical Museum

Full Professorship in Systematic Botany and Plant Geography

Applications are invited for the joint tenured position of Full Professor of Systematic Botany and Plant Geography at the Department of Biology, Chemistry, Pharmacy and Managing Director of the Botanic Garden and Botanical Museum. The successful candidate will be required to provide teaching and research in the said areas. The initial contract for the position of Managing Director of the Botanic Garden and Botanical Museum is for a period of five years

In line with article 100 of the Higher Education Act of the land of Berlin (Berliner Hochschulgesetz), a post-doctoral lecturing qualification (Habilitation) or comparable qualifications for a teaching career in higher education are required

The successful candidate will have an internationally recognized research profile in the field of Phytodiversity and teaching experience in Systematic Botany. In addition, the candidate should have pertinent experience and expertise in maintaining scientific collections and managing research institutes as well as in securing external funding and in managing externally funded projects. He or she will be also expected to collaborate with colleagues in other departments of the Freie Universität, especially within interdisciplinary research clusters. Furthermore, the candidate should be involved in national and international research ventures

In general, the language of instruction will be German, but some activities may be offered in English. A non-German speaking appointee will be expected to be able to teach in German within two years

The successful candidate will be offered civil servant or public sector employee status (Professorial Grade "W3"). Applications must reach the

Freie Universität Berlin, Fachbereich Biologie, Chemie, Pharmazie, Dekanat, Takustr. 3, 14195 Berlin, Germany,

by March, 22nd 2007 Applications should include the following: a letter describing your interest in the position and pertinent experience, a curriculum vitae, the names and addresses of three referees, a list of publications, and copies of the certificates of academic qualifications held.

The Freie Universität Berlin is a state-funded university. It has some 35,000 students and 350 professors, excluding Medicine. The University has 11 departments structured into more than 70 institutes, plus the Medical Faculty Charité, made up of the former medical departments of Freie Universität and Humboldt Universität. Detailed information is available at the following web sites:

<http://www.fu-berlin.de> <http://www.bcp.fu-berlin.de> and

<http://www.bgbm.org> Dr. Birgit Gemeinholzer
Botanic Garden and Botanical Museum Berlin-Dahlem
Free University Berlin Königin-Luise-Straße 6-8 D-14195 Berlin Germany Phone: (+4930) 838-50152 Fax: (+4930) 841-72924 E-mail: b.gemeinholzer@bgbm.org
<<mailto:b.gemeinholzer@bgbm.org>>

"Gemeinholzer,
<B.Gemeinholzer@BGBM.org>

Birgit"

KansasStateU Bioinformatics

Computer Specialist / Bioinformatics Specialist

Kansas State University, Manhattan, Kansas

Immediate opening exists for a bioinformatics specialist in the KSU Bioinformatics Center to collaborate with faculty scientists in the application of bioinformatics to basic biological research, provide training, and lead workshops in bioinformatics. Relevant interests include genomics, gene expression analysis, machine learning, data mining, and relational databases. Requires an M.S. in Computer Science or related field (Ph.D. preferred), and demonstrated accomplishments in bioinformatics such as developing bioinformatics tools, data management, data mining, or database development and curation. Preferred qualifications include project management experience (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 June 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 March 1, 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.

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

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, Manhattan, KS 66506-4901

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.bioinformatics.k-state.edu/>>

/www.ksu.edu/agc> www.ksu.edu/agc
dmerrill@ksu.edu dmerrill@ksu.edu

LaurentianU PlantEvol

The Department of Biology at Laurentian University invites applications for a tenure-track position at the Assistant Professor level in ecology commencing July 1, 2007. The preferred candidate should have research expertise in the ecology of plants, including interactions with other organisms such as mycorrhizae or herbivores and an interest in addressing questions on large-scale phenomena at the ecosystem, watershed or landscape level. The successful applicant would establish an externally funded research program studying boreal ecosystems, restoration of mining-influenced ecosystems and watersheds, or effects of climate change.

The successful applicant will have a strong commitment to excellence in teaching and research. He/she would teach undergraduate courses in Biology and an upper year course in his/her area of specialization. The successful candidate will contribute to the M. Sc. program in Biology and the Ph. D. program in Boreal Ecology.

A completed PhD is required. Preference will be given to applicants who have appropriate teaching and post-doctoral research experience.

This position is subject to budgetary approval.

Laurentian University (LU) is located in Sudbury, an attractive modern city offering unique cultural, recreational, and educational opportunities. For further info see <http://www.sudburytourism.ca>. LU is a bilingual institution and an equal opportunity employer. It has a policy of passive bilingualism (English/French) as a condition of tenure. LU is committed to equity in employment and encourages applications from all qualified applicants, including women, aboriginal peoples, members of visible minorities and persons with disabilities. In accordance with Canadian immigration requirements, priority will be given to Canadian citizens and permanent residents. Applications will be reviewed commencing in January 2007 but will be accepted until the position is filled. Ph.D. in the related field is essential unless otherwise indicated. Applicants should provide a covering letter clearly indicating the Ad number, a curriculum vitae, a list of publications, a summary of research interests, a research proposal indicating equipment needs and three letters of reference addressed to:

Dr. J.D. Shorthouse Chair, Department of Biology
Laurentian University 935 Ramsey Lake Road Sudbury,
ON P3E 2C6

or by e-mail to asr@laurentian.ca.

dlesbarreres@laurentian.ca dlesbarreres@laurentian.ca

NewMexico FieldAssist

Hi Evoldir community,

I and Daniel Ortiz-Barrientos (Loren Rieseberg's lab) are planning a field experiment in New Mexico starting in April/2007. We will plant wild sunflower seeds along with interspecific artificial hybrids and back-crosses. We need help to set up the experiment and/or to collect data after we leave New Mexico in May/2007. The experiment can potentially go up to September/2007.

We are looking for a very responsible and independent individual who can undertake these activities, has a car, and is able to drive to the Seville National Wildlife Refuge in a regular basis to collect our data. The ideal person lives within a reasonable distance from our field site ([http://www.fws.gov/southwest/refuges/-newmex/ sevilleta/](http://www.fws.gov/southwest/refuges/-newmex/sevilleta/)). The task also includes data-entry and the commitment to send the collected data in a regular schedule.

We can pay for the mileage and per hour of work. This is an opportunity to have a hands-on experience in a large-scale transplant experiment while learning sunflower evolution and ecology.

If you are interested in the job please contact either

Julianno Sambatti: jbmsamba@interchange.ubc.ca

or

Daniel Ortiz-Barrientos: danielo@interchange.ubc.ca

Julianno Sambatti <jbmsamba@interchange.ubc.ca>

NewMexicoStateU EvolutionaryImmunology

The Department of Biology at New Mexico State University invites applications for a 9-month tenure-track assistant professorship. The Department is interested

in individuals who employ innovative approaches and model systems to tackle fundamental questions in immunology. Applicants using non-mammalian or cellular model systems are especially encouraged to apply. The successful candidate will be expected to develop an independent research program, teach an Immunology course, and contribute course offerings related to his/her area of expertise at the undergraduate and graduate levels. The successful candidate will have the opportunity to interact with colleagues who work in a variety of sub-disciplines from cell and organismal biology to ecology. The department offers undergraduate degrees in Microbiology and Biology and M.S and Ph.D degrees in Biology. Opportunities are available to participate in the graduate program in Molecular Biology and in NIH- and NSF-sponsored minority research programs such as MBRS-RISE, MARC, Bridges, INBRE, AMP, and MICCP, and the HHMI Undergraduate Scholars Program. For more information about the department, see our website at <http://biology-web.nmsu.edu/>. Applicants should have a Ph.D. in an appropriate field and post-doctoral experience, research productivity commensurate with experience, and a commitment to mentoring undergraduate and graduate students at a minority-serving institution. Send a curriculum vitae, statements of teaching and research philosophies, and three letters of reference to: NMSU Immunology Search Committee, Biology Department MSC 3AF, Box 30001, Las Cruces, NM. 88003. Screening of applications will begin on March 9, 2007 and will continue until filled. New Mexico State University is an equal opportunity/affirmative action employer. Requisition # 2007001058.

Michele K. Nishiguchi, PhD Associate Professor Department of Biology - MSC 3AF New Mexico State University PO Box 30001 Las Cruces, NM 88003-8001 505-646-3721 (office) 505-646-4123 (lab) 505-646-5665 (FAX) email: nish@nmsu.edu <http://biology-web.nmsu.edu/> nish@nmsu.edu

NorthCarolinaStateU
EvolPlantPathology

ASSISTANT PROFESSOR OF PLANT PATHOLOGY

The Department of Plant Pathology at North Carolina State University, Raleigh, NC invites applications for a tenure-track, 12-month position in plant pathology.

This position is primarily research at the assistant professor level. The individual must have a Ph.D. with training in epidemiology, ecology, plant pathology or a closely related field. The successful candidate will build a program that will provide leadership in advancing the understanding of plant disease epidemiology at the population or ecosystem level. The incumbent is expected to develop analytical or simulation modeling methods that will further our understanding of the spatio-temporal trends in epidemic development in agricultural or natural ecosystems. The individual will have the opportunity to collaborate with strong ongoing programs in epidemiology, disease forecasting and population biology. The successful candidate is expected to participate in the graduate program by developing and teaching a course in advanced epidemiology, mentoring graduate students and participating in other academic programs within the Department of Plant Pathology. The candidate filling this position will have a competitive start-up package including technical support. Applications will only be received electronically, and the position will remain open until a suitable candidate is identified. For priority consideration, applicants must submit NC State's online application form and attach to that application a curriculum vitae including a list of relevant publications, transcripts, a description of research and teaching interests and goals, the names and contact information for three professional references, and a cover letter by March 31, 2007. To submit the required application materials, candidates should visit: jobs.ncsu.edu/applicants/Central?quickFindt948 and follow the instructions there.

For additional information concerning this position contact James Moyer (james_moyer@ncsu.edu) Head, Department of Plant Pathology, NCSU. AA/EEO. NC State welcomes all persons without regard to sexual orientation. Persons with disabilities who need accommodations in the application process should contact Marci Walker, Department of Plant Pathology, via telephone (919) 515-6498, or via e-mail: Marci.Walker@ncsu.edu.

Marci Walker University Administrative Manager Department of Plant Pathology 3419 Gardner Hall Raleigh, NC 27695-7616 919-515-6498 919-515-7716 (fax) Marci.Walker@ncsu.edu

Marci Walker <marci_walker@ncsu.edu>

OpenUUK MolecularEvolution

Lectureship in Molecular Ecology

The Open University, UK

£29,138 - £31,840 or £32,795 - £39,160, depending on qualifications and experience

For details see: <http://www.jobs.ac.uk/jobfiles/-YV046.html> Closing Date for applications: 12 March 2007

J.Silvertown@open.ac.uk J.Silvertown@open.ac.uk

OregonStateU EvolComputGenom

Faculty Research Assistant or Postdoctoral Research Associate in Zoology at Oregon State University available 05/07 to investigate evolutionary genomic processes using computational approaches. Specific project will include analysis of full-genome tiling array data for *C. elegans*, and phylogenomic analyses of DNA repair protein evolution in eukaryotes. Experience in computer programming required, specific knowledge in Perl and R/BioConductor applications, Unix/Linux operating systems preferred. BA/BS required. Candidates seeking postdoctoral experience will also be considered in the context of a postdoctoral research associate position and must possess a PhD. View Complete announcement at: <http://oregonstate.edu/jobs/>. Qualified candidates are invited to electronically submit an application, including: (1) letter of interest, (2) current vita, (3); contact information for 3 professional references, and (4) 1-page statement of professional and research objectives. For additional information contact: Dr. Dee Denver at email:denver@cgrb.oregonstate.edu. To learn more about the Denver lab, go to <http://denverlab.science.oregonstate.edu/>. For full consideration apply by 3/15/07. OSU is an AA/EOE employer.

Dee R. Denver Department of Zoology Center for Genome Research and Biocomputing Oregon State University 2000 Cordley Hall Corvallis, OR 97331 USA

phone: 541-737-3698 fax: 541-737-0501
email: denver@cgrb.oregonstate.edu web:

<http://www.cgrb.oregonstate.edu/faculty/-denver>

denvedee@cgrb.oregonstate.edu
denvedee@cgrb.oregonstate.edu

RoyalZooSociety Antwerp PopulationBiol

The Centre for Research and Conservation (CRC) of the Royal Zoological Society of Antwerp (RZSA) is seeking to employ a full time conservation scientist / population biologist

The successful candidate will be involved in applied zoo-research and related activities of the Centre for Research and Conservation (CRC). The CRC is a government-funded research division of the Royal Zoological Society of Antwerp (RZSA) and is active both within the society's grounds (Antwerp Zoo, Wild Animal Park Planckendael and the local nature reserve De Zegge), in its own field-based conservation projects in Cameroon and Brazil, and as a research partner in various other projects with an in situ component. Performing scientific research helps the Royal Zoological Society of Antwerp accomplish its mission to contribute to worldwide nature conservation and education.

The post holder will be a fully participating member of the CRC, and will be expected to develop interdisciplinary research projects particularly bridging the interests of the CRC departments of ethology and conservation biology, perform research activities and collaborate in existing projects of all four research units of the CRC (ethology, conservation biology, functional morphology and veterinary medicine). Other tasks include teaching and supervising undergraduate students, co-supervising PhD students, actively contributing to applications for external funding, actively participating in activities to bring science to the public and supporting the general conservation and education activities of the RZSA.

The successful candidate should have: A demonstrable interest in zoo-related research; A PhD in Biology in (a) relevant field(s); A special interest for - and preferably experience in - applied scientific research in the fields of behavioural and evolutionary ecology and/or population biology/ population dynamics; Experience with statistical data analysis. Knowledge of ARKS, SPARKS, PM2000 is an asset. A stern discipline in, and experience with the publication of research results in scientific journals; An higher knowledge of English

and preferably a basic knowledge of Dutch (or the willingness and commitment to learn within a time period to be agreed); A talent to mentor students and be an enthusiastic teacher; The ability to work independently though in close collaboration with fellow researchers; An interest and enthusiasm for popular science writing;

The post-holder will have a full-time fixed term RZSA contract for one year of which six months on proof, with the possibility for an extension. This is a newly created position and the post will available immediately.

Review of applications will begin on 26 February 2007 and will continue until the position is filled. Candidates should apply by sending a full CV, a publication list and a cover letter, explaining why they are interested in this position, what particular skills they will bring, and why they are interested in zoo-related research.

Please send your application before 26 February 2007 to: Greta Thewis Human Resources Royal Zoological Society of Antwerp Koningin Astridplein 26 2018 Antwerp, Belgium Greta.Thewis@zooantwerpen.be

For more information about this job please contact Zjef Pereboom by e-mail (zjef.pereboom@zooantwerpen.be) or by telephone (+32(0)32024580). Visit the CRC website at <http://webh01.ua.ac.be/crc/> for information about the CRC's activities.

Zjef Pereboom <Zjef.Pereboom@zooantwerpen.be>

RuhrU PopGenetics

Ruhr-University Bochum, Faculty of Biology, Department of Systematic Zoology (Spezielle Zoologie)

We are inviting applications for an* Research Associate (wissenschaftlicher Mitarbeiter/in) *position (EG 13 TV-L) to work in the field of* Population Genetics and Molecular Evolutionary Ecology.

*

The Department of Systematic Zoology (with research focus on Animal Ecology, Evolution and Biodiversity) is seeking highly motivated candidates with documented experience (group leader, post-doc) and research interests in the area of population genetics and molecular evolutionary ecology. The successful candidate will be able to build up a molecular working group and run the molecular lab. He/she will establish independent externally funded projects, supervise students and conduct a

moderate amount of teaching (English or German language).

The position is available starting March 2007 (a later start is possible) for up to six years, with evaluation after three years. Ruhr-University Bochum is committed to equal opportunity in employment and gender equality in its working environment. We strongly encourage applications from qualified women. Applications from appropriately qualified handicapped persons are also encouraged.

To apply, please send a complete CV, a description of current research interests with an outline of future projects, three major papers and arrange at least two letters of reference to be sent, either by email or mail. Review of applications will begin on 20. February 2007, and will continue until the position is filled.

Please send your application to:

Prof. Dr. Ralph Tollrian Ruhr-University Bochum Department of Systematic Zoology (Spezielle Zoologie) Universitaetsstr. 150 /Gebaeude ND05 D-44780 Bochum phone: +49 (0)234-3224998; 3224563 fax: +49 (0)234-3214114 email: tollrian@rub.de

Smithsonian Panama Butterfly Assistant

Butterfly Research Intern Position

Position: Intern, Heliconius Research Facility

Location: Smithsonian Tropical Research Institute, Panama

Salary: \$800 per month stipend

Start date: Immediate

Length of contract: One year, with the possibility of extension

Background: We are looking for a research assistant to work in Panama for the Heliconius Research Facility. This project is a collaboration between Owen McMillan (North Carolina State University), Chris Jiggins (University of Cambridge, UK) and Eldredge Bermingham (Smithsonian Tropical Research Institute, Panama). We are studying the genetic basis of colour pattern diversification in Heliconius butterflies, in particular concentrating on two species, *H. melpomene* and *H. erato* that are mutual co-mimics. For more information see www.heliconius.org. Responsibilities: To include

maintenance of host plants and butterfly stocks, dissection of tissue for genetic studies and local collecting of butterflies. The intern will also be expected to assist visiting researchers with short term research projects.

Selection criteria: The potential applicant should have a keen interest in butterfly biology. Experience rearing butterflies would be advantageous.

Although not a requirement, this position would potentially be suitable for a Masters student whose dissertation project could be carried out in parallel with the responsibilities of maintaining the stock centre. We would be happy to assist with such a project where possible.

Contact: Potential applicants should contact Chris Jiggins (cj107@cam.ac.uk) or Owen McMillan (womcmill@ncsu.edu) as soon as possible. Please note that applicants may apply in Spanish if preferred.

Chris Jiggins Department of Zoology University of Cambridge Downing Street Cambridge CB2 3EJ Tel: (+44)(0)1223 769021 Fax: (+44)(0)1223 336676 Home: 01223 578 371 <http://www.heliconius.org/> Chris Jiggins <cj107@cam.ac.uk>

StanfordU HumanEvolBiol

The Program in Human Biology at Stanford University seeks a full-time lecturer to coordinate our sophomore core course sequence, beginning September 2007. Human Biology is an interdisciplinary undergraduate major blending the biological, social and behavioral sciences, with a focus on applications to environmental, health and other public policies that influence human welfare. The core is two parallel year-long course sequences, drawing faculty from diverse departments and schools. Responsibilities of the coordinator include training and supervision of teaching assistants, course administrative support and coordination with faculty and an academic technology specialist to develop innovative teaching tools. The coordinator may also teach an interdisciplinary junior/senior level seminar in his/her area of interest. Candidates should have a Ph.D. in the biological, social, or behavioral sciences, teaching experience at the introductory level, interest in interdisciplinary teaching, and excellent communication and organizational skills. Use of innovative teaching and assessment techniques, and experience supervising and training teaching assistants is desirable, but not required. The position is for one year, re-

newable for at least two more years. For more information, see http://www.stanford.edu/dept/humbio/-core_course_coordinator.html Deadline: March 19 or until filled.

Please send a CV, statement of teaching philosophy, interests and experience including experience in interdisciplinary courses, teaching evaluation summaries if available, and the names and addresses of three references to: Core Coordinator Search Committee, Program in Human Biology, 450 Serra Mall, Building 80, Stanford University, Stanford, CA 94305-2160, or by e-mail to humbio-director@lists.stanford.edu. Stanford is an AA/EOE.

cboggs@stanford.edu cboggs@stanford.edu

TexasAMU EvolBiol

Texas A&M University

Department of Wildlife and Fisheries Sciences

Faculty Positions in Mammalogy and Ornithology

The Department of Wildlife and Fisheries Sciences at Texas A&M University seeks outstanding individuals to join our faculty as Assistant Professor of Ornithology and Assistant Professor of Mammalogy. These positions are charged with building successful teaching and research programs in their respective area of emphasis and will also serve as Curator of Birds and the Curator of Mammals for the Texas Cooperative Wildlife Collection. In this role, they will supervise and develop their respective collections, including frozen tissue collections. Successful candidates must have a PhD in an appropriate field and demonstrated research excellence in ecology, evolutionary biology, systematics, genetics, or conservation biology as evidenced by a record of peer reviewed publications. Records of extramural research funding and experience in teaching are desirable. Additional information on these positions, the department, and Texas A&M University can be found at <http://www.wfsc.tamu.edu> To apply: Indicate clearly the position you are applying for (separate applications are necessary for each position) and submit an electronic CV, statements of teaching and research interests, and philosophy regarding collections management and curation, plus contact information for three references to: Dr. Michael L. Morrison, Search Committee Chair, mlmorrison@ag.tamu.edu. Electronic submission deadline is 31 March 2007. The Texas A&M University System

is an Equal Opportunity Employer and strongly encourages women and minorities to apply.

t.lacher@conservation.org

U Akron Integrative Biol

Title: UAkron.IntegrativeBiologist

Assistant Professor The University of Akron

The University of Akron, Department of Biology, invites applications for a tenure track Assistant Professor position in the area of Integrated Bioscience to begin preferably Fall 2007. We seek a biologist who will play a central role in supporting our newly established Ph.D. program in Integrated Bioscience.

Candidates must hold a Ph.D. in a biologically-related field and post-doctoral experience is preferred. They should be able to interact effectively with another discipline, such as (but not limited to) chemistry, computer science, geology, math, biomedical/chemical engineering, and materials/polymer science. Successful candidates will be effective instructors of both undergraduate and graduate students and be able to develop an externally-funded research program. Review of applications will begin immediately and continue until the position is filled. Please submit a cover letter, statement of research and teaching interests, current CV, and three letters of reference to:

Dr. Bruce Cushing Chair of Biology and Director Integrated Biosciences Doctoral Program, The University of Akron, Dept Biology, Akron, OH 44325-3908 USA
cbuce@uakron.edu.

Electronic submission of application materials, followed by hardcopy mailing, is encouraged. The University of Akron is committed to a policy of Equal Employment Opportunity and to the principles of Affirmative Action in accordance with state and federal laws.

Todd A. Blackledge Assistant Professor Department of Biology University of Akron Akron, OH 44325-3908

Voice: (330) 972-7264 Fax: (330) 972-8445 Email: blackledge@uakron.edu <http://www3.uakron.edu/-biology/blackledge/index.htm> "Blackledge, Todd Alan" <tab27@uakron.edu>

UC Berkeley Manager Genomics Facility

Specialist Series: The Environmental Genomics Facility, a shared molecular biology laboratory housed in the UC Berkeley Department of Environmental Science, Policy and Management, seeks a part-time Facility Manager. Reporting to the facility directors, the manager will administrate this facility, which offers the use of standard molecular laboratory equipment (thermal cyclers, gel diagnostic systems, quantitative PCR system, etc.) to constituents across campus. Will help design experiments and optimize the use of PCR and DNA techniques, train graduate and undergraduate students in their application and use, and proactively help to secure funding for the maintenance and expansion of this facility. Proposed annual full-time salary range is \$37,548 - \$50,112. Proposed appointment is expected to start on April 13, 2007.

Ph.D. preferred in the biological sciences and technical proficiency in a range of molecular biological techniques is required. Specifically, the individual should have experience extracting nucleic acids (DNA and RNA) and proteins from microbial, plant and animal samples, be familiar with a wide array of PCR protocols used in systematics, molecular ecology, evolution and functional genomics and troubleshooting methods, be capable of designing quantitative (real time) PCR experiments. Techniques that will be required periodically include microsatellite and related fragment analyses and DNA sequencing, PCR primer design and troubleshooting, cloning and subcloning of amplified DNA, and gene expression studies.

Because of the multi-user nature of the Environmental Genomics Facility, a training component is also required for this position. The candidate should have a demonstrated ability to train students in all of the above techniques. The Facility Manager is expected to keep abreast of new technical developments in the fields of ecology, evolutionary and environmental biology. Continued publication in the applicant's major research area is expected. Excellent oral and written communication skills are a must. The ability to grasp the research objectives of various Principal Investigators and help design effective experiments to meet them are critically important to the success of this position.

The Facility Manager will, in collaboration with the

co-directors, attempt to secure internal and external funding to maintain and expand this facility. Writing proposals, such as NSF equipment grants, to fund initiatives that expand user research ability is required. Send curriculum vitae, publication list, and names of three professional references to: Dr. Patrick O'Grady, Dept. Environmental Science, Policy and Management, 137 Mulford Hall, University of California, Berkeley, CA 94720-3114 by March 30, 2007; E-mail: ograde@nature.berkeley.edu. The University of California is an Equal Opportunity/Affirmative Action Employer. Applicants should ask referees to review the UC Berkeley Statement of Confidentiality found at:

<http://apo.chance.berkeley.edu/evaltr.html>

Rosalyn Farmer <rfarmer@nature.berkeley.edu>

UCaliforniaMerced SystemsBiol

Although the specific examples given in this advertisement are relatively narrow, this position is open to evolutionary biologists with relevant expertise and broad interests.

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Assistant Professor Life Sciences - Systems Biology
The University of California is creating a dynamic new university campus and campus community in Merced, California, which opened in September 2005 as the tenth campus of the University of California and the first American research university built in the 21st century. In keeping with the mission of the University to provide teaching, research and public service of the highest quality, UC Merced will be providing new educational opportunities at the undergraduate, masters and doctoral levels through three academic schools: Engineering, Natural Sciences and Social Sciences/Humanities/Arts.

Schools of Natural Science and Engineering are seeking an assistant professor (tenure track) in the areas of experimental or computational systems biology. Systems biology is used here to mean a research approach that uses comprehensive datasets and multiple types of analysis to relate the overall function of an organism, organelle, or regulatory pathway to the underlying biochemical or biophysical processes, with an ultimate goal of a predictive understanding of the system's behavior. Applications of special relevance to research emphases at UC Merced include the mechanisms of cell

fate decisions, complex diseases such as diabetes or inflammation, and microbial systems relevant to human disease.

The University of California at Merced is an affirmative action/equal opportunity employer with a strong institutional commitment to the achievement of diversity among its faculty, staff, and students. The University is supportive of dual career couples. Qualifications: Applicants should have a Ph.D. in the biological sciences or related field, a record of research, publication and teaching commensurate with a faculty appointment at the University of California, and should have demonstrated the potential to develop a strong research program in systems biology. Applicants should have the ability to interact with colleagues from a broad range of disciplines, and a strong interest in developing interdisciplinary and multidisciplinary undergraduate and graduate curricula and research programs. We require a commitment to excellence and innovation in undergraduate and graduate education and training, and a commitment to education and outreach for students of diverse backgrounds, particularly disadvantaged or underrepresented students. Salary: Negotiable, based on University of California salary scales Closing Date: 02/15/2007 To Apply: Interested applicants are required to submit 1) a cover letter 2) curriculum vitae 3) statement of research 4) statement of teaching 5) a list of five references with contact information including mailing address, phone number and e-mail address and 6) three representative publications.

Please do not submit individual letters of recommendation.

Applications must be submitted via this website. <http://jobs.ucmerced.edu/n/academic/-position.jsf?positionId=732>

For more information: Please contact Professor David Ojcius (dojcius@ucmerced.edu) or Professor Marcos Garcia-Ojeda (mgarcia-ojeda@ucmerced.edu), search committee co-chairs.

Michael N Dawson <mdawson@ucmerced.edu>

UGuelph 3 EvolutionaryBiol

The department of integrative biology, University of Guelph, is inviting applications for 3 evolution positions in: functional genomics, evolutionary biology, and co-evolutionary ecology.

Candidates must have a PhD, preferably with post-doctoral experience, a strong record of publications in peer-reviewed journals, and ideally some experience in undergraduate/graduate teaching. Further details on specific positions can be obtained by contacting the individuals indicated with each position description. Applicants should submit three copies of their curriculum vitae, including the names of three referees, and a letter of application to the Dean's Office, College of Biological Science University of Guelph Guelph, ON, Canada N1G 2W1. Committees will be looking at applications from March 31st. For more information and a complete list of all 13 College of Biological Science tenure track positions, visit the University of Guelph's faculty jobs website: <http://www.uoguelph.ca/facultyjobs/postings/ad07-01.htm>

Functional Genomics We seek individuals with expertise in integrating broad gene and/or protein expression data sets to understanding complex processes of physiological regulation and evolutionary adaptations in animals. Opportunities exist to collaborate with a large group of comparative animal physiology, ecology and evolutionary biology researchers with a strong focus on aquatic organisms. Contact Dr. Patricia Wright, email patwri@uoguelph.ca

Evolutionary Biology We seek individuals with expertise in evolutionary biology, particularly those that use theoretical and modeling approaches, which complement our existing strengths in evolutionary ecology, evolutionary genetics and molecular systematics. Opportunities exist to participate in new graduate teaching and research initiatives in bioinformatics, biodiversity, and applied evolution. Contact Dr. Moira Ferguson, email mmfergus@uoguelph.ca

Co-evolutionary Ecology We seek individuals with a research focus on interactions, dynamics and reciprocal co-evolution among species in ecological communities. We are particularly interested in novel applications of co-evolution, such as emerging problems in the evolution of infectious disease, pests, pathogens and/or non-native species as well as the ability to span multiple levels of organization. Contact Dr. John Fryxell, email jfryxell@uoguelph.ca

berenrob@uoguelph.ca

UHelsinki TheoEvolutionaryEcology

The Major Subject Division of Ecology and Evolution-

ary Biology at the Department of Biological and Environmental Sciences of the University of Helsinki invites applications for a fixed-term University Lectureship in Theoretical Ecology

The term of appointment for this replacement position is from 1 September 2007 to 31 July 2011.

The salary for the post will be based on a job-specific demands level to be confirmed, as well as on personal work performance.

The duties of the appointee will include participation in the teaching theoretical ecology within the major subjects of ecology and evolutionary biology, student guidance, the supervision of theses, and conducting theory-oriented research in ecology and/or evolutionary biology. The emphasis of the duties of the post is on research, but the appointee is also expected to assume some responsibility for the development of teaching in the field of theoretical ecology. The field of teaching of the post includes, in particular, theoretical thinking, approaches and methods, as well as the development of teaching in ecology and evolutionary biology.

For required qualifications, instruction for applications and other information, see http://www.helsinki.fi/bio/-hallinto/ilmoitus_ekologialehtori_eng.pdf Written applications, together with the required enclosures, should be addressed to the Faculty of Biosciences and sent to the Registrar of the University of Helsinki, P.O. Box 33 (Yliopistonkatu 4), 00014 University of Helsinki, to arrive no later than Wednesday 21 February 2007, by 3.45 p.m. Further information is available from Professor Veijo.Kaitala@Helsinki.fi or tel. + 358 9 191 57723.

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Many thanks! Hanna Kokko –

Hanna Kokko, Department of Biological and Environmental Science PO Box 65 (Viikinkaari 1), 00014 University of Helsinki, Finland Tel. +358-9-1915 7702, fax +358-9-1915 7694 www.helsinki.fi/~hmkokko/ hmkokko@mappi.helsinki.fi

UKwaZulu-Natal EvolParasitology

The University of KwaZulu-Natal is committed to employment equity and will give preference to appointable candidates from the designated groups. All appointments are based on individual merit, relative to criteria mentioned below. Candidates who do not meet all the

minimum criteria will not be considered. The university reserves the right not to fill the post or to extend the recruitment process through re-advertising and head-hunting in order to meet its equity targets.

PROFESSOR: PARASITOLOGY SCHOOL OF BIOLOGICAL & CONSERVATION SCIENCES DURBAN CENTRE REF NO.: SA54/2006

The School, based at the Durban and Pietermaritzburg centres, is well established with one of the strongest research records in the University and a substantial graduate school. Its research facilities are rapidly expanding and modern instrumentation is available.

The School seeks a leader for the subdiscipline of parasitology, who will contribute actively to research, curriculum development and teaching in the field. The successful candidate will have an exceptional record in parasitology, preferably utilising molecular techniques. Research supervision at all levels and establishment of a strong independent research programme will be essential. The appointee will also be responsible for co-ordination of the undergraduate degree programme in Biomedical Sciences in collaboration with the School of Health Sciences and Nelson R. Mandela School of Medicine.

MINIMUM REQUIREMENTS: A PhD focussing on parasitology; An excellent record of independent research evidenced by current publication in the peer-reviewed international parasitology literature; Proven ability to attract competitive research grants; A substantial record of successful supervision of doctoral students; Proven academic leadership in teaching and research; Experience in academic administration.

ADVANTAGES: Research interest in medical parasitology; Experience in undergraduate curriculum development; Experience in the application of modern molecular techniques.

The position is available from 01 July 2007. Shortlisted candidates will be required to make a presentation.

For further information see the School website at <http://www.ukzn.ac.za/biology> or contact Dr Jenny Lamb at lambj@ukzn.ac.za

The remuneration package offered includes benefits and will be dependent on the qualifications and experience of the successful applicant. The selection process will commence on 12 January 2007 and will continue until a suitable candidate is appointed or a decision is taken not to fill the post. (This is still open.)

Applicants are required to submit a covering letter highlighting their experience in, and providing evidence for, each of the minimum requirements and any ad-

vantages listed above, together with a detailed CV including the names, full addresses, fax numbers and e-mail addresses of three referees, to Mrs S Gellately, Human Resources Administration, Howard College Campus, University of KwaZulu-Natal, Durban, 4041, Fax No +27 031 260 2139. E-mail Gellatel@ukzn.ac.za

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

ULibreDeBruxelles EvolTropicalPlants

ACADEMIC FULL-TIME POSITION IN TROPICAL BOTANY UNIVERSITE LIBRE DE BRUXELLES, BELGIUM

The official version of this advertisement is in French; see <http://www.ulb.ac.be/docs/greffe/vacances/-academique/index.html> The Free University Brussels invites applications for a full-time position in Tropical Botany to begin in fall 2007.

Title required: PhD in Science or in Agronomy (or equivalent)

The candidate must demonstrate his/her capacity to conduct high quality research in tropical botany. A field work experience in the tropics is desired.

He/she will join the teaching staff in plant biology in the "Académie Universitaire Wallonie-Bruxelles" and participate to the teaching of botany and plant sciences (including lectures, practicals, field work and supervision of Master and PhD theses), especially related to tropical botany. He/she will develop a research activity focused on one or several of the following areas: plant biodiversity in tropical regions, systematics and evolution of plants, conservation biology and ecology, preferably on flowering plants and using molecular tools.

The candidate is expected to develop cooperation with developing countries.

For further details, please get in touch with Prof. Yves ROISIN, Departement de Biologie des Organismes, Tel +32 2 650 4512, yroisin@ulb.ac.be, or Prof. Pierre MEERTS (pmeerts@ulb.ac.be).

The applicant should provide: * A complete curriculum vitae (presented as required in the following webpage: <http://www.ulb.ac.be/tools/CV-type.rtf>) * A teaching project * A research project (max. 3500 signs) * A

commented list of his/her most significant publications.

Applications should be sent in duplicate to the Rector, Université Libre de Bruxelles, Avenue FD Roosevelt, 50, B-1050 BRUSSELS, Belgium.

Deadline for applications: 15th March 2007

Please refer to the French version of this document for further details (<http://www.dev.ulb.ac.be/greffe/files/-1582.pdf>)

yroisin@ulb.ac.be yroisin@ulb.ac.be

UMaryland HumanEvolGenomics

Research Technician Position in Human Evolutionary Genomics

A research technician position is available in a human population genetics laboratory in the Department of Biology at the University of Maryland at College Park for NIH and NSF funded research. Projects in the lab focus on a unique resource of >6,000 DNA samples from ~100 ethnically and geographically diverse African populations. These samples are being used for genome-level analyses of diversity at both coding and non-coding loci (including high throughput resequencing and whole genome SNP and STRP genotyping). For many of these samples we also have phenotype data for a number of traits that are likely important in adaptation, including those with a complex pattern of inheritance. We are using these data (1) to infer population structure and demographic history and test models of modern human evolution (2) to identify regions of the genome that are targets of selection using whole genome scans (3) to identify functionally significant variants using genotype/phenotype association studies as well as gene expression analyses (4) to study the genetic basis of resistance against infectious disease (with a focus on malaria) and co-evolution of the human and Plasmodium falciparum genomes. Collaborators on these projects include Jonathan Pritchard, Molly Przeworski, Carlos Bustamante, Josh Akey, Greg Wray, Philip Awadalla, Gil McVean, and Anna Tramontano. Additional information about the Tishkoff lab can be found at <http://www.life.umd.edu/biology/-tishkofflab/> .

UMCP is located in a suburb of Washington D.C. with easy access to a number of research institutions in the Baltimore/D.C. area including NIH, the Smithsonian, TIGR, George Washington University and Johns

Hopkins University. More information about the Biology Department and the Behavior, Ecology, Evolution, and Systematics (BEES) program at UMCP is available at <http://www.life.umd.edu/biology/> and <http://www.life.umd.edu/biology/>

Candidates for the research assistant position must have a B.S. degree or higher in a biological sciences field. A minimum of one year laboratory research experience is required with knowledge of basic molecular biology and genetic analysis techniques. Experience with high throughput sequencing and/or genotyping and database management would be a plus. Job duties will include assistance in research projects in the lab as well as laboratory management and maintenance. Starting dates are flexible. Salaries are commensurate with qualifications and experience.

Please send curriculum vita and contact information for three references to Dr. Sarah Tishkoff, Dept. of Biology, Biology/Psychology Building #144, Univ. of Maryland, College Park, MD 20742 or e-mail to tishkoff@umd.edu. Women and minority members are strongly encouraged to apply. The University of Maryland is an equal opportunity/affirmative action employer.

Sarah Tishkoff, Ph.D. Associate Professor
Dept. of Biology Biology/Psychology Building
Univ. of Maryland College Park, MD 20742
Tel: 301-405-6038 Fax: 301-314-9358
email: <BLOCKED::mailto:tishkoff@umd.edu>
tishkoff@umd.edu

<BLOCKED::<http://www.life.umd.edu/biology/-tishkofflab/>> <http://www.life.umd.edu/biology/-tishkofflab/> **NOTE NEW E-MAIL ADDRESS LISTED ABOVE**

UMassLowell GeneticsPopGenetEvol

Assistant/Associate Professor

Department of Biological Sciences

The University of Massachusetts Lowell Department in Biological Sciences invites applications for a full-time tenure-track position, rank negotiable, to start Fall 2007. The successful candidate will be expected to build a vigorous, externally funded research program, and collaboration within this and other departments is encouraged. Current faculty research interests in-

clude bioinformatics, genetics, plant science, neurobiology, cancer biology, invertebrate biology, developmental biology, virology, microbial ecology, and biogeochemistry. Our campus is located very near the vibrant academic and commercial biotechnology centers of Boston, Cambridge and Worcester.

We are seeking individuals with expertise in one or more of the following areas: Genetics, Population Genetics and/or Evolution.

Teaching obligations include development of upper level undergraduate/graduate courses in his/her expertise and participation in the teaching of core undergraduate courses as needed.

MINIMUM QUALIFICATIONS:

- Earned doctorate
- Demonstrated ability teaching at the undergraduate and graduate levels
- Commitment to develop and sustain an externally funded research program
- Demonstrated potential for publications in scholarly journals
- Excellent communication and interpersonal skills
- Demonstrated ability working with diverse student and faculty population

Applicants should submit the following materials by BOTH mail and electronic submission by March 16, 2007:

A curriculum vita, copies of several recent research publications, a statement of research and teaching interests, not to exceed three pages, and arrange for three letters of recommendation to be sent to:

Biological Sciences Faculty Search

Department of Biological Sciences

University of Massachusetts Lowell

One University Avenue

Lowell, MA 01854

Job Reference #FC04020701

Email materials to biology_search07@uml.edu.

Please include reference number in subject line of e-mail.

The University of Massachusetts is an Equal Opportunity/Affirmative Action Title IX, H/V, ADA 1990 Employer.

bbettenc69@gmail.com

UMontpellier PaidStage TroutGenetics

Dear colleagues, Sorry, this message is for French speaking M1/M2 students.

Bonjour, Je cherche urgemment un(e) stagiaire pour un stage rémunéré sur la gestion et la génétique de la truite française. Mieux pour un stage professionnalisant. SVP faites circuler la fiche descriptive jointe. Merci

Hi, I'm looking urgently a student for a paid stage on French trout management and genetics. Better if the student is in a professional formation Please dispatch around you this demand and the accompanied descriptive file Thanks

Patrick BERREBI UMR 5554 "Institut des Sciences de l'Evolution" Equipe Métapopulations, Conservation et Co-évolution Université Montpellier II CC 065. Place E. Bataillon 34095 Montpellier Cedex 5 (France)

Mél: berrebi@univ-montp2.fr Tél. France 04 6714 3732
- International 33 4 6714 3732

Patrick BERREBI <berrebi@univ-montp2.fr>

UNottingham ResAssoc MicrobialPops

School of Biology - Institute of Genetics, University of Nottingham, UK

Research Associate/Fellow (3 years)

'The importance of non-genotypic diversity for the fitness of microbial populations'

Funded by the Natural Environmental Research Council (NERC), applications are invited for the above post to work on a project aimed at elucidating the importance of non-genotypic diversity for the fitness of laboratory and wild yeast isolates. The research will exploit the *S. cerevisiae* model as well as yeasts isolated from the natural environment, applying novel culture strategies to address this important question. Excellent facilities for the research are available at the University of Nottingham. The successful candidate will join a well-

funded research group within the RAE 5 rated Institute of Genetics, School of Biology.

Candidates with expertise in one or more of the following techniques are particularly welcome to apply: microbial/yeast physiology and culturing techniques, cellular stress responses, DNA fingerprinting, flow cytometry/cell sorting, isolation of microorganisms from the field. Candidates must have a relevant degree; a PhD is desirable.

Salary will be within the range £21,682 - £30,913 per annum, depending on qualifications and experience (salary can progress to £34,793 per annum, subject to performance) - (£23,692 maximum without PhD). This post will be offered on a fixed-term contract for a period of three years.

Informal enquiries may be addressed to Dr S V Avery, tel: +44 (0)115 951 3315, Email: Simon.Avery@Nottingham.ac.uk or Dr P S Dyer, tel +44 (0)115 951 3203, Email: Paul.Dyer@Nottingham.ac.uk.

Candidates should send a detailed CV, together with the names and addresses of two referees, to Dr S V Avery, School of Biology, The University of Nottingham, University Park, Nottingham, NG7 2RD. Email: Simon.Avery@Nottingham.ac.uk. Please quote ref. MED/118. Closing date: 26 February 2007.

Key references Bishop AL, Rab FA, Sumner ER and Avery SV (2007). Phenotypic heterogeneity can enhance rare-cell survival in 'stress sensitive' yeast populations. *Mol. Microbiol.* 63, 507-520.

Avery SV (2006). Microbial cell individuality and the underlying sources of heterogeneity. *Nature Rev. Microbiol.* 4, 577-587.

This message has been checked for viruses but the contents of an attachment may still contain software viruses, which could damage your computer system: you are advised to perform your own checks. Email communications with the University of Nottingham may be monitored as permitted by UK legislation.

McElligott Alan <Alan.Mcelligott@nottingham.ac.uk>

UOslo EvolBiol

Dear Colleagues,

I want to bring to your attention a vacant position at the Department of Biology, University of Oslo. Al-

though the position includes administrative responsibility for the alpine research station at Finse, it is a normal faculty position with full freedom to pursue research, and the station itself has a part-time manager. The position is open in regard to research topic, and I encourage both ecologists and evolutionary biologists with interest in any alpine system to apply. Note deadline 13 March.

The position is announced in Nature (also pasted below): <http://naturejobs.nature.com/taxis/jobsearch/-details.html?id=45db01094a0610;lookid=nature>

Sincerely,

Thomas Hansen (thomas.hansen@bio.uio.no)

University of Oslo Associate Professor

UNIVERSITY OF OSLO

ASSOCIATE PROFESSOR (F) POSITION IN BIOLOGY (including the management of Finse research center) is available at THE DEPARTMENT OF BIOLOGY, UNIVERSITY OF OSLO

Additional information: professor Tore Slagsvold, tel. + 47 22 85 75 38 e-mail: tore.slagsvold@bio.uio.no instituttleder Trond Schumacher, tel. + 47 22 85 46 61 e-mail: trond.schumacher@bio.uio.no

Pay grade: 56 - 67 (NOK 403 500,- NOK 494 000,-) depending on qualifications Application deadline: 13 March 2007

REF. NO.: 07/1158

Four sets of the application (marked with REF.NO.), including CV, scientific publications, certified copies of testimonials and a complete list of all documents submitted should be forwarded to:

Faculty of Mathematics and Natural Sciences, University of Oslo, Attn.: Senior Executive Officer Bente Schjoldager, P.O.Box 1032, NO-0315 OSLO, e-mail: bente.schjoldager@matnat.uio.no

Application documents, except original publications, will not be returned

The position is at the Department of Biology, under Faculty of Mathematics and Natural Sciences, University of Oslo.

This post comes under the Department of Biology, Program for experimental behaviour and population ecology (EBE). Currently there are 5 full professors, 3 post doc researchers, 3 Ph.D. students, 7 M.Sc. students and 1 technician working within the research program. The research program has strength in studies of population and behavioural ecology of terrestrial invertebrates, mammals, birds and lichens. The EBE staff has

a close collaboration with the companion research programs at the Department. The Department has long traditions in the alpine ecosystem of the Finse area (Hardangervidda), in particular in studies on adaptations and on life history traits and population dynamics of key organisms of the alpine tundra.

The post includes the administrative leadership (management) of Finse research center, established in 1972 and owned by the University of Oslo (UiO) and the University of Bergen (UiB). The center is located in the northwestern corner of the Hardangervidda plateau, 1200 m asl. The center activities include research projects, field courses for students at all levels and procurement of all disciplines of natural sciences, in particular in high mountain ecology. The center serves as a field station for researchers and students from UiO, UiB, and other national and international universities.

The manager is expected to administrate the various activities, including practical and economical responsibilities, and expects to develop university courses and research projects in his/her field of science and to supervise MSc and PhD students doing their work at the station. The manager is also expected to participate in the daily activities at the center, in particular during the summer months. The remote localisation of the center calls for an independent and self-willed person with practical skills being familiar with outdoor activities in the arctic-alpine zone.

A requirement for the post is that the successful candidate initiates projects and research activities at the center, and connects these to his/her research group at the Department of Biology, UiO. The successful candidate is expected to develop research activities of high international standard and to collaborate with the existing research environments at the Department. The applicant is therefore asked to present his/her own plans for the future work at the center. Furthermore, the applicant must document an ability to finance his/her own research activities. Administrative experience, in particular in research funding and planning, and teaching experience, will give an advantage.

A doctor's degree, strong publication record, postdoctoral experience and teaching experience are required. Experience from field work in alpine environments, and in the discipline of entomological ecology and population biology are advantageous.

The post is announced as an associate

— / —

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>

URochester ResTech BacterialMolEvolEcol

Research Technician III Molecular Ecology of Bacteria
Wolbachia are among the most abundant and widespread bacteria on the planet. We are investigating their diversity and effects on insects using molecular methods. This work involves molecular and genetic research, and data analysis to study the global diversity of these bacteria and their insect hosts. The position is in the evolutionary genetics laboratory of Professor John Werren, Dept. of Biology, University of Rochester.

Responsibilities include conducting molecular genotyping of bacteria and insects, bioinformatics, computers, and genetic analyses of sequences from strains of the intracellular bacterium Wolbachia collected from around the world. Other work includes routine administrative laboratory duties and assistance in training laboratory personnel in routine computer, bioinformatics, and genomic procedures. Strong organizational skills are required for this position.

Please contact Rachel Edward (redward2@mail.rochester.edu) or Crystal Allen (crit*rose@yahoo.com) if you are interested in this position (585-275-3889).

Jack Werren <werr@mail.rochester.edu>

URochester Tech MolGeneticsSpeciation

Lab Tech - Molecular Genetics of Speciation

Conduct studies of genetic and molecular evolution in insects. This position is part of a 4-year NIH grant funded project to investigate molecular genetics and evolution of male-specific differences in wing size between closely related species of *Nasonia*. The project exploits the recently sequenced genome of *Nasonia*, an emerging model for the genetics of complex traits. Familiarity with standard molecular techniques involving DNA and RNA, PCR, and QPCR, cloning and conducting sequence reactions and alignments is desired.

RNAi methods will also be used to study the role of genes in species differences. The person will also assist in administrative aspects of the project. Good organizational skills are a plus. BS in Biology is preferred. Salary will be commensurate with experience. The position is in the evolutionary genetics laboratory of Professor John Werren, Dept. of Biology, University of Rochester.

Please contact Rachel Edward (redward2@mail.rochester.edu) or Jon Giebel (jgiebel@mail.rochester.edu) if you are interested in this position (585-275-3889).

John (Jack) Werren Professor of Biology University of Rochester Rochester, NY 14627 Office: 585-275-3694 Lab: 585-275-3889 Fax: 585-275-2070 web:

<http://www.rochester.edu/College/BIO/-labs/WerrenLab/index.html> Jack Werren
<werr@mail.rochester.edu>

UTuebingen EvolBiolOfPlantsFungi

FULL PROFESSOR ORGANISMAL BOTANY-MYCOLOGY TUEBINGEN

The Faculty of Biology of the Eberhard-Karls-University Tuebingen invites applications for the post of

Full professor (W3) in "Organismal botany and mycology" (Successor Prof. Dr. F. Oberwinkler)

available from 1st April 2008. The successful applicant will pursue an internationally high-ranking research agenda in the field of evolutionary biology of plants, fungi or their interaction. Teaching obligations cover all aspects of organismal botany and mycology. Close collaborations within the interfaculty teaching and research platform "Evolution and Ecology Forum" EvE are expected. EvE integrates organismal biology in Tuebingen and offers cooperation with the faculties of Biology and Geosciences and the Max-Planck-Institute for Developmental Biology. The post includes management of the botanical garden and the "Herbarium Tubingense".

A formal requirement for appointment is a "Habilitation" or equivalent level of scientific and academic teaching qualifications.

The University of Tuebingen is committed to strengthen the proportion of women in research and

teaching and strongly encourages applications of qualified female scientists.

If this is a candidate's first professorship, the appointment is limited to three years initially, with tenure being granted after positive evaluation. Exceptions can be made for foreign applicants or candidates from the private industry. Tenure does not require another appointment procedure.

Disabled applicants with equal qualification will be considered with higher preference.

Please send your application letter including c.v., certificates, list of publications and a summary of teaching experience by 15 March 2007 to Dekanat fuer Biologie der Universitaet Tuebingen, Auf der Morgenstelle 28, 72076 Tuebingen, Germany

Nico K. Michiels (Prof.) Animal Evolutionary Ecology Zoological Institute, Faculty of Biology U niversity Tuebingen Auf der Morgenstelle 28 E 72076 Tuebingen Germany

Tel. +49 7071 29 74649 Mobile +49 170 4758003 Fax +49 7071 29 5634

nico.michiels@uni-tuebingen.de <http://www.uni-tuebingen.de/evoeco> <http://eve.uni-tuebingen.de>

Nico Michiels <nico.michiels@uni-tuebingen.de>

UTuebingen VertebrateEvol

The Faculty of Biology of the Eberhard-Karls-University Tuebingen invites applications for the position of

Full professor (W3) in "Evolutionary Biology of Vertebrates"

available from 1st of April 2008.

The successful applicant will pursue an internationally high-ranking research agenda in the field of organismal zoology, preferably with a focus on vertebrates. Teaching obligations cover all aspects of zoology, with emphasis on vertebrate evolution. Close collaborations with the interfaculty teaching and research platform "Evolution and Ecology Forum" (EvE) are expected. EvE integrates organismal biology in Tuebingen and offers cooperation with the faculties of Biology and Geosciences and the Max-Planck-Institute for Developmental Biology. The position includes management of the zoological collection and the limnological field station

“Federsee”.

A formal requirement for appointment is a “Habilitation” or equivalent level of scientific and academic teaching qualifications.

The University of Tuebingen is committed to strengthen the proportion of women in research and teaching and strongly encourages applications of qualified female scientists.

If this is a candidate’s first professorship, the appointment is limited to three years initially, with tenure being granted after positive evaluation. Exceptions can be made for foreign applicants or candidates from the private industry. Tenure does not require another appointment procedure.

Disabled applicants with equal qualification will be considered with higher preference.

Please send your application letter including CV, certificates, list of publications and a summary of teaching experience by 10 th of April 2007 to Dekanat fuer Biologie der Universitaet Tuebingen, Auf der Morgenstelle 28, 72076 Tuebingen, Germany

Nico K. Michiels (Prof.) Animal Evolutionary Ecology Zoological Institute, Faculty of Biology University Tuebingen Auf der Morgenstelle 28 E 72076 Tuebingen Germany

Tel. +49 7071 29 74649 Mobile +49 170 4758003 Fax +49 7071 29 5634

nico.michiels@uni-tuebingen.de <http://www.uni-tuebingen.de/evoeco> <http://eve.uni-tuebingen.de>

Nico Michiels <nico.michiels@uni-tuebingen.de>

UWalesBangor Head Biol

UNIVERSITY OF WALES, BANGOR

COLLEGE OF NATURAL SCIENCES SCHOOL OF BIOLOGICAL SCIENCES

Head of Biological Sciences

Salary negotiable in Professorial Range (minimum £46,624 p.a.)

The University of Wales, Bangor provides research, teaching and learning of the highest quality. The RAE 4 rated School of Biological Sciences (SBS), within the newly created College of Natural Sciences, is at the forefront of delivering this vision with its acknowl-

edged delivery of world-class research and excellence in teaching. As part of a University-wide commitment to research, we seek a research-active Head of School with drive and vision to promote and coordinate high quality and distinctive output within our key research areas (<http://biology.bangor.ac.uk>). The appointment coincides with a period of major University expansion of research supported by considerable funding (£11M) from the Higher Education Funding Council for Wales and the Welsh Assembly Government, which underpin an innovative research and enterprise partnership between Bangor and the University of Wales, Aberystwyth. Such activity is enhanced by the Natural Environment Research Council’s (NERC) recent investment in the partnership between the University of Wales, Bangor and the NERC Centre for Ecology and Hydrology to create the Environment Centre for Wales (<http://biology.bangor.ac.uk/school/-environment-centre/>), within which SBS will play a leading role. Applications will be especially welcome from candidates who can contribute to the zoological or environmental aspects of our research portfolio. An appropriate package consistent with a research-active Head (including a Deputy Head plus the support of an experienced administrative and technical team led by the School’s Administrator, Teaching Administrator and Chief Technician) will be offered.

Bangor now seeks an outstanding individual as Head of School with commensurate research credentials and the ability to lead a thriving and dynamic academic community. They will be excited by the prospect of working within the pioneering multidisciplinary College structure (SBS, Schools of Ocean Sciences, and the Environment and Natural Resources), and will contribute to the overall vision of the University. Bangor is adjacent to the Snowdonia National Park, an area of outstanding natural beauty, with a diverse range of natural environments from rocky coastlands to alpine vegetation, and is well served by major routes and two international airports within 1.5 h.

Application forms and further particulars should be obtained by contacting Human Resources, University of Wales, Bangor; tel: + 44 (0)1248 382926/388132; e-mail: personnel@bangor.ac.uk; web: <http://www.bangor.ac.uk>. Electronic applications are encouraged using the on-line Application Form and should be submitted, along with a covering letter, C.V. and any other supporting documents, by email to Human Resources. (There is no need to duplicate information on the Application Form that is already in your C.V.)

Please quote reference number 07-6/114 when applying.

Closing date for applications: Wednesday 28th February, 2007.

A request for further information and/or an informal enquiry can be made to Dr M.A. Lock, Acting Head of School, tel: +44 (0)1248 382310, e-mail: m.a.lock@bangor.ac.uk

The Information Package relating to this post is available directly from the School. Please contact Mrs Karen Goodwin, School Administrator, tel: +44 (0)1248 382430, e-mail: k.r.goodwin@bangor.ac.uk

Dr Martin Taylor Brambell Building School of Biological Sciences University of Wales, Bangor Gwynedd LL57 2UW Tel: 01248 382344 email1: m.taylor@bangor.ac.uk email2: nitram8@hotmail.com Web page. <http://biology.bangor.ac.uk/~bss214/nitram8@hotmail.com>

UWalesBangor Reader EnvGenomics

UNIVERSITY OF WALES, BANGOR

COLLEGE OF NATURAL SCIENCES SCHOOL OF BIOLOGICAL SCIENCES

Reader / Chair of Environmental Genomics

Reader Grade: £46,624 - £49,167 p.a. or Salary negotiable in Professorial Range (minimum £46,624 p.a.)

Applications to the School of Biological Sciences are invited from candidates with a proven world-class record of research in environmental genomics. We expect applicants to investigate organism function within the environment in its broadest context by exploiting state-of-the-art genomic and post-genomic technology. The successful candidate will advance evolutionary and ecological theory, or an understanding of ecosystem structure and function, utilising existing and new genomic knowledge and technology. Achieving this will be facilitated by linkage with the strong research base in molecular ecology and evolution, gene regulation, metabolite profiling, ecosystem function and conservation already present in Bangor and collaborating institutions. This is enhanced by NERC's recent investment in the partnership between the University of Wales, Bangor and the NERC Centre for Ecology and Hydrology to create the Environment Centre for Wales.

Applicants will have a strong track record of research funding, academic leadership and collaboration. Re-

search themes of particular interest include genomic regulation of ecological interactions between species (e.g. symbiosis, pathogen-host, herbivore-plant or resource competition), or of biological response to environmental change (e.g. climate, pollution, land use) and the evolution of adaptive variation.

The post is permanent, but is funded in the first instance by the new £11m Research and Enterprise Partnership between the University of Wales, Aberystwyth and the University of Wales, Bangor. The appointee will join the Centre for Integrative Research in the Rural Environment programme within the partnership which links Bangor's research with the recently strengthened international expertise in bioinformatics, metabolomics and molecular and environmental plant genetics in Aberystwyth. In addition, the successful candidate will contribute to teaching in the School of Biological Sciences within their own specialisation and perform relevant administrative duties.

Application forms and further particulars should be obtained by contacting Human Resources, University of Wales, Bangor; tel: + 44 (0)1248 382926/388132; e-mail: personnel@bangor.ac.uk; web: <http://www.bangor.ac.uk>. Electronic applications are encouraged using the on-line Application Form and should be submitted, along with a covering letter, C.V. and any other supporting documents, by email to Human Resources. (There is no need to duplicate information on the Application Form that is already in your C.V.)

Please quote reference number 07-6/97 when applying.

Closing date for applications: Wednesday 28th February, 2007.

Informal enquiries can be made to Professor Gary Carvalho, tel: +44 (0)1248 382100; e-mail: g.r.carvalho@bangor.ac.uk or Professor Roger Thorpe, tel: +44 (0)1248 382312, e-mail: r.thorpe@bangor.ac.uk

The Information Package relating to this post is available directly from the School. Please contact Mrs Karen Goodwin, School Administrator, tel: +44 (0)1248 382430, e-mail: k.r.goodwin@bangor.ac.uk

nitram8@hotmail.com

Umelbourne BehaviouralEvol

LECTURER (Level B, Fixed-Term) in Behavioural

Ecology Position No: 0016511 Department of Zoology, University of Melbourne, Australia Salary: \$65,630 - \$77,934 p.a.+ 9% Employer superannuation contributions

This full-time (fixed-term) position is a staff replacement and is available until the end of 2009. It provides immediate opportunities for collaboration in existing research programs within the Animal Behaviour and Evolution research cluster, particularly in the fields of signalling, sexual selection or animal mating systems. In addition to participating in general undergraduate biology teaching, the appointee will contribute to specialised higher-level undergraduate and postgraduate courses including those in animal behaviour, evolutionary biology and ecology. In line with our commitment to facilitating research opportunities for the successful candidate, the teaching load will be less than that expected for faculty on a continuing appointment.

Further information about this position, including details on how to apply, is available at www.jobs.unimelb.edu.au (Use the above position number as the keyword in the Job Search screen). For enquiries, contact Prof Mark A Elgar, tel. +61 3 8344 4338, email m.elgar@unimelb.edu.au

Closing Date: 2 March 2007

Mark Elgar <m.elgar@unimelb.edu.au>

WillametteU AnimalEvol

Please post the following tenure track job opportunity for someone with background in Animal Evolution with a molecular and whole organism background. We look forward to applications.

Thanks much!

Animal Evolutionary Ecologist Assistant ProfessorThe Department of Biology at Willamette University invites applications for a tenure-track position at the level of assistant professor for an Evolutionary Ecologist to begin August 2007. Proficiency with molecular techniques is required. Preference will be given to candidates who research whole animal level questions and whose interests complement our existing field-

based strengths. Specific areas of interest include, but are not limited to, comparative morphology, population genetics, adaptation, speciation, and the evolution of species' interactions. The successful applicant will be expected to develop an externally funded research program that involves undergraduates. Teaching duties include introductory biology, an intermediate course in Evolution, and a research methods course including molecular techniques and/or strong computational skills. Candidates must have a PhD, postdoctoral training, a record of peer-reviewed publications and scholarly accomplishments commensurate with experience. Applicants should submit a letter of application, curriculum vitae, a concise description of research and teaching interests, and three reference letters to Barbara Stebbins- Boaz, PhD, Chair, Department of Biology, Willamette University, 900 State St., Salem, OR 97301. Applications should be received by March 15, 2007. Please visit our website for more information at <http://www.willamette.edu/>. Willamette maintains a strong institutional commitment to diversity and strives to recruit and retain candidates from communities of color and ethnic groups.

skephart@willamette.edu skephart@willamette.edu

WoodsHole SummerUndergrad BacterialSymbiosis

Undergraduate research opportunity in bacterial symbiosis - Woods Hole

We seek a highly motivated undergraduate student for an NSF REU (Research Experience for Undergraduates) position at the Marine Biological Lab in Woods Hole, MA. The student will join the lab of Jennifer Wernegreen to explore population dynamics and potential functions of bacterial endosymbionts associated with ants. This 10-week position (late May to early August) will include support for housing at the MBL, travel, and a summer stipend. The position is contingent upon receipt of funding.

For details, please see: http://www.mbl.edu/hr/-job_search.php?func=detail&par=job_id=532

Jennifer Wernegreen <jwernegreen@mbl.edu>

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18srRNA alignment

Hello All, I am working on phylogenetic study which uses 18S rRNA, and I am trying to make a secondary structure rRNA alignment for 30+ sequences (invertebrates). I found out that many papers refer to DCSE (Dedicated Comparative Sequence Editor) written by Peter De Rijk, however all internet links direct to a site which is dead. I have also tried (and failed) to reach the author. I have therefore these questions:

1) does anyone know if this software is still in use and if yes where I can get it? 2) if there is an alternative package which can read/edit or assist in alignment of rRNA with secondary structure (i.e. what do YOU use?) 3) if

any of you came across any good “practical” guide on how to do the secondary structural alignment for 18S rRNA, whether it is “by hand” or computer software assisted.

Thank you in advance, Anton

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School of Environment and Society, University of
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Tel. +44 (0) 1792 205678 ext 4603 or 4421 mailto:
202871(at)swansea.ac.uk

atsyganov@gmail.com

Application Pathogen Evol

Dear EvolDir readers,

I am looking for examples of molecular evolutionary studies of pathogens that have led to actual treatments or vaccines.

I am particularly interested in dN/dS ratios of pathogen genes and evidence of horizontal gene transfer within/between pathogen species. There seem to be many interesting studies that find, for example, some codons evolving under diversifying selective pressures, and conclude with "this research will be useful in vaccine development," but have any of these ideas been picked up by researchers in drug/vaccine development?

Thanks for any references that you can point me towards (or good search terms if I've been completely blind!).

Sara Sandstedt

Sara A. Sandstedt, Ph.D. Department of Epidemiology
School of Public Health University of Michigan, Ann Arbor

Sara Amelia Sandstedt <sandsted@umich.edu>

Beagle Project

The Beagle Project:

The Beagle Project aims to build a sailing replica of HMS Beagle and recreate the Voyage of the Beagle that inspired Charles Darwin's big idea. <http://www.thebeagleproject.com/> The replica Beagle is not intended to be a museum ship; she will be equipped with laboratories and equipment to allow overlapping crews of practising and aspiring scientists to carry out specific programmes of research. The circumnavigation will offer opportunities for science worth doing, and worth communicating.

Research aboard the Beagle will be: * original, question-driven science of international scope and relevance that demonstrably robust to the peer-review process * a vehicle for communicating science to a range

of audiences, students and young adults in particular

The Beagle Project will issue a call for research project proposals in late 2007/early 2008, but until then we invite researchers to send us their ideas on an informal basis. All projects must support the aims listed above (original research, science communication, science education). Projects funded in whole or in part by peer-reviewed granting agencies will be given priority. People wishing to sail with us and use the Beagle for scientific research will need sea legs, be prepared to do some science mentoring and rope-hauling (emeriti not excepted).

<http://www.thebeagleproject.com/> The HMS Beagle Project - Celebrating Darwin - Inspiring science- Building evolution's inspiration web: www.thebeagleproject.com blog: www.thebeagleproject.com/beagleblog.html A not for profit company registered in the UK The Stableyard Lawrenny Pembrokeshire SA68 0PW UK reg. no. 6025763

Charitable status pending

karen@thebeagleproject.com

Beetle phylogeography

Dear all,

I am working on beetle phylogeography using mitochondrial DNA sequences (cytochrome oxidase I and II).

My problem is concerning heteroplasmy (i.e. for one individual, the presence of two kinds of DNA in one mitochondrion, or two kinds of mitochondria). Indeed, half analysed individuals showed double peaks at 1 to 8 nucleotide sites. This was confirmed by the reverse sequences.

I have tried to perform analyses by coding these ambiguous sites using the IUPAC code. However softwares such as PAUP have difficulties while the analyses are running.

I am interested in defining the potential haplotypes without having to clone them.

Is anyone aware of suitable analyses and/or softwares providing mitochondrial DNA haplotypes when heteroplasmy is involved?

Any help will be appreciated.

Best regards,

Fotini Koutroumpa

Fotini KOUTROUMPA Porte 128 Laboratoire de Biologie des Ligneux et des Grandes Cultures UPRES EA 1207 Université d'Orléans Rue de Chartres BP 6759 45 067 ORLEANS Cedex 2 FRANCE

Tel.: 02 38 49 43 32

Fotini.Koutroumpa@univ-orleans.fr

Fotini KOUTROUMPA <fotini.koutroumpa@univ-orleans.fr>

Boa constrictor micros

I am a PhD student at DICE (Durrell Institute of Conservation and Ecology) at the University of Kent, England and would like to know if anyone is currently developing microsatellite primers for *Boa constrictor*.

I am working with Hog Island Boas (*Boa constrictor imperator*) and have so far had very limited success in cross amplifying markers in this subspecies. I was, therefore, wondering if anyone was either in the process of developing specific markers for *Boa constrictor* or would be interested in collaborating/partially funding the development of a microstellite library?

Regards

Steve Green

sewg2@kent.ac.uk

CNRS FrenchPyrenees Volunteers EvolOfDispersal

Volunteer Opportunity

We are looking for volunteers on a new project looking at the evolution of dispersal and sociality. The themes of this work are centered on the evolution of sociality and meta-population dynamics. This project seeks to experimentally manipulate parameters in dispersal behavior and social aggregations to understand trade-offs and key determinants of the evolution of these behaviors. The project is lab based in nature using *Tetrahymena thermophila*, a unicellular ciliated protist, as a model organism. Volunteers are expected to partici-

pate in maintenance of cultures, experimental manipulations, and the best candidates will also be capable of helping to plan experiments and process data.

This project is run in Dr. Jean Clobert's lab and students will work with both Dr. Clobert and Dr. Alexis Chaine. The lab is situated in the foothills of the French Pyrenees Mountains at a CNRS field station (Moulis / Saint Girons). Students will be provided with housing but will be expected to cover their other expenses. Work is ongoing and volunteers can begin at a negotiated date. Duration of work is flexible, and while volunteers are expected to commit to a minimum of 4 weeks, priority will be given to those who can commit to longer periods.

For more information, please contact Alexis Chaine (alexis.chaine@lsm.cnrs.fr)

Alexis Chaine <alexis.chaine@lsm.cnrs.fr>

Callosobruchus maculatus specimen

Hello, we are chasing some black *Callosobruchus maculatus*. If anyone has some we'd greatly appreciate some. Origin not an issue. Any help or advice appreciated (reply to D.J.Hosken@ex.ac.uk) Thanks a lot. David Hosken, Tom Tregenza & Laurene Gay

Dr DJ Hosken Centre for Ecology & Conservation School of Biosciences University of Exeter, Cornwall Campus Tremough, Penryn, Cornwall TR10 9EZ UK

Tel: +44 (0) 1326 371843 D.J.Hosken@exeter.ac.uk
<http://www.uec.ac.uk/biology/research/staff-research-interests/david-hosken.shtml>

D.J.Hosken@exeter.ac.uk

Ceratodon purpureus samples

Dear all, I'm currently looking at the dispersal of the moss *Ceratodon purpureus* in the Southern Hemisphere as part of my PhD. I have populations from Australia, the subantarctic and Antarctica, however to complete the project I desperately need populations from southern South America, southern Africa and New Zealand. I'm using microsatellite allele frequencies, so I need at

least 10 specimens for each population. Either recent herbarium samples or freshly collected material is best and only small amounts of sample are needed (10-20 shoots). I can also cover all postage costs. If you can help or know of someone who might be able to, please contact me via e-mail on ljc03@uow.edu.au for more details. Apologies for cross-postings. Thanks very much, Laurence

Laurence Clarke PhD candidate Institute of Conservation Biology University of Wollongong Northfields Ave., Wollongong NSW Australia 2522 E-mail: ljc03@uow.edu.au

ljc03@uow.edu.au ljc03@uow.edu.au

ChicagoBotanicGarden PlantEvol SummerRes

Summer field research experience for undergrads or recent graduates

Are you interested in gaining field research experience and learning about the ecology and evolution of plants and plant-animal interactions in fragmented prairie? We are looking for 3-5 field research assistants for an NSF-funded research project on habitat fragmentation of the tallgrass prairie. We are investigating how small plant population sizes influence inbreeding, demography, pollination, and herbivory in the purple coneflower (*Echinacea angustifolia*). This is a great summer internship or co-op for those interested in field biology or conservation.

No experience is necessary, but you must be enthusiastic and hard-working. You will survey natural plant populations, measure plant traits in experimental plots, hand-pollinate plants, observe & collect insects, and assist in all aspects of research. Housing is included and there is a stipend. There are options for doing an independent project and being an REU participant.

If you want more information or wish to apply, please visit this website <http://echinacea.umn.edu/> or contact Stuart Wagenius. Applications due 9 March 2007.

— Stuart Wagenius, Ph.D. Conservation Scientist
Institute for Plant Biology & Conservation Chicago
Botanic Garden 1000 Lake Cook Road Glencoe, IL
60022

phone: 847 835 6978 fax: 847 835 5484

email: swagenius@chicagobotanic.org web: <http://->

echinacea.umn.edu SWagenius@chicagobotanic.org

Climate change

Hi all,

Today (February 2) a milestone was reached in the climate change debate as the IPCC (Intergovernmental Panel on Climate Change; <http://www.ipcc.ch>) had a press release to announce its 4th Assessment Report on climate change. The previous Assessment Report was from 2001. Based on a wealth of scientific data, the new report provides by far the strongest warning on human mediated climate change to date. More information, including the “Summary for Policymakers” (pdf) and a link to a web cast of the press conference, can be found at:

<http://ipcc-wg1.ucar.edu/index.html> Amongst other points, the “Summary for Policymakers” projects that average global temperature will rise by 1.8-4 degrees and sea levels will rise by 18-58 centimeters by 2100. Importantly, such a temperature change may push the global climate beyond a threshold at which feedback mechanisms (e.g., reduced polar ice caps leading to increased heat absorption; release of methane from melting tundra adding to the greenhouse effect) will make the climate change irreversible.

Obviously, the time for politicians and policymakers to catch on to reality is now. I believe that as evolutionary scientists we have a moral responsibility to spread the word on this issue. Let your students and colleagues know - the more climate change is discussed the better!

Sincerely,

Johan Lindell

– Johan Lindell, PhD candidate Department of Ecology & Evolutionary Biology University of Toronto

Address of correspondence: Department of Natural History (Section for Herpetology) Royal Ontario Museum
100 Queen’s Park Toronto, Ontario M5S 2C6 Canada
johan.lindell@utoronto.ca johan.lindell@utoronto.ca

DNA extraction from seeds CTAB

Hi

I would like to extract DNA from some plant seeds and have some methodological questions that I hope someone out there can help with.

1) When I browse the internet for common methods I see that many use CTAB. Can any one tell me why this seems to be so popular, and what it does? I know its a detergent, but what makes it special compared to SDS or alternatives

2) Would digestion with a CTAB buffer be more efficient (well better overall) than simply grinding the seeds and then digesting them in a buffer containing Tris, NaCl, DTT, SDS and proteinase k?

3) I was going to follow either of the above with an organic purification then precipitation. Does anyone have any feel how any of the commercial kits perform compared to such traditional methods?

Thanks for your help!

Tom Gilbert

mtpgilbert@gmail.com

DNA extraction from seeds CTAB answers

I recently posted a query about plant DNA extractions namely what exactly does CTAB contribute to the process, and what methods do people recommend. Thanks for the replies I received, they were extremely useful. Particularly I wish to thank the following:

Donovan Bailey Anders S Larsen Joe Staton Andreas Zipperle Sara Good-Avila Polly Spencer-Vellacott

With respect to CTAB itself

>>>>

I believe that CTAB was developed for use with mucilaginous bacteria to get rid of the very gooey glycoproteins that SDS will not.

>>>>

CTAB is so popular in plant extractions because early published approaches illustrated its broad utility and so people stuck with it. Most commercially available Plant extraction kits now use protocols much more akin to a typical phage lysis extraction. To the best of my knowledge nobody uses proteinase K in plant extractions - that approach is generally restricted to animal based

systems (but it may be useful in some groups).

Whether or not to use CTAB or another approach often depends on the quality of DNA you recover from either - they are such different approaches that one will often work well in a particular group of plants while another fails miserably - I would try both and see what works best for you seeds.

>>>>

Although with regards to Prot K.

All of the traditional recipes we have used include CTAB. CTAB binds to the cell wall debris, proteins and polysaccharides in the homogenate: once you perform a phenol-chloroform extraction after the CTAB step, the CTAB/debris/polysaccharide/protein mix is removed. We also include proteinase K to facilitate digestion of the relatively compact tissue in the seeds.

>>>>>

One other thing I learnt, that may be useful to some of you who might be as naïve with plants as I am

I extracted DNA from seeds of *Fraxinus excelsior* (ash tree). I used a kit (Qiagen) but what may be important (you probably know it already) is that if you are interested in the seed genotype you separate the embryo from the endocarp etc, which might have the maternal genotype.

With respect to different method (and here I include names in case anyone needs to chase up anything with the original responder)

>>>>

We (Donovan Bailey) have recently published a very inexpensive and high throughput method that mimics commercially available kits (who claim to have proprietary approaches - all components of which were actually published many years ago). You can see our paper in molecular ecology notes -

<http://www.blackwell-synergy.com/doi/abs/10.1111/j.1471-8286.2006.01549.x>

>>>>

Qiagens plant extraction kits work fine for baobab seeds (scant endosperm) I've experienced, but be aware of the quantity - you easily reduce your yield if adding too much material here!

I've seen one protocol where you simply put the required amount of seed into water overnight and extract the desired way (kits or CTAB) afterward, saving the nitrogen. Can't remember the details, but can come back with the protocol next week (Anders Larsen).

>>>>

I am using microsatellites and I used both, CTAB and a SDS based methods for DNA extraction from seeds. I do not exactly know what CTAB does, but the quality of DNA that I got using a commercial (Sephaglas) and homemade glasmilk is much better with CTAB. Nevertheless, using glasmilk from the really fine-fraction of silica resulted in good quality DNA as well (at least for msats). While CTAB extracted DNA can be stored for at least two years in a -20 freezer this might not be true for SDS. I never used a kit, because our home made method performs pretty good, is streamlined for a 96 well format, can be used with CTAB or SDS and is much cheaper than a kit. If you are interested Elphinstone et al. (2003) Mol Ecol Notes 3, 317 - 320 is the basis for our extraction method and the method itself will be published soon. (Andreas Zipperle)

>>>>

I've pasted the protocol we are currently using below. This protocol works brilliantly for us - it is fast and gives high yields and very reliable post-PCR. Although it is preferable to remove the seed coat, this isn't always practically feasible or necessary. Currently, we are using this protocol on apple seeds.

Modified slightly from Kang et al. 1998. Our (Sara Good-Avila's) protocol for extraction from apple

You can start with the whole seed, or the seed - minus the seed coat. Depending on the size of the seed use all or part of it. For apples we use one whole seed/extraction. You can adjust the volume of extraction buffers and final eluate for other seed sizes.

- Place the seed in a microcentrifuge tube (1.5 ml). - Add 200 ul of extraction buffer containing proteinase K (50 ug), incubate at 37 C for 1 h.

— / —

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>

DNase DNA cDNA

Hi,

We're studying expression of single-exon genes using PCR and cDNA isolated from different sea urchin tissues. But, PCR with an intron-containing sequence (a control) shows that there's DNA contamination. We're

using the Bio-Rad PureZol and iScript kits. DNase treatment is part of the protocol, but in some samples it doesn't seem to do the job. Has anyone had this problem (with this kit or others) and is there a solution? We've thought of using only a poly-T primer (rather than the poly-T plus random hexamers), but it seems to me that getting rid of DNA shouldn't be impossible. Suggestions?

Thanks,

John Taylor University of Victoria BC, Canada

taylorjs@uvic.ca

Double sequence after cloning

Hi all,

We have been using TOPO TA cloning (kit from invitrogen) to sequence from a number of enriched microsatellite libraries and we were encountering a high percentage of what looked like double sequence or contaminated sequence in our chromatographs. After a while, we noticed that in all of these cases, one of the two overlapping sequences was our target insert and the other corresponded to vector that appears to have been cut in two places (thus excising a small fragment) and re-ligated by Vaccinia topoisomerase I (which recognizes the sequence CCCTT but in this case appears to have also cut at a CCCT site further along in the vector). There is obviously a lot more to this, but my question is whether anyone has noticed a similar problem? We designed a primer that eliminates the double sequence problem and would like to publish our methods but reviewers have been skeptical about how widespread the problem might be. We do know of a couple of other labs that have experienced this problem but we would like to expand our sample size (especially interested in any pertinent information that has been published or is available online).

cheers,

Andrew Forbes (aforbes@nd.edu)

aforbes@nd.edu

Ensis directus E americanus samples

Dear Evoldir members,

I have recently started my PhD thesis at the University of La Coruña (Spain), looking at the population genetics of a few species of bivalves. I'm currently working on a razor clam species called */Ensis directus/* (syn. */Ensis americanus/*). This species is present on the North American East Coast, and it ranges from the Baltic Sea to France and Great Britain in Europe. I'm currently trying to get material from a wide range of locations. I would really appreciate if you have any samples of this species suitable for DNA analyses that you may be able to share with me or if you may be able to collect some individuals and send them to University of La Coruña. We would of course provide the cost of postage.

Thank you very much for you help.

Best regards, Joaquín Vierna

– Joaquín Vierna (PhD student) Department of Cell and Molecular Biology Universidade da Coruña A Zapateira s/n. E-15071. La Coruña. SPAIN. Tel. +34 981167000 Ext. 2030 Fax +34 981167065 <http://www.udc.es/dep/bm/genetica/a/joaquin/indice.htm> – jvierna@udc.es

Estimating Divergence Times answers

A few weeks ago I posted a question re: estimating divergence times. A number of people requested that I forward the responses. The most popular response was to use the program BEAST, which allows a relaxed molecular clock. Thank you to all who replied.

You may want to try the software package BEAST which I am one of the authors of.

It does Bayesian MCMC estimation of divergence times without assuming a particular tree topology. The paper to look at is:

DRUMMOND, A.J., HO, S.Y.W., PHILLIPS, M.J., RAMBAUT, A., 'Relaxed phylogenetics and dating with confidence.' PLoS Biol 4, e88, 2006

<http://biology.plosjournals.org/perlserv/?request=get-document> <<http://biology.plosjournals.org/perlserv/?request=get-document&doi.1371/journal.pbio.0040088>>

There has been a workshop on dates and rates in Ade-

laide just last week, after which I have decided to use BEAST to calculate divergence dates. I have similar situation to yours: mtDNA, some estimates of divergence rates (from 2 to 12% per mln yrs), no calibration points, and rejected molecular clock. BEAST implements the model of "relaxed clock" which allows each branch on the tree have its own specific mutation rate.

Given mutation rates (or strong mutation rate priors) it spits out an ultrametric tree with estimates of the age for major nodes and 95% credibility intervals around them (thus incorporating uncertainties in the phylogeny). Also, BEAST estimates parameters of population growth (if the model of growth is chosen by you as the most appropriate model for your organisms) and population size, because age of the nodes depends on pop size ($\tau = N_e \cdot \mu$).

You have to be patient with BEAST, though: there are thousands of models to navigate through, you have to have strong apriori priors and think of the best model for your data.

Have you tried the program BEAST? That's what I used when I was in a similar situation. It incorporates uncertainty in your phylogeny by sampling over many different trees, weighted according to their posterior probability. It can give you an estimate, with a 95% confidence interval, of the divergence time between two or more groups. You can specify different evolutionary models (e.g. relaxed clock, or allowing different lineages to evolve at different rates, if that fits your data best). The program can be found at <http://evolve.zoo.ox.ac.uk/beast/> Hope that helps.

Sincerely, my advice is : do not try to calculate divergence times without good fossil calibration. Even if they are fashionable, phylogenetic methods cannot do better than fossils for estimating divergence times. So if you do not have any fossils, your estimations will have no meaning at all.

You must be very careful when estimating divergence times with a single locus. Even if the gene is clocklike, what you will really be measuring is the locus specific divergence time, not the true species divergence time. This will vary throughout the genome due to stochastic processes governed by population parameters like population sizes, rates of divergence etc... How deep are the relationships you are trying to reveal? Species level, genus level, family level, etc? For just COI, you may have a difficult time getting good estimates of divergence, no matter what optimality criterion you use. I have used a simple 2% /million years rate before to get an estimate of divergence times, but this was for a small group of very recently derived species, and I was more interested in relative differences rather than ab-

solute. A sweepingly broad estimate may be the best you can hope for given your poor resolution and single locus. You might check out "Estimating divergence times from molecular data on phylogenetic and population genetic timescales" by Arbogast et al 2002 for ideas.

FWIW, in my research on Hawaiian bees I found that COI was evolving at a rate of up to 13% per million years (9% in *amino acids*). That's a minimum rate (though based on the fastest-evolving species) calibrated by populations within a species on islands of known age. That of course is assuming that the bug arrived as soon as the island emerged, which is unlikely. Not that your things are necessarily that weird, but just pointing out that the real rate might be quite different from 1.4%, and to be wary if you're attaching absolute dates to it.

Cheers Claire

Claire McClusky Postgraduate Research School of Life and Environmental Sciences Deakin University Warrnambool VIC Australia clairefi@deakin.edu.au

Claire McClusky <clairefi@deakin.edu.au>

EuropeanEvolBiol JohnMaynardSmithPrize

The European Society for Evolutionary Biology has established The John Maynard Smith Prize to be awarded to outstanding young researchers in the field of evolutionary biology

The prize is named after John Maynard Smith (6 January 1920 - 19 April 2004), eminent evolutionary biologist, and author of many books on evolution, both for scientists and the general public. He was professor emeritus at University of Sussex, UK, Fellow of the Royal Society, winner of the Darwin Medal, and laureate of the Crafoord Prize of the Swedish Academy of Sciences.

The sixth prize winner will be announced at the 2007 congress of the society in Uppsala, Sweden.

Previous winners * 2005: Daven Presgraves - Speciation genes & selfish genes in *Drosophila*. * 2003: Patricia Beldade - The genetic basis of phenotypic variation: evolution and development of butterfly wing patterns. * 2001: Alexander Badyaev - Paradox of rapid evolution of sexual size dimorphism: the role of ontogeny and

maternal effects. * 1999: Nicolas Galtier - Non stationary models of nucleotide substitution and the evolution of base composition. * 1997: Marie-Charlotte Anstett - Facilitation and constraints in the evolution of mutualism?

Nomination

The prize is open to any field of evolutionary biology. Candidates for the prize must be nominated by a senior colleague; the nomination must be accompanied by the candidate's CV, a list of publications, a short description of future research plans, the names and addresses of two referees, and a letter from the candidate approving the nomination. Candidates for the 2007 prize must have received a PhD (or equivalent) degree no earlier than January 2005.

The nominations should be received by email and sent to: Prof. Paul Schmid-Hempel, ETH Zürich Institute for Integrative Biology, ETH-Zentrum, CHN, Universitätsstrasse 16 CH-8092 Zürich, Switzerland e-mail: psh@env.ethz.ch

They should arrive no later than March 1, 2007. Please take care to limit the size of attachments (total < 5 MB) in any one email (use sequels if necessary). The winner is expected to attend the 2007 congress, where he or she will deliver the John Maynard Smith Lecture. The society will pay registration, accommodation, and travel expenses (economy fare).

Dieter Ebert Secretary ESEB University of Basle, Switzerland

dieter.ebert@unibas.ch dieter.ebert@unibas.ch

Faecal DNA

I'm trying to optimise preservation of DNA in faecal samples and I was wondering if anyone had any experience of preserving otter spraint and knew of any non-ethanol preservation methods. Does anyone have any experience of using RNAlater for preserving DNA in faecal samples?

Robert.Pickles@ioz.ac.uk

Fennel pondweed beds

Dear members of EvolDir,

As a PhD student I'm currently involved in a project concerning among other factors the genetic diversity of the freshwater macrophyte fennel pondweed (or sago pondweed, *Potamogeton pectinatus*, *Stuckenia pectinata*) in relation to herbivory. I am particularly looking for shallow wetlands with beds or large patches of this plant in Mediterranean or temperate Europe. Ideally, I would like to know if these localities are visited by Bewick's swans or Whooper swans that may forage on the tubers of fennel pondweed. Both localities receiving many of these birds or close to none at all are suitable. I would be very grateful if you have information that you would like to share with me.

Yours sincerely, Bert Hidding

Bert Hidding NIOO - CL, Department of Plant- Animal Interactions, P.O. Box 1299, 3600 BG, Maarssen, the Netherlands. e-mail: b.hidding@nioo.knaw.nl Telephone: + 31 (0) 294 23 93 40 Mobile phone: + 31 (0) 6 55 13 39 08 Home address: Transvaalstraat 93 B1, 1092 HE, Amsterdam.

Freshwater to Marine Colonisations

Dear All

We are looking for examples in which a species has undergone population size expansion sometime in the past; for example as when an island species colonises the mainland. Ideally we would like these events to have occurred within the last 10 million years but not within the last million, but we will accept just about anything for consideration since we are very short of data. We are looking for further examples of island to mainland colonisation and examples of freshwater species invading the marine environment. The cases of island to mainland colonisation we have so far looked at are chameleons, anole lizards, the plant *Coraria*, *Monarcha* birds and *Eleutherodactylus* frogs.

Any help would be greatly appreciated. Thanks

Adam

Adam Eyre-Walker Centre for the Study of Evolution & School of Biological Sciences University of Sussex Brighton BN1 9QG

a.c.eyre-walker@sussex.ac.uk
walker@sussex.ac.uk

a.c.eyre-

GenClone odd results

I am getting an unusual result with GenClone 1.0 on one of 11 plant populations that I am analyzing. One of the smaller population samples (n 11) analyzed across 16 SSR loci has 9 multi-locus genotypes with only a single one-allele pairwise difference (i.e., 8 of the 9 MLGs are quite distinct). Shannon-Weiner diversity is reasonably high (2.098) and Shannon Evenness is 0.955. Simpson diversity is 0.945, but for some reason Simpson evenness = 0. I have run the analysis several times, and always with the same result. This makes little sense to me. Is it something to do with my sample size (I have another population for which n = 11 and it did not have a similar problem), or have I perhaps uncovered a bug? Any one have any ideas?

Thanks.

Alan W. Meerow, Ph.D., Research Geneticist and Systematist USDA-ARS-SHRS, National Germplasm Repository 13601 Old Cutler Road, Miami, FL 33158 USA voice: (305) 254-3635 fax: (305) 969-6410 email: ameerow@saa.ars.usda.gov

ameerow@saa.ars.usda.gov

Genemapper problems

Genemapper 4.0 and AFLPs

Hello everyone,

I am using Genemapper 4.0 to analyse my AFLP data (ABI 3730) and have encountered following problem:

Samples with a red symbol in the SQ column need correcting manually in the Size Match Editor. I exactly follow all the steps outlined in the 'AFLP System Analysis Getting Started Guide' and I can successfully manually correct mislabelled peaks. After clicking 'Apply' and 'OK' I need to reanalyse the corrected sample. That's where the problem starts. Having done so the red symbol appears again in the SQ column and when I check the Size Match Editor all the changes I have made before are undone and the peaks show the same mislabels as before correcting them. All this happens

in the AFLP Default Analysis Method.

If I do the same in the Microsatellite Analysis Method then the changes are saved and a green symbol appears after reanalysing in the SQ column. But unfortunately I am running AFLPs and not microsatellites so I need to be able to change mislabelled peaks in the AFLP Analysis Method.

Has anybody encountered a similar problem in Genemapper 4.0?

Thank you

Markus

Markus Ruhsam PhD Student University of Edinburgh
m.ruhsam@sms.ed.ac.uk

s0231272@sms.ed.ac.uk

Genetic Cartography History

Dear Evoldir members,

I have accepted to write an entry titled "Genetics and Cartography," (750 words, 5 references, and 1 to 3 illustrations) to appear in the sixth volume of the encyclopedia "History of cartography" <<http://www.geography.wisc.edu/histcart/>> . More or less I know what I will write but I would like to know if someone can provide any valuable reference of the first genetic maps. I mean, when and where they were published. Maps not in terms of symbols or written frequencies on a maps but more advanced representations like interpolation curves of frequencies, PCA components against long/lat coordinates etc. The entry should provide an overview of the last century. If anyone has an idea or can send a suggestion it will be highly appreciated.

With kind regards

Franz Manni <manni@mnhn.fr> "

Dr. Franz Manni Maître de conférences / Lecturer
UMR 5145 - Eco-Anthropology Group National Museum of Natural History MNHN - Musée de l'Homme
17, Place du Trocadéro 75016 Paris - France Tel. 0033 1 44 05 72 84 Fax. 0033 1 44 05 72 41 Telex Musethno

Franz Manni <manni@mnhn.fr>

GeneticDistance with linkage

Hi all,

I am working with some nuclear sequences that show heterozygous positions for most individuals. Since I cannot ascribe the 2 sequences of each individual I would like to use these heterozygous positions to estimate genetic distances between individuals. But, to do that I should take into consideration linkage between these loci.

Does anyone know of a program that estimates genetic distances correcting for linkage between loci?

Any help will be appreciated.

Thanks!

Vera S. Domingues UEE-ISPA Rua Jardim Tabaco,
34 1149-041 Lisboa Portugal http://www.ispa.pt/-ui/uee/eetf/vera_domingues.asp Vera Domingues
<Vera.Domingues@ispa.pt>

Honeysuckle micros

Dear colleagues,

I was wondering if anybody has developed or knows of microsatellite primers for the Amur honeysuckle, *Lonicera maackii* (or any other honeysuckle, assuming that they would cross-hybridize with Amur honeysuckle DNA). I am studying gene flow in the Amur honeysuckle and therefore am interested in loci that are likely to be polymorphic. Hence the need for micros. But if any other markers have been developed and are suitable for this purpose, I would love to hear of it.

Finally, I have already collected the samples, but I'd have to outsource the bench work since I don't have a wet-lab. Any suggestions for outsourcing that would be good and fairly inexpensive?

Thanks very much.

Sudhindra Gadagkar

Sudhindra R. Gadagkar, Ph.D. Department of Biology
University of Dayton 300 College Park Dayton, OH
45469-2320

Ph: (937) 229-2410 Fax: (937) 229-2021 Email: gadagkar@notes.udayton.edu

Sudhindra.Gadagkar@notes.udayton.edu Sudhin-
dra.Gadagkar@notes.udayton.edu

Human Nucleotide ratios

NUCLEOTIDE RATIOS:

The following question seems quite elementary but I found no answers for it.

I would be grateful for any answers:

What are the ratios between the four nucleotides A,C,G,T in humans in:

The whole genome. The exons, the introns, non coding DNA, and junk DNA.

In genetically variable loci.

Thanks in advance,

Yair Yuval

moranuri@gmail.com

Intragenic Recombination in fungi

EvolDir community,

I have a question:

Does anybody know of any published papers demonstrating direct evidence of intragenic recombination within or between loci in a natural or agricultural ecosystem of a fungal species? O¹Donnell et al (2000) in a PNAS paper (97:7905-7910) suggested that they were the first to their knowledge.

Thanks, Greg

Greg W. Douhan Plant Pathology University of California Riverside, CA 92521 951-827-4130

Micro identification

Dear EvolDir members,

I have a methodological question that deals with the assessment of clonal diversity with microsatellite loci. Could we consider that each observed multilocus genotype (MLG) mirrors reality? Or is it more realistic to consider two or more MLG differing by only one allele at a locus (out of several) as a unique MLG? For example, could one consider the two following MLG to be different or identical? :

(1) 0102 0202 0405 0405 0103 0203 0405 0405 (2) 0102 0202 0405 0405 0103 0202 0405 0405

Does someone know papers, methods or softwares that could help to take a decision by taking into account allelic frequencies or genotyping error rates?

thank you very much for any help and advices!

Stef

sfenart@vub.ac.be – Stephane Fenart

Algemene Plantkunde en Natuurbeheer (PlantBiology and Nature Management) Room 7F416 Vrije Universiteit Brussel Pleinlaan, 2 B-1050 Brussels Belgium

tel: + 32 2 629 3057 fax: + 32 2 629 3413

Visit our website: <http://www.vub.ac.be/APNA/>
Stéphane Fénart <sfenart@vub.ac.be>

Microarray problem

Hi,

I am working on a microarray project using fish liver as a source for RNA. I did Trizol extractions, including 2 isopropanol steps and 2 ethanol washes before drying and resuspending in RNase free water and RNase-inhibitor. I then cleaned the extraction over a Microcon filter. I measured the quantity of RNA, which is exactly in the range of what we expect for liver. The 260-280 absorbance ratios are between 1.8 and 1.95, suggesting no protein contamination. The 230-260 ratios are in the same range, suggesting no phenol contamination. After running the RNA on an Experion chip (same as Bioanalyser), there is no sign of RNA contamination. There is, though, sign of genomic contamination, showed by a little bump or “shoulder” after the 28S peak (this is clearly not RNA degradation).

My samples have been flash frozen in -80°C ethanol (cooled by dry ice) but some ethanol entered the tubes, which means that my samples have been in presence

of ethanol for something like 3 months at -80oC. I do believe that ethanol has penetrated the livers.

Now, I did microarrays (using Genisphere Array 50 kit) with my samples and positive control samples (that had already worked for microarrays). The controls worked but not my samples, although I treated them exactly the same way (I did the two in parallel). This test was repeated twice with the same results. This excludes the possibility of some reagent/kit/microarray not being fonctionnal.

I also proceeded to test the retro-transcription by running a quantitative PCR on the samples before and after the retro-transcription. This shows that the RT works well and that there could be a little bit of genomic DNA as well, but that one ensured only 1/1000 to 1/4000 times the amount of amplified material compared to the cDNA after the retrotranscription.

And now the questions :

Would someone have any idea how to explain these results?

Can genomic DNA contamination affect the microarray, even though the retro-transcription worked very well? If yes, in what way? (hybridization, labelling...)

Could the presence of ethanol in the sample livers be enough to ensure carry-over of genomic DNA in a Trizol extraction?

Thanks very much for any help!

Eric

Eric Normandeau

Étudiant au deuxième cycle Département de biologie
Pavillon Charles-Eugène Marchand Université Laval,
Quebec QC G1K 7P4 Canada

Tél: 418 656-2131 poste 8455

eric.normandeau.1@ulaval.ca

eric.normandeau.1@ulaval.ca

Microarray problem 2

Hi,

Following suggestions, I changed some information in the description of my problem. If you answer (you can do so at : eric.normandeau.1@ulaval.ca), please consider this version. Thank you :)

I am working on a microarray project usign fish liver

as a source for RNA. I did Trizol extractions, including 2 isopropanol steps and 2 ethanol washes before drying and resuspending in RNase free water and RNase-inhibitor. I then cleaned the extraction over a Microcon filter (YM-30). I measured the quantity of RNA, which is exactly in the range of what we expect from liver. The 260-280 absorbance ratios are between 1.8 and 1.95, suggesting no protein contamination. The 230-260 ratios are in the same range, suggesting no phenol contamination. After running the RNA on an Experion chip (same as Bioanalyser), there is no sign of RNA degradation. There is, though, sign of genomic DNA contamination, showed by a little bump or "shoulder" after the 28S peak (this is clearly not RNA degradation).

My samples have been flash frozen in -80oC ethanol (cooled by dry ice) but some ethanol entered the tubes, which means that my samples have been in presence of ethanol for something like 3 months at -80oC. I do believe that ethanol has penetrated the livers. Ethanol is believed to increase carry-over of genomic DNA in a phenol-chlorophorm RNA extraction.

Now, I did microarrays (using Genisphere Array 50 kit) with my samples and positive control samples (that had already worked for microarrays). The controls worked but not my samples, although I treated them exactly the same way (I did the two in parallel). *****On the microarrays I did with my extractions, virtually nothing shows on the array. It is even hard to see the spots on the chip. So there is no signal for both channels (Cy3 and Alexa).***** This test was repeated twice with the same results. This excludes the possibility of some reagent/kit/microarray not being fonctionnal.

I also proceeded to test the retro-transcription by running a quantitative PCR on the samples before and after the retro-transcription. This shows that the RT works well and that there could be a little bit of genomic DNA as well. Without retro-transcription, only 1/1000 to 1/4000 times product was generated, compared to the amount of amplified material from cDNA after the retrotranscription. The primers and probe were designed across an intron/exon limit, so they should not be very efficient in amplifying genomic DNA. Thus, it is possible that there is a non-negligible amount of genomic DNA in the sample when compared to the mRNA quantity.

And now the questions :

Would someone have any idea how to explain these results? (failling microarrays in the context described?)

Can genomic DNA contamination affect the microarray, even though the retro-transcription worked very well?

If yes, in what way? (hybridization, labelling...)

Could the presence of ethanol in the sample livers be enough to ensure carry-over of genomic DNA in a Trizol extraction?

Thanks very much for any help!

Eric

You can reply directly at:

eric.normandeau.1@ulaval.ca

Eric Normandeau

Étudiant au deuxième cycle Département de biologie
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Microsatellite Alleles

I amplified and genotyped an individual DNA sample and found 3 separate microsatellite alleles (as evidenced by 3 separate peaks on the electropherogram output from the 3730 Sequencer) at 3 out of the 5 tetranucleotide loci I am scoring. This same sample at the other two loci have a "normal" 1 or 2 allele pattern. I thought my sample may have been contaminated and so I re-extracted and re-amplified my original DNA sample with the same result, 3 peaks at 3 of the 5 loci. Has anyone ever encountered this before (3 alleles at a locus) and have an explanation? I do not see 3 peaks at any loci for the other ~2000 DNA samples I have run.

josephdibattista@hotmail.com

Microtus brachycercus samples

Dear Evoldir members,

I saw recently in the new edition of "Mammal Species of the World" by Wilson & Reeder that *Microtus* (*Terricola*) *brachycercus*, initially described as a subspecies of *M. savii*, was elevated at the species rank on the basis of gonosomal differences and morphological traits.

I am working on *Microtus* (*Terricola*) phylogeny. So I would like to know if one of you could provide me with some tissue samples of this vole in order to determine its phylogenetic position.

Thanks in advance, Christelle Tougard.

Christelle TOUGARD UMR CNRS 5561
Biogéosciences-Dijon Equipe "Forme, Evolution,
Diversité" Université de Bourgogne 6 boulevard
Gabriel 21000 Dijon (France) Tél: +33 (0)3 80
39 63 79 - Fax = +33 (0)3 80 39 63 87 E-mail:
Christelle.Tougard@u-bourgogne.fr

Mismatch distribution analysis

Dear evoldir members

I have a trouble with my analysis of mismatch distribution. Results that the curve is unimodal but the significance of raggedness index is not significant under the null hypothesis of neutral evolution. The analysis was performed in DNAsp with coalescent simulations considered no-recombination and observed theta values. The answer is: The populations suffer or not an expansion? Sorry for my english.

Any reply send to juan_jmart@yahoo.com.ar

Juan José Martínez Cat. Genética de Poblaciones y Evolucion FCEFYN UNC. Cordoba, Argentina.

juan_jmart@yahoo.com.ar

NatHistMus Dublin UREKA Programme 2007

Applications for the 2006 summer undergraduate research programme are now open.

If you know of any students who are qualified to apply for this summer's programme, please pass on the information below!! Cheers

Julia

Undergraduate Research in the Natural History Museum, Dublin <http://www.ucd.ie/ureka> CoBiD-UREKA is a research summer programme in Dublin,

Ireland for international undergraduate students to work with the National Museum of Ireland (Natural History) and University College Dublin.

Full funding is available for a limited number of students to attend this 10-week course, beginning 11 June 2007. All applications must be received by 25 March.

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

Term dates: June 11th to August 17th 2007

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

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

All materials must be received by: Sunday 25 March

Research Projects | fossil birds | stonefly ecology | genomic imprinting | carboniferous coral "reefs" | evolution of mammalian "hearing" | molecular markers in coastal fish | plant evolution and extinction | vertebrate paleontology | extreme environments |

For more details, please see <http://www.ucd.ie/ureka/> or e-mail: ureka@ucd.ie

The CoBiD summer school programme is funded by Science Foundation Ireland.

ureka@ucd.ie

New *Drosophila* stocks

ANNOUNCEMENT OF NEW DROSOPHILA SPECIES STOCKS BOTH ISOFEMALE AND MULTIFEMALE STRAINS

can be ordered from <http://stockcenter.arl.arizona.edu/>

NEW DROSOPHILA ISOFEMALE LINES: The Tucson *Drosophila* Species Stock Center has recently received new isofemale lines from different species. These Isofemale lines are available until May 1st 2007: *Drosophila simulans*: (59) 26-isofemale lines from Magdalena, Sonora, Mexico (2006) 17-isofemale lines from San Carlos, Sonora, Mexico (2006) 7-isofemale lines from South Africa (2007) 6-isofemale lines from Nogales, Sonora, Mexico (2006) 2-isofemale lines from Flagstaff, Arizona (2006)

Drosophila arizonae: (50) 40-isofemale lines from San Carlos, Sonora (2006) 10-isofemale lines from Tucson, Arizona (2006)

Drosophila pseudoobscura: (32) 21-isofemale lines from Magdalena, Sonora, Mexico (2006) 4-isofemale lines from Tucson, Arizona (2006) 3-isofemale lines from Nogales, Sonora, Mexico (2006) 3-isofemale lines from Flagstaff, Arizona (2006) 1-isofemale line from Catalina Island, California (2006)

Drosophila melanogaster: (31) 19-isofemale lines from San Carlos, Sonora, Mexico (2006) 10-isofemale lines from South Africa (2007) 1-isofemale line from Flagstaff, Arizona (2006) 1-isofemale line from Magdalena, Sonora, Mexico (2006)

Drosophila hydei: (15) 6-isofemale lines from San Carlos, Sonora, Mexico (2006) 5-isofemale lines from Magdalena, Sonora, Mexico (2006) 4-isofemale lines from Tucson, Arizona (2006)

Drosophila buzzatii: (8) 8-isofemale lines from Sardinia, Italy (2006)

Zaprionus indianus: (9) 9-isofemale lines from Tucson, Arizona (2006)

Drosophila hamatofila: (1) 1-isofemale line from Tucson, Arizona (2006)

NEW DROSOPHILA STOCKS PERMANENT COLLECTION: The Tucson *Drosophila* Species Stock Center has incorporate several strains of wild type flies. Check website for collection info: **MULTIFEMALE STOCKS:** *Drosophila pseudoobscura* 14011-

0121.125 (Pinal de Amoles, Queretaro, Mexico 2002) *Drosophila pseudoobscura* 14011-0121.126 (Chiapas, Mexico 2002) *Drosophila pseudoobscura* 14011-0121.127 (Durango, Mexico 2001) *Drosophila pseudoobscura* 14011-0121.128 (Filo de Caballo, Guerrero, Mexico 2001) *Drosophila pseudoobscura* 14011-0121.129 (Centro Nuclear, Estado de Mexico, Mexico 2001) *Drosophila pseudoobscura* 14011-0121.130 (Tlaxcala, Mexico 2003) *Drosophila pseudoobscura* 14011-0121.131 (Amecameca, Estado de Mexico, Mexico 2000) *Drosophila pseudoobscura* 14011-0121.132 (Veracruz, Mexico 2001) *Drosophila pseudoobscura* 14011-0121.133 (Chilpancingo, Guerrero, Mexico 2001) *Drosophila pseudoobscura* 14011-0121.134 (Guanajuato, Mexico 2001) *Drosophila pseudoobscura* 14011-0121.135 (Torreon, Coahuila, Mexico 2003) *Drosophila pseudoobscura* 14011-0121.136 (Tierra Nueva, Guanajuato, Mexico 2001) *Drosophila pseudoobscura* 14011-0121.137 (El lobo, Queretaro, Mexico 2002) *Drosophila pseudoobscura* 14011-0121.138 (Hidalgo, Mexico 2000) *Drosophila pseudoobscura* 14011-0121.139 (Juriquilla, Queretaro, Mexico 2004) *Drosophila pseudoobscura* 14011-0121.140 (Zacatecas, Mexico 2000) *Drosophila pseudoobscura* 14011-0121.141 (Matehuala, Nuevo Leon, Mexico 2003) *Drosophila pseudoobscura* 14011-0121.142 (Cola de Caballo, Nuevo Leon, Mexico 2000) *Drosophila pseudoobscura* 14011-0121.143 (Chiflon, Coahuila, Mexico 2004) *Drosophila pseudoobscura* 14011-0121.144 (Huimilpan, Queretaro, Mexico 2000) *Drosophila pseudoobscura* 14011-0121.145 (Michoacan, Mexico 2000) *Drosophila pseudoobscura* 14011-0121.146 (Puebla, Mexico 2001) *Drosophila pseudoobscura* 14011-0121.147 (Los Reyes, San Luis Potosi, Mexico 2001) *Zaprionus indianus* 50001-1031.04 (Tucson, Arizona 2006)

ISOFEMALE STOCKS: *Drosophila aldrichi* 15081-1251.18 (Tucson, Arizona 2006) *Drosophila buzzatii* 15081-1291.63 (Sardinia, Italy 2006) *Drosophila hydei* 15085-1641.65 (Tucson, Arizona 2006). *Drosophila hydei* 15085-1641.66 (Magdalena, Sonora, Mexico 2006). *Drosophila hydei* 15085-1641.67 (San Carlos, Sonora, Mexico 2006). *Drosophila melanogaster* 14021-0231.49 (Flagstaff, Arizona 2006) *Drosophila melanogaster* 14021-0231.50 (Magdalena, Sonora, Mexico 2006) *Drosophila melanogaster* 14021-0231.51 (South Africa 2007) *Drosophila pseudoobscura* 14011-0121.120 (Flagstaff, Arizona 2006) *Drosophila pseudoobscura* 14011-0121.121 (Catalina Island, California 2006) *Drosophila pseudoobscura* 14011-0121.122 (Magdalena, Sonora, Mexico 2006) *Drosophila pseudoobscura* 14011-0121.123 (Nogales, Sonora, Mexico 2006) *Drosophila pseudoobscura* 14011-0121.124 (Sinaloa, Mexico 2002) *Drosophila pseudoobscura*

14011-0121.148 (San Francisco, California 2006) *Drosophila pseudoobscura* 14011-0121.149 (San Luis Potosi, Mexico 2000) *Drosophila repleta* 15084-1611.11 (Tucson, Arizona 2005). *Drosophila simulans* 14021-0251.251 (Flagstaff, Arizona 2006) *Drosophila simulans* 14021-0251.252 (Magdalena, Sonora, Mexico 2006) *Drosophila simulans* 14021-0251.253 (Nogales, Sonora, Mexico 2006) *Drosophila simulans* 14021-0251.254 (South Africa 2007)

— / —

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>

Ornate chorus frog tissue samples

Hello,

Does anyone have tissue or DNA samples of the ornate chorus frog (*Pseudacris ornata*)? Does anyone have specific location data on ponds which have *P. ornata* choruses? Any replies would be greatly appreciated.

Reply to

Jack Degner jdegner@pegasus.cc.ucf.edu

All the best,

Jack

jdegner@pegasus.cc.ucf.edu

Paracentrotus lividus samples

Dear all,

Im just beginning my PhD at the center of oceanology of Marseille (France), at the laboratory diversity, evolution and marine functional ecology (DIMAR). My work deals with the common sea urchin *Paracentrotus lividus*, for which Im studying some aspects of population genetics and life history. So Im looking for samples from different places (Mediterranean Sea and north eastern Atlantic) and Im wondering if someone could send me some in order to integrate them to my study.

I would be very obliged if you could help me or if you know somebody that could. Dont hesitate to contact me to know more about my needs and my work.

Cordially

<<http://www.com.univ-mrs.fr/DIMAR/>>

PENANT Gwilherm, PhD Student

UMR 6540 CNRS DIMAR Centre d'Océanologie de Marseille Station Marine d'Endoume Chemin de la Batterie des Lions 13007 MARSEILLE - France

phone : 33 (0)4 91 04 16 18 fax : 33 (0)4 91 04 16 35

Mail : gwilherm.penant@univmed.fr Web : <http://www.com.univ-mrs.fr/DIMAR/>
herm.penant@univmed.fr gwil-

2. If Parentage can't do it, is it safe to modify the input to make it compatible with Parentage? This would be based on the assumption that alleles present in the families but not in the population sample have low frequencies in the population. For example, there are some inferred paternal alleles, which are missing from the population sample. Is it ok to add fake genotypes to the population sample, which would provide one copy of each missing paternal allele; i.e. assign an arbitrary low frequency to the missing alleles? Then, some of the known mothers also carry alleles, which are missing from the population sample. Can I include the mothers in the population sample?

Thanks and regards, Kristina

Kristina Sefc Department of Zoology University of Graz
kristina.sefc@uni-graz.at kristina.sefc@uni-graz.at

Parentage problems

Hi,

I was hoping that somebody could help me with an analysis in the program "Parentage". According to the manual, the program should be able to cope with the situation that alleles were found in the tested families, which do not occur in the population sample used for calculating background frequencies.

>From the manual:

Freqmodel: Used to determine the modelling used for sampling parents from background frequencies. The models can be simple multinomial sampling if the background frequencies contain all the alleles that are seen in the data, or multinomial-Dirichlet, if there are alleles in the data that are not in the background frequencies. If background frequencies are not provided then a multinomial-Dirichlet model should be used. Input either 0 (Dirichlet) or 1 (multinomial) default 0

Using the setting freqmodel: 0, the program exits with a polite excuse printed on the screen. Same with freqmodel: 1, when I run the families with the 'extra' alleles.

Increasing the population sample is not possible in the short run, current N is about 50 individuals. All fish (maternal families and population sample) were sampled at the same location and the species is known to be highly philopatric.

My questions: 1. If it is possible to use 'Parentage' in this situation, how do I get it to work?

Particle counter sizer

Dear Evoldir members, I am in the process of purchasing an instrument to count and measure the size of particles. I will be using this mainly for pollen, although some colleagues might want to use it to measure population growth of yeast. I have received bids from three companies, and I would appreciate your comments on any of them regarding 1) limitations of the instrument, 2) difficulty level of samples preparation, 3) cleaning and maintenance, 4) user support, 5) any other comments you may have. The instruments are: a) Beckman-Coulter - Multisizer 3 Coulter Counter b) Micromeritics (Folio Instruments Inc. in Canada) - Elzone II 5390 Automated particle size analyzer c) Brightwell Technologies (Spectra Research Corporation in Canada) - DPA 4100 Micro Flow Imaging (MFI) Particle Analysis System

I am most familiar with b), and I understand a) uses the same principle (and possibly was the original particle counter. I have no experience with c), and I am particularly curious to hear from users who have gone from a) or b) to using c).

I will be glad to collect and compile your messages and send them back to the list for everybody's benefit. Please send your responses to german.avilasar@msvu.ca. Thank you.

Germán Avila Assistant Professor Mount Saint Vincent University 166 Bedford Highway Halifax, Nova Scotia B3M 2J6

<http://faculty.msvu.ca/germanavila/> Tel: (902)-457-6251 Fax: (902)-457-6134

German.Avila-Sakar@msvu.ca
Sakar@msvu.ca

German.Avila-

Phylemon web server

Dear members of EvolDir, we would like to inform you that “Phylemon: a suite of web-tools for molecular evolution, phylogenetics and phylogenomics” is available at:

<http://phylemon.bioinfo.cipf.es> Phylemon is an online platform for phylogenetic and evolutionary analysis of molecular sequence data. It has been developed as a web server that integrates a suite of different tools selected among the most popular stand alone programs in phylogenetic and evolutionary analysis. It has been conceived as a natural response to the increasing demand of data analysis of many experimental scientists willing to add a molecular evolution and phylogenetics insight into their research. Tools included in Phylemon cover a wide range of programs, from the most basic for multiple sequence alignment to elaborate statistical methods of phylogenetic reconstruction and the evolutionary analysis of rates to test adaptation in molecular sequences. Phylemon has several features that differentiates from other web servers:

- 1- It offers an integrated environment that enables the direct concatenation of evolutionary analyses, the storage of results and the required data format conversions,
- 2- Once an outfile is produced, Phylemon suggests the next possible analyses, thus guiding the user and facilitating the integration of multi-step analyses, and
- 3- Users can define and save complete pipelines for specific phylogenetic analysis to be automatically used on many genes in subsequent sessions or multiple genes in a single session (phylogenomics).

The Phylemon web server is at <http://phylemon.bioinfo.cipf.es> Sincerely, H –

Hernán J. Dopazo, PhD Pharmacogenomics & Comparative Genomics Unit, Bioinformatics Department, Centro de Investigación Príncipe Felipe c/ ep Avda. Autopista del Saler 16 (Junto al Oceanográfico), 46013, Valencia, España. Tfn: (34) 96 328 96 80 ext: 1008 Fax: (34) 96 328 97 01 hdopazo@cipf.es <http://www.cipf.es/> <http://bioinfo.cipf.es/hdopazo/> hdopazo@ochoa.fib.es

QA agarose

Hi Everyone

I have been using a 10% Acrylamide gel to run PCR products of approximately 96-100bp in size. In trying to avoid using acrylamide, I have converted to use a product call “QA agarose, high resolution” at 6% and encountered some problems. Has anyone have any experience, with running fragments of approx. the above size, using the QA agarose? I'd appreciate any input at all on the matter.

Thank you.

Nga Dang. Teaching technician Dept. of Biological sciences Monash University Clayton 3800 VIC Australia.

Nga.Dang-Lien@sci.monash.edu.au

QA agarose answers

Thank you everyone for your help in response to my querie:

Hi Everyone

I have been using a 10% Acrylamide gel to run PCR products of approximately 96-100bp in size. In trying to avoid using acrylamide, I have converted to use a product call “QA agarose, high resolution” at 6% and encountered some problems. Has anyone have any experience, with running fragments of approx. the above size, using the QA agarose? I'd appreciate any input at all on the matter.

Thank you.

Nga Dang. Teaching technician Dept. of Biological sciences Monash University Clayton 3800 VIC Australia.

I've used NuSieve agarose at 6% for fragments a little bit bigger (150bp) - and this worked fine for distinguishing between fragments about 6 bp apart. I found that the most important 'tricks' are to make sure you heat the agarose really well (and add it slowly to the buffer so it does not clump) since it melts much more slowly

than traditional agarose. Second is that you have to run the gel much more slowly (not over 90v) to avoid warping the fragments.

I hope this helps. Alexis

Every time I've tried using one of the supposed high-resolution agaroses, I end up cursing them and going back to acrylamide, though I've never used it at 10%; we've gone as high as an 8% (0.35mm thickness)- to resolve microsatellite polymorphisms in fragments ranging in size from 100-200bp. More recently, we tried using NuSieve at 4%, but again, could not resolve the size differences. And making gels that thick is a pain.

We have been silver-staining the acrylamide gels, but will try a DNA stain called FMC Gel-Star.

I'm curious to know what sort of apparatus you are running your acrylamide gels in. We typically use the Bio-Rad Sequi-Gen 38x30cm setup, because we can load 48 samples across. We tried using their protein-oriented Protean II system, but the gels are thicker, and not set up to run at high enough temperatures, or at least I think that's what our problem was. Bio-Rad tech support could offer no help b/c they said the unit is meant for proteins.

I'd very much like to know what your experience is, and what you learn from others.

Best wishes, Bob Marra

We don't use QA agarose but we do use NuSieve GTG Agarose to resolve fragments that size. We usually use 2.8% gels to resolve fragments 80-120 bp in size. It is low melting too so you can cut out the bands and use them for reamplification, cloning etc.

Cheers, Anne

Nga.Dang-Lien@sci.monash.edu.au

oping among evolutionary and population biologists on the use of the "false discovery rate" (Q-value) in multiple comparisons instead of the various forms of the Bonferroni correction. Since Rice's 1989 paper (Evolution 43:223), the Bonferroni correction has been widely used for adjusting the significance level of multiple comparisons to minimize type I errors. In fact, in some fields, as I have learned the hard way, it has become a virtual requirement for publication. But with these corrections, the power of the analyses are lowered, perhaps artificially and unnecessarily, and some biologists have argued that they probably should not be used (e.g. Moran,2003; Oikos 100:443). My own work often involves large numbers of comparisons of gene frequencies by chi-square or related statistics, to evaluate the significance of allelic frequency differences among populations or the potential reality of linkage disequilibrium detected by programs like LinkDos. I have used the Bonferroni correction in the past, but often with the feeling that I was throwing many babies out with the bathwater, especially with preliminary surveys, which are often "fishing expeditions."

It seems to me that use of the Q value instead of the Bonferroni correction could restore a great deal of power to multiple comparisons. [see Verhoeven et al., 2005; Oikos 108:643 for a discussion and review of literature]. Yet I see relatively few papers, particularly in population genetics, that use the Q value, and many that still use the Bonferroni correction. Of course, this apparent delay could simply reflect the fact that most papers that are in the current issues of journals were submitted around a year ago or more. Or it could simply stem from the conservatism of research communities (including referees of journal articles) that don't spend a lot of time worrying about type I vs type II errors.

I cordially invite comment from anyone who has a viewpoint or experience with this issue. Bruce J. Turner Dept. Biol. Sci. VPISU Blacksburg, VA 24061 (540)-231-7444 (V) (540)-231-9307 (F)

fishgen@vt.edu

Qvalue vs Bonferroni

[Note: this message will be posted on Evoldir, Ecolog-L, and the popbiol listservs, and I apologize in advance if you get multiple copies. I will post summaries of replies to all three lists.]

I am try to get a sense of whether a consensus is devel-

SSB Graduate Student Research Awards

Awards for Graduate Student Research

The Society of Systematic Biologists (SSB) announces its sixth annual Graduate Student Research Award competition. The purpose of these awards is to as-

sist students in the first two years of their systematics projects and in the collection of preliminary data needed to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: <http://systbiol.org/join.html>). Previous awardees may not re-apply, but previous applicants who were not selected for funding are eligible. Awards will range between \$1,000 and \$2000.

Applicants must submit 1) a curriculum vitae (one page) 2) brief research proposal including objectives, methods, significance, and schedule (max. three single-spaced pages including literature cited and any figures and tables) 3) budget and budget justification (1 page) 4) and arrange for two letters of recommendation; one letter must be from the student's current graduate advisor.

The research proposal must clearly state the current stage of the proposed research and the current year and status of the student. Please include e-mail contacts for the applicant in the application itself. Both Masters and Ph.D. students are eligible. Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work.

All applications materials must be in electronic format. Applicants and their recommenders are strongly encouraged to use pdf format, rather than Word or some other application, to minimize difficulties in file transfer. We strongly recommend that applicants send all materials (except letters of reference) in a single pdf file. Letters of recommendation should be sent separately by the referees in pdf format or in the text of an e-mail; please include the full name of applicant in letters of recommendation.

Please email all application materials and queries to Dr. Kelly Zamudio at krz2@cornell.edu

To be considered for this year's award, application materials, including letters of recommendation, must be received electronically no later than March 31, 2007.

Additional Information can be found at: <http://systbio.org/?q=node/22> -

krz2@cornell.edu krz2@cornell.edu

Software BayesianPhylogenetics GeneiousPlugin

Bayesian phylogenetics without tears!

I am pleased to announce the availability of a free MrBayes plugin for the Geneious molecular sequence platform. Running on top of Geneious (version 2.5.4 or greater), this plug-in provides:

An easy-to-use graphical interface for performing Bayesian phylogenetic reconstruction using MrBayes.

One can seamlessly integrate blast searches, multiple sequence alignment and Bayesian phylogenetic reconstruction with simple clicks of the mouse. Currently available through the plug-in are the nucleotide- and codon-based models, JC, HKY, GTR and CodonM0, all with or without molecular clock assumptions, and invariant and site-specific rate variation.

Importantly, the plug-in also provides interactive graphical viewers to examine the resulting posterior distributions. These viewers generate publication-quality summaries of the tree and other model parameter distributions, including:

1. Marginal summary statistics, histograms and density plots,
2. Bi-variate correlation plots to explore hidden structure in the posterior, and
3. Effective sample size estimates and time-series plots to assess convergence.

The plug-in is open source, so researchers interested in extending it should contact me (msuchard@ucla.edu) to receive the source code. While the current choices of reconstruction models are limited, upcoming extensions include:

1. multiple data partitions,
2. amino acid models,
3. flexible prior specification, and
4. site-specific codon models with direct plotting of positive selection probabilities in Geneious.

Following the cross-platform ideal of Geneious for molecular sequence analysis, the plug-in runs under Windows, Mac OSX and Linux.

MrBayesPlugin v0.2 is available for download from: <http://www.biomath.ucla.edu/msuchard/software/-software.htm> Geneious v2.5.4 can be obtained at: <http://www.geneious.com> Marc A. Suchard, MD, PhD Assistant Professor Departments of Biomathematics, Biostatistics and Human Genetics David Geffen School

of Medicine at UCLA, and UCLA School of Public Health 6558 Gonda Building 695 Charles E. Young Dr, South Los Angeles, CA 90095-7088 (310) 825-7442 msuchard@ucla.edu

Software MSA

A new version of the Microsatellite Analyzer (MSA) has just been uploaded. MSA is a user friendly, platform independent software for the analysis of microsatellite data.

New features: - Estimates the variance in FST in relation to a specified number of loci. This feature is helpful to compare QST and FST if an estimate for the number of loci affecting the trait is available. - Generation of an input file for the IM Software (Hey & Nielsen) - GST and GST, which allows the comparison of loci with different levels of variability (Hedrick 2005) - Allelic richness - moment estimator beta (Weir & Hill) - file conversion to: IM (Hey & Nielsen)

Further features of MSA are:

ADVANTAGES Simple input format With only a few modifications the output file of a genotyping software could be converted into a MSA input file

Large data files are allowed Within the limits of available memory, no constraints on the number of loci

Platform independent Executables for Mac and PC are available

FEATURES Calculates basic summaries (e.g. observed and expected heterozygosity, number of alleles, expected number of alleles, variance in PCR product size, variance in repeat number

Several genetic distances are calculated (including Fst, delta mu squared, proportion of shared alleles, Neis distances etc.) Bootstrap and permutation options are available to test for statistical significance. Distances can be calculated for populations, individuals, across loci and for each locus separately.

Provides input files for other software (e.g.: Arlequin, Structure, Migrate)

Random discarding of alleles: this option is useful for researchers working with inbred strains (e.g.: Drosophila isofemale lines)

DOWNLOAD http://i12server.vu-wien.ac.at/MSA/-MSA_download.html click on the icon with the desired

OS

Christian Schlotterer 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://i12server.vu-wien.ac.at/> christian.schlotterer@vu-wien.ac.at christian.schlotterer@vu-wien.ac.at

Software NewTreefinder

A new unpaid TREEFINDER version is online at www.treefinder.de.

New features are:

- parametric bootstrapping from a dialog - simulation of partitioned sequences - sequence simulation along reports - mtArt protein model - various other improvements

Testing of phylogenetic hypotheses and substitution models is very easy now. One can examine the stochastic variation of all parameters under a particular null model and compute all kinds of statistics.

I still have no position in Munich.

Gangolf Jobb

Gangolf Jobb <gangolf@treefinder.de>

Tissue Storage for Morphological work

Please excuse the cross-posting.

I would like to know about any recent literature and people's personal experiences with storing specimens, particularly insects and spiders, for morphological work. There has been recent discussion regarding tissue preservation for molecular work which appeared to come to a consensus (majority rule?) that 95-100% EtOH and -80 degrees C is optimal. But this is not optimal for morphological work. Moreover, many of us do both molecular and morphological work and need to find a balance.

Personally, I like to have a long series of specimens that can be stored in several different ways for different pur-

poses (I work with insects so I can do this). But for soft-bodied critters (spiders, termites, larvae, etc.) and/or the very small (mites, aphids, etc.), what do people recommend for collection and storage? The answer to this will be somewhat dependent on the taxon (eg. caterpillars often turn black if killed in EtOH and should be killed in very hot water), and what the ultimate purpose will be (eg. study of internal organs, clearing-staining-slide mounting, etc.). Meanwhile, new methods are continually being tested (and old ones remembered).

Given all these caveats, I would like to hear your opinions, experiences, references and preferences.

Please reply off list and I will compile the results and repost.

Thank you,

Pete

Peter T. Oboyski, PhD candidate University of California ESPM Insect Biology 137 Mulford Hall MC3114 Berkeley CA 94720-3114

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/www.cnr.berkeley.edu/
pt_oboyski@hotmail.com

http://poboyski/

TrinityCollege Dublin UREKAProgramme 2007

Dear Colleagues,

Please forward to any undergraduates who you think might be interested.

Thanks,

Mark Brown Zoology, Trinity College Dublin

Undergraduate Research in the School of Natural Sciences, Trinity College Dublin <http://www.tcd.ie/naturalscience/ureka> "Integrating Ecology and Evolution in a Changing World" is a summer, undergraduate research programme based in Dublin, Ireland. Its aim is to provide research training and experience, as well as an introduction to Ireland, to national and international undergraduate students. Students will work within active research groups in Trinity College Dublin, Ireland's premier university.

Full funding is available for ten students to participate

in this 10-week programme, from 2 July - 7 September 2007. International students are also entitled to assistance with travel costs.

All applications must be received by 16 March.

The new School of Natural Sciences, comprising the departments of Botany, Geography, Geology and Zoology, and the Centre for the Environment, hosts internationally acclaimed biological, physical and social scientists. It provides a dynamic and exciting research environment, with ~40 academic staff, ~20 post-doctoral fellows, and ~120 graduate students. The summer undergraduate research programme cuts across the ecology and evolution research strands within the School, and offers projects ranging from climate change to behaviour to phylogenetics, and training in both practical laboratory and field skills, as well as generic science communication skills. Students will be embedded within active research groups and receive direct training from PIs, as well as post-doctoral fellows and graduate students. A weekly seminar programme will cover research ethics, the transition to graduate school, current topics in ecology and evolution, and science communication. At the end of the programme students will both write up and present their research project at a one-day symposium.

In addition to the science, an active social programme will introduce students to the delights of Dublin, and the beauty and history of Ireland.

Requirements: - completion (in 2007) of the penultimate year of an undergraduate biological science degree - proficiency in English (written and spoken) - willingness to work hard, and ability to work independently - strong interest in the project of choice - aspiration to pursue research in ecology or evolution

Your application must include a CV (with 2 referees) and a completed application form, which you will download from the website (www.tcd.ie/naturalscience/ureka). Details for the application process can be found on the website. All materials must be received by Friday 16 March 2007

Research Projects: Host-parasite molecular phylogeny; Grass phylogenetics; Parasite morphology; Shrimp feeding ecology; Plant biodiversity in conservation areas; Plant biodiversity in managed forestry; Phylogeny of Thai plants; Management and respiration in crops; Crop greenhouse emissions; Foraging and competition in bivalves

For more details, please see: <http://www.tcd.ie/naturalscience/ureka> or e-mail: fimolony@tcd.ie

mabrown@tcd.ie

Tripneustes samples

Dear all EvolDir users,

We are studying the large scale population structure of *Tripneustes gratilla*, a sea urchin species distributed all over the Pacific and Indian Ocean, as well as the Red Sea. We are looking to expand our sample sizes, and we would like to know if one of you could provide us with some tissue samples of this species in order to achieve better resolution for our analyses. So far we were collecting a couple of tubular feet kept in ethanol.

Thanks in advance, Catherine Lippé.

– Catherine Lippé Research Assistant 2538 McCarthy Mall, Edmondson Hall #152 University of Hawaii at Manoa Honolulu, HI 96822 (USA) Tel: (808) 956-4722 Fax: (808) 956-9812 E-mail: lippe@hawaii.edu –

lippe@hawaii.edu

Trizol RNA extraction

Hi all,

I do microarray work with Atlantic salmon livers. I collected my samples by putting the livers in cryotubes and flash freeze them in ethanol that was at -80C. Unfortunately, the tubes took some ethanol in and now my small livers (50-150mg) (as well as brains, white muscle and whole fish) have been in presence of small amounts of 95% pure ethanol for some time. Their is good reason to believe that the ethanol has penetrated the tissues.

I did Trizol RNA extractions with some of these livers, whipping the excess ethanol before putting the samples in Trizol and homogenizing them. Following the normal microarray protocol (Array 50 kit from Genisphere), I did 2 chips. 1 control with material from an extraction that had successfully used for microarray and one with 2 of my samples. The control is superb whereas mine didnt work.

My only suspect is the sample itself, and its only particularity is this presence of ethanol in the tubes.

Anyone has any reason to suspect how this ethanol could be bad for the retro-transcription of mRNAs in cDNAs, the hybridization of cDNAs on the chip or hybridization of the fluorochromes on the cDNAs, I'd be more than happy to know.

I also need a way of getting rid of the ethanol from all my samples. Some have suggested to put them in RNA later so as to extract the ethanol. Would that work?

Cheers and thanks a lot

Eric Normandeau

Étudiant au deuxième cycle Département de biologie Pavillon Charles-Eugène Marchand Université Laval, Quebec QC G1K 7P4 Canada

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eric.normandeau.1@ulaval.ca

cDNA AFLP fragments

Hi all,

I am currently working with cDNA AFLP and I get some troubles at re-amplifying the long fragments generated by the technique (beyond 400 bp). My selective amplification products are electrophoresed on polyacrylamide gels and silver-stained according to the procedures used by Bassam et al (1991).

I collect the fragment of interest by scraping gel away from around band of choice, then let sit the fragment in 50 ul sterile 1X TE buffet at least 5 hours in 4C.

After this step, I set up PCR reactions with appropriate primers and use 5 ul of the designer DNA as the target.

Finally, I load a 2% agarose gel for confirmation of the presence of the correct band.

So far, I have not been able to extract and reamplify the fragments above 400 bp.

Too much of the silver stained fragment could inhibit the PCR reaction? In vain, I tried to set the PCR reaction with different kind of Taq. Maybe the largest fragments can't get out of the gel. I tried longer time and various temperatures when letting sit in the 1X TE.. No better results.

I'd appreciate any advice or comment on the question.

Nicolas Taris PostDoc USDA-ARS Shellfish Genetics

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Nicolas.Taris@oregonstate.edu

Nico-

las.Taris@oregonstate.edu

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Barcelona ConservationGenetics

A POSTDOCTORAL POSITION IN ANIMAL CONSERVATION GENETICS GROUP (IRTA - INSTITUTE of RESEARCH & TECHNOLOGY FOOD & AGRICULTURE - in Cabrils, Barcelona, Spain)

The main goal of Animal Conservation Genetics group is to contribute to the conservation of endangered mammalian species by applying population genetics and molecular biology techniques in order to elucidate phylogenetics relationships, population history and reproductive patterns.

We are seeking a postdoctoral scientist to participate in the next call for the Juan de la Cierva programme of the Science and Technology Department of Spanish Government. More information about this programme is available in http://www.mec.es/ciencia/-jsp/plantilla.jsp?area=delacierva_eng&id=2

To apply for this position, please send a cover letter of no more than a page outlining your special interests and your cv before 9th March 2007.

For further information, contact Dr. Montserrat Bosch.

Dr. Montserrat Bosch Head of Animal Conservation Genetics IRTA Crta. Cabrils km 2 08348 Cabrils (Barcelona, Spain) montse.bosch@irta.es

“Bosch, Montserrat” <montse.bosch@irta.es>

Barcelona speciation

POSTDOC JOB IN BARCELONA: GENETIC ARCHITECTURE OF SPECIATION

A postdoctoral position is available to study genetic architecture of hybrid male sterility in *Drosophila*. Work in our lab has shown that experiments using introgressed hybrids support that the threshold additive model (apparently many genetic additive factors) is the most plausible to explain hybrid sterility. However, these results do not discard the existence of unique factors of major effect and/or epistatic interactive factors mapping in different chromosomes. We plan to saturate the genome with species specific AFLP markers in order to detect candidate sequences responsible for hybrid sterility. At the moment we have selected at least 20 AFLP markers associated to hybrid male sterility that are being sequenced and mapped to unveil candidate genes. Combining genomic, molecular, cytogenetic and bioinformatic techniques we want to distinguish between additive and epistatic actions of these genetic factors. This work is carried out in hybrids between *D. koepferae* and *D. buzzatii*, but we plan to extend it to other species pairs in earlier stages of differentiation. Applicants must have either a strong background in *Drosophila* molecular evolutionary genetics or in molecular genetics with a high interest in evolution and speciation. Applicants must contact immediately Dr. Antonio Fontdevila sending a cover letter, a CV and the names, affiliation, address, e-mail address, and telephone number of two persons of reference. Deadline for submission is March 5, but immediate notice is encouraged. Annual salary range is 24750-32600 euros (before taxes) and duration is 3-5 years. The successful applicant is expected to start working on September 2007 (or earlier), but, if justified, his/her incorporation can be delayed.

Antonio Fontdevila Grup de Biologia Evolutiva Departament de Genètica i Microbiologia Edifici C Universitat Autònoma de Barcelona 08193 Bellaterra, Spain Phone: 34-93-5811083 Fax: 34-93-5812726 e-mail: antonio.fontdevila@uab.es

antonio.fontdevila@uab.es

BonnGermany MolSystematics

The Zoological Research Museum Alexander Koenig in Bonn (<http://www.zfmk.de/index.en.html>) is a center for biodiversity research, where traditional taxonomy, molecular methods and testing of phylogenetic, biogeographic, and evolutionary hypotheses are combined to a nearly holistic approach to understanding biodiversity. The institute has projects especially in tropical hot spot areas, but also in temperate Eurasia and in Polar Seas.

We are seeking a person interested in molecular systematics, familiar with a programming language (e.g. C++), to develop methods for the evaluation of the information content of DNA alignments. The 3-year position is immediately available. Salary is equivalent to the German grade BAT IIa (roughly 3100.- \hat{a} -/monthbeforetax, dependingonage).

Bonn is located in the romantic landscape of the Rhine valley and has an agreeable climate. The university has a strong tradition for organismic biology including palaeontology and systematics and is strengthening this area of research (<http://www.uni-bonn.de/en/Institutions/Faculties.html>).

Please send your application and names and contact details for two referees to:

Prof. Dr. J. Wolfgang Wägele Director Zoologisches Forschungsmuseum Alexander Koenig und Lehrstuhl für Spezielle Zoologie Rheinische Friedrich-Wilhelms-Universität Bonn

Adenauerallee 160 53113 Bonn, Germany

w.waegle.zfmk@uni-bonn.de Tel.: 0049 (0) 228 9122 200 Fax: 0049 (0) 2289122 202 <<http://www.zfmk.de>> <http://www.zfmk.de>> w.waegle.zfmk@uni-bonn.de

CardiffU 2 MolEvolEcol

TWO MARIE CURIE POSTDOCTORAL RESEARCH FELLOWSHIPS IN MOLECULAR ECOLOGY

SCHOOL OF BIOSCIENCES, CARDIFF UNIVER-

SITY

Application deadline 28th February 2007.

EU funded positions, salary dependent on EU experienced researcher qualifications: £28,000 (Marie Curie Fellow 1) or £41,928 p.a., (Marie Curie Fellow 2). Each position is for 24 months.

In a global economy, the transfer of parasites to novel hosts can pose a major threat to both farmed and wild animal stocks. The effects of parasite invasion can have significant impacts on rural economies and biodiversity, but are difficult to evaluate in the short-term, since adaptation to new hosts occurs over an evolutionary time-scale. This project will study neutral genetic variation and adaptive evolution of morphology and virulence of gyrodactylid parasites associated with historical translocations of the guppy (*Poecilia reticulata*).

This group of fish-parasites may comprise ca. 20,000 species, the majority of which are still unknown to science. Gyrodactylids are renowned for their colonization abilities and pathogenicity, and one species alone, *Gyrodactylus salaris* has cost the Norwegian Salmon Industry >500 million in 25 years. Gyrodactylids demonstrate biological plasticity including host-shifts, an evolutionary characteristic important for parasite invasion.

We will utilize a multi-disciplinary approach integrating morphometrics, molecular ecology and experimental parasitology to identify and describe novel species, to study their invasion potential, and to establish DNA barcoding for this group.

The successful candidates must have PhDs and have a strong background in evolutionary biology, genetics, ecology and/or epidemiology. They will join a team of parasitologists (Cardiff and Oslo) and evolutionary biologists (Cardiff and Hull) engaged in a four year Transfer of Knowledge (ToK) Marie Curie Programme (GYROSCOPE). The successful candidates will both be based in Cardiff for two years, but there will be the possibility of short periods of fieldwork in Trinidad and/or Tobago. For Marie Curie Fellow 1, expertise in parasitology/microscopy or molecular biology is required. For Marie Curie Fellow 2, experience of microsatellite, AFLP and/or SNP analysis is essential.

To comply with EU ToK appointment regulations, UK candidates are not eligible, unless they have worked outside the country for the last five years.

For further information, contact Dr. Jo Cable (e-mail: cablej@cardiff.ac.uk), Prof. Mike Bruford (BrufordMW@cardiff.ac.uk) and/ or Dr. Cock van Oosterhout (C.van-oosterhout@hull.ac.uk). For general information on the Schools of Biological

Sciences at Cardiff University visit our website at <http://www.cardiff.ac.uk/biosi/research/biodiversity/-index.html> Joanne Cable <cablej@Cardiff.ac.uk>

FloridaStateU phylogenetics

A postdoctoral position is available in the laboratory of Dr. Mark Holder. The research will focus on theoretical and computational issues in systematics (particularly phylogenetics). Projects in the lab include: extending models of character evolution to allow for dependence in the evolutionary process across characters; the development of improved heuristics for tree searching; and the application tree-based analyses to other fields in biology (for example in biogeographic analyses). Candidates will be expected to have completed a PhD in Biology, Statistics, Computer Science or a related field. Preferably the candidate will exhibit competence in at least one programming language (C, C++, Python, Java, or Perl are preferred). The ideal candidate will be enthusiastic, motivated, have a strong background in phylogenetics, and have experience implementing statistical inference techniques in software.

The earliest start date for the position September 1, 2007.

Application details =====To apply, go to <https://jobs.ku.edu> and search for position 00206267.

You will be asked to provide: * current CV * statement of research interests, and * the names (and email contact information) for three references.

First consideration will be given to application materials received by the initial review date (03/15/2007).

Links =====For further information, see: <http://www2.ku.edu/~eeb/documents/postdoc-phylogenetics.pdf> or contact Mark Holder (who is at Florida State University until summer, 2007): <http://www.scs.fsu.edu/~mholder/> mtholder@ku.edu

Mark Holder mtholder@ku.edu

<http://www.scs.fsu.edu/~mholder> current address (until summer 2007):

School of Computational Science 150-F Dirac Science Library Florida State University Tallahassee, Florida 32306-4120 Tel. (850) 645-0305

mtholder@ku.edu mtholder@ku.edu

IndianaU EvoDevo

Evolution of Development Postdoctoral Fellowship Opportunity, Indiana University School of Medicine at the University of Notre Dame, South Bend, Indiana A postdoctoral position is available starting August 2007 in the Indiana University School of Medicine-South Bend at the University of Notre Dame, which has recently built new research facilities. The lab has a number of research interests, including analysis of nervous system development, with emphasis on axon growth, in *Drosophila* and other arthropods. Funding is available for three years. A background in *Drosophila* genetics, cellular growth regulation, or evolution of development (especially RNAi) is beneficial, though not required. Motivated individuals with excellent technical and communication skills are encouraged to apply by sending a letter of interest, CV, and the names/contact information of three references to Molly Duman-Scheel by e-mail (mscheel@albion.edu). Applications will be reviewed on a rolling basis until the position is filled.

Dr. Molly Duman Scheel, Asst. Professor Department of Biology Albion College Albion, MI 49224 Phone: (517) 629-0572 FAX: (517) 629-0888 email: mscheel@albion.edu

Institut Pasteur HumanPopGenet

POST-DOCTORAL POSITION Human Population Genetics, INSTITUT PASTEUR, Paris

Population genomics of human immune response: genetic diversity and natural selection

A postdoctoral position is available in the Unit of Human Evolutionary Genetics directed by Lluís Quintana-Murci, in the Department of Genomes and Genetics at Institut Pasteur in Paris (www.pasteur.fr). Research projects in our lab focus on empirical and modeling studies of the role of population demography and natural selection in shaping the patterns of human genome variability. We are particularly interested in the study and dissection of the relative influence of population history, variable temporal and geographic host exposure to pathogen pressures, and different lifestyles (from

hunter-gathering to farming economy) on the patterns of variability of human immunity-related loci. We focus on genes or gene families involved in innate immunity, which constitutes the first line of host defence against pathogens (ex. Toll-like receptors, C-type lectins, scavenger receptors, etc.). These studies, which integrate molecular biology, population genetics and bioinformatics, will allow us to determine the extent to which natural selection has shaped the patterns of variation of these genes, and to identify those genes or gene families, variations in which may affect susceptibility to infectious diseases. Institut Pasteur hosts geneticists, microbiologists, immunologists and computational biologists under this broad research agenda, providing a working interdisciplinary research environment.

The candidate should be highly motivated, with good communication skills and a high level of commitment. He/She is expected to have a Ph.D. in the relevant field (population genetics, genomics, human genetics), and a strong background in molecular genetics and/or population genetics. Bioinformatics and computational skills are desirable. A willingness to engage in interdisciplinary research in population genetics, evolution and immunology is essential. The starting date is negotiable, but the position is available immediately.

Applicants should send their CV, a summary of work experience and interests, and contact information for three references to Dr. Lluís Quintana-Murci by email to (quintana@pasteur.fr).

Lluís Quintana-Murci, PhD Unit of Human Evolutionary Genetics CNRS-URA3012 INSTITUT PASTEUR 25, rue du Dr. Roux 75724 Paris Cedex 15 France

Tel +33 1 45 68 89 20 Fax +33 1 45 68 86 39 e-mail: quintana@pasteur.fr

Lluís Quintana-Murci <quintana@pasteur.fr>

LifeSpan research

The Network of Excellence LifeSpan is seeking postdocs and PhD students.

The overall aim of the network is to establish the relationship between early-life events, and late-life survival and health, and to identify the mechanisms that underpin this relationship. In LifeSpan we will move to and fro between observations in humans and experiments in (in)vertebrate models, to test effects detected in one species in the context of candidate longevity mecha-

nisms in the others.

The LifeSpan consortium consists of the leading European laboratories that are crucial to studying mechanisms of ageing and development, and their interplay. In all these laboratories positions are open now, and others will become available over the coming five years.

We are encouraging people to apply that are excited by the LifeSpan initiative and whom can contribute expertise relevant to the network. This will result in an enthusiastic and synergistic group of scientists that cover all relevant fields of expertise. How to apply? On the LifeSpan website (www.lifespannetwork.nl) the complete list of positions and full job descriptions are available.

More general information on the Network can be obtained by contacting, Dr. Bas Zwaan (b.j.zwaan@biology.leidenuniv.nl, tel., +31 71 527 4877) or Prof. Dr. Rudi Westendorp (r.g.j.westendorp@lumc.nl, tel., +31 71 526 2642).

Recently, the EU funded a Network of Excellence "LifeSpan" that integrates research into development and ageing.

B.J.Zwaan@biology.leidenuniv.nl
B.J.Zwaan@biology.leidenuniv.nl

Madrid MatingSystems

Dear colleagues,

We are seeking a postdoctoral scientist to participate in the next call for the Juan de la Cierva programme (<http://www.mec.es/ciencia/jsp/-plantilla.jsp?arealacierva&cid=4>). The applicants will be associated to the project REPROFOR (Breeding systems, effective gene flow and parental effects: application to management and conservation of forest genetic resources), coordinated by Centro de Investigaciones Forestales (INIA, Madrid) and Centro de Investigaciones sobre Desertificación (CSIC, Valencia) and participated by several researchers at Universidad de Cádiz, University of Oxford, Université de Montpellier and INRA (France).

As a result of the above mentioned project, several of our research lines have converged towards the issue of the phylogenetic structure of the plant communities. We want to face such topic with the help of different molecular markers. We hope the candidate to help in

the development of such line of research.

To see our publications, please click on <http://www.uv.es/~verducam/publications> The work will be done in the CIDE (Valencia, Spain) and the applicant should have a strong empirical and theoretical research background in areas related to population genetics and evolutionary biology and large expertise in molecular biology labs.

Please, send an email with a CV to Miguel.Verdu@uv.es.

Thanks,

Miguel Verdú

Centro de Investigaciones sobre Desertificación -CIDE- (CSIC/UV/GV) Apartado Oficial 46470 ALBAL, VALENCIA (SPAIN) phone: (+34) 961220540 ext. 110 fax: (+34) 961270967 Miguel.Verdu@uv.es

santiago@inia.es

MaxPlanckLeipzig EvolAnthro

Max Planck Institute for Evolutionary Anthropology: Post-Doctoral Position for Individual-Based Modeling

A post-doctoral position is available in the Junior Research Group of Julia Ostner Integrative Primate Socio-Ecology at the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany. The successful applicant will build an individual-based model of demographic events in primate populations to test hypotheses concerning the ecological bases of primate behavior. Requirements for the position are a Ph.D./Dr. in Theoretical Biology, Ecology & Evolution, Biology, Animal Behavior, Physical Anthropology or a related field, a firm theoretical background in social evolution/population biology and prior experience with building agent-based models in behavior and ecology. The position will initially be for one year, with a possibility of extension based on successful progress.

The Junior Research group on Integrative Primate Socio-Ecology develops and tests conceptual models on the evolution of social relationships. Information on the group can be found at our webpage: <http://www.eva.mpg.de/ipse/>. The group gains from close affiliation with the Primatology Department (<http://www.eva.mpg.de/primat/>) at the MPI for Evolutionary Anthropology in Leipzig. The working language at the institute is English. Leipzig offers a dynamic cultural

and social life.

Applications including a cover letter stating research experience and interests, curriculum vitae, and the names and e-mail addresses of two referees should be sent electronically to Julia Ostner (ostner@eva.mpg.de). The first evaluation of applications will start on April 1st 2007 and applications will be accepted until position is filled.

The Max Planck Society is an equal opportunity employer.

Dr. Julia Ostner Integrative Primate Socioecology MPI for Evolutionary Anthropology Deutscher Platz 6 04103 Leipzig Germany Phone: ++49-341-3550-260 Fax: ++49-341-3550-299 Email: ostner@eva.mpg.de www.eva.mpg.de/ipse/ ostner@eva.mpg.de

Montpellier EvoOfHandednessInHumans

Evolution of handedness in human populations

Institute of Evolutionary Sciences of Montpellier (France) CNRS UMR 5554

Part 1. Social status and handedness Social status is a fitness component in humans, as in other social species with dominance relationships. Associations between socio-economic status and handedness have been found in a western society in a population of children and in several large cohorts of adults. We propose to investigate this relation in other cultures, especially in traditional or sub-traditional societies that have not experienced the demographic transition.

Part 2. Sex and handedness There are more left-handed men than women, in most societies so far investigated. Why left-handed women still exist is not well understood, in light of the advantage found, in fighting interactions, which does not concern women. One possible explanation is an indirect advantage for women, through their sons, because there is a maternal component in the inheritance of left-handedness. This aspect has only been explored theoretically, and requires empirical evidence.

These two parts are to be completed with other aspects, according to competence and expertise, e.g. the temporal variation of handedness (through bilateral asymmetries in past remains), and the investigation of the evolutionary causes of historical and geographical vari-

ations.

Duration: 24 months (including at least 6 months of field work)

Salary: monthly, net : 1430-1741 (according to experience)

Application: CV, list of publications, names and email addresses of at least two research scientists able to fully evaluate the candidate, and cover letter should be sent to Michel Raymond (raymond@isem.univ-montp2.fr).

Dr. Charlotte Faurie Department of Animal and Plant Sciences University of Sheffield Western Bank, Sheffield S10 2TN United Kingdom

work. +44 114 222 0117 home. +44 114 273 8220 mobile UK. +44 773 829 1951 mobile FR. +33 616 729 228

The Human Life History Project <http://www.huli.group.shef.ac.uk/index.html>
c.faurie@sheffield.ac.uk

Montpellier MolPopGenet

Mouse molecular population genetics.

A post-doctoral position is open at the Institut des Sciences de l'Evolution, (CNRS-Université Montpellier II), Montpellier, France.

The project aims at understanding the historical and selective determinants of the differentiation of the house mouse subspecies, leading to partial incompatibility and reproductive isolation. The approach will combine the study of the patterns of coalescence of genes within and among subspecies with that of the patterns of introgression across a hybrid zone between the subspecies, and will take advantage of the growing knowledge of the mouse genome sequence variation and functional genomics. The team has long experience in mouse population biology, population genetics, chromosome evolution, archaeological, morphometric and behavioural studies. A large collection of mouse DNA samples and wild-derived strains are available for the project. The project is funded by ANR (Agence Nationale pour la Recherche). The Post-Doc will work in direct collaboration with one researcher (Dr. Pierre Boursot), one bench-work technician, and one PhD student.

The Institut des Sciences de l'Evolution offers a rich environment of evolutionary biologists covering many disciplines from palaeontology to molecular evolution

and population genetics. It offers access to platforms for robotics, automatic capillary sequencing and real-time PCR, as well as computer clusters, with dedicated staff for operation and assistance. Montpellier is a hot spot for evolutionary biology, biodiversity and genomic studies in France.

Candidates should have a strong background in molecular population genetics and/or molecular genetics. Skills in bioinformatics and programming are desirable. Experience of high throughput polymorphism detection methods would also be favourable. Strong motivation, communication skills and commitment are expected.

The position is for one year with possible extension, depending on starting date and progress of the project.

Applicants should send a CV including summary of past research, current interests and motivation for the present project, as well as contact information for three references to Pierre.Boursot@univ-montp2.fr <mailto:Pierre.Boursot@univ-montp2.fr>

—

Dr. Pierre BOURSOT Institut des Sciences de l'Evolution (UM2-CNRS UMR 5554) Universite Montpellier II Case Courrier 063 34095 Montpellier cedex 5 FRANCE tel: +33 (0)4 67 14 46 86 fax: +33 (0)4 67 14 45 54 Email: Pierre.Boursot@univ-montp2.fr

Pierre Boursot <Pierre.Boursot@univ-montp2.fr>

Muenster EvolEcolImmunity

Postdoc: Muenster (Germany) - Evolutionary Ecology of Immunity and Host-Parasite Coevolution

A postdoctoral research associate position is available in the group of Animal Evolutionary Ecology at the newly founded Institute for Evolution and Biodiversity, University of Muenster, Germany (www.uni-muenster.de/Evolution) from April 2007.

Research projects will be in the areas of Evolutionary Ecology of Immune Defence, Host-Parasite Coevolution or Evolution of Immune Systems. Current projects of the group focus on the evolution of specific memory and phenotypic plasticity in immune responses, adaptations of parasites to host immune defences and the adaptation of hosts to their natural parasite fauna. We use diverse immunological, genetical and parasitological methods. Our current model species include flour beetle and stickleback fish.

Requirement for the position is a PhD degree and research experience in a biological field (which should be detailed in the application). Experience in one or several of the fields of evolutionary biology, ecology, immunology, parasitology or genetics will be an advantage.

Positions are paid according to TVOED, level TV-L 13 (approximately 35.000-45.000 Euro p.a., cf. <http://paul.schubbi.org/bat/>). The position will include some teaching and administrative duties, however these are generally relatively low. Working and teaching language is English.

Muenster hosts many excellent scientific institutions and is a dynamic city with a world-famous heritage centre. It is very lively, last not least because of the high number of students (around 20% of the residents) and the rich choice of social, cultural and sporting facilities (see www.muenster.de for further details).

Interested candidates should, from now on, send applications (preferentially as E-mail attachment) containing a CV, a list of publications, a research statement and the addresses of 3 potential referees to:

Prof. Joachim Kurtz Institute for Evolution and Biodiversity University of Muenster Huefferstr. 1 D-48149 Münster joachim.kurtz@uni-muenster.de

Tel. +49 (0)30 89001266

Closing date is the February 28th 2007.

***** Prof. Dr. Joachim Kurtz

University of Muenster Institute for Evolution and Biodiversity, Animal Evolutionary Ecology Group Huefferstr. 1, D-48149 Muenster, Germany Phone: + 49 251 83 21 027 (Secretary, Ms. Doberenz) Fax: + 49 251 83 24 668 <http://www.uni-muenster.de/Evolution/>
PLEASE NOTE: From Oct 2006 - March 2007 I will be located at:

Wissenschaftskolleg zu Berlin (Institute for Advanced Study) Wallotstrasse 19, D-14193 Berlin, Germany Phone: + 49 30 89 001 266 Fax: + 49 30 89 001 300 <http://www.wiko-berlin.de> E-mail: joachim.kurtz@wiko-berlin.de joachim.kurtz@env.ethz.ch

NewMexicoStateU MolPopGenetics

ANNOUNCEMENT OF POSITION AVAILABILITY

Title: Postdoctoral Research Associate

Effective: XXX

Salary: \$30,000 - \$32,000/yr + university benefits (up to three year appointment contingent upon research project funding)

Location: New Mexico State University, Las Cruces and U.S. Fish and Wildlife Service, Dexter National Fish Hatchery and Technology Center, Dexter, New Mexico

Education: Requires Ph.D. in Genetics or related discipline

Experience: Familiarity and practical genetic experience in one or more of the following: 1) single nucleotide polymorphism analysis or; 2) pathogens of fish, reptiles or amphibians, including isolation of genetic variants, sequencing, phylogeography, genomics or; 3) development, sequencing and application of microsatellite libraries or; 4) development and/or application of advanced statistical analysis to complex genetic questions or; 5) environmental PCR, for chytrid fungus or other target organisms or; 6) population genetic assessment of natural populations.

Duties: Will be required to design sampling protocols and implement genetic projects and data collection on native species throughout the desert southwest. The research will include existing projects, and the development of new technology. The selectee must be able to communicate orally and in writing, to develop project guidelines, investigation results, and preparation of scientific technical reports, proposals and manuscripts. They will conduct genetic studies in a laboratory setting, including DNA isolation, PCR, and operation of an ABI 3130 genetic analyzer for different projects, as well as analyzing and interpreting data. Operate, configure, and maintain specialized molecular genetics laboratory equipment such as thermocyclers, DNA analyzer, and Real Time PCR system. Provide direction to biological technicians, university student assistants and volunteers in executing assigned duties.

To Apply: Submit resume or curriculum vitae, copy of transcripts, and name, address, and phone, FAX, and email contacts for three references familiar with your professional capabilities.

Dr. Colleen A. Caldwell, Acting Leader U.S. Geological Survey, New Mexico Cooperative Fish and Wildlife Research Unit Department of Fishery and Wildlife Sciences P.O. Box 30003, MSC 4901 Las Cruces, NM 88003 (Office: 505-646-8126, FAX 505-646-1281, or ccaldwel@nmsu.edu)

NEW MEXICO STATE UNIVERSITY IS AN

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Connie Keeler-Foster, Ph.D. Research Leader Dexter National Fish Hatchery and Technology Center 7116 Hatchery Road, P. O. Box 219 Dexter, NM 88230 Phone 505.734.5910 ext 16, Fax 505.734.6130

Connie_KeelerFoster@fws.gov

OxfordU ProtozoanMolecularEvol

Oxford University: Protozoan Molecular Evolution

3 year NERC-funded postdoctoral position supervised by Professor T. Cavalier-Smith FRS in the Department of Zoology

Starting 1 October 2007. Open to all with a recent PhD in an appropriate biological subject or who expect to be awarded one before 1st October 2007.

THE PROJECT: Evolution, biodiversity, and molecular ecology of apusozoan protozoa

Remarkably little is known of the biology, species diversity, and ecology of the recently established phylum Apusozoa, which are free-living predators on bacteria in all major habitats. The position of this phylum in the eukaryote phylogenetic tree is also obscure, as they do not clearly belong to any of the recently defined six major assemblages of eukaryotes, and might represent a distinct lineage, possibly being the most divergent among bikont eukaryotes. Whether the five groups currently assigned to this phylum (apusomonads, ancyromonads, breviate, diphyllids, Micronuclearia) are all genuinely mutually related is also controversial.

A keen and independently minded postdoctoral researcher with experience in PCR, DNA sequencing and phylogenetic analysis is sought for two related projects: [1] testing the relationships of all the major apusozoan groups by multigene phylogenies; and [2] studying the biodiversity and habitat preferences of each of them by subgroup-specific PCR and sequencing of environmental DNA samples and isolation of new cultures. Skills in bioinformatic methods and/or an interest in protozoa and microscopy or cell evolution (or in learning much more about them) are desirable.

We provide an excellent environment for this research,

as the postdoctoral researcher will work alongside a graduate student carrying out EST sequencing projects on apusozoans, with much opportunity for exchange of ideas and mutual help, and several other experienced researchers in the lab are using similarly diverse approaches for two large and important protozoan phyla: Amoebozoa and Cercozoa.

The appointment will be on the RA1A scale (Grade 7 starting at £25,889 per annum) and subject to a probationary period.

REFERENCES

Cavalier-Smith, T. (2003). Protist phylogeny and the high-level classification of Protozoa. *Eur. J. Protistol.* 39, 338-348. Cavalier-Smith, T. & Chao, E. E. (2003). Phylogeny of Choanozoa, Apusozoa, and other Protozoa and early eukaryote megaevolution. *J Mol Evol* 56, 540-563.

To apply send a cover letter of no more than a page outlining your special interests and explaining why this project interests you, your cv and publication list, and contact details for three referees, to Personnel Office, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS, E-mail: HYPERLINK "mailto:recruit@zoo.ox.ac.uk" recruit@zoo.ox.ac.uk If sent electronically please copy to both tom.cavalier-smith@zoo.ox.ac.uk and cedric.berney@zoo.ox.ac.uk. We expect to hold interviews in April.

INFORMAL ENQUIRIES ABOUT THE PROJECT TO EITHER OF: Dr Cedric Berney, EMAIL: cedric.berney@zoo.ox.ac.uk Professor Tom Cavalier-Smith FRS, EMAIL: tom.cavalier-smith@zoo.ox.ac.uk Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS, UK Tel: +44 1865 281 065 Fax: +44 1865 281 310

FORMAL APPLICATIONS should be received no later than 23 March 2007

Best wishes, Tom Professor T. Cavalier-Smith FRS, Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS, UK Tel: +44 1865 281 065 Fax: +44 1865 281 310

tom.cavalier-smith@zoo.ox.ac.uk

Smithsonian PhylogeneticsHawaiianSongbirds

Postdoctoral Position: Phylogenetics of Hawaiian Song-

bird Lineages

A postdoctoral research position to conduct molecular and morphological phylogenetic analyses of Hawaiian songbird lineages is available for up to two years beginning as early as June 2007 (the second year of funding is contingent upon satisfactory performance in the first year). Most of the species under study are extinct or endangered, so museum specimen and subfossil bone material will be analyzed using "ancient DNA" methods. Applicants should have a background in molecular methods (PCR, DNA sequencing) and phylogenetic analysis. Experience with ancient DNA methods and morphological character analysis are a plus. Some paleontological fieldwork in Hawaii is expected, as well as museum sampling visits. Please send a letter of application detailing your experience in the relevant areas, a full curriculum vitae, examples of your work (pdfs), and the names, addresses, phone numbers and email addresses of at least two references who know your research experience and abilities. Research will be conducted in the Genetics Program located in the National Zoological Park and the National Museum of Natural History, both located in Washington, DC. Email application materials to Dr. Rob Fleischer (fleischerr@si.edu) and Dr. Helen James (jamesh@si.edu). Review of applications will begin on 15 March 2007.

FleischerR@si.edu FleischerR@si.edu

TrinityCollegeDublin GeneticDataAnalysis

A new project, funded by Science Foundation Ireland Research Frontiers programme, requires a suitably qualified post-doctoral candidate. The focus of the project is the study of the spread of the Neolithic in Europe.

The project requires substantial study in the area of genetics, but will include archeology and perhas linguistics. As it is relatively unstructured with regard to the exact statistical methods required, the ideal candidate will have considerable experience of independent research. The ideal candidate would be well-versed in Bayesian methods and may have some background in the study of genetic data.

Further details are at <http://www.tcd.ie/Statistics/-JHpersonal/Archeogenetics.htm> This is a readvertisement.

John Haslett E-mail John.Haslett@tcd.ie Professor
Phone +353 1 8961114 (direct) Department of Statistics +353 1 8961767 (sec) School of Computer Science
Fax +353 1 6770711 and Statistics Room 146 Trinity College Dublin 2,Ireland

WWW: <http://www.tcd.ie/Statistics/JHpersonal/-research.htm> John.Haslett@tcd.ie John.Haslett@tcd.ie

TurkuU EvolEcol

Position for a Post-Doc (or a PhD -student) at the Section of Ecology, Turku University

I'm looking for a highly motivated person with a substantiated interest in evolutionary ecology for a Post-doc (or a PhD) post on marine alga-grazer interactions. The research focuses on feeding strategies of littoral mesoherbivores (isopods and amphipods). The main research issues are 1) how the variation in feeding strategies of herbivores translates into variation in their fitness, 2) how feeding strategies and the host exploitation ability vary in a system of naturally fragmented, geographically separated populations, and 3) what is the evolutionary potential of feeding strategies. The nearby research environment, the brackish-water Archipelago Sea at the southwestern coast of Finland, with over 20 000 islands with a varying level of isolation provides a unique environment for research on species interactions in the rocky littoral habitat.

The person I am looking for can be either at the stage of initiating PhD -studies, or, may have a PhD on related issues (plant-herbivore interactions, optimal foraging, benthic ecology). The position is available from March-April, initially to the end of the year 2007, with a possibility for extension for additional two years conditional to continuation of funding. Salary for a postdoc will be about 2300-2700 eur/month, and for a PhD -student 1700-2300 eur/month depending on performance.

Details on the research environment can be found in <http://www.sci.utu.fi/biologia/en/> and on the team in <http://users.utu.fi/veijor/project/-fuindex.html> Please send queries and applications (CV including list of publications, outline of research interests and motivation for this project, and contact information for 2 referees) in the mail or as email attachments to: Veijo Jormalainen Section of Ecology

Department of Biology University of Turku FIN-20014 Turku Finland

Veijo Jormalainen (veijo.jormalainen@utu.fi)

UAdelaide PlantBiogeography

Postdoc in plant biogeography

A highly motivated candidate is sought to undertake a 2.5 year postdoctoral research position in plant biogeography.

The role of long distance dispersal in the evolution of the Australasian and southwest Pacific flora is hotly contended, but appropriate tests of alternative hypotheses are still lacking. This position will develop a new comparative method for biogeography, combining phylogeny, fossils, mutation rate estimation, and statistical analysis tools. This approach will be applied to the Podocarpaceae, southern pines, to test central premises of biogeographic theory, examine differences in long distance dispersal dynamics and evolutionary potential between groups, and coincidence with major past geological or climatic changes.

Specifically the postdoc will be expected to :

1. Integrate existing phylogenetic data on Podocarpaceae and undertake new sampling, phylogenetic and phylogeographic analysis for specific groups.
2. Integrate existing macro and fossil pollen data for Podocarpaceae
3. Examine the utility of preserved macrofossil sequences for developing mutation rate analyses using ancient DNA
4. Develop statistical methods for long distance dispersal and divergence time estimations to test the influence of geological and climatic changes in the Australasian and SW Pacific region

This position is part of an ARC discovery project

Contact Andrew Lowe for further details (andrew.lowe@adelaide.edu.au).

Andrew Lowe Professor of Plant Conservation Biology Head of Science, State Herbarium and Biosurvey Plant Biodiversity Centre Dept. of Ecology and Evolution Adelaide Botanic Gardens School of Earth and Environmental Science Hackney Road North Terrace Adelaide SA5000 Adelaide SA5005 Australia Australia Tel: +61 (0)8 8222 9326 Tel: +61 (0)8 8303 5280 Fax: +61 (0)8 8222 9326 Fax: +61 (0)8 8303 6222 Mob: 0434 607 705

Email: lowe.andrew@saugov.sa.gov.au
 or andrew.lowe@adelaide.edu.au Email:
 lowe.andrew@saugov.sa.gov.au or an-
 drew.lowe@adelaide.edu.au

UArizona VertebrateSystematist

Vertebrate Systematist/Curator - University of Arizona

The Department of Ecology and Evolutionary Biology seeks to fill postdoctoral level curator positions beginning Fall 2007. We anticipate filling three positions over the next two years. The positions are part of a renewed investment in natural history collections on the University of Arizona campus and a new initiative in biodiversity informatics. The holdings of the EEB collections, ichthyology, herpetology, ornithology, mammalogy and invertebrates, demonstrate a strong taxonomic focus on the fauna of the southwest United States, northwest Mexico, the Gulf of California and the Eastern Pacific. We seek individuals engaged in collections-enabled research. Responsibilities of the positions will include research, curation (including participating in database and other informatics activities), and may include teaching one course per year in the candidate's taxonomic specialty. Salary is \$35-40,000 (depending on experience) plus benefits. Position is renewable up to three years based on satisfactory performance.

Applicants should apply online at the University of Arizona Human Resources website (<https://www.uacareertrack.com>; look for job #37205). Position is open until filled, but we anticipate reviewing applications beginning on Feb. 26, 2007. Contact Dr. Peter Reinthal (pnr@email.arizona.edu) or Dr. Michael Sanderson (sanderem@email.arizona.edu) for further information.

Michael J. Sanderson

New Address: Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721

New Email: sanderem@email.arizona.edu

Phone:520-626-6848

lab web site: <http://ginger.ucdavis.edu> Phylota
 project: <http://www.phylota.org> r8s software: <http://ginger.ucdavis.edu/r8s> sanderem@email.arizona.edu
 sanderem@email.arizona.edu

UArizonaPopulationEvolGenetics

POSTDOC IN POPULATION GENETICS, UNIVERSITY OF ARIZONA

A postdoctoral position in population genetics is available in Michael Hammer's group at the University of Arizona.

Research projects are flexible and can be tailored to suit individual interests. However, they must contribute to the group's overall focus. Current studies include inferring human demographic history from genomic data (primarily DNA re-sequencing datasets), and distinguishing the roles of natural selection and demographic processes in shaping patterns of genomic variability. Our research group already hosts geneticists, computational biologists, applied mathematicians and anthropologists under this broad research agenda, and provides a working interdisciplinary research environment.

A major resource of the lab is a large, novel DNA re-sequencing database that represents 90 independent regions of the genome. Each 'neutral' genomic region, spanning approximately 20kb, maps to regions of moderate to high recombination far from coding DNA. Sampling is consistent across each genomic region and includes data from several indigenous populations in Africa, Eurasia and the Americas. Additional projects focus on sequencing candidate genes for complex traits such as resistance to disease and skin pigmentation on the same sample panel as the 'neutral' genomic regions. This study design creates an essentially unique genomic dataset.

Our group enjoys close ties with the laboratory of Jeffrey Wall at USC as well as other labs at the University of Arizona, notably those of Michael Nachman (EEB), Joseph Watkins (Math) and Stephen Lansing (Anthropology). Moreover, it benefits from an excellent extended community of researchers in population genetics, computer science, statistics and genomics at the University of Arizona.

Applicants for the position must have: a PhD in relevant field; a graduation date no later than 30 April 2007; training in evolutionary biology and/or population genetics; a background in either theoretical population genetics or a quantitative field such as statistics with a strong interest in genetics; and advanced computational skills, including at least one programming

language.

The ideal candidate will have a strong background in theoretical population genetics or in relevant areas of mathematics and statistics, skills in computer modeling by simulation or exact mathematical analysis, and be self-motivated and independent.

This position includes outstanding UA benefits including health, dental, and life insurance; paid vacation, sick leave, and holidays; UA/ASU/NAU tuition reduction for the employee and qualified family members; access to UA recreation and cultural activities; state retirement; and more.

All applicants must apply on-line by completing an appointed personnel application and attaching a CV and letter of interest. To view the on-line posting and to apply, go to www.uacareertrack.com/applicants/Central?quickFind6454 <<http://www.uacareertrack.com/applicants/Central?quickFind6454>> or go to www.uacareertrack.com <<http://www.uacareertrack.com>> and search postings using job #37181.

All applicants must also email copies of relevant publications and two letters of recommendation to David Shropshire at shrop@email.arizona.edu.

Michael Hammer <mfh@email.arizona.edu>

UBritishColumbia AlgalMolEvol

Research Associate Position in Algal Molecular Evolution

University of British Columbia

Vancouver, Canada

We are looking for a well-trained highly motivated and enthusiastic individual interested in exploring the evolutionary biology of complex algae and their organelles using molecular techniques.

The applicant must have a PhD or equivalent and at least three additional years of research experience. Expertise in algal culturing and environmental sampling, molecular evolutionary analyses, eukaryotic biodiversity and evolutionary history, and the interpretation of molecular phylogenetic data are essential. The applicant must have excellent written and oral communication skills and be highly organised. Molecular biology and cell biology techniques including microscopy and

cell culture are also highly desirable.

The position is available starting May 1 2007 for an initial period of one year with a possibility for extension subject to a satisfactory performance and funding. If interested, please send a cover letter outlining research experience and interest, a curriculum vitae and the names and contact information for 3 referees to Patrick Keeling, Department of Botany, University of British Columbia, 3259-6270 University Boulevard, Vancouver, B. C. V6T 1Z4, Canada. Email pkeeling@interchange.ubc.ca. Fax (604) 822-6089. Closing date is March 8 2007.

UBC hires on the basis of merit and is committed to employment equity. We encourage all qualified persons to apply, however, Canadians and permanent residents of Canada will be given priority.

pkeeling@interchange.ubc.ca

pkeeling@interchange.ubc.ca

UBritishColumbia ProtistEvol

Research Associate Position in Molecular Evolution of Protistan Parasites

University of British Columbia

Vancouver, Canada

We are looking for a well-trained highly motivated and enthusiastic individual interested in exploring the evolutionary cell biology of Microsporidia parasites.

The applicant must have a PhD or equivalent and at least three additional years of research experience. Expertise in molecular biology and parasite cell biology techniques including heterologous protein expression in yeast and bacterial cells, microscopy of parasite cells and microsporidia cell culture are essential. The applicant must have excellent written and oral communication skills. Experience of genomic data analysis and willingness to take some responsibility for the running of the lab are highly desirable.

The position is available immediately for an initial period of one year with a possibility for extension subject to a satisfactory performance. If interested, please send a cover letter outlining research experience and interest, a curriculum vitae and the names and contact information for 3 referees to Patrick Keeling, Department of Botany, University of British Columbia, 3259-6270 University Boulevard, Vancouver, B. C. V6T

1Z4, Canada. Email pkeeling@interchange.ubc.ca. Fax (604) 822-6089. Closing date is Feb. 15 2007.

UBC hires on the basis of merit and is committed to employment equity. We encourage all qualified persons to apply, however, Canadians and permanent residents of Canada will be given priority.

pkeeling@interchange.ubc.ca
ing@interchange.ubc.ca

pkeel-

UCaliforniaSanDiego ConservationBiogeo

“Biogeography, ecology and conservation of terrestrial vertebrates in a changing world”

Division of Biological Sciences, University of California San Diego

DESCRIPTION: One NSF funded postdoctoral position (two years) will be available starting spring/summer 2007 to work on the conservation and broad-scale ecology of terrestrial vertebrates. The research will draw on a number of ecological, environmental, phylogenetic and distributional databases. An intended core focus will be the impacts of global environmental change on species' ranges, and their associated ecological and evolutionary context. There are some obvious additional research opportunities, and there is potential for the postdoctoral scientist to develop new directions.

RESEARCH GROUP: The position is based in the Lab of Walter Jetz. In this group, the successful candidate will interact with two PhD students (broad-scale conservation of mammals and birds, macroecology of vertebrate energy use), two affiliated postdoctoral fellows (cross-scale bioenergetic models of herptiles, global biogeography of vertebrates), and several graduate and undergraduate level students. There is the potential to develop and co-supervise undergraduate and graduate research projects.

LOCATION: University of California, San Diego. The position is based at the Section of Ecology, Behavior & Evolution in the Division of Biological Sciences - a research community of ca. 100 faculty (including 14 members of the National Academy), 140 postdoctoral fellows, and 250 graduate students, which is further strengthened by the neighboring Scripps Institute of Oceanography.

REQUIREMENTS: A Ph.D. in ecology, biogeography or evolution with research experience in the analysis of spatial data and strong quantitative skills. Evidence of research productivity as indicated by scholarly publications is required. Sound skills and experience in the use of GIS, the analysis of distribution data, relational databases and statistical analysis of spatial data are a prerequisite. Evidence of strong communication and teamwork skills is highly desired. Experience in environmental niche modeling, spatial statistics, the analysis of phylogenetic data, R and/or MatLab, a Programming language (e.g. C, Visual Basic) is a plus.

APPLICATION: Please email brief letter of interest, C.V., and the names and contact details of three referees by March 15, 2007 to Romel Hokanson, rhokanson@ucsd.edu, subject line: “Postdoctoral Position Jetz Lab”. Phone: +1 (858) 822-4862. For questions about the position contact Walter Jetz, wjetz@ucsd.edu. Review of applications will begin March 15, and continue until the position is filled.

wjetz@ucsd.edu wjetz@ucsd.edu

UChicago EvolHeatShockGenes

POSTDOCTORAL FELLOWSHIP *** THE UNIVERSITY OF CHICAGO

Contingent on anticipated final approval of NSF funding, a postdoctoral fellowship will be available with a negotiable starting date, but preferably between 1 June 2007 and 1 September 2007.

The postdoctoral scholar will participate in an ongoing project to elucidate the role of transposable elements in the evolution of heat-shock genes in natural populations. Prior work in the lab has discovered that transposable elements are abundant, diverse, and consequential in the proximal promoter regions of many heat-shock genes of *Drosophila melanogaster* (see, for example, PLoS Genetics Vol. 2, No. 10, e165), probably due to the unique chromatin organization of heat-shock promoters (see, for example, Genetics 178:809-820 (2006)). Next steps will involve tests of the generality of these findings by examining species progressively more distantly related to *Drosophila melanogaster*, and by examining the phenotypes of recently-discovered transposon insertions.

The ideal candidate will be a recent Ph.D. with expertise in informatics, basic molecular biology (PCR,

sequencing, cloning, cell transfection, reporter constructs), and/or *Drosophila* genetics and phenotype analysis – or interests in and aptitude for acquiring these skills and others as needed. Also important is interest in interacting with a diverse and large community of scholars and trainees, including evolutionary biologists (<http://pondside.uchicago.edu/ceb/> <http://pondside.uchicago.edu/ecol-evol/>), geneticists (<http://cg.bsd.uchicago.edu/> , <http://cg.bsd.uchicago.edu/>), and integrative and systems biologists (<http://pondside.uchicago.edu/oba/>).

Appointment will be initially for 12 months at an annual salary of approximately \$37,000 plus fringe benefits, and be renewable contingent on satisfactory performance and availability of funding. The University of Chicago is an Affirmative Action/Equal Opportunity Employer. Review of applications will commence on 26 March 2007.

Please direct applications by email/attachments (including letter of application detailing your fit to the position, CV, research statement, and contact information for 3 references) and inquiries (by email or telephone) to: –

Dr. Martin E. Feder E-Mail: m-feder@uchicago.edu

Professor Department of Organismal Biology & Anatomy; Programs in Evolutionary Biology, Genetics, and Molecular Medicine The University of Chicago 1027 East 57th Street Chicago, IL 60637 USA E-Mail: m-feder@uchicago.edu Telephone: 773 702-8096 Fax: 773 702-0037 <http://pondside.uchicago.edu/~feder/Martin.Feder.html> m-feder@uchicago.edu m-feder@uchicago.edu

UDusseldorf EvolSystemsBiol

The Bioinformatics Institute (Prof. Martin Lercher) of the Heinrich Heine University of Düsseldorf, Germany, invites applications for

2 Postdoc positions (EGr.13 TV-L)

(fixed-term) to be filled as soon as possible.

Research area: Applied bioinformatics: evolutionary genomics and systems biology. Topics of interest include the evolution of biological networks (metabolism, protein interaction, regulation), and the function of non-coding RNA.

Qualifications: We invite applications from individ-

uals with a PhD in biology, computer science, or physics/mathematics.

The Heinrich Heine University of Düsseldorf is an equal opportunity employer and is attempting to increase the percentage of women in research and teaching, and therefore explicitly invites applications by women. These will be given preference when qualifications are equal between candidates. Disabled candidates with the necessary qualifications are also strongly urged to apply for the position.

Applications, including CV and list of publications, should be sent (preferably via email) to the following address:

Lehrstuhl Bioinformatik, Prof. M. Lercher Heinrich-Heine-Universität Düsseldorf Universitätsstr.1 40225 Düsseldorf, Germany lercher@cs.uni-duesseldorf.de

lercher@cs.uni-duesseldorf.de

lercher@cs.uni-duesseldorf.de

www.uni-duesseldorf.de

UFlorida Adaptive Life History Evol

A postdoctoral position at the University of Florida is available to study the physiological basis of adaptive shifts in life history timing in the apple maggot, *Rhagoletis pomonella*.

R. pomonella is a model system for studying the evolution of insect-host plant associations and sympatric speciation. Historically, *R. pomonella* larvae fed on the fruits of hawthorns (*Crataegus* sp.) but radiated onto domesticated apple (*Malus pumila*) after its introduction to North America. In areas where both hosts occur, apple and hawthorn populations form genetically distinguishable host races. The timing and depth of diapause (overwintering dormancy) are critical life-history traits differentially adapting apple and hawthorn-infesting populations of *R. pomonella* to differences in the fruiting times of their respective hosts, generating reproductive isolation in the process. Physiological traits such as nutrient storage and metabolic rate affect diapause length and timing in other insects. We will test the hypothesis that adaptive differences in diapause length between the apple and hawthorn host races are mediated by energetics, particularly the accumulation of metabolic fuel prior to diapause and its utilization during diapause.

We will determine the functional importance of nutrient storage and metabolism to diapause length and timing

for apple and hawthorn host races of *R. pomonella* in the field and lab; and then equate any observed difference in fuel storage, body size, and metabolic rate with allelic variation at loci that have diverged between the host races. Linking allele frequencies to diapause-associated nutrient storage and metabolism will provide the basis for our ultimate goal of identifying the specific physiological, biochemical, and genetic alterations underlying adaptive host plant-mediated life history evolution in the two *R. pomonella* host races.

The postdoc will join Dan Hahn's group in the Department of Entomology and Nematology at the University of Florida (<http://danhahn.ifas.ufl.edu/>) and will have significant interactions with Jeff Feder's group in the Department of Biological Sciences at Notre Dame (<http://www.nd.edu/~biology/JeffreyFeder.shtml>).

Ideally a candidate would start in June 2007. Salary and benefits will range between \$33,000 and \$40,000 and are available for 3 years, contingent on performance. Excellent family medical/dental health plans are available. Applicants should provide a formal letter of application, a complete biographical CV, transcripts of college courses, three letters of reference (note: the letter of application and C.V. should arrive electronically). Review of applications will begin March 5th and applications will be accepted until a suitable applicant is found.

For more information, contact Dan Hahn at the e-mail below.

Daniel A. Hahn Assistant Professor Department of Entomology and Nematology The University of Florida P.O. Box 110620 Gainesville, FL 32611-0620 dahahn@ifas.ufl.edu Phone: 352-392-1901x156 Fax: 352-392-0190

dahahn@ufl.edu dahahn@ufl.edu

UKwazulu-Natal PlantEvol

POSTDOCTORAL POSITION IN PLANT EVOLUTIONARY ECOLOGY, UNIVERSITY OF KWAZULU-NATAL, SOUTH AFRICA

The Forest Biodiversity Research Unit is recruiting a postdoctoral scientist to contribute to a study of regeneration dynamics in coastal dune forests. The project will investigate the reproductive biology of a dominant understorey shrub, *Isoglossa woodii*, and seeks to determine the evolutionary and ecological advantages of

monocarp in this species. Familiarity with techniques in cross-pollination, measuring seed set, and quantifying pre- and post-dispersal seed predation and advantage but not essential. There will also be opportunities to develop independent research projects exploring other aspects of the dynamic and chronically stressed coastal dune forest ecosystem.

A Ph.D in ecology, plant biology, or equivalent is required. The expected length of the appointment is one year, commencing in early to mid -2007. The position will be funded at a rate of R100,000 (approx. US\$14,000) per annum, which is enough for an individual or small family to live comfortably in South Africa.

To apply send a current CV, copies of relevant publications, a statement of research interests, and the names and contact information for two references by email to Prof. Mike Lawes. Closing date: 9 March 2007 or until a suitable candidate is selected.

Prof. Mike Lawes School of Biological and Conservation Sciences Forest Biodiversity Research Unit University of KwaZulu-Natal Private Bag X01 Scottsville, 3209, Pietermaritzburg, South Africa

Telephone +27 33 260 5443 Facsimile +27 33 260 5105

Email: Lawes@ukzn.ac.za <http://www.ukzn.ac.za/-Biology/MikeLawes214.aspx> Michael Lawes <Lawes@ukzn.ac.za>

UMaryland HumanEvolGenomics

Postdoctoral Positions in Human Evolutionary Genomics

Postdoctoral positions are available in a human population genetics laboratory in the Department of Biology at the University of Maryland at College Park for NIH and NSF funded research. Projects in the lab focus on a unique resource of >6,000 DNA samples from ~100 ethnically and geographically diverse African populations. These samples are being used for genome-level analyses of diversity at both coding and non-coding loci (including high throughput resequencing and whole genome SNP and STRP genotyping). For many of these samples we also have phenotype data for a number of traits that are likely important in adaptation, including those with a complex pattern of inheritance. We are using these data (1) to infer population structure and demographic history and test models of modern human evolution (2) to identify re-

gions of the genome that are targets of selection using whole genome scans (3) to identify functionally significant variants using genotype/phenotype association studies as well as gene expression analyses (4) to study the genetic basis of resistance against infectious disease (with a focus on malaria) and co-evolution of the human and *Plasmodium falciparum* genomes. Collaborators on these projects include Jonathan Pritchard, Molly Przeworski, Carlos Bustamante, Josh Akey, Greg Wray, Philip Awadalla, Gil McVean, and Anna Tramontano. Additional information about the Tishkoff lab can be found at <http://www.life.umd.edu/biology/tishkofflab/>. UMCP is located in a suburb of Washington D.C. with easy access to a number of research institutions in the Baltimore/D.C. area including NIH, the Smithsonian, TIGR, George Washington University and Johns Hopkins University. More information about the Biology Department and the Behavior, Ecology, Evolution, and Systematics (BEES) program at UMCP is available at <http://www.life.umd.edu/biology/> and <http://www.life.umd.edu/biology/>. Candidates with either a strong molecular and/or statistical genetics background are encouraged to apply (computational and laboratory positions are available). Familiarity with population genetics theory and/or computer programming is a plus. Salaries are commensurate with qualifications and experience.

Please send curriculum vita, a statement of interest, and contact information for three references to Dr. Sarah Tishkoff, Dept. of Biology, Biology/Psychology Building #144, Univ. of Maryland, College Park, MD 20742 or e-mail to tishkoff@umd.edu. Women and minority members are strongly encouraged to apply. The University of Maryland is an equal opportunity/affirmative action employer.

Sarah Tishkoff, Ph.D. Associate Professor
Dept. of Biology Biology/Psychology Building
Univ. of Maryland College Park, MD 20742
Tel: 301-405-6038 Fax: 301-314-9358
email: BLOCKED::mailto:tishkoff@umd.edu
tishkoff@umd.edu

[BLOCKED::http://www.life.umd.edu/biology/tishkofflab/](http://www.life.umd.edu/biology/tishkofflab/)
<http://www.life.umd.edu/biology/tishkofflab/> **NOTE NEW E-MAIL ADDRESS LISTED ABOVE**

tishkoff@umd.edu tishkoff@umd.edu

UMass PathogenMolecularEvol

UMass.PathogenMolecularEvolution

We are seeking a post-doctoral research fellow with experience in molecular biology (PCR, cloning, genotyping, etc) and quantitative analyses of genomic data (statistics, custom programming, phylogenetics, etc.) to join our expanding lab group at the University of Massachusetts, Amherst. Several well-funded, ongoing projects in the lab pertain to study of the molecular adaptation of zoonotic pathogens and their host/vector species, including human malaria parasites, tick-borne Lyme borreliosis, Toxoplasmosis, and raccoon rabies.

Candidates with either a strong molecular and/or statistical genetics background are encouraged to apply (computational and laboratory positions are available). Familiarity with population genetics theory and/or computer programming is a plus. Salaries are commensurate with qualifications and experience of the incumbent. Initial appointments may be made for up to two years with possibility of extension based on satisfactory performance.

Please send (1) current vitae, (2) a statement of research interest, and (3) contact information for three references to: Stephen Rich, 209 Fernald Hall, Department of PSIS, 270 Stockbridge Rd., University of Massachusetts, Amherst, MA 01003. Women and minority members are strongly encouraged to apply. The University of Massachusetts is an equal opportunity/affirmative action employer.

"Dr. Stephen Rich" <smrich@psis.umass.edu>

UParis13 AntPhylogeny

Post-doctoral Fellowship in ants phylogenetics.

A position is available to explore the phylogeny and social structure of species in the *Ectatomma* genus, in collaboration with Dr C. Poteaux (U. of Paris 13) at the Laboratory of Experimental and Comparative Ethology (LEEC-CNRS UMR 7153) beginning Fall 2007. The applicant is expected to: 1/ determine genetic variation to reconstruct the phylogeny of *Ectatommini* ants using molecular methods (DNA sequence analysis) 2/ analyse socio-genetic structure of *Ectatomma ruidum* with microsatellite loci, in collaboration with Dr J-P Lachaud (CRCA-CNRS UMR 5169). Candidates should have experience in phylogenetics and/or population genetics. Prospective applicants should, in the first instance, send a curriculum vitae including a brief state-

ment of previous research experience, and the names and contact informations of 2 personal references to C. Poteaux (poteaux@leec.univ-paris13.fr) before March, 07th 2007. In a second step, the team and the selected applicant will apply jointly for a grant from the Fyssen Foundation. Salary will be approximately 2000 euros net per month.

The study grants will be awarded to foreign or French research scientists holding a foreign doctorate (Ph.D). Study grants are intended to help young research scientists less than 35 years of age.

For details about the host lab, please see: <http://www-leec.univ-paris13.fr/> and about the Fyssen Foundation: <http://www.fondation-fyssen.org/-bourseUS.html> Chantal Poteaux, Ph.D. LEEC-CNRS UMR 7153 Université Paris 13 Avenue J-B Clément F-93430 Villetaneuse poteaux@leec.univ-paris13.fr Chantal.Poteaux@leec.univ-paris13.fr Chantal.Poteaux@leec.univ-paris13.fr

applicants will begin March 15, 2007.

The Penn Genomics Institute offers an outstanding intellectual environmental. Research at the Institute addresses questions in biology and medicine through genomic, computational, and modeling approaches. Collaborations among research groups and across the broader Penn community are common. The Institute is housed in the newly constructed Lynch research building.

Highly motivated applicants are encouraged to email a statement of research interests, CV, and contact details for three references to jplotkin@sas.upenn.edu.

Joshua B. Plotkin Department of Biology The University of Pennsylvania 415 S University Avenue Philadelphia, PA 19104

jplotkin@fas.harvard.edu jplotkin@fas.harvard.edu

USGS NewMexico PopGenetics

UPennsylvania TheoBiol

POSTDOCTORAL POSITIONS – THEORETICAL BIOLOGY

Two postdoctoral fellow positions are available in the theoretical biology group of Dr. Joshua Plotkin at the University of Pennsylvania.

The specific research project is flexible and can be tailored to the interests of the individual, but it will fall under the broad purview of evolutionary theory. Areas of research in the Plotkin lab include theoretical population genetics, the evolutionary ecology of viral populations, mathematical models for the evolution of robustness, the structure of fitness landscapes and epistasis, and the determinants of protein evolutionary rates.

Requirements for the position include (1) a proven record of self-motivated research; (2) a PhD in biology, mathematics, statistics, physics, or related area; (3) excellent quantitative and computational skills. The ideal candidate should be familiar with scientific programming.

Postdoctoral positions provide a competitive annual stipend (minimum \$38,000) plus benefits and health insurance. Start date is negotiable. Applications are welcome from candidates in any country. Screening of

Position Available: Postdoctoral Research Associate: U.S. Geological Survey, New Mexico Cooperative Fish & Wildlife Research Unit, Department of Fishery and Wildlife Sciences. PhD. in genetics or related discipline required. Salary commensurate with education and experience. Familiarity and practical genetic experience in one or more of the following: single nucleotide polymorphism analysis; pathogens of fish, reptiles or amphibians; development of sequencing and application of microsatellite libraries, application of advanced statistical analysis to complex genetic questions or environmental PCR for chytrid fungus or other target organisms; population genetic assessment of natural populations. Up to a three year appointment contingent upon research project funding. For complete job description visit: <http://www.nmsu.edu/~personel/-postings> NMSU #2007001052. Reply to: Dr. Colleen A. Caldwell, Leader, U.S. Geological Survey, NM Cooperative Fish & Wildlife Research Unit, Dept. of Fishery & Wildlife Sciences, NMSU, MSC490, Las Cruces, NM 88003. Telephone (505) 646-1281, email: ccaldwel@nmsu.edu. Review of letter of application, resume, unofficial transcripts, and three letters of reference will begin: April 1, 2007 and continue until position is filled. NMSU is an EEO/AA employer.

Connie Keeler-Foster, Ph.D. Research Leader Dexter National Fish Hatchery and Technology Center 7116 Hatchery Road, P. O. Box 219 Dexter, NM 88230 Phone

505.734.5910 ext 16, Fax 505.734.6130

Connie_KeelerFoster@fws.gov

UTurku MultiSpeciesCyclicPops

Postdoctoral research post

Project: Multi-species cyclic vole populations: inter-specific competition, and prey choice and emergent impacts of multiple predators for one year (starting in Apr-May 2007) at Dept. Biol., Univ. Turku, Finland.

The objective is to study multi-prey multiple predator interactions among voles and their avian and mammalian predators in the field. Main questions: 1) competition and predation risk vs. reproductive performance of voles, 2) prey selection of predators in multi-predator situations, 3) risk by avian predators vs. hunting behaviour of small mustelid predators, 4) impacts of multiple native and alien predators on prey populations. (see, for example, Korpimäki et al. 2005, Proc. R. Soc. Lond. B 272: 193-202, Ahola et al. 2006, Proc. R. Soc. Lond. B 273: 1261-1265, and Koivisto et al. 2007, Oikos 116:156-162).

Details on the research environment, research projects and their productivity can be found in <http://users.utu.fi/ekorpi/> <http://vanha.sci.utu.fi/biologia/ekologia/korpimaki.htm> The postdoctoral researcher will take part in the planning and execution of the project, in analysing the existing long-term observational and experimental data sets, in writing papers, and in supervision of the Ph.D. students, etc. (grant approx. EUR 1500 per month)

Queries and applications (CV, list of publications, a summary of research interests and motivation for this project) to Erkki Korpimäki, e-mail ekorpi@utu.fi fax +358-2-3336550

Deadline for applications is 20 Feb 2007. Address: Section of Ecology, Department of Biology, University of Turku, FIN-20014 Turku, Finland.

Erkki Korpimäki <ekorpi@utu.fi>

UVirginia PlantEvoEcol

Postdoctoral position is available in plant evolutionary ecology at the University of Virginia: We currently have a project evaluating the age-dependent and age-independent influences on the demography of *Plantago lanceolata*. This project involves several large experiments in the field and in the greenhouse. This post-doc position will include collaboration on this project, funded by NIH Institute of Aging, and the development of an independent research project related to this project will be encouraged. The University of Virginia has a highly interactive group of population/evolutionary biologists, and Charlottesville is an attractive place to live.

The starting date for this position is flexible, but applications should be completed by mid-February. To apply, send a cover letter explaining your interest in the position, a CV, and names of three references, to Deborah Roach, Biology Department, Gilmer Hall, University of Virginia, Charlottesville, VA, 22904-4328. Informal email inquiries about the position are also welcome at droach@virginia.edu

Deborah Roach Associate Professor Department of Biology 266 Gilmer Hall University of Virginia Charlottesville, VA 22904 phone: (434)982-4858

Deborah Roach <dar2x@virginia.edu>

UWindsor AquaticInvadersPopGenet

Post-Doctoral Researcher Great Lakes Institute for Environmental Research (GLIER).

We invite applicants for a Post-Doctoral Researcher Position in the field of population genetics/phylogenetics of aquatic invaders. The position is funded by the Canadian Aquatic Invading Species Network (CAISN). The project involves analysis of hierarchical genetic structure of invasive tunicates from at different spatial scales and aims to i) characterize spatial and temporal patterns of genetic structure during the establishment and subsequent spread of two invasive tunicates; ii) identify potential sources and vectors of invasions; and iii) address taxonomic problems related to color morphospecies.

The candidate should have proven skills in molecular biology including DNA sequencing, genotyping, gene cloning, and knowledge of bioinformatics related to evolutionary analyses. The individual should also have a

good track record in publishing and the ability to work well in a collaborative research atmosphere.

The GLIER offers a collaborative environment, with faculties in the field of aquatic invasions, evolutionary genetics, genomics and toxicology. The CAISN network offers ample opportunities for interactions with researchers across Canada. The post-doctoral researcher will have access to excellent genomics facilities housed at GLIER.

The position is for one year, but can be renewed, and can begin as early as May 2007. Review of applications will begin March 1st, 2007. Interested applications should send their CV, a brief statement of research interest, and at least two supporting letters of reference to:

Dr. Melania Cristescu Great Lakes Institute for Environmental Research University of Windsor Windsor, Ontario Canada N9B3P4

Phone: 519-253-3000 x 3763 Email: mcris@uwindsor.ca

Melania E. Cristescu Assistant Professor University of Windsor Great Lakes Institute for Environmental Research 401 Sunset Ave Windsor Ontario Canada N9B 3P4

Phone: (519) 253-3000 Ext. 3763 FAX: (519) 971-3616 E-Mail: mcris@uwindsor.ca

mcris@uwindsor.ca

UWisconsinMadison CommunityGenetics

Postdoctoral Position

Community/Ecosystem Genetics and Chemical Ecology

University of Wisconsin - Madison

A postdoctoral Research Associate position will be available summer 2007 as part of a large, multi-investigator, multi-institutional project funded under NSF's Frontiers in Integrative Biological Research (FIBR) program. This research explores the genetic basis of community dynamics and ecosystem processes. Specifically, it evaluates how genetic and chemical variation in naturally occurring and synthetic hybrids of cottonwood species mediates ecological structure and function at population, community and ecosystem levels. (See the feature article on genes to ecosystems

by Whitham et al. [2006. *Nature Reviews Genetics* 7:510-523].) Field sites include a number of riparian habitats throughout the Intermountain West. Project PIs include T.G. Whitham, S. Shuster, C.A. Gehring, G.J. Allan, J.C. Marks, S.C. Hart, P.S. Keim, R.L. Lindroth, S.P. DiFazio, and B.M. Potts. For more information about the collaborative project, go to: <http://www.poplar.nau.edu/> Primary responsibilities of the Research Associate are to coordinate and conduct the chemically-related components of the research program. Collaborative projects underway relate cottonwood chemistry to arthropod communities, mycorrhizal communities, mammalian foraging, and litter decomposition. Results from this work will be integrated with that of other project coordinators to understand the influence of cottonwood genetic structure on chemical variation, and the linkages between chemical variation and community and ecosystem function at local and regional scales. The Research Associate will also be expected to initiate and conduct research projects related to his/her area of expertise (e.g., quantitative genetics, G x E interactions, etc.)

Qualifications include expertise in plant chemical analyses and/or quantitative genetics, and interest in the chemical ecology of trophic interactions and ecosystem function. Strong interpersonal, laboratory, statistical and writing skills are essential. Extended collecting trips to field sites in the western U.S. will likely be required.

Salary and benefits: \$31,500 - 33,500, commensurate with experience. Excellent family medical/dental health plans available at minimal cost.

Application: Preliminary inquiries are welcome, preferably by phone or e-mail. Applications will be accepted through Feb. 28, 2007, or until a suitable applicant is found. To apply, send c.v., names/addresses of three references, representative reprints, and a letter detailing your fit to the position to:

Dr. Rick Lindroth Phone: 608-263-6277 Dept. of Entomology E-mail: lindroth@entomology.wisc.edu 1630 Linden Dr. Madison, WI 53706

For additional information about the Lindroth research group, visit <http://entomology.wisc.edu/~lindroth/> UW - Madison is an equal opportunity employer

Richard L. Lindroth, Ph.D. Dept. of Entomology 1630 Linden Dr. University of Wisconsin Madison, WI 53706 U.S.A.

Phone: 608-263-6277 Fax: 608-262-3322 E-mail: lindroth@entomology.wisc.edu <http://entomology.wisc.edu/~lindroth/>

lindroth@entomology.wisc.edu

Umea 2 ForestGenetics

TWO POST-DOC POSITIONS IN FOREST GENETICS AT SLU, UMEÅ, SWEDEN

The two postdoc positions are for two years and part of a common project that will evaluate the efficiency of molecular markers as a tool for improved breeding of Scots pine (*Pinus sylvestris*). One position is directed towards development of molecular marker techniques (SNP and AFLP) and the other towards development of statistical methods, but opportunities for collaboration both within the project and with other groups exists. The positions will be situated at Umeå Plant Science Centre, SLU, Sweden, which is a very strong research institution for plant molecular biology and forest genetics. The net salary is based on a stipend (17 500 SEK/month). The positions will be open until the right candidates have been found.

(1) The molecular marker position aims at finding SNP and AFLP markers for breeding traits in one of the most advance breeding populations of Scots pine in Sweden. The applicant should have a PhD in molecular genetics and preferably be familiar with SNP and AFLP marker development. Experience in conifer genetics and knowledge of quantitative genetics is positive, but not mandatory.

Contact for this position: Dr. Rosario Garcia-Gil
E-mail: M.Rosario.Garcia@genfys.slu.se
http://www.upsc.se/index.php?option=-3Dcom_content&task=3Dview&id=3D2971&ItemidC

(2) The other postdoc will be working on developing and applying new statistical/computational methods for marker assisted selection and analysis of function valued traits in Scots pine. The candidate should have a Ph.D. in genetics, bioinformatics, statistics, or related field. Knowledge of quantitative genetics and/or tree breeding is a plus, but not mandatory.

Contact for this position: Dr. Patrik.Waldmann
E-mail: Patrik.Waldmann@genfys.slu.se
<mailto:Patrik.Waldmann@genfys.slu.se>
http://www.upsc.se/index.php?option=-3Dcom_content&task=3Dview&id=3D2818&ItemidC

Patrik.Waldmann@genfys.slu.se

UppsalaU CichlidBrainEvol

Post-doctoral position at the Evolutionary Biology Centre, Uppsala University: Comparative analyses of brain evolution in Lake Tanganyikan cichlid fishes.

A one year (with possibility of extension to a total of two years) post-doctoral position is hereby open within my group at the department of Animal Ecology. The project aims at investigating how brain structure has evolved in relation to ecology, life histories, sexual selection and speciation patterns across the highly diverse Tanganyikan group of cichlid fishes.

The project will start with collection of data on brain structure based on analyses on wild-caught specimens of both sexes using a combination of sectioning on a microtome and MRI (Magnetic Resonance Imaging) analysis. These analyses will be undertaken in collaboration with Professor Svante Winberg, renowned expert on the fish brain. This detailed data will then be compared to an already existing data base containing information on a number of ecological variables using formal comparative methods that account for phylogenetic relationships. A substantial fish lab (>100 aquaria) is also available for experiments investigating cognitive ability across key species identified through the comparative analyses. Together, these approaches aim at providing novel insights regarding patterns of brain evolution in vertebrates.

The successful applicant should have a PhD in evolutionary biology. Experience in modern comparative methods is considered a strong merit. Experience in brain morphology, general fish ecology and fish dissection is also welcome but not essential. The salary is 20000 SKr/month (2200 Euros) net (not subject to Swedish income tax).

The Evolutionary Biology Centre at Uppsala University is one of Europe's finest institutions in its field and hosts 15 departments working on the levels of genes, organisms and communities. This provides for outstanding possibilities for cross-disciplinary interactions. See http://www.ebc.uu.se/index_eng.php for further information.

Applications (2 copies) should include a brief description of research interests and past research experience, Curriculum vitae and the name and contact information of 2 personal references. Relevant publica-

tions should be attached to the application. Application dead-line is 1st of March 2007 and the project is planned to start 15th of April 2007. Please contact Niclas Kolm (niclas.kolm@ebc.uu.se) for further information about the position.

Please submit your applications to: Dr Niclas Kolm, Assistant Professor Animal Ecology/Department of Ecology and Evolution Evolutionary Biology Centre (EBC) Uppsala University Norbyvägen 18D, 75236 Uppsala, Sweden

Dr Niclas Kolm, Assistant Professor Animal Ecology/Department of Ecology and Evolution Evolution-

ary Biology Centre (EBC) Uppsala University Norbyvägen 18D 75236 Uppsala, Sweden

e-mail: niclas.kolm@ebc.uu.se tel: 46(0)184712639 mobile: 46 (0)730980809 fax: 46(0)184716484 homepages with pdf' s:

<http://www.iee.uu.se/zooekol/default.php?type=-3Dpersonalpage> <<http://www.iee.uu.se/zooekol/default.php?type=personalpage&id=86&lang=sv>> &id&lang=sv

<http://www.uea.ac.uk/bio/kolm/Kolm.html>

niclas.kolm@ebc.uu.se niclas.kolm@ebc.uu.se

WorkshopsCourses

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LaColle-sur-Loup France GenomicsOfComplexTraits May20-25

Dear Colleague,

Here is an announcement for an "Ecole-chercheurs" on Genomics of Complex Traits, to be held in La Colle-sur-Loup (France), in May 20-25, 2007.

Sincerely yours.

The organizing committee: Franoise Clerget-Darpoux
Christine Dillmann Denis Milan Xavier Montagutelli
Dominique de Vienne

Genomics of Complex Traits

Contexte et enjeux L???intérêt pour les caractères à déterminisme complexe n???est plus ??? comme cela a longtemps été le cas ??? l???apanage des seuls sélectionneurs et évolutionnistes. Les technologies de la génomique ont ouvert la voie à l???analyse de leurs bases physiologiques et à l???isolement des gènes en cause, si bien qu???aujourd???hui un nombre croissant de laboratoires les étudient, dans le cadre de problématiques très variées : maladies génétiques humaines, génétique évolutive et écologique, amélioration des espèces, biotechnologie, etc. Une des difficultés de la génétique multifactorielle est que les outils et concepts à mettre en ??uvre sont nombreux et empruntés à des domaines divers, de la génétique des populations à la biologie moléculaire, en passant par la modélisation et la génétique quantitative « classique ». Mais un de ses atouts est d???être par nature intégrative, et de proposer une démarche cohérente et des méthodes

pour l'analyse de la variation et de l'évolution des systèmes biologiques complexes.

Objectifs de l'école Cette Ecole-Chercheurs a pour ambition de : - Faire le point sur la génétique multifactorielle actuelle, dans le contexte des développements les plus récents de la génomique, de la génétique des populations et évolutive, et de la biologie intégrative. /Cet objectif suppose une présentation détaillée des concepts et méthodes de base et de la terminologie qui, selon les domaines et les modèles, peuvent présenter des différences à expliciter. / - Favoriser les échanges entre chercheurs travaillant sur des modèles différents, (animaux, végétaux, humains, micro-organismes), dont les matériels génétiques et les outils d'analyse spécifiques peuvent susciter des synergies.

Public L'Ecole-Chercheurs est ouverte à tout scientifique (chercheurs, ingénieurs, post-doctorants, doctorants) désireux de compléter sa formation dans le domaine, voire d'acquérir les bases pour son projet de recherche, et de rencontrer des chercheurs travaillant sur d'autres modèles.

Programme 1. Introduction historique à la génétique multifactorielle Présentation des principales notions : caractère « complexe », gène à effets quantitatifs, génotype et phénotype, hérédité, épistasie. D. de Vienne, P. Darlu, J.-M. Elsen

2. Cartographies génétique et physique Descendances et populations utilisées pour la cartographie, métriques de cartes, techniques de génotypage, hybrides d'irradiation, cartographie comparée. M. Falque, X. Montagutelli, C. Julier, L. Schibler, H. Roest-Crolius

3. Structure des populations Déséquilibre de liaison (mesures, causes de la l'apparition et de la disparition, inférences) ; paramètres de la diversité dans les populations naturelles. E. Genin, B. Servin, C. Bourgain, R. Petit

4. Détection de gènes contrôlant les caractères à déterminisme complexe Utilisation de croisements contrôlés, de données familiales, de populations ; cartographie fine ; gènes candidats. F. Clerget, F. Demenais, L. Moreau, P. Le Roy, O. Loudet, A. Eggen

5. Réseaux de gènes et réseaux métaboliques La notion de réseau ; modélisation des réseaux et génétique des caractères complexes ; QTL d'expression. S. Robin, C. Dillmann, V. //Schachter, G. Yvert

6. Intégration de données Méta-analyse ; hybridation génomique comparative ; statistiques des séquences biologiques. A. Char//cosset, P. Broët, B. Prum

7. Evaluation des risques / Evaluation des valeurs

génétiques Pharmacogénétique des populations humaines ; génomique et sélection ; aspects éthiques de la médecine prédictive. A. Sabbagh, D. Boichard, J.-L. Mandel

Ateliers Quels logiciels pour quoi faire ? Animatrice : B. Mangin Avenir des technologies de génotypage. Animateur : Ivo Gut

Lieu La Colle-sur-Loup (06) France

Dates Du lundi 21 mai 9h (arrivée dimanche 20 soir) au vendredi 25 mai 13h00.

Coûts /Personnels INRA /(y compris doctorants). Frais pédagogiques et d'hébergement pris en charge à hauteur de 50% par la formation permanente nationale INRA et 50% par le programme agroBI, les DS APA et PPV et les départements GAP, GA et EFPA ; seuls les frais de transport sont à la charge des unités. /Autres personnels/. Participation aux frais de séjour et pédagogiques

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LaFouly Switzerland DemoGenetics Jun6-10

A workshop on "ESTIMATING DEMOGRAPHIC PARAMETERS FROM GENETIC DATA" will be held in La Fouly, Valais, Switzerland, from June 6th to June 10th 2007.

The workshop aims at familiarizing participants with emerging statistical methods (likelihood, Bayesian, MCMC, ABC, etc) allowing the estimation of demographic parameters (e.g. migration, dispersal, densities, bottlenecks, expansions, etc) from various types of molecular data.

Invited speakers: —————

David Balding: Likelihood vs. Bayesian demographic inferences. Principles of MCMC and ABC

Gil McVean: Estimating evolutionary parameters and demography from DNA sequence data taking into account recombination. Composite-likelihood and RJ-MCMC.

Rasmus Nielsen: Estimating evolutionary parameters

and demography from SNP data.

Andrew Rambaut: Demographic inference from fossil DNA data, skyline plots

Arnaud Estoup: Demographic and historical inference from recent invasions

Kent Holsinger: Hierarchical Bayesian models in geographical genetics, or what in the Fst is going on?

Invited speakers and participants will also have the opportunity to present their own research. Ample time will be allowed for discussions.

Registration fees are CHF 300.-, including local accommodation and food. Fees are waived for students from the Swiss universities affiliated to the CUSO (Geneva, Lausanne, Neuchatel, Fribourg and Berne), which will be given priority.

Deadline for registration is March 31st 2007.

Please register directly on our web site: <http://www.unil.ch/dee/page11644.en.html> Note that the workshop is limited to 30 participants, and a final selection will be done at the beginning of April.

Organizers : J, Goudet & N. Perrin, University of Lausanne L. Excoffier, University of Berne

Workshop location: <http://www.dolent.ch/> – Laurent Excoffier Computational and Molecular Population Genetics (CMPG) Zoological Institute, University of Bern 6, Baltzerstrasse, CH-3012 Bern, Switzerland Tel: +41 31 631 30 31 Fax: +41 31 631 48 88 Email: laurent.excoffier@zoo.unibe.ch URL: <http://cmpg.unibe.ch/people/excoffier.htm> Laurent Excoffier <laurent.excoffier@zoo.unibe.ch>

LakeheadU AncientDNA May22-Jun9

Ancient DNA Training Program

A training program focused on training participants in the analysis of degraded, difficult, ancient or low copy number DNA.

The ancient DNA training program is a three week intensive course in DNA. This year we are delivering the program from May 22nd to June 9th, 2007 at the Paleo-DNA laboratory Lakehead University.

During the program, participants will work in small groups (one instructor to 4 participants) and are given

a project depending upon their interests. This may be genetic analysis of museum specimens, genetic analysis of degraded samples, disease in ancient mummified tissue, genetic analysis of archived specimens or forensic profiling of a remains or many other such projects. As a participant, you will learn a variety of different extraction methods to compare and contrast on both your own DNA and other samples. You will generate your own DNA profile, determine your own mitochondrial haplogroup/haplotype, your own STR profile, confirm your own sex genetically and learn numerous techniques for the analysis of DNA.

The lectures will include the history of various types of analytical techniques, detailed mechanisms of each method and an large array of techniques that can be used in a genetic project. Participants will learn about the different types of DNA that can be analyzed: mitochondrial, nuclear, chloroplast and pathogenic DNA. You will be taught different methods of analysis PCR-RFLP, multiplex PCR, sequencing, regular PCR and electrophoresis. You will learn different methods of sample preparation from a number of different tissue types like bone, teeth, hair, archived specimens, museum specimens, blood residues and mummified tissue.

You will understand the use of genetic analysis and its potential in archaeozoology, palaeopathology, archaeology, forensic science, palaeobotany and palaeontology. Lectures by professors and senior analysts in the fields of archeology, genetics, ancient DNA, forensic science, palaeopathology and more are integrated with the laboratory sessions.

If you would like further information, please visit our website at <http://www.ancientdna.com/> or feel free to contact me at cjaspers@lakeheadu.ca.

With many thanks,

Cheryl Jaspers Administrator Ancient DNA Training Program Paleo-DNA Laboratory Lakehead University Thunder Bay, ON 1-807-343-8862

cjaspers@lakeheadu.ca

MBL WoodsHole MolEvol Jul22-Aug3

Workshop on Molecular Evolution

<http://workshop.molecularevolution.org/> Michael P. Cummings, Director

22 July - 3 August 2007 plus extended topics session 4
August - 10 August 2007

Application Deadline 1 March 2007

The Workshop on Molecular Evolution has been the finest course of its type in the world since it was started in 1988. The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. A distinguishing feature of the Workshop is a well-equipped computer laboratory with Linux workstations and servers for comparative analysis of molecular data. Authors and experts in the use of computer programs and packages such as Clustal W and Clustal X, FASTA, GARLI, GCG, LAMARC, MrBayes, PAML, PAUP*, and PHYLIP provide demonstrations and consultations. This two-week program is designed for established investigators, postdoctoral fellows, and advanced graduate students with prior experience in molecular evolution and comparative genomics. Scientists with a strong interest in molecular evolution, systematics, and population genetics are encouraged to apply. Enrollment is limited to 60 students, and 15 students will be admitted to an extended topics session for the purpose of analyzing their research data sets. Many participants find the extended topics session to be especially useful.

Topics to be covered include:

* Databases and sequence matching: database searching; protein sequence versus protein structure; homology; mathematical, statistical, and theoretical aspects of sequence database searches * Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis, hypothesis testing * Character analysis in a phylogenetic context: analysis of quantitative and discrete characters; hypothesis testing * Maximum likelihood theory and practice in phylogenetics and population genetics: coalescent theory; maximum likelihood estimation of population genetic parameters * Bayesian methods in phylogenetic analysis * Molecular evolution integrated at different levels: population biology; biogeography; ecology; systematics and conservation * Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution * Comparative genomics: genome content; genome structure; genome evolution * Transposable elements: types; history; evolutionary dynamics; as a major component of genomes

Fee: \$2150 (room and board at no additional charge), plus an additional \$850 for the extended topics session.

Application Form at <http://www.mbl.edu/education/-admissions/applications/> Further information at

<http://workshop.molecularevolution.org/> Preliminary list of faculty

Peter Beerli Joseph Bielawski Michael Cummings Alexei Drummond Scott Edwards Joseph Felsenstein Mary Kuhner Paul Lewis Axel Meyer Michael Miyamoto William Pearson David Rand Fredrik Ronquist David Swofford Steven Thompson Paul Turner Daniel Voytas Anne Yoder Shozo Yokoyama Derrick Zwickl

mike@umiacs.umd.edu mike@umiacs.umd.edu

PortalAZ AntEvol Aug2-12

ANT COURSE 2007

Southwestern Research Station (SWRS), Portal, AZ, August 2-12, 2007

DEADLINE FOR APPLICATION: April 1, 2007

http://www.calacademy.org/research/entomology/-ant_course/ COURSE OBJECTIVES. ? ANT COURSE is designed for systematists, ecologists, behaviorists, conservation biologists, and other biologists whose research responsibilities require a greater understanding of ant taxonomy. Emphasis is on the classification and identification of more than fifty ant genera of North America. Lectures will include background information on the ecology, life histories and evolution of ants. Field trips are structured to teach collecting and sampling techniques, and associated lab work provides instruction on specimen preparation, sorting and labeling. Information on equipment/supply vendors, literature, and myrmecological contacts are also presented.

COURSE SIGNIFICANCE. ? Ant Course is a unique opportunity to acquire training that is unavailable elsewhere. This course will provide students with 1) the confidence and skills to identify the major ant genera of North America; 2) an understanding of modern specimen processing and curation techniques; 3) an appreciation for the biological diversity of ants, and 4) experience keying to the species level.

SPONSORS. ? California Academy of Sciences and Museum of Comparative Zoology, with partial funding from the National Science Foundation.

BACKGROUND INFORMATION. ? ANT COURSE will be taught from August 2 ? 12, 2007 at the Southwestern Research Station (SWRS) in Portal Arizona (

<http://research.amnh.org/swrs/>). The Station is centered amid the richest ant fauna in North America. This is an ongoing course, offered annually.

PARTICIPANT ACCEPTANCE CRITERIA. ? ANT COURSE is open to all interested individuals. Priority will be given to those biologists for whom the course will have a significant impact on their research with ants. An entomological background is not required. We aim to include students with a diverse interest in biology, including ant systematics, ecology, behavioral biology and conservation. The high instructor to student ratio will allow students to receive individual attention. ANT COURSE is presented in English and limited to 25 participants

COSTS. ? Tuition for the 10-day COURSE is \$475 for current students and \$675 for non-students. In addition, Southwestern Research Station (SWRS) fees for this period, covering dormitory room and board, are estimated at \$460. Transportation costs between home and Tucson (air) or SWRS (auto) are to be borne by all participants.

FELLOWSHIPS. ? Four fellowships are available for 2007. Two fellowships cover tuition fees and two fellowships cover station fees. Foreign students may apply for additional fellowships to assist in travel. Those interested in attending the course should seek all possible avenues to secure funding for the course. You should only apply for the Ant Course fellowship if you can not find other support and it is essential for your participation in the course. Beware that if you apply for an ant course fellowship it implies that fellowship funding is essential to your participation in the course. Thus, if you are not selected for a fellowship, you might not be accepted into the course. Please notify the course if your funding request status changes before the application due date.

POSSIBLE INSTRUCTORS: Brian Fisher (Coordinator), Dept. of Entomology, California Academy of Sciences, San Francisco, CA, bfisher@calacademy.org Stefan Cover (Coordinator), Museum of Comparative Zoology, Harvard University, Cambridge, MA, cover@oeb.harvard.edu Lloyd Davis, Gainesville, FL, ants@gru.net Mark Deyrup, Archbold Biological Station, Lake Placid, Florida, mdeyrup@archbold-station.org André Francoeur Université du Québec, Saguenay, Québec, andre_francoeur@uqac.ca Bob Johnson, Dept. of Biology, Arizona State University, Tempe, Arizona, atraj@imap1.asu.edu Jack Longino, Lab I, The Evergreen State College, Olympia WA, longinoj@evergreen.edu Mike Kaspari, Dept. of Zoology, University of Oklahoma, Norman OK, mkaspari@ou.edu Corrie Moreau, Museum of Compar-

ative Zoology, Harvard University, Cambridge, MA, cmoreau@oeb.harvard.edu Andrew Suarez, Departments of Entomology and Animal Biology, University of Illinois, Urbana, IL, avsuarez@life.uiuc.edu James Trager, Shaw Nature Reserve, Gray Summit MO, James.Trager@mobot.org Walter Tschinkel Department of Biological Science Florida State University Tallahassee, FL, tschink@bio.fsu.edu Gary Umphrey, Dept. of Mathematics and Statistics, University of Guelph, Guelph, ON, University of Guelph, umphrey@uoguelph.ca Phil Ward, Department of Entomology, University of California, Davis, CA, psward@ucdavis.edu

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Roscoff MarineGenomics Jun25-Jul6

The European Network of Excellence “Marine Genomics Europe” invites applications for the third annual summer course “Marine Evolutionary & Ecological Genomics” at the Station Biologique, Roscoff (Brittany), France June 25 July 6, 2007 The deadline for application is April 30, 2007

For information and registration: <http://www.marine-genomics-europe.org> (training and education)

Contact person: Ulrika Hjelm Training and Education Programme Manager NoE Marine Genomics Europe Kristineberg Marine Research Station S-450 34 Fiskebäckskil Sweden Phone: ++46 (0) 523 18548 Fax: ++46 (0) 523 18502 Mobil: ++46 (0) 70 344 2371 E-mail: <blocked::mailto:ulrika.hjelm@kmf.gu.se>ulrika.hjelm@kmf.gu.se

Disclaimer: http://www.kuleuven.be/-cwis/email_disclaimer.htm Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

Sarawak Malaysia BorneoBiodiversity Jul23-Aug26

** Course announcement: Harvard University/CTFS-AA Field Biology Course: 'The Biodiversity of Borneo'
**

In association with the Harvard University Summer School, the Center for Tropical Forest Science and the Arnold Arboretum (CTFS-AA) will offer a field biology course to be held in Sarawak and Sabah (East Malaysia) from 23 July to 26 August 2007. Southeast and South Asian participants will join Harvard University students to study terrestrial and marine biodiversity, ecology and conservation, with instructors from Harvard University and other institutions.

The forests and reefs of northwest and north Borneo have some of the highest levels of alpha diversity in the world. The forests are home to orang-utans, hornbills, rhinos and thousands of tree species, and the reefs offer some of the best diving in the world. We will visit world-class parks and reserves (e.g., Lambir, Kinabalu and the Maliau Basin), to gain a thorough understanding of abiotic controls on species composition, and will contrast processes that maintain biodiversity in forests with those operating on coral reefs. Throughout Borneo, intensive logging and marine harvesting have occurred for many years. Our course will explore the complexities of conservation today, including trips to sustainably-managed, carbon-traded, and restored forests. We will also provide opportunities for the students to meet people living in and off the forest, to understand their motivations for forest conversion and conservation, and to consider the human health dimensions of forest change.

A key feature of the course will be the development of skills in research project design, execution and analysis, based around the statistical platform R. The students will complete two independent projects, from conception to presentation, and participate in a group project on the coral reef. The students will gain database and web publishing skills by developing a community digital record of the trip.

The course is aimed at advanced undergraduates, recent graduates currently active in biological research, and postgraduate entry-level students. For more information on the course (including instructions for application) see:

<http://www.summer.harvard.edu/2007/programs/-abroad/borneo/> Queries and completed application materials should be directed to Cam Webb (cwebb@oeb.harvard.edu). Please note: the application deadline has been extended for US students to 15 March 2007.

cwebb@oeb.harvard.edu cwebb@oeb.harvard.edu

UAlaskaFairbanks PlantEvolEcol Jul9-Aug16

We are offering an undergraduate summer course in Field Methods in Plant Ecology at the University of Alaska Fairbanks from July 9 August 16, 2007. This field course is separated into different weekly research modules in which we will explore topics in spatial vegetation analysis, ecological genetics, herbivory, and disease incidence, to name a few. All students also will participate in self-motivated group research projects at the end of the course. For more information visit UAF summer sessions at <http://www.uaf.edu/summer/index.html> or email the instructors Matt Olson <matt.olson@uaf.edu> or Christa Mulder <ffcpm2@uaf.edu>. Registration begins February 19 2007 and in-state tuition is charged for everyone. The course description as in the course catalog is shown below.

BIOL F395F71 4 credits CRN 50616 Mulder/Olson 1:00-4:40 p.m., MR, Irving 303 July 9August 16 9:00 a.m.-4:30 p.m., W, Irving 103 Lab Concepts and methods to conduct and communicate the results of field research in Alaskan plant communities. Includes hypothesis development, experimental design, field sampling, data analysis and oral and written presentation of results. Topics may include pollination, hybrid zones, spatial patterning, herbivory, competition, and demography. Prerequisite: BIOL 105x and BIOL 106x or permission of instructor. Recommended: BIOL 271. \$100 field trip fee.

Thanks

Matt Olson

Matthew S. Olson Associate Professor Institute of Arctic Biology and Department of Biology and Wildlife University of Alaska at Fairbanks

Mailing address: PO Box 757000 UAF Fairbanks, AK 99775-7000

Courier address (FedEx): 311 Irving 1 902 Koyukuk Dr. UAF Fairbanks, AK 99775-7000

Phone: 907.474.2766 Fax: 907.474.6967 web: http://www.iab.uaf.edu/~matt_olson/

Matt Olson <matt.olson@uaf.edu>

UBasel Evol June

Graduate course in evolutionary biology.

It my pleasure to announce this years Guarda workshop in Evolutionary Biology for master and PhD students. The main aim of the course is to develop the skills to produce an independent research project in evolutionary biology.

The course takes place in the June 2007 (1 week course) in the Swiss mountain village Guarda. Faculty includes Mark Kirkpatrick, Janis Antonovics, Sebastian Bonhoeffer, Tad Kawecki and Dieter Ebert (organizer).

The course is intended for master (Diploma) students and early PhD students.

The web page with all the details can be found under:

<http://www.evolution.unibas.ch/teaching/guarda/-index.htm> Please communicate this information to interested students.

With best wishes,

dieter ebert

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UCopenhagen PopulationStructureAndProcesses May21-25

Invitation for Ph.D. course “Molecular marker analysis of plant population structure and processes”, 21-05-2007 - 25-05-2007 at Faculty of Life Sciences, University of Copenhagen (formerly the Royal Veterinary and Agricultural University).

The course provides the participants with advanced knowledge of the analysis of genetic structure, mating patterns, and population processes in plant

populations, using molecular marker data. The course includes theoretical lectures, discussions of student projects, and exercises with various computer programs. This course is Module 3 of the course package: “Molecular plant breeding and genetic resources”, <http://www.kursus.kvl.dk/shares/-phdmarker/index.htm> . Course content Estimation of diversity, inbreeding level, restricted gene flow, population admixture, hybridization, selfing rate, paternity assignment, and allocation to parental populations and hybrids. Assumptions and limitations behind diverse procedures used in relevant computer programmes, such as: GenAlEx, Spagedi, Structure, MLTR, Two-gener, Population Graph, Split tree, New Hybrids, AFLPOP, Famos, Cervus, etc. Discussion of student projects (use this opportunity to discuss your Ph.D. research!). Practical computer analysis with various software.

Course credit 3 ECTS points. Requirement for obtaining credit: approval of a written synopsis of the course content.

Course material All course material, such as discussion articles, presentations and software, will be available through a restricted web site. All software to be used is freely available.

Practicals Maximum number of participants is twenty. Ph.D. students have preference until 15/4; after that, remaining seats’ are open to non-PhD students. The course will take place at the Faculty of Life Sciences, University of Copenhagen, 1958 Frederiksberg C (part of Copenhagen). Computers will be available for all; if you prefer to bring your own laptop computer, do that. Coffee and tea will be served. Travel, lodging, and accommodation are to be organised and paid by the participants on their own; suggestions for hostels and hotels will be posted on the web. Course fee To be decided, maximum 500 DKK.

Organisers and teachers Gunter Backes, Associate Professor in Plant Breeding, guba@life.ku.dk Ole Kim Hansen, Ph.D. in Forest Genetics; okh@life.ku.dk Thure Hauser, Associate Professor in Plant Ecology, tpha@life.ku.dk Erik D. Kjær, Professor in Forest Genetics, edk@life.ku.dk

Registration and questions Write an e-mail to Thure Hauser, tpha@kvl.dk, containing the following information: Full name, sex, e-mail address, mobile phone no., institution, full mailing address, country, whether you are a Ph.D. student, title of present research project, whether you would like to present your project during the course; in that order and on separate lines.

tpha@life.ku.dk

UFlorida MolecularMarkers Apr9-13

Molecular Markers Workshop April 9-13, 2007. Early registration deadline March 23, 2007.

Register at www.biotech.ufl.edu/WorkshopsCourses or contact Teresa Benton at 352-273-8035

University of Florida- Interdisciplinary Center for Biotechnology Research Education and Training Core Laboratory offer a hands-on workshop:

Microsatellites are a powerful class of genetic markers used in a variety of molecular studies such as determining fine scale population structure, parentage, and individual identification. The genomes of most eukaryotes contain thousands of loci containing short nucleotide sequence motifs tandemly repeated many times, such as (CT/GA)_n. The repeat units tend to be highly polymorphic, and several loci taken together produce a genetic fingerprint that is consistent and unchanging from one individual to the next. While readily used and analyzed, it is generally necessary to develop a new set of markers for each species, as there tends to be little crossover between species unless fairly closely related.

Developing a microsatellite library can be a long and troublesome task, especially for those with limited molecular background. This workshop will take participants through the steps used to build an enriched microsatellite library using DNA from their species of interest using a variety of molecular techniques such restriction enzyme digestion, ligation, PCR, and several screening protocols to find loci containing polymorphic repeat motifs. Participants will also learn about primer design and statistical analyses.

Sharon E. Norton Scientific Education Coordinator
University of Florida ICBR Education and Training Core Laboratory PO Box 103622 Gainesville, FL 32610 office:(352) 273-8048 lab: (352) 273-8047 fax: (352) 273-8069 <<http://www.biotech.ufl.edu>>
www.biotech.ufl.edu

Sharon Norton <norton@biotech.ufl.edu>

UWashington StatGenetics Jun11-29

Details are now finalized for the 12th Summer Institute in Statistical Genetics. They are shown on the web page <http://www.biostat.washington.edu> The Institute will offer a total of 21 modules between June 11 and 29, including new modules in clinical trials, proteomic data analysis, biomarker evaluation and computing for statistical genetics. Registration is limited in all modules.

Please send all enquiries, including requests for electronic or hard copies of the Institute Brochure, to sisg07@u.washington.edu

– Bruce S. Weir Professor and Chair, Department of Biostatistics University of Washington Seattle, WA 98195-7232 Phone (206) 221-7947. Fax (206) 543-3286.

Bruce Weir <bsweir@u.washington.edu>

Valencia MolEvol May21-25

Second Course on Molecular Evolution, Phylogenetics and Phylogenomics

21 - 25 May 2007, Valencia. Spain

Hernán Dopazo, Co-ordination

The course aims to provide the necessary background to understand the basic concepts from comparative and evolutionary biology that are frequently used in molecular biology and bioinformatics analyses. The course consists in five full-day sessions with an adequate balance between theory and computer practice, oriented to solve frequent problems and hypothesis testing. The course includes a session of phylogenomic analysis and functional annotation including the most recent developments in this area. Among other tools, attendees will become familiar with Phylip, Phyml, PAML, TreePuzzle, MrBayes, Modeltest programs and tools developed in our department such as Phylemon, FatiGO, FatiScan, and ETE. The course is mainly intended for professionals in the field of biology and chemistry who work on areas related to biological sequence analysis.

Course fee is 250 euros, a limited number of grants will be available.

Teachers Fátima Al-Shahrour, Jaime Huerta, Leonardo Arbiza, Toni Gabaldón y Hernán Dopazo. Departamento de Bioinformática. Centro de Investigación Príncipe Felipe (CIPF)

Invited Professors Arcadi Navarro, UPF (Barcelona) Fernando González, UV (Valencia) Rafael Zardoya

(MNCN, Madrid)

More information: <http://bioinfo.cipf.es/docus/-courses/coursesCIPF/II.CIPF.Evo-Filo.htm> Application Deadline 1 May 2007

Language: the official language of the course will be english unless all attendees speak spanish.

More information at <http://bioinfo.cipf.es/docus/-courses/coursesCIPF/II.CIPF.Evo-Filo.htm> Phylemon web server: <http://phylemon.bioinfo.cipf.es> Centro de Investigación Príncipe Felipe (<http://www.cipf.es>)

[/www.cipf.es](http://www.cipf.es)) Bioinformatics Department (<http://bioinfo.cipf.es>) Valencia, Spain.

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Hernán J. Dopazo, PhD Pharmacogenomics & Comparative Genomics Unit, Bioinformatics Department, Centro de Investigación Príncipe Felipe c/ ep Avda. Autopista del Saler 16 (Junto al Oceanográfico), 46013, Valencia, España. Tfn: (34) 96 328 96 80 ext: 1008 Fax: (34) 96 328 97 01 hdopazo@cipf.es <http://www.cipf.es> <http://bioinfo.cipf.es/hdopazo/> hdopazo@ochoa.fib.es

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 sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

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