
E v o l D i r

February 1, 2008

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

Forward

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

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

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



Forward	1
Conferences	2
GradStudentPositions	12
Jobs	27
Other	41
PostDocs	56
WorkshopsCourses	75
Instructions	82
Afterward	83

Conferences

Ascona Switzerland Silene Evolution May4-9	2	NHM London Speciation Mar12-13	8
Barcelona SMBE Jun5-8	2	RoyalSociety London Phylogenetics Apr28-29	8
Barcelona SMBE Jun5-8 2	3	Seattle EarlyCareer Female EvolutionaryBiologists	
Barcelona SMBE Jun5-8 Registration	4	Oct19-22	8
Berlin IntlCongressGenetics Jul12-17	4	Slovakia PlantSystematics July	9
Copenhagen GrassSystematicsEvolution Aug11-15 ..	5	UIowa Evolution of Sex Jun16-19	9
FloridaStateU SEEC Evolution Mar28-30	5	Vancouver CanadianSocEcolEvol May11-14	10
Halifax PhylogeneticNomenclature July21-23	5	Winchester ArtificialLife and Evolution Aug5-8	10
KansasCity ArthropodGenomics Apr11-13	6		
MadisonWI CelegansEvolution Jun11-15	7		

Ascona Switzerland Silene Evolution May4-9

1st announcement

International Workshop Silene: from populations to genes

Monte Verità, Ascona, Switzerland 4-9 May 2008

Invited speakers:

Janis Antonovics, Arjen Biere, Deborah Charlesworth, Lynda Delph, Dmitry Filatov, Tatjana Giraud, Gabriel Marais, John Pannel, Jacqui Shykoff, Doug Taylor, Boris Vyskot, Lorne Wolfe

Closing date for registration and abstract submission: February 1st, 2008

Website: www.unil.ch/silene The genus *Silene* is emerging as a study case for plant evolutionary ecology, with current research questions covering among others local adaptation, sex determination, sex ratio variation, sexual dimorphism, mating systems, population genetics, the epidemiology of fungal diseases and nursery pollination. The aim of the workshop is to bring together scientists working on various aspects of the biology of the genus *Silene* (and of interacting agents such as pathogenic fungi and herbivores) for an exchange of experiences and to initiate and continue collaborative

projects. The meeting will include invited and contributed talks as well as posters and discussions. The conference is open to researchers working on *Silene*, *Mycrobotryum*, *Hadena*, but *we welcome anyone interested in the system, working with related or similar systems, or addressing similar questions or developing conceptual issues that may be tested with this system.*

Organisers: Giordina Bernasconi, Jérôme Goudet, Alex Widmer

Giordina Bernasconi <Giordina.Bernasconi@unil.ch>

Barcelona SMBE Jun5-8

Barcelona, SMBE 2008 Meeting

CALL FOR MENTORS-SMBE UNDERGRADUATE DIVERSITY MENTORING PROGRAM AWARDS

2008 Annual Meeting of the Society for Molecular Biology and Evolution June 5-8, Barcelona, Spain <http://www.smb2008.com> PROGRAM OUTLINE

The Society for Molecular Biology and Evolution (SMBE) is offering 10 awards to 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 attending 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). WE ARE SEEKING INDIVIDUALS INTERESTED IN BEING A MENTOR. Specific 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.

CONFERENCE PARTICIPATION

In addition to the activities outlined above, mentors will be invited to attend a special reception / poster session on Friday June 6, along with undergraduates, supervisors and other interested conference attendees.

If you are interested in mentoring an undergraduate at this year's SMBE meeting please email Laura Katz (Lkatz[at]email.smith.edu) and John Archibald (john.archibald[at]dal.ca).

Julio Rozas Carmen Segarra www.smb2008.com
jroz@ub.edu jroz@ub.edu

Barcelona SMBE Jun5-8 2

Barcelona, SMBE 2008

The Organizing Committee is pleased to invite you

to attend the 2008 annual meeting of the Society for Molecular Biology and Evolution (SMBE) that will be held on June 5-8, in Barcelona, Spain.

Conference registration and abstract submission is now available online at the SMBE 2008 website (<http://www.smb2008.com/>). The site also contains additional information on accommodation and travel, confirmed speakers, as well as the Walter M. Fitch Prize competition for young investigators, postdocs and graduate student travel awards, and the Undergraduate Diversity Mentoring Program awards.

IMPORTANT DATES

Abstract Submission Deadline: March 3 Early Registration From January 17 to March 10. Walter Fitch Prize Deadline: March 3 Undergraduate Diversity Mentoring Program Awards Deadline: February 15

SYMPOSIUM TOPICS

Animal domestication genomics Animal molecular Evo-Devo Beyond scans for selection: Studying the phenotypes Bioinformatics for molecular evolution Dating divergence: The Tower of Babel of geneticists and paleontologists? Drosophila population genomics Evolution of gene regulation Evolutionary comparative genomics Evolutionary genomics of human and pathogen interactions Evolutionary radiations and molecular phylogeny Genetics and molecular biology of speciation Genome variation: Lessons from the human genomes Genomic evidence for natural selection and implications Genomics for crop evolution and improvement Models of genome evolution and phylogenomics Molecular and evolutionary epidemiology Molecular phylogeography and population genetics Network evolution and systems biology Popgen in space! Theory and inference in spatial population genetics RNA world: Emergence of life on earth Spontaneous mutations and their evolutionary consequences The ancestral eukaryotic cell The crossroads between prokaryotic genomics, ecology and adaptation The X - an eXceptional chromosome! Transposable elements: diversity, dynamics and evolutionary impact on host genomes What would/should we do with a million DNA barcodes?

ORGANIZING COMMITTEE

Chairs Carmen Segarra (Universitat de Barcelona)
Julio Rozas (Universitat de Barcelona)

Members Montserrat Aguade (Universitat de Barcelona) Pere Arus (Institut de Recerca i Tecnologia Agroalimentàries) Jaume Bertranpetit (Universitat Pompeu Fabra) Jose Castresana (Consejo Superior de Investigaciones Científicas) Roderic Guigo (Universitat Pompeu Fabra) Elvira Juan (Universitat de Barcelona)

Marta Riutort (Universitat de Barcelona) Alfredo Ruiz (Universitat Autònoma de Barcelona) Mauro Santos (Universitat Autònoma de Barcelona) Lluís Serra (Universitat de Barcelona)

Julio Rozas Carmen Segarra www.smbe2008.com
jrozas@ub.edu jrozas@ub.edu

Barcelona SMBE Jun5-8 Registration

Barcelona, SMBE 2008

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Julio Rozas Carmen Segarra

www.smbe2008.com SMBE <info@smbe.org>

Berlin IntlCongressGenetics Jul12-17

The International Congress of Genetics, organized under the auspices of the International Genetics Federation (IGF) is one of the most important international congresses in the field of genetics and genomics. Ever since 1899, it has been held every five years in different countries of the world with the last one taking place in, Australia (2003).

The IGF has elected the German Genetics Society (GfG) to host the XX International Congress of Genetics in 2008.

JOIN THE WORLD MOST PROMINENT GENETICISTS IN BERLIN SUBMIT YOUR ABSTRACT BEFORE JANUARY 15, 2008

DON'T MISS THE EARLY BIRD DEADLINE

REGISTER BEFORE JANUARY 15, 2008

The Scientific Program of the XX International Congress of Genetics 2008 may be viewed and downloaded at the following link: < <https://www2.kit.de/downloads/ICG.Symposia.pdf> > <https://www2.kit.de/downloads/ICG.Symposia.pdf>

For more information about registration or abstract submission, please consult the official congress website at www.geneticsberlin2008.com < <http://www.geneticsberlin2008.com/> > .

eblin@kit-group.org

Copenhagen GrassSystematicsEvolution Aug11-15

The 2nd Circular for

“The Fourth International Conference on the Comparative Biology of the Monocotyledons & The Fifth International Symposium on Grass Systematics and Evolution”

to take place in Copenhagen, Denmark, 11-15 August 2008 is now available at www.monocots4.org . We look forward to seeing you in Copenhagen in August! Note: Dead-line for early registration is April 4th.

On behalf of the organizing committee

Ole Seberg, Chairman of the Organizing Committee - Monocots IV/Grasses V Laboratory of Molecular Systematics The Natural History Museum of Denmark

oles@snm.ku.dk

FloridaStateU SEEC Evolution Mar28-30

2008 Southeastern Ecology and Evolution Conference
Florida State University Call For Abstracts

Florida State University will host the 2008 Southeastern Ecology and Evolution Conference and is announcing a call for abstracts for presentations of research. This is a scientific symposium aimed at graduate, post-doctoral, and undergraduate researchers in the fields of ecology, systematics, and evolutionary biology. The conference will be held on the campus of Florida State University in Tallahassee, Florida on March 28-30, 2008.

Abstract Submission Information

Researchers interested in presenting posters or 15-

minute talks are invited to submit abstracts pertaining to: - Animal Behavior - Conservation - Ecology - Evolution - Functional Morphology - History and Philosophy of Science - Systematics

The deadline for the submission of abstracts is Friday March 14, 2008 at 5:00 PM, EST. Please submit your abstract along with registration at the SEEC website, found at <http://bio.fsu.edu/~eerdg/seec/> . Abstracts should be limited to 250 words, and please include any primary and co-authors as well as session preference. Information about poster and talk requirements is available on the SEEC website.

Please contact David McNutt (dmcnutt@bio.fsu.edu) for questions regarding registration or abstract submission, or general questions about SEEC to Amanda Buchanan (abuchanan@bio.fsu.edu) or Eric Jones (ejones@bio.fsu.edu).

jfjerst@bio.fsu.edu jfjerst@bio.fsu.edu

Halifax PhylogeneticNomenclature July21-23

3rd Meeting of the International Society for Phylogenetic Nomenclature Halifax, Nova Scotia, July 21 - July 23, 2008

We are pleased to announce that the 3rd Meeting of the International Society for Phylogenetic Nomenclature (ISPN) will be held in conjunction with a joint meeting of the International Society of Protistologists and the International Society for Evolutionary Protistology (<https://protist2008.dal.ca/>). In addition to featuring communications on the theory and practice of phylogenetic nomenclature, this meeting will be an opportunity to discuss the forthcoming release of the PhyloCode and publication of the Companion Volume, as well as development of the on-line registration database (RegNum). All systematists interested in the development of phylogenetic nomenclature are welcome. Discussions and presentations at this meeting may influence the future development of the PhyloCode.

Venue: The meeting and associated social gatherings will be held on the campus of Dalhousie University, in the centre of Halifax. In order to make the meeting accessible to all scientists, on-campus dormitory-style accommodation will be available, in addition to nearby hotels. Note that U.S. Citizens traveling to Canada will be required to carry passports.

Conference Language: English

ISPN Organizing Committee: Harold Bryant, Chair, Royal Saskatchewan Museum, Canada Nico Cellinese, University of Florida, U.S.A. Walter Joyce, Yale University, U.S.A. Michel Laurin, CNRS, Paris, France

Registration and Abstract Submission: Instructions on how to register and submit abstracts will be provided in the second circular, which will be distributed in the very near future.

Contact Harold Bryant Chief Curator and Curator of Earth Sciences Royal Saskatchewan Museum 2340 Albert Street Regina, Saskatchewan S4P 2V7 Canada 306-787-2826; FAX 306-787-2645 email: hbryant@royalsaskmuseum.ca

Nico Cellinese <ncellinese@flmnh.ufl.edu>

KansasCity ArthropodGenomics Apr11-13

SYMPOSIUM: NEW INSIGHTS FROM ARTHROPOD GENOMES

April 11-13, 2008, in Kansas City

Registration is now open to attend the 2nd Annual Arthropod Genomics Symposium, April 11 - 13, 2008, in Kansas City. A brochure and complete information with links for registration and hotel reservations can be downloaded at www.ksu.edu/agc/symposium.shtml.

SYMPOSIUM PROGRAM: The main symposium sessions will take place on Friday-Saturday, April 11-12. Speakers will present new insights from genomic approaches in arthropods and describe the development of tools for genomic analysis. Optional workshops are scheduled for Thursday and Friday evenings. An evening of jazz and KC barbeque is planned for Saturday night. On Sunday morning, participate in a roundtable discussion with the ArthropodBase Consortium. Activities will conclude by noon on Sunday.

FEATURED SPEAKERS:

John Kenneth Colbourne, Indiana University, Preservation, expansion and invention of crustacean genes with reference to insect genomes.

Christine G. Elsik, Georgetown University, Unusual base composition of the honey bee genome.

Sarjeet S. Gill, University of California, Riverside, Mosquito midgut interactions with bacterial toxins.

Catherine A. Hill, Purdue University, Tick genome organization and evolution.

Thomas Kaufman, Indiana University, The latest news from CNN: What the 12 sequenced *Drosophila* genomes have told us about rapidly evolving genes and positive selection.

J. Robert Manak, University of Iowa, Empirical annotation of arthropod genomes using tiled genomic microarrays.

Subbaratnam Muthukrishnan, Kansas State University, Functional genomics of insect chitin metabolism.

Hugh M. Robertson, University of Illinois at Urbana-Champaign, What we've learned about the insect chemoreceptors from arthropod genome projects.

Bruce R. Schatz, University of Illinois at Urbana-Champaign, BeeSpace: Interactive functional analysis of arthropod genomic data.

Jeff Stuart, Purdue University, Avirulence, sex determination, and a physical map of the Hessian fly genome.

Judy Willis, University of Georgia, Insect cuticular proteins: Annotation, proteomics, expression, evolution.

Evgeny Zdobnov, University of Geneva, Medical School, Switzerland, A comparative perspective on insect genomes.

POSTER SESSIONS: There will be two poster sessions, limited to first 150 abstracts received before Friday, February 29. A few platform presentations will be chosen from submitted poster abstracts.

WORKSHOPS AND ROUNDTABLE DISCUSSION: On Thursday evening, a workshop on "Community Contributions to Genome Annotation" will feature a presentation on use of the Apollo Genome Annotation Curation Tool by Dr. Chris Elsik (BeeBase). On Friday evening, Dave Clements (NESCent) and Scott Cain (CSHL) will lead a workshop, "Chado Databases and Integration with GMOD Tools." Throughout the meeting, arthropod genome database and bioinformatics tool developers will be available for individual training. On Sunday morning, participate in a roundtable discussion led by members of the ArthropodBase Consortium regarding the generation of integrated arthropod genome databases and tools for genome analysis, and community curation. Symposium attendees are invited to participate in these additional events.

VENUE: The symposium will take place at the historic Muehlebach Hotel (operated by Marriott) in downtown Kansas City.

KANSAS CITY JAZZ AND BARBEQUE: Participants are encouraged to stay Saturday night for an op-

tional evening of jazz and KC barbeque in the historic 18th and Vine district.

REGISTRATION: The registration fee will be \$275 (\$150 for graduate and undergraduate students), and will include a welcome reception Thursday evening, breakfast and lunch on Friday and Saturday, and light refreshments at the Friday poster session. Additional fees apply for the Apollo Workshop Thursday evening and Saturday night dinner.

INFORMATION: Contact Doris Merrill at dmerrill@k-state.edu or 785-532-3482. To receive future Symposium announcements, send your contact information to dmerrill@k-state.edu.

SYMPOSIUM WEBSITE: www.k-state.edu/agc/-symposium.shtml

DEADLINES:

February 29, 2008 - Poster abstracts (limited to first 150 received)

February 29, 2008 - Early registration

March 20, 2008 - Hotel reservations

Please share this announcement with colleagues and students!

SYMPOSIUM FUNDING: Symposium funding provided by the Center for Genomic Studies on Arthropods Affecting Human, Animal and Plant Health with support from Targeted Excellence at Kansas State University.

Susan J. Brown, Professor

Director, Center for Genomic Studies on

Arthropods Affecting Human, Animal and Plant Health

by

Doris Merrill, Program Coordinator

K-State Arthropod Genomics Center

Division of Biology, Kansas State University



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>

Madison WI C.elegans Evolution Jun11-15

Hello!

We are pleased to announce a special session on Evolution at this year's C. elegans topic meeting 11-15 June 2008 in Madison, Wisconsin, USA. This symposium will provide an exceptional opportunity to exchange ideas and to present current research on the evolutionary analysis of C. elegans and its congeners, and of comparative work with other model nematodes (e.g. Pristionchus, Oscheius, Heterorhabditis). The session is a sequel to the 2006 C. elegans Evolution Workshop held in Oeiras, Portugal, that was organized by Henrique Teotonio, Marie-Anne Félix, Patrick Phillips, and Ricardo Azevedo. We are also proud to have Scott Emons as the keynote speaker for the Evolution topic session.

The session on evolution will cover diverse fields within evolutionary biology, including: * comparative evolutionary genetics and genomics * experimental evolution * ecologically important traits (chemotaxis, learning, resistance, etc.) * genetic variation: population and quantitative genetics, gene family evolution * reproductive biology and sexual selection

In addition, the meeting will also host a Workshop on Caenorhabditis Evolution with the aim of facilitating discussion of salient problems in evolutionary biology through use of C. elegans and its relatives. We intend the workshop to focus on 3 themes: 1. Understanding diversity in Caenorhabditis: variation in morphology, behavior, and sequences 2. Fundamental problems in evolution to which C. elegans can be applied 3. Synergism and resources for studying evolution in Caenorhabditis

Other sessions in this year's C. elegans Development & Evolution topic meeting will provide a rich complement of talks relating development and evolution, and the meeting features an outstanding line-up of keynote speakers.

Deadline for abstract submission is 7 April 2008 (online registration will commence shortly). For further details, see the conference website: <http://www.union.wisc.edu/celegans/> Best wishes and hope to see you in Madison!

Asher Cutter / Hinrich Schulenburg
asher.cutter@utoronto.ca / hinrich.schulenburg@uni-tuebingen.de (Co-organizers, Evolution session)

Dr. Hinrich Schulenburg

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

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

NHM London Speciation Mar12-13

Speciation Symposium, London 12-13 March 2008

The third Natural History Museum Speciation Symposium will be held from 1pm on 12 March to 3pm on 13 March in the Museum's Flett Lecture Theatre, Exhibition Road, London. The Keynote Address will be by Prof. Leo Beukeboom on 'Speciation in *Nasonia* wasps'.

We still have room for contributed papers. Please send a proposed title and brief abstract to the organisers, Ralph Harbach (reh@nhm.ac.uk) and Roger Butlin (r.k.butlin@sheffield.ac.uk).

Bookings for participants will be taken nearer the time. There will be a small charge to cover refreshments. We will not be providing accommodation so you might like to look at London hotels now. We can supply a list of hotels within easy reach of the Museum.

Ralph Harbach and Roger Butlin

r.k.butlin@sheffield.ac.uk r.k.butlin@sheffield.ac.uk

RoyalSociety London Phylogenetics Apr28-29

Royal Society Discussion Meeting: Statistical and computational challenges in molecular phylogenetics and evolution

Royal Society, London, UK 28-29 April 2008

Invited speakers include: Dr Nicolas Galtier, Professor Olivier Gascuel, Dr Mark Holder, Professor John Huelsenbeck, Dr Ari Loytynoja, Professor Rasmus Nielsen, Professor Mark Pagel, Dr Tal Pupko, Professor Bruce Rannala, Professor Allen Rodrigo, Dr

Alexandros Stamatakis, Dr Marc Suchard, Professor Jeff Thorne, Professor Arndt von Haeseler, Dr Simon Whelan and Professor Ziheng Yang FRS.

Royal Society website and registration details: <http://royalsociety.org/event.asp?id=6067> Beautifully-produced flyer for you to give to all your friends: http://www.ebi.ac.uk/goldman-srv/tmp/RS_Flyer_2.pdf

The rapid growth of genetic sequence data has provided much-needed power for resolving controversial species relationships and studying the evolutionary process, but has also posed many statistical and computational challenges to the field. This meeting will bring together scientists with a diverse range of backgrounds, and in particular researchers actively developing statistical methods and computational algorithms used in modern phylogenetics software.

Statistical and computational challenges facing the field will be discussed in the meeting, for example, efficient tree search algorithms under likelihood, Markov chain Monte Carlo algorithms for Bayesian phylogenetics, estimation of species divergence dates by incorporating uncertainties in the fossil record and statistical tests of phylogenies.

Organisers: Nick Goldman and Ziheng Yang

Nick Goldman tel: +44-(0)1223-492530 EMBL - European Bioinformatics Institute fax: +44-(0)1223-494468 Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK

goldman@ebi.ac.uk goldman@ebi.ac.uk

Seattle EarlyCareer Female EvolutionaryBiologists Oct19-22

Dear Colleagues,

We are writing to introduce you to WEBS (Women Evolving Biological Sciences), an annual three-day symposium aimed at addressing the retention of female scientists and issues related to the transition of women from early career stages to tenure track positions and leadership roles in academic and research settings. The inaugural WEBS symposium in October 2007 was a huge success. Early career participants as well as our senior scientist panelists reported feeling inspired and equipped with new connections and tools that they expect will help them in their career in the years to come. WEBS targets early career women in the Biological Sci-

ences with an emphasis on ecology and evolutionary biology. In particular, it focuses on women who have earned their doctoral degrees within the past two to eight years and who do not have tenure in order to address the critical transition period from graduate studies and post-doctoral positions to permanent research and teaching positions. The symposia provide a forum for professional development, including awareness and improvement of academic leadership skills; opportunities to establish mentoring relationships; and resources for developing professional networks. The 2008 symposium will be held at the Pack Forest Conference center near Seattle, WA from October 19-22, 2008.

Please visit our website (<http://www.webs.washington.edu>) for details and application materials. Feel free to contact us with any questions you might have (webs@u.washington.edu). Applications will be due April 15, 2008.

Sincerely, Samantha Forde, Ph.D. Claire Horner-Devine, Ph.D. Joyce Yen, Ph.D. University of California Santa Cruz University of Washington University of Washington

forde@biology.ucsc.edu

Slovakia PlantSystematics July

Following a really successful meeting of the International Organisation of Plant Biosystematists (IOPB, now interest group of the International Association for Plant Taxonomy) in Valencia in 2004 (www.jardibotanic.org/iopb.html) the next IOPB meeting in July 2008 will be held in the Vysoke Tatry Mts. in Slovakia. The meeting will be devoted to the Evolution of Plants in Mountainous and Alpine Habitats. We would like to cover a wide span of topics ranging from the traditional biosystematic studies to the application of the most advanced molecular techniques addressing evolutionary, phylogenetic, phylogeographic, ecological and other questions. The idea is to present the results of studies of the mountain and alpine flora from different parts of the world.

Following the symposium there will be a possibility to stay for few days in the Vysoke Tatry Mts. and visit some interesting localities of the mountain and alpine flora in the Tatry National Park.

The 2008 symposium in the Vysoke Tatry Mts. is organised by the Institute of Botany of the Slovak

Academy of Sciences, Slovak National Taxonomic Facility, and the Department of Botany, Charles University in Prague in cooperation with the International Association for Plant Taxonomy and International Organisation of Plant Biosystematists.

We invite you to take part at this meeting, which will be an excellent opportunity to become aware of the most recent developments in the study of the high mountain flora, but also to see interesting examples of the Carpathian flora just few metres from the symposium venue.

For further information and registration please visit the symposium web page www.guarant.cz/iopb2008

Karol Marhold

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Tel.: (+421) 2 5942 6128 Fax: (+421) 2 5477 1948
E-mail: karol.marhold@savba.sk <http://ibot.sav.sk/Karol01.html> see also <http://www.iopb.org> &

Department of Botany, Charles University, Benatska 2, CZ-128 01 Praha, Czech Republic
Fax: (+420) 2 2195 1645

Karol Marhold <karol.marhold@savba.sk>

UIowa Evolution of Sex Jun16-19

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

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

<http://cgg.biology.uiowa.edu/sexrec> The Roy J. Carver Center for Comparative Genomics and the Department of Biology at the University of Iowa announces an international conference on the evolution of sex & recombination. This conference will immediately precede the 2008 Evolution meeting taking place in nearby Minneapolis, Minnesota (June 20-24).

Talks will be given by invited speakers at both the junior and senior level. There will also be opportunities for contributed talks and posters to be given by conference attendees at all levels of seniority. A number of travel awards (10-15) will be provided to deserving students and postdocs.

Topics will include: -Advantages of sexual reproduction

-Experimental evolution of sex -Estimating recombination rates -Mating types & sex determination -Linkage, selection & population size -Sex chromosomes -Sex & pathogenesis -Sexual selection -Sexual conflict

Confirmed speakers include: Philip Awadalla University of Montreal Doris Bachtrog University of California, San Diego Graham Bell McGill University Rhona Borts University of Leicester Bernardo Carvalho Universidade Federal do Rio de Janeiro Andy Peters University of Wisconsin-Madison Brian Charlesworth University of Edinburgh Nick Colegrave University of Edinburgh Tim Cooper University of Houston Ursula Goodenough Washington University-St. Louis Joe Heitman Duke University Michael Hood Amherst College Alex Kondrashov University of Michigan Curt Lively Indiana University Stephanie Meirmans University of Bergen Bill Rice University of California, Santa Barbara Isa Schön Royal Belgian Institute of N.S. Marcy Uyenoyama Duke University Jerry Wilkinson University of Maryland Cliff Zeyl Wake Forest University

Check the conference website for details regarding registration, accommodation, etc.: <http://ccg.biology.uiowa.edu/sexrec/registration.php> A symposium issue to be published in Journal of Heredity is being planned.

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

On behalf of the organizing committee,

John Logsdon –

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

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

john-logsdon@uiowa.edu john-logsdon@uiowa.edu

nual Meeting, Vancouver, BC, May 11-14

We are pleased to announce that the CSEE annual meeting will be held at the University of British Columbia from May 12-14 2008 (opening reception on May 11). Registration is now open at:

<http://www.ecoevo.ca/ubc2008/en> Please register early to obtain the best rates and to be eligible for student travel awards. Registration closes March 1 2008. Registration fees remain very low for members of CSEE, and you may pay your 2008 membership at the same time that you register.

We hope to see you there!

Local Organizing Committee: Brad Anholt (University of Victoria), Leah Bendell-Young (Simon Fraser University), Kathy Martin (UBC), Blake Matthews (UBC), Douglas Morris (Lakehead University), Sally Otto (UBC), Jon Shurin (UBC)

INSCRIPTION EN COURS

Société Canadienne d'Écologie et d'Évolution Réunion annuelle 2008, Vancouver, C.-B., 11-14 mai

Nous avons le plaisir d'annoncer la tenue de la réunion annuelle de la SCEE à l'Université de Colombie-Britannique du 12 au 14 mai (réception d'ouverture le 11 mai). L'inscription est maintenant en cours à:

<http://www.ecoevo.ca/ubc2008/fr> Veuillez vous inscrire à l'avance pour bénéficier des meilleurs tarifs et afin d'être éligible aux bourses de voyage pour étudiants. L'inscription prend fin le 1 mars 2008. Les frais d'inscription sont très avantageux pour les membres de la SCEE et vous avez l'option de payer vos frais d'adhésion lors de votre inscription à la réunion annuelle.

En espérant vous y voir!

Comité organisateur: Brad Anholt (University of Victoria), Leah Bendell-Young (Simon Fraser University), Kathy Martin (UBC), Blake Matthews (UBC), Douglas Morris (Lakehead University), Sally Otto (UBC), Jon Shurin (UBC)

otto@zoology.ubc.ca otto@zoology.ubc.ca

Vancouver CanadianSocEcolEvol
May11-14

Winchester ArtificialLife and
Evolution Aug5-8

REGISTRATION NOW OPEN

Canadian Society for Ecology and Evolution 2008 An-

Dear Brian,

Presumably you get a lot of this sort of request, but was wondering whether you would allow us to announce an upcoming conference on the Evolution Directory? The conference is ALIFE XI, the 11th International Conference on Artificial Life, which some colleagues and I are organizing for this summer.

As you may know, Artificial Life investigates the fundamental properties of living systems through simulating and synthesizing biological entities and processes in artificial media. As such it engages with many interesting questions in theoretical biology, evolutionary biology, ecology, synthetic biology, computational biology, etc.

A general call for participation follows, but some points of note are:

The conference has some great keynote speakers: Stuart Kauffman, Eva Jablonka, Peter Schuster, Takashi Ikegami and Andrew Ellington, see <http://www.alifexi.org/keynotes/> It allows for abstract as well as full paper submission, but with no distinction in presentation time at the conference (details below).

The organisers are committed to keeping the costs of registration and accommodation as low as possible. Details will be available shortly at <http://www.alifexi.org/registration/> The event will perhaps be especially beneficial to PhD students who would benefit from exposure to a wider range of biological ideas.

Several themed sessions on biological issues are scheduled: microbial systems, major transitions, synthetic biology, cell signalling, etc. (more details below).

If you see this as an appropriate meeting to be announced on EvoDir, we'd be very grateful for the help in publicizing it.

Thanks very much for your time, Jason Noble.

CFP:

–Please forward this call responsibly.–

2nd CALL FOR PAPERS: Artificial Life XI

The Eleventh International Conference on the Simulation and Synthesis of Living Systems

5th - 8th August 2008, Winchester, UK www.alifexi.org

You are invited to submit papers to the upcoming Eleventh International Conference on Artificial Life, to be hosted by the University of Southampton and held in Winchester, UK.

NEWS - Keynote speakers announced! - ALIFE XI goes online and open-access with MIT Press! - ALIFE XI themes announced! - ALIFE XI wiki and discussion forums launched!

See www.alifexi.org for details, and www.alifexi.org/new4alifexi/ for information.

IMPORTANT DATES - 29 February 2008: Full paper submission deadline - 18 April 2008: Notice of acceptance for full papers - 25 April 2008: Abstract submission deadline - 9 May 2008: Camera ready deadline - 5-8 August 2008: Conference dates

OVERVIEW Artificial life investigates the fundamental properties of living systems through simulating and synthesizing biological entities and processes in artificial media. Summer 2008 will see the international Alife conference hosted by the University of Southampton, UK, bringing the meeting to Europe for the first time in its 21-year history. Over the last two decades, some of the highly speculative ideas that were discussed at the field's inception have matured to the extent that new conferences and journals devoted to them are being established: synthesising artificial cells, simulating massive biological networks, exploiting biological substrates for computation and control, and deploying bio-inspired engineering are all now cutting-edge practice. The ALIFE XI conference provides an opportunity for those working across these topics to get together and exchange ideas and results. To this end, the conference will present a selection of the best current work in the field, highlight new directions for investigation, and present high-profile keynote speakers.

Papers are welcome in all areas of the field, including:
 * Synthesis and origin of life, self-organization, self-replication, artificial chemistries
 * Evolution and adaptation, evolutionary dynamics, evolutionary games, co-evolution, major evolutionary transitions, levels of selection, ecosystems
 * Development, differentiation, and regulation; generative representations
 * Synthetic biology
 * Self-organizing technology, self-computing and computational ecosystems
 * Unconventional and biologically inspired computing
 * Bio-inspired robots and embodied cognition, autonomous agents, evolutionary robotics
 * Collective behaviour, communication, cooperation
 * Artificial consciousness; the relationship between life and mind
 * Philosophical, ethical, and cultural implications
 * Mathematical and philosophical foundations of Alife, new and creative syntheses

All authors are encouraged to explain how their work sheds light on the fundamental properties of living systems and makes progress on the important open questions identified at previous meetings.

Several artificial life themes have been proposed as live research

— / —

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

GradStudentPositions

ColoradoStateU SexualSelection	12	UCalgary EvolutionaryEcology	20
EAWAG Switzerland 2 HostParasiteInteractions ...	13	UFlorida GeneticsGenomics	20
ETH Zurich AlpineGeneticAdaptation	13	UFlorida LifeHistoryEvolution	21
IowaStateU SexGenomics	59	UGuelph rDNA Evolution	22
KentStateU SexDifferencesInRecombination	14	UJyvaskyla EvolutionaryBiol	22
LaurentianU EvolutionaryBiology	15	ULausanne EvolutionSymbiosis	23
LaurentianU MolEvol	15	UManchester EvolGenomics	23
PennsylvaniaStateU MarineEvolution	16	UMunich EvolEcolSystematics	24
StAndrews SystemsBiology	16	UNottingham SticklebackSpeciation	24
Sundsvall ConservationGenetics	17	UOttawa Sexual selection	25
TrentU CarnivoreEvolution	17	UOxford Evolution Of Virulence	25
TrentU PathogenCoEvolution	18	VanderbiltU Evolutionary Diversification	26
UAlaskaAnchorage ArcticMustardFlowerColor	19		
UBath BacterialORFans	19		

ColoradoStateU SexualSelection

* PhD Student in Evolutionary Sexual Selection *

A graduate student position is available in the lab of Lisa Angeloni in the Biology Department at Colorado State University. Motivated students who are interested in working on mating behavior and sexual selection in Trinidadian guppies are encouraged to apply. Guppy populations experience different levels of predation pressure in their natural habitats, which affects male color patterns, life history strategies and female preferences for male traits. In collaboration with Dr. Cameron Ghalambor, we will investigate how reproductive behavior depends on several factors, including the history of predation in the natural population, the presence of predator cues during development and the presence of predator cues during mating. There are many possible questions to ask with this system, and the graduate student will have the opportunity to determine the scope of the project.

Graduate students will have the opportunity to partici-

pate in the interdisciplinary Graduate Degree Program in Ecology at CSU. Please send a statement of interest and a CV or resume including GPA and GRE scores, research experience and research interests by February 11, 2008 to Lisa Angeloni (angeloni@lamar.colostate.edu). Reference letters for top candidates will be solicited at a later date. Applications will be reviewed as they come in and may also be reviewed after the target date if the position has not been filled.

Lisa Angeloni Assistant Professor of Biology Colorado State University Fort Collins, CO 80523-1878 (970) 491-0562 angeloni@lamar.colostate.edu <http://rydberg.biology.colostate.edu/angelonilab/Site/-Home.html> –

Lisa Angeloni Assistant Professor Department of Biology Colorado State University E441 Anatomy-Zoology Building Fort Collins, CO 80523-1878 Phone: 970-491-0562 Fax: 970-491-0649

Lisa Angeloni <angeloni@lamar.colostate.edu>

EAWAG Switzerland 2 HostParasiteInteractions

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

The Department Aquatic Ecology (groups of Piet Spaak, respectively Bas Ibelings) seeks for

2 PhD students in evolution of host-parasite interactions

The PhD students will participate in a collaborative research project GEDIHAP with host-parasite researchers from the ETH Zürich and the Swiss Federal Institute for Forest Snow and Landscape Research, WSL, to study the influence of environmental factors (natural and human induced) on host - parasite interactions. In the first project a hybrid *Daphnia* species complex and its parasites are studied. We are interested in the population genetics of the host as well as of the parasite. Experimentally genotype (host) x genotype (parasite) x environment interactions will be studied. In the second project the impact of 2 environmental stress factors (climate change and water pollution) on the co-evolution of the diatom *Asterionella formosa* and parasitic chytrid fungi is studied.

For this, from CCESS (Competence Center Environment and Sustainability of the ETH Domain) financed project, we are looking for 2 highly motivated candidates with interests in evolutionary biology, population genetics and host-parasite interactions. Although field work is also involved, most of the work will be done in the lab (conducting experiments and screening hosts and parasites using molecular tools). Some of the work will be done in Germany (*Daphnia*) and the Netherlands (*Asterionella*).

We offer a stimulating research environment in a lively and social institute in Dübendorf (near Zürich). In a department with several other evolutionary and ecological research groups with a focus on host parasite interaction. Both PhD candidates will be actively involved in workshops and courses organized within the GEDIHAP framework. The position will be for a period of three years, and should start as soon as possible (April 2008 or soon thereafter). The ideal candidate has both experimental as well as molecular skills (PCR,

sequencing, genotyping). A Diploma or Master degree (or equivalent) in biology or related subject is necessary for admission. The working language in the group is English.

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

Please submit your application by 1 March 2008 as one PDF file to Sandra Isenring, Eawag, Human Resources Department: recruiting@eawag.ch, indicating reference number 084401. For further information, consult <http://www.cces.ethz.ch/projects/feh/GEDIHAP> or contact Piet Spaak (Tel. +41 44 823 5617), spaak@eawag.ch or Bas Ibelings (Tel + 41 41 349 2174), bas.ibelings@eawag.ch

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

ETH Zurich AlpineGeneticAdaptation

The Swiss Federal Institute for Forest, Snow and Landscape Research WSL is part of the ETH Domain. Approximately 500 people work on topics related to the sustainable use and protection of the environment and on an integrated approach to handling natural hazards. Species respond to climate change by either adaptation or migration. The Research Unit Ecological Genetics and Evolution is thus investigating the genetic adaptation of alpine species to temperature as well as their migration capacity by using molecular methods. We are searching for a

PhD Student in Ecological Genetics

You will identify genetic markers of adaptive significance by using genome scans on *Arabis alpina* and *Arabidopsis thaliana* and by transplant experiments in alpine environments, analyze the data, co-operate with other groups within the CCES-BIOCHANGE initiative and write scientific publications. Data from a pre-project are at your disposal.

Your profile: Master thesis in population or ecological genetics of plants, experience with genetic lab techniques and statistics, fluent in written and spoken English, used to work in alpine terrain.

Interested? Please send your complete application

including a photo, using reference number 513 to Mrs. Monika Huber, WSL, Human Resources WSL, Zuercherstrasse 111, CH-8903 Birmensdorf, Switzerland. Dr Rolf Holderegger, tel. +41 (0)44 739 25 27 or Dr Felix Gugerli, tel. +41 (0)44 739 25 90, will be happy to answer any questions or offer further information.

Felix Gugerli Künzle, PhD Biologist / Group leader Swiss Federal Research Institute WSL Research Unit Ecological Genetics & Evolution Zuercherstrasse 111 CH-8903 Birmensdorf

SWITZERLAND

phone: +41-(0)44-739-2590 fax: +41-(0)44-739-2215
<http://www.wsl.ch/staff/felix.gugerli/> Felix Gugerli
 <felix.gugerli@wsl.ch>

IowaStateU SexGenomics

PhD GRADUATE STUDENT POSITION in Genomics at Iowa State University.

A PhD graduate student position is available to study the gene expression response to naturally fluctuating temperature in turtles with alternative sex determining mechanisms. The position is part of an NSF-funded project in the laboratory of Nicole Valenzuela, Department of Ecology, Evolution, and Organismal Biology, Iowa State University. The project calls for field and laboratory developmental experiments to help elucidate the effect that naturally-fluctuating temperature has on the expression of genes involved in gonadal formation in turtles with temperature-dependent and genotypic sex determination, and how males and females are produced in nature. For additional information concerning this and other research projects, please refer to the laboratory web site (<http://www.public.iastate.edu/~nvalenzu>).

Prospective candidates should have strong academic records and some research experience is preferred. Review of applications will begin immediately and continue until a candidate is selected.

Iowa State University offers a stimulating environment and excellent resources for ecological, evolutionary, developmental, and molecular biologists through its interdepartmental programs in Ecology and Evolutionary Biology <http://www.grad-college.iastate.edu/-EEB/> and Genetics <http://www.genetics.iastate.edu/> . To apply, please contact Dr. Nicole Valenzuela

(nvalenzu@iastate.edu), and send materials to the EEB or IG programs at Iowa State University.

Dr. Nicole Valenzuela Assistant Professor Dept. of Ecology, Evolution, and Organismal Biology Iowa State University 239 Bessey Hall Ames, IA 50011 (515) 294-1285 <http://www.public.iastate.edu/~nvalenzu/>
nvalenzu@iastate.edu

KentStateU

SexDifferencesInRecombination

Evolution of Sex Differences in Recombination Rates

One doctoral student position is available for a motivated individual to study the evolution of behavior in the Biological Sciences Department at Kent State University in Ohio.

The project will focus on the evolution of sex-differences in recombination rates on autosomes using *Drosophila ananassae* as a model system (see my web page for background) and will involve lab work (including molecular genetics and immunostain-based cytology) and some theory: - Quantitative PCR will be used to measure sex-differences in expression of genes known to affect recombination in females. - This will involve primer design for candidate genes. - Immunostaining techniques will be developed to show the centromere, synaptonemal complex and cross-over events in *D. ananassae* meiotic cells. - Models for how sex differences in recombination rates can evolve will be developed. - Predictions from several hypotheses will be tested including the hypothesis that sexual selection causes the observed sex-differences in recombination rates.

Previous experience in animal behavior, with *Drosophila*, and/or with molecular techniques or immunostaining would be an asset; a strong interest in evolution and behavior is required.

Position will remain open until filled.

For more information contact:

Patrick Lorch Biological Sciences Dept. Kent State University 256 Cunningham Hall Kent, OH 44242-0001 USA O: 330-672-7888 Lab: 330-672-2514 <http://bioweb.biology.kent.edu/facultypages/lorch/lorch.html>
 Patrick Lorch <plorch@kent.edu>

LaurentianU EvolutionaryBiology

MSc Position at Laurentian University, Ontario

Evolutionary Ecology and Amphibian Emerging Infectious Diseases

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

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

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

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

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

Dr. David Lesbarrères Associate Professor & Graduate Coordinator

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

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

dlesbarreres@laurentian.ca dlesbarreres@laurentian.ca

LaurentianU MolEvol

Graduate Student Position: The Molecular Evolution of Metabolic Enzymes and Networks

Merritt Lab, Department of Chemistry & Biochemistry, Laurentian University

Graduate positions to study the molecular evolution of metabolic enzymes and networks are available in the Merritt Lab in the Department of Chemistry & Biochemistry, Laurentian University (<http://web.mac.com/tjsmerritt>). I welcome applicants for both MSc and PhD positions to start September 2008. Current projects in my lab use naturally occurring and laboratory generated genetic variation, sequence comparisons, and direct experimentation to quantify interactions among enzymes and downstream phenotypes. My research program also examines changes in biochemistry that result from genetic variation and the physiological impact of these changes. Successful applicants will be expected to develop research projects of their own while building current projects in the lab, especially targeting novel phenotypes and functional variation across species. Student interactions and collaborations across both the Departments of Chemistry & Biochemistry and Biology will be encouraged.

Laurentian University is a bilingual institution offering courses in both French and English, with the fastest growing research program in Canada. The Merritt Lab is funded by grants from the Natural Sciences and Engineering Research Council (NSERC) and the Canadian Foundation for Innovation (CFI) Leaders Opportunity Fund. The city of Sudbury is one of the globe's greatest ecological recovery stories, includes over 300 lakes, and offers immediate access to wilderness and outdoor recreation activities.

Applicants should be independently motivated, have a good academic record, and have demonstrated both an interest in and aptitude for research. Please send an application with unofficial transcripts, a one page CV including contact information for two references, to: Thomas Merritt (tmerritt@laurentian.ca), Department of Chemistry & Biochemistry Laurentian University 935 Ramsey Lake Road Sudbury, ON, P3E 2C6, Canada.

Thomas Merritt, PhD Assistant Professor Department of Chemistry and Biochemistry Laurentian University

935 Ramsey Lake Road Sudbury, Ontario P3E 2C6
Canada e-mail: tmerritt@laurentian.ca phone:705-675-
1151 ext. 2189

tmerritt@laurentian.ca tmerritt@laurentian.ca

PennsylvaniaStateU MarineEvolution

Graduate Assistantships (M.Sc. or Ph.D.) are available in the labs of Iliana Baums and Todd LaJeunesse at the Pennsylvania State University in the areas of marine ecology and evolution. Prospective candidates should have strong academic records and some research experience is preferred. In addition to laboratory bench work, periodic field expeditions are an important part of our research and involve collecting and experimental work using SCUBA often in remote locations. Motivation, self-discipline, creativity, and good interpersonal skills are essential.

Baums and her students work on dispersal, connectivity and reproductive biology of marine organisms, with a focus on tropical corals. Molecular tools are used to address ecological and evolutionary questions with conservation applications. Currently, we are studying the effects of climate change on dispersal in corals and other reef taxa. Research on conservation genetics of elkhorn corals in the Caribbean includes quantification of heritable genetic variation and the role of asexual reproduction. (<http://www.bio.psu.edu/people/faculty/baums/Index.htm>.)

LaJeunesse and his students work primarily on the ecology and evolution of endosymbiotic microbes. Research is currently focused on a diverse group of photosynthetic dinoflagellates that live in the tissues of corals and related taxa. Molecular approaches are utilized to investigate the biodiversity, host-symbiont specificity, and geographic distributions in order to address questions related to co-evolutionary processes and to learn how these systems respond to severe environmental change.

Penn State (<http://www.psu.edu/>) offers a stimulating environment and excellent resources for ecological and evolutionary biologists through the Huck Institute for the Life Sciences (www.huck.psu.edu). PSU is a world-renown research institution with a strong reputation in the field of evolutionary genetics through both the Institute of Molecular Evolutionary Genetics and the Intercollege Graduate Program in Genet-

ics (<http://www.genetics.psu.edu/>) many members of which belong to the Department of Biology (<http://www.bio.psu.edu/home>). The interdepartmental program in Ecology brings together 49 faculty from across the campus and has a very active graduate student organization (<http://www.ecology.psu.edu/>). Students may apply through the Department of Biology or through Interdepartmental Programs by Dec 31, 2007 for admission in Fall of 2008.

For more information contact Iliana B. Baums, Ph.D. Assistant Professor Department of Biology The Pennsylvania State University 208 Mueller Laboratory University Park, PA, 16802 baums@psu.edu <http://www.bio.psu.edu/people/faculty/baums/> Todd LaJeunesse, Ph.D. Assistant Professor Department of Biology The Pennsylvania State University 208 Mueller Laboratory University Park, PA, 16802 tcl3@psu.edu
ibb3@psu.edu

StAndrews SystemsBiology

Dear EvolDir Members,

Please share the below PhD studentship advertisement with any interested parties. (And yes, I have sent out two messages – this is for a different studentship).

Thank you, Anne Smith

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

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

Gene and protein networks related to breast cancer

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

In this studentship, you will examine gene and protein regulatory networks related to breast cancer. You will both build computational models and perform biological experiments. The project will lever two systems biology methods-dynamical systems modelling (DSM) of large cellular networks and Bayesian network (BN) inference of network structure-to produce data-driven models of gene and protein regulation networks relevant to breast cancer. DSM handles well the sparsity of data; however, networks are manually described and uniqueness is difficult to verify. BNs complement this by recovering network structure de novo from data and predicting several alternative structures; however, they have high data demands. You will use these two complementary methods to suggest structures consistent with the data and to identify the key experiments required to discriminate between alternative solutions.

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

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

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

Sundsvall ConservationGenetics

PhD-position

Mid Sweden University with about 15 000 students and 1 000 employees have its main activities in Härnösand, Sundsvall, and Östersund. Mid Sweden University offers education and conduct research connected to conservation biology aiming to contribute to the develop-

ment of a sustainable forestry.

Mid Sweden University and the Department of Natural Sciences, Campus Sundsvall looks for a PhD-student For the project “Population establishment of wood fungi on fire influenced pine wood” ref.nr MIUN 2007/1892

Research task: After more than 100 years of efficient fire control, many fire associated species have strongly declined. Species living on pine wood has experienced severe fragmentation and many occur in isolated populations where the ability to disperse and establish is crucial for populations viability. The project aims to study the colonization of wood fungi after forest fire. To identify the species we will use both traditional methods and newly developed molecular approaches. As a PhD-student you will take part in developing these tools to study the population dynamics wood fungi.

Qualifications: The applicant for the 4-year position (aiming for a PhD-degree) should have a bachelors degree in biology related to the research field described above. For example knowledge of wood fungi, population dynamics and experience from laboratory work with DNA-applications are valued.

Position place: Sundsvall

Information on the position is given by Professor Bengt Gunnar Jonsson tfn. +46 (0)60-148941, e-mail bengt-gunnar.jonsson@miun.se Worker Union representative: Lars Nilsson, SACO, +46 (0)60-14 88 32 and Lollo Ljuslin, ST, +46 (0)63-16 57 14. Application: Welcome with you application at latest 24 January 2008 to: Registrar, Mid Sweden University, SE-851 70 Sundsvall. Include a verified CV and other documentation you considered of value.

Svante Holm svante.holm@miun.se Mid Sweden University +46 (0)60-148537 Sweden

Svante.Holm@miun.se Svante.Holm@miun.se

TrentU CarnivoreEvolution

Conservation/Landscape Genetics of North American Carnivores

I will have positions available for MSc and/or PhD candidates to investigate the conservation/landscape genetics of North American carnivores, primarily focusing on North American black bears, but with opportunities to investigate other species.

Resolving the underlying factors influencing the movement of animals and genetic variation across complex landscapes is critical to understanding their ecology, evolution, effective conservation and management. Using a landscape genetics approach, correlations between genetic discontinuities (gene flow or local adaptation) with landscape and environmental features (mountains, lakes, road systems) can be revealed. New statistical and analytical tools are now emerging to enhance our understanding of the distribution of genetic variation on finer scales and statistically test hypotheses (e.g. quantify barrier effects of roads/unsuitable habitat and certain forestry practices) using detailed GIS-based geographical and environmental data, along with high-resolution molecular markers. Black bears are harvested for sport, food, fur, and other derivatives (bones, urine, and gall for traditional medicines). It is not always clear how many animals, and from what populations, we can harvest in a sustainable manner. This project involves using DNA profiling to define populations and non-invasively census black bears using baited hair-traps. These same data will be applied to further our understanding of black bear ecology through landscape genetics and enhance DNA databanks to enforce wildlife laws in illegal harvest and trade.

Research will take place within the new DNA Building at Trent University that houses the Natural Resources DNA Profiling and Forensics Centre and the Wildlife Research and Development Section of the Ontario Ministry of Natural Resources. This venue provides an exciting collaborative research environment with field and lab-based researchers and unsurpassed infrastructure for wildlife genetic and wildlife disease research. Refer to the websites below for further information. < <http://web.nrdpfc.ca> > < <http://www.wildliferesearch.mnr.gov.on.ca/spectrasites/internet/wrds/wrds.cfm> > < <http://www.trentu.ca/dnabuilding> >

Candidates are expected to commence their studies between May - September 2008. Interested individuals should provide a recent CV with referee contact information, copies of any publications, approximate GPA, and a brief description of their interest in the position. A review of applications will begin on February 1, 2008 and continue until the positions are filled.

Contact: Dr. C. J. Kyle Research Chair in Wildlife Genetics and Forensics Natural Resources DNA Profiling and Forensics Centre Trent University, 2140 East Bank Drive Peterborough, ON, K9J 7B8 chris.kyle@nrdpfc.ca <<mailto:chris.kyle@nrdpfc.ca>>

chris.kyle@nrdpfc.ca

TrentU PathogenCoEvolution

Coevolutionary Mechanisms in Pathogen/Vector Complexes

I will have positions available for MSc and/or PhD candidates to investigate coevolutionary mechanisms using the raccoon rabies virus and its vectors as a model system.

The dynamic interaction between species and their pathogens plays a pivotal role in their adaptation, evolution, and persistence. Conventional belief suggests that rabies is a lethal disease with no potential for evolution within its hosts. Disease challenge and vaccination experiments, however, indicate that variability exists in the immune response of raccoons to rabies. This project will involve an investigation of selective responses of raccoons to rabies via genes that are intimately associated with the initiation of an immune response and studied in relation to the absence, presence and duration of rabies exposure. These data will be used to empirically test theories of balancing selection, frequency-based selection, the geographic mosaic theory of co-evolution, and contribute to our understanding of mechanisms involved in disease spread and maintenance.

Research will take place within the new DNA Building at Trent University that houses the Natural Resources DNA Profiling and Forensics Centre and the Wildlife Research and Development Section of the Ontario Ministry of Natural Resources. This venue provides an exciting collaborative research environment with field and lab-based researchers and unsurpassed infrastructure for wildlife genetic and wildlife disease research. Refer to the websites below for further information. < <http://web.nrdpfc.ca> > < <http://www.wildliferesearch.mnr.gov.on.ca/spectrasites/internet/wrds/wrds.cfm> > < <http://www.trentu.ca/dnabuilding> >

Candidates are expected to commence their studies between May - September 2008. Interested individuals should provide a recent CV with referee contact information, copies of any publications, approximate GPA, and a brief description of their interest in the position. A review of applications will begin on February 1, 2008 and continue until the positions are filled.

Contact: Dr. C. J. Kyle Research Chair in

Wildlife Genetics and Forensics Natural Resources
DNA Profiling and Forensics Centre Trent University,
2140 East Bank Drive Peterborough, ON, K9J 7B8
chris.kyle@nrdfpc.ca <mailto:chris.kyle@nrdfpc.ca>

chris.kyle@nrdfpc.ca

UAlaskaAnchorage ArcticMustardFlowerColor

Arctic Mustard Flower Color Evolution

Fully Funded MS Position in Flower Color Evolution
in the Arctic: Integrating Genomic and Ecological Research

Dear Prospective Students,

We are currently recruiting a new Master's Degree student to study ecological genomics and reproductive ecology of the arctic mustards *Parrya* and *Cardamine* for an NSF-funded International Polar Year project. The student will be responsible for investigating spatial patterns of flower color polymorphisms across Alaska and their relationships to pollinator preferences and non-pollinator agents of selection (climate, herbivory, etc.). The student will also work closely with Dr. Justen B. Whittall, assistant professor of Biology at Santa Clara University, who will be isolating and quantifying expression of the anthocyanin biosynthetic pathway genes and comparing these results to whole-genome microarray hybridizations. The research will involve extensive fieldwork from southern Alaska to the North Slope, beginning this summer (2008). Support for summer research is included for the first year, followed by a full year of support the second year, including a tuition waiver. Previous experience in pollination ecology or molecular ecology is preferred.

The University of Alaska Anchorage is Alaska's largest university whose Biological Sciences Department faculty has nearly doubled since 2000. The UAA Master's Degree is a research-intensive, thesis-based degree program. This MS studentship in the UAA Biological Sciences Department affords unique opportunities to interact closely with the Alaska Natural Heritage Program, Alaska EPSCoR, and the faculty and research at the University of Alaska Fairbanks. More information about the Biological Sciences Department at the University of Alaska Anchorage can be found at <http://www.uaa.alaska.edu/biology/>. If interested, please send a brief statement of interest and CV to Matt Carl-

son (afmlc2@uaa.alaska.edu) and Justen B. Whittall (jwhittall@scu.edu) by February 20, 2008.

Matthew L. Carlson Assistant Professor - Biological Sciences Department & Program Botanist - Alaska Natural Heritage Program University of Alaska Anchorage 707 A Street Anchorage, Alaska 99501 Phone: (907) 257-2790 afmlc2@uaa.alaska.edu

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Justen B. Whittall Assistant Professor Department of Biology Santa Clara University Santa Clara, CA 95053 Phone: (408) 554-4808 www.jbwhittall.com jwhittall@scu.edu

Justen Whittall <jwhittall@scu.edu>

UBath BacterialORFans

Bioinformatics PhD available on bacterial "ORFans"

This is a collaborative project supervised jointly by Dr Edward Feil (University of Bath, UK), and Dr Dawn Field (University of Oxford, UK).

Our collection of genomes and metagenomes continues to grow at an increasing pace. These data provide great potential for understanding both evolutionary and ecological processes, but new software tools and statistical approaches are required to manage and to fully exploit the datasets. Each newly sequenced genome reveals a number of previously unknown genes (?ORFans?). These genes are likely to be of central importance to bacterial adaptation, yet they remain largely understudied. You will join the microbial adaptation group led by Dr Ed Feil at the University of Bath, and the evolutionary bioinformatics group at CEH Oxford led by Dawn Field, to further develop comparative genomic software to understand the evolutionary significance of newly identified hypothetical gene sequences. It is envisaged that most of your time will be spent in Oxford. You will use your programming and database skills to extend the current infrastructure, including the provision of a public web server from cached and uploaded data sets. In addition to gaining extensive bioinformatics expertise, the project will also involve a strong appreciation of bacterial population biology and microevolution. In undertaking these studies you will work with a range of existing collaborators in the USA and Europe and build new suitable collaborations in the course of your PhD research.

This project has funding associated with it. It is a 4-year studentship. Eligible candidates are UK or EU applicants, who have been resident in the UK for at least the 3 years prior to the start of the research programme.

It is envisaged that this studentship will start in early 2008.

Applicants can download an application form, together with advice on the application procedure, from the University of Bath website at <http://www.bath.ac.uk/-grad-office/apply/index.html>. Alternatively, please contact the Postgraduate Administrator, Dr Emma Lawrence for further information and advice on the project and the application procedure.

Alternatively please contact Ed Feil directly at e.feil@bath.ac.uk.

Recent Publications:

G.A. Wilson, E.J. Feil, A. Lilley & D. Field 2007 The large-scale comparative genomic ranking of lineage-specific predicted proteins in bacterial and archaeal genomes. *PLoS ONE*. 2(3):e324
 Wilson, G.A., Feil, E.J., Field, D. 2005. Databases and Software for the comparison of prokaryotic genomes. *Microbiology*. 151:2125-32.
 Wilson, G.A., Bertrand, N., Patel, Y., Hughes, JB, Feil, E.J., Field, D. 2005 Orphans as taxonomically restricted and ecologically important genes. *Microbiology*. 2005 151:2499-501

e.feil@bath.ac.uk e.feil@bath.ac.uk

UCalgary Evolutionary Ecology

I am currently seeking a graduate student (PhD or exceptional MSc) to start in Sept. 2008 or Jan. 2009. I am seeking bright, motivated, independent, question-driven students interested in any area of evolutionary, population, or community ecology. Students with strong quantitative skills and/or an interest in relating theory to data are particularly encouraged to apply. Ongoing and planned research in the lab uses both mathematical theory and a variety of lab and field systems (microbial microcosms, aquatic mesocosms, alpine plants, rocky intertidal communities) to address questions concerning population dynamics, community dynamics, and adaptive evolution in an ecological context.

Full funding of approximately \$21,000/year is guaranteed for 2 years (MSc) or 4 years (PhD) through a com-

bination of TAships and RAships.

The University of Calgary is a large research university in a growing city (pop. 1 million) located close to the beautiful Canadian Rockies. The Dept. of Biological Sciences has approximately 140 graduate students and 50 faculty, with approximately half the faculty pursuing research in ecology and evolution.

For more information on my lab see <http://homepages.ucalgary.ca/~jefox/Home.htm> < <http://homepages.ucalgary.ca/%7Ejefox/Home.htm> >

Interested students should contact me via email, including a cover letter describing background and interests (including specific interests in my lab), cv, transcripts (unofficial is fine), and contact details for 3 referees.

Jeremy Fox

Asst. Professor and Alberta Ingenuity New Faculty Dept. of Biological Sciences University of Calgary 2500 University Dr. NW Calgary, AB T2N 1N4 Canada <http://homepages.ucalgary.ca/~jefox/Home.htm> Jeremy Fox <jefox@ucalgary.ca>

UFlorida Genetics Genomics

We are seeking some additional outstanding applicants for the 2008-2009 entering class in Genetics & Genomics at the University of Florida, Gainesville.

Our new graduate program in Genetics & Genomics is truly interdisciplinary in nature and involves faculty from more than six colleges, including Agriculture, Engineering, Liberal Arts & Sciences, Medicine, Pharmacy, and Veterinary Medicine. Students receive broad training in genetics and genomics, including participating in a first-year rotation program designed to ensure a good fit of students and advisors as well as breadth of training. Our program spans virtually every area of genetics, from the most applied (human gene therapy and crop design) to the most basic (evolution of mutation rate). We have particular strengths in evolutionary genetics and genomics, including molecular systematics, bioinformatics, population genetics, and systems biology. The UF Interdisciplinary Center for Biotechnology Research provides state-of-the-art services in genomics, proteomics, and bioinformatics to UF researchers.

Gainesville is a pleasant, family-friendly college town in north-central Florida, with a wide variety of outdoor recreational opportunities, and a vibrant cultural

life (<http://www.cityofgainesville.org/about/>). The Atlantic and Gulf coasts are both within a 90-minute drive.

Application information is available at <http://www.ufgi.ufl.edu/Graduate-training1.htm> Marta L. Wayne, PhD Director, UF Genetics & Genomics Graduate Program Associate Professor P.O. Box 118525 Department of Zoology University of Florida Gainesville, FL 32611-8525 (courier: B30 Bartram Hall) vox: 352-392-9925 fax: 352-392-3704 <http://www.zoo.ufl.edu/mlwayne> mlwayne@zoo.ufl.edu mlwayne@zoo.ufl.edu

UFlorida LifeHistoryEvolution

Are you interested in understanding the mechanisms underlying adaptive life history evolution and phenotypic plasticity? I am currently seeking graduate students to join our research group at the University of Florida. We take an integrative approach to understanding life history plasticity and life cycle evolution in insects that includes combining analyses of costs and benefits, organismal and cellular physiology, molecular genetics, and population genetics. Examples of possible projects include:

- 1) Mechanisms of phenotypic plasticity in insect hibernation/diapause (combining organismal biology, physiology, microarray genomics, and high-throughput proteomics)
- 2) Consequences of body size and nutrient storage on the costs and benefits of diapause.
- 3) Physiology of reproductive plasticity including identifying and testing candidate molecules and pathways for the control of reproductive timing and allotment and diapause.
- 4) Evolution of diapause strategies and the role of diapause strategies in diversification and speciation.

A possible project would be 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. (yes, the one from all the textbooks!) 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.

Additional projects could include addressing similar questions about plasticity in diapause responses and the physiological basis of costs of diapause on reproduction and dispersal in flesh flies.

The student would 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>). Interdisciplinary training at UF could include coursework, research, and interactions across campus including the Department of Zoology, the USDA Center for Medical and Veterinary Entomology, various departments in the medical school, and more. Tuition, health care, and a competitive salary are included.

Interested students please contact Dan Hahn (dahahn@ufl.edu) right away including a copy of your resume and a short statement of interests.

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

<http://danhahn.ifas.ufl.edu/>

dahahn@ufl.edu dahahn@ufl.edu

UGuelph rDNA Evolution

I am looking for PhD candidates who are interested in conducting research on the evolution of ribosomal DNA to start in May or September 2008. Some experience in the use of molecular techniques is desirable. Interested students should contact Teresa Crease at tcrease@uoguelph.ca. Additional information about the Zoology graduate program at the University of Guelph can be found at http://www.uoguelph.ca/ib/-graduate_zoology2.shtml. A description of my research interests is provided below.

Ribosomal DNA (rDNA) is an important multigene family that codes for the structural RNA molecules that make up ribosomes. One unit of rDNA consists of 3 genes encoding ribosomal RNA (rRNA) separated by intergenic spacers. The spacers contain sequences that control the expression of the rRNA genes. Some regions of these genes evolve very slowly while other regions, known as expansion segments, and the intergenic spacers evolve very rapidly. Despite this rapid evolution in their sequence, they still maintain their function. In addition, it has been observed that sequence similarity among the members of this multigene family is high within species relative to similarity between copies from different species. This phenomenon is known as CONCERTED EVOLUTION.

Due to variation in the rate of evolution in different parts of the same repeat unit, rDNA is an excellent model system with which to study the interaction between the molecular processes that cause concerted evolution, and natural selection to maintain the structure and function of the molecule. I use freshwater crustaceans in the genus *Daphnia* as a model organism for this work as they contain unusually long expansion segments, and show variation in breeding system with some populations reproducing by cyclical and others by obligate parthenogenesis.

The current goals of my research program are to:

- 1) identify proteins that bind to the ribosomal intergenic spacer, and determine the impact of intra- and interspecific variation on the interaction between this sequence and these proteins
- 2) determine the impact of breeding system and genomic location on the evolution of a *Daphnia* transposon, Pokey, that is found both inside and outside of the

rDNA.

3) test the hypothesis that rates of recombination and rDNA copy number differ between *Daphnia* species, and thus cause differences in their rates of concerted evolution

4) test the hypothesis that natural selection is acting on rRNA gene expansion segment length variation within species

– Dr. Teresa Crease Professor Department of Integrative Biology University of Guelph Guelph, Ontario N1G 2W1 Canada

Phone: 519-824-4120 ext 52723 Fax: 519-767-1656
Email: tcrease@uoguelph.ca

UJyvaskyla EvolutionaryBiol

Open PhD position

Centre of Excellence in Evolutionary Research, Department of Biological and Environmental Sciences at the University of Jyväskylä invites applications for a doctoral student position in the field of evolution of warning signals and mimicry. The planned work includes both field and laboratory work on three trophic level interactions between plants, insects and their enemies. The model species is an Arctiid moth *Parasemia plantaginis*. We are looking for an individual with a master's degree or equivalent, who is highly self-motivated and can work both independently and in a team. A successful candidate for this position will have background in ecology and evolutionary ecology. The work will be conducted in collaboration with chemists, chemical ecologists and geneticists. Thus, we encourage candidates with good communication skills to apply. The assignment will begin in the early 2008 (start date is flexible) and end in the end of 2011. Experience on population genetics and quantitative genetics is considered an asset! The working language will be English.

An overview of our past and current research can be found at <http://users.jyu.fi/~mappes/aposematism/>. The salary will start on level 2 of the demands level chart for teaching and research personnel in the salary system of Finnish universities, and the job specific component of the salary will thus be EUR 1 678 per month. In addition, the appointee will be paid a salary component based on personal work performance.

The application should include: 1) A complete CV 2)

Publication list (if available) 3) A scanned academic transcript (list of grades in university courses) 4) A statement of research interests and motivation for applying this position not exceeding two pages 5) Two references

Applications should be addressed to Professor Johanna Mappes mappes@bytl.jyu.fi by e-mail to arrive no later than 31st January 2008. More information about Finland, University of Jyväskylä, and Department of Biological and Environmental Sciences can be found at <http://www.jkl.fi/lang/> (city) and <http://www.jyu.fi/> (university).

Johanna Mappes <mappes@bytl.jyu.fi>

ULausanne EvolutionSymbiosis

PhD studentships in Lausanne: Evolution & Symbiosis

We are seeking several highly motivated students with an interest in molecular biology and/or evolutionary ecology to join our group working on symbiotic mycorrhizal fungi. These important fungi form mutualistic symbioses with most plants, improving plant growth and influencing diversity of ecosystems. Although the fungi grow clonally, they have a highly unusual genome organization, harbouring genetically different nuclei that are passed from one generation to the next (see Hijri & Sanders, Nature 2005; Kuhn, Hijri & Sanders, Nature 2001). The main goals of our research are to understand how selection, drift, genetic exchange and recombination act on these fungi and how this can be used to create more beneficial strains of the fungi for use in sustainable agriculture.

A selection of possible projects include: - Stability/heritability of fungal traits associated with improved growth of rice - Population genetics of mycorrhizal fungi in natural or agricultural systems - Linking quantitative changes in genetically different nuclei with important phenotypic traits - Exploring natural variation in mycorrhizal fungal populations for improvement of plant growth

The candidate should be familiar with molecular biology and have an interest in applying this knowledge to evolutionary & ecological questions. He/she should also be willing to interact with the other group members working on evolution and population biology of mycorrhizal fungi (see list of recent papers on our web site).

The successful candidate must have a Masters degree (MSc) in order to qualify for our PhD program. We are located in the Department of Ecology and Evolution at the University of Lausanne (Switzerland). The Dept. of Ecology and Evolution in Lausanne is situated on the shores of Lake Geneva and provides a pleasant & exciting research environment and a strong PhD program. It is also one of the largest institutions in Europe for research in ecology and evolutionary biology, comprising 17 different research groups. A genomics research centre also exists at the same site.

The studentships are for a period of 3 years. Starting date ideally by late spring 2008 but this date can be extended for exceptional candidates. Closing date for application is 28 February 2008. To apply, applicants should send a CV plus a letter of motivation by EMAIL to Ian Sanders, Dept of Ecology and Evolution, University of Lausanne, Switzerland. Email: ian.sanders@unil.ch: Tel: +41 21 692 4261. More details can be found about our group at: <http://www.unil.ch/dee/page7238.html> Ian R. Sanders Professor of Evolutionary Biology Dept. of Ecology & Evolution University of Lausanne Biophore Building 1015 Lausanne Switzerland

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

http://www.unil.ch/dee/page7238_en.html Ian Sanders <Ian.Sanders@unil.ch>

UManchester EvolGenomics

MSc in Evolutionary Genetics and Genomics, University of Manchester, UK

Please bring this new MSc course to the attention of potentially interested students.

This course is aimed largely at students with an interest in evolution who are thinking about going on to do a PhD in some aspect of evolutionary biology e.g. conservation, molecular evolution, speciation, population genetics, ecological genomics, bioinformatics. The taught component of the course (~one third) covers the principles of evolutionary genetics and genomics and some of the statistical approaches used. Engaging in full-time research in active laboratories is a key part of this programme and each student will undertake two full-time research projects (~two thirds of the course). Projects,

which can be lab-based, field-based, bioinformatics or theoretical, will be on offer from a large number of academic staff with a wide range of research interests.

Several fully, or partially, funded BBSRC studentships are available for UK and EU students and will be awarded on merit. Timely applications are encouraged as studentships will be awarded as suitable candidates apply.

Apply online: www.manchester.ac.uk/lifesciences/postgraduate/apply Further information: www.manchester.ac.uk/lifesciences/evolutionarygeneticmsc Enquiries for applications: Tel: 0161 275 5608 Fax: 0161 275 5657 Email: pg.lifesciences@manchester.ac.uk

Enquiries for further information on the course: Tel: 0161 275 1533 Email: Cathy Walton (Catherine.walton@manchester.ac.uk) or Richard Preziosi (Richard.Preziosi@manchester.ac.uk)

Catherine.Walton@manchester.ac.uk Catherine.Walton@manchester.ac.uk

others who don't need a visa to study in Germany).

For more information, please have a look at our website (<http://www.eeslmu.de>) or contact me by e-mail.

Best wishes, Pleuni Pennings

–

Pleuni S. Pennings

* Program Coordinator of the Munich Graduate School for Evolution, Ecology, and Systematics

* Postdoc in theoretical evolutionary biology

Evolutionary Biology, Department Biologie II University of Munich (LMU) Großhaderner Str. 2 D-82152 Planegg-Martinsried

Tel: 0049 89 2180 74 234 <http://www.eeslmu.de/eeswiki> <http://www.biologie.uni-muenchen.de/ou/theopopgen/index.htm> pennings@lmu.de

Pleuni Pennings <pennings@zi.biologie.uni-muenchen.de>

UMunich EvolEcolSystematics

Master Program in Evolution, Ecology and Systematics in Munich

The University of Munich (LMU) offers a 2-year, international master program for highly motivated students from Germany and abroad with a background in biology or a related subject. All courses are offered in English. The program started in October 2007 with 11 students from North America, South-America and Germany. Applications are now welcome to start in October 2008.

The EES Master program contains many innovative elements such as a mentoring program, integrated skills courses and individual research training. We also apply a feedback and revision system instead of simple grading. Classes are small and students have a lot of contact to the teachers. Thanks to funding by the Volkswagen Foundation, students can apply for their own research and travel money and for money to invite international speakers. Unfortunately, we cannot provide grants to cover costs of living. Students pay appr. 500 Euro tuition fees per semester.

Application deadlines in 2008: 30th of April (for non-EU students) and 30th of June (for EU-students and

UNottingham SticklebackSpeciation

Speciation in three-spined sticklebacks.

Funding may be available, on a within department competitive basis, for a PhD studentship to investigate the relative importance of different ecological factors in the divergence and speciation of three-spined sticklebacks.

Speciation can be viewed as the evolution of reproductive isolation between related taxa. Recent research has begun to investigate the ecological conditions that favour selection for reproductive isolation as well its genetic basis. This project will investigate the relative importance of different sources of reproductive isolation in speciation in three-spined sticklebacks.

On the island of North Uist in the Scottish Outer Hebrides three-spined sticklebacks occur as isolated freshwater populations, freshwater populations that hybridise with marine three spined sticklebacks in defined hybrid zones, sympatric, isolated population pairs of marine and freshwater 'species' and collapsed 'hybrid swarms'. This project will use this natural variation and combine field work, lab based mate choice tests and molecular genetics to explore the relative importance of different pre- and post-mating isolating mechanisms during stickleback divergence and speciation.

Applicants should have a good degree in a relevant sub-

ject, and an interest and enthusiasm for evolutionary ecology. Previous field work experience and a full driving licence would be beneficial but are not required.

Prospective students should, as soon as possible, send a CV and a one page outline of how they would tackle the project to Andrew MacColl (Andrew.maccoll@nottingham.ac.uk <<mailto:Andrew.maccoll@nottingham.ac.uk>>).

Andrew MacColl School of Biology University of Nottingham University Park Nottingham NG7 2RD U.K.

Andrew.Maccoll@nottingham.ac.uk

UOttawa Sexual selection

Graduate positions in sexual selection, adaptation, and speciation

Rundle lab, Department of Biology, University of Ottawa

Funding is available for graduate students (MSc, PhD) to join my evolutionary ecology lab. Working with various drosophila species, we use experimental evolution, quantitative genetics, and behavioural assays to address a diversity of research topics including the role of sexual selection in adaptation and speciation, the evolution of mate preferences, the use of social information within populations, sexual conflict, the evolution of genetic architecture (G matrix), and more. For further information, consult my website (<http://www.science.uottawa.ca/~hrund050/>)

Interested candidates should send their CV, a short (1 page) description of their research interests, and an (informal) copy of their transcripts to me via email (hrundle@uottawa.ca).

Located at the confluence of English and French Canada, Ottawa is a rich and vibrant national capital of approximately 1 million inhabitants (<http://www.ottawatourism.ca> <<http://www.ottawatourism.ca/>>). The city offers a wide range of cultural activities in the visual and performing arts, as well as easy access to green spaces and wilderness. The University of Ottawa is located next to the historic Rideau Canal, steps from Parliament and within easy access to a wide range of research facilities of interest to evolutionary biologists including the Canadian Museum of Nature, the National Wildlife Research Center, Health Canada,

and Environment Canada.

Cheers,

Howard

Howard D. Rundle Assistant Professor & Canada Research Chair

Department of Biology University of Ottawa

30 Marie-Curie Priv. Ottawa, Ontario, K1N 6N5

CANADA

Office: +1 613-562-5800 x2835; Fax: +1 613-562-5486; Lab: +1 613-562-5800 x6837

Email: hrundle@uottawa.ca; Skype: howarddrundle

<http://www.science.uottawa.ca/~hrund050/> <http://www.science.uottawa.ca/~hrund050/>

UOxford Evolution Of Virulence

Dear Evoldir members, Please distribute this PhD studentship advertisement to any interested parties. Best wishes, Sam Brown

PHD STUDENTSHIP (with funding for EU citizens) SOCIAL EVOLUTION AND VIRULENCE Supervisors: Sam Brown and Angus Buckling, Oxford University

Here's the advertisement (to appear in New Scientist, and available at <http://www.findaphd.com/search/showproject.asp?projectid=16130>). If you're interested, please first get in touch with me (sam.brown@zoo.ox.ac.uk) as soon as possible. I'm happy to discuss any questions about possible research topics and the application process.

Simultaneous selection on multiple microbial social traits and the evolution of virulence

Microbes have complex social lives, both cooperating and acting spitefully. For example, bacteria produce numerous "public goods" (shared resources that are released into the environment), such as iron-scavenging siderophores and glue that coats surface dwelling bacteria to form a resistant "biofilm"; as well as producing anti-competitor toxins (bacteriocins). Recent theoretical and empirical studies have provided key insights into the ecological conditions under which different social behaviours evolve, and how these behaviours may affect the severity of microbial infections. Despite this progress, our understanding of microbial social be-

haviours has to date been limited by the study of single social traits in isolation. Microbes, however, typically perform multiple social behaviours simultaneously. For example, a cooperative behaviour may be directed towards some individuals, whereas a spiteful behaviour may be simultaneously directed towards others.

Here we propose to theoretically address how natural selection acts on multiple social traits simultaneously, and the consequences of this for disease virulence (the damage caused to hosts by pathogens). The theory will be developed in close conjunction with an experimental program led by Angus Buckling, using the highly social, opportunistic animal and plant pathogen, *Pseudomonas aeruginosa*, as a study organism.

To apply please complete the University application form (available from: www.admin.ox.ac.uk/gsp/) and include two references from academic referees (follow procedure in Booklet A). Please submit two copies of the application forms and all supporting material to the Graduate Administrator, Department of Zoology, University of Oxford, South Parks Road, Oxford, OX1 3PS (and NOT the address detailed on the application form). Closing date: 29 February 2008

The University of Oxford is an Equal Opportunities Employer.

Funding Notes UK Research Council Funded

Sam Brown Wellcome Trust Career Development Fellow Department of Zoology University of Oxford South Parks Rd Oxford OX1 3PS, UK

+44 (0)1865 281062 <http://www.zoo.ox.ac.uk/staff/academics/brown.s.htm> sam.brown@zoo.ox.ac.uk
sam.brown@zoo.ox.ac.uk

VanderbiltU Evolutionary Diversification

GRADUATE STUDIES IN ECOLOGY AND EVOLUTION AT VANDERBILT, 2nd Announcement

Dear colleagues and prospective students,

The Department of Biological Sciences at Vanderbilt University seeks interested and highly motivated graduate students to join a group of laboratories with complementary research interests focusing on ecological and genetic mechanisms of evolutionary diversification. Ongoing research investigates all stages of diversification (population differentiation, reproductive isolation, spe-

ciation, evolutionary radiation) and several fundamental ecological and evolutionary processes (adaptation, ecological specialization, symbiosis, social interactions).

Online application to the graduate program is FREE and can be filed electronically at < <http://sitemason.vanderbilt.edu/biosci/grad/application>

> The deadline for submission of applications is JANUARY 15TH.

Our group occupies a modern (2002) building complete with our own DNA sequencing facility, numerous environmentally controlled rooms, and an adjoining state-of-the-art greenhouse. Vanderbilt researchers enjoy the participation of excellent undergraduates, the resources of a thriving medical center and full access to a super-computing facility. Our beautiful campus is located in the heart of Nashville, a friendly and inexpensive city situated amidst the lush rolling hills of biologically diverse middle Tennessee. Graduate students receive generous stipends and are trained in a highly interactive scientific community.

The research interests of the Ecology & Evolution faculty are listed below. Please note that all faculty are actively recruiting new graduate students:

Patrick Abbot (patrick.abbot@vanderbilt.edu) – social evolution, symbioses, molecular evolutionary genetics in insects and microbes

Dan Funk (daniel.j.funk@vanderbilt.edu) – ecological specialization and speciation, phylogenetics, herbivorous insect biology

Dave McCauley (david.e.mccauley@vanderbilt.edu) – population biology, population structure, local adaptation in plants and insects

Antonis Rokas (antonis.rokas@vanderbilt.edu) – phylogenetics, molecular evolution, comparative genomics, origins of multicellularity, evolution of genetic pathways in fungi

Additionally, we are presently conducting a faculty search for an evolutionary ecologist.

For further information on research and graduate study at Vanderbilt, please consult our departmental web page at < <http://sitemason.vanderbilt.edu/biosci> > Specific questions can be directed to any of the above faculty.

Antonis Rokas Department of Biological Sciences
Vanderbilt University VU Station B 351634, Nashville,
TN 37235 Email: antonis.rokas@Vanderbilt.Edu
Tel: +1-615-936-3892 Fax: +1-615-343-6707
<http://people.vanderbilt.edu/~antonis.rokas/> antonis.rokas@vanderbilt.edu

Jobs

ChicagoBotanicGardens Summer PlantEvolution .. 27	UCaliforniaBerkeley EvolutionOfDisease 34
DalhousieU MolEvol 27	UCaliforniaIrvine Specialist Position DrosEvolGe- nomics 35
Dublin Summer2008 EvolutionaryBiology 28	UNebraska LabTech PlantViralEvolution 35
EmoryU LabTech HostParasite 29	UOxford AvianMalariaEvolution 35
FortHood Texas FieldTech Mar-Jun ConsGenet ... 29	UPennsylvania LabManager HumanEvolGenomics . 36
France FieldAssist BehaviouralEvolution 30	UPennsylvania Programmer HumanEvolGenomics . 36
GeorgiaInstTech 12Month IntroEvolBiol 30	US EPA ResTechnician QuantPopGenetics 37
GettysburgCollege OneYear StatisticalGenetics 31	USydney MarineAnimalEvolutionaryBiology 38
GrinnellCollege 1year EvolBiol 31	UTexasElPaso EvolutionaryGenetics 38
ImperialCollegeLondon AdaptationToClimateChange 32	UUtah HerbariumCurator 39
LaJolla FishEvolution 32	WoodsHole ResAssist ComparativeEvolution 39
Mexico Bee PopGenet and MolPhylogeny 33	WoodsHole ResAssist MarineGenomics 40
UBath PopBioLectureship 33	
UBern VolunteerFieldAssist BirdPredation 34	

ChicagoBotanicGardens Summer PlantEvolution

Summer field research experience for undergrads (REU) and recent graduates

Are you interested in gaining field research experience and learning about the evolution of plants and plant-animal interactions in fragmented prairie? We are looking for 3-5 summer field researchers for an NSF-funded project on habitat fragmentation of the tallgrass prairie. We are investigating how small plant population size influences 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 provided and

there is a stipend. Undergraduate students have the opportunity to do an independent project as 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 7 March 2008.

Stuart Wagenius, Ph.D. Conservation Scientist Division of Plant Science and 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> Stuart Wagenius
<SWagenius@chicagobotanic.org>

DalhousieU MolEvol

DALHOUSIE UNIVERSITY

DEPARTMENT OF BIOCHEMISTRY & MOLECULAR

LAR BIOLOGY

ASSISTANT PROFESSOR POSITION

The Department of Biochemistry & Molecular Biology invites applications for a probationary tenure-track position at the rank of Assistant Professor to begin July 1, 2008. The ideal candidate will have expertise in molecular biology or biochemistry with a research emphasis on microbial molecular evolution and/or comparative genomics. Specific research areas of interest include, but are not limited to: molecular biology and evolution of organelles, microbial genome structure and function, biochemical/cellular diversity in prokaryotes and eukaryotes. The candidate must have a research track record that will be highly competitive in attracting external research funding. The successful candidate will join an internationally recognized group of researchers at Dalhousie working on microbial molecular evolution, comparative genomics, bioinformatics and biodiversity. The candidate will have the opportunity to mentor undergraduate honors and graduate students as well as postdoctoral fellows, and be expected to teach undergraduate and graduate courses in molecular biology/biochemistry consistent with her/his background and interest.

The ability to collaborate across disciplines is encouraged. The Department is closely affiliated with the recently established Program in Integrated Microbial Biodiversity (IMB) of the Canadian Institute for Advanced Research (CIFAR) and with a newly created interdisciplinary Centre in Comparative Genomics and Evolutionary Bioinformatics (CGEB) at Dalhousie University. The successful applicant will be nominated as a Scholar in the CIFAR IMB program (information on this program can be found at www2.cifar.ca). More details about the research activities of the Department of Biochemistry and Molecular Biology and the Faculty of Medicine can be found on our web sites: www.biochem.dal.ca and www.medicine.dal.ca.

Applicants must have a Ph.D., at least 2 years of postdoctoral experience and a strong publication record. Please submit curriculum vitae, reprints of several recent publications, one- to two-page statements outlining teaching and research plans, and arrange for three references to be sent under separate cover to:

Dr. D.M. Byers Head, Department of Biochemistry & Molecular Biology Faculty of Medicine Sir Charles Tupper Medical Building Dalhousie University Halifax, NS B3H 1X5.

Closing date for receipt of applications is March 31, 2008. The Academic Planning and Appointments Committee will commence reviewing applications in March.

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority.

Dalhousie University is an Employment Equity/Affirmative Action employer. The University encourages applications from qualified Aboriginal people, persons with a disability, racially visible persons and women.

posted by: Andrew J. Roger Associate Professor, Fellow CIFAR Program in Integrated Microbial Biodiversity, Dept. of Biochemistry and Molecular Biology, Dalhousie University Rm 8B1, 5850 College St., Halifax, N.S. B3H 1X5 Canada tel:902-494-2620 (office) tel:902-494-2881 (lab) fax:902-494-1355 lab webpage: <http://rogerlab.biochem.dal.ca> Andrew.Roger@Dal.Ca

Dublin Summer2008 EvolutionaryBiology

Dear all,

Please circulate this notice to your colleagues who may be in contact with potential students (3rd years), as well as to any relevant groups. Note the closing date for applications is March 30th 2008.

Summer Research in Dublin

Collections-Based Biology in Dublin (CoBiD) Undergraduate Research Experience & Knowledge Award

This summer programme offers research projects and activities for students in organismal biology using biological collections

Research Projects extreme environments | fire ecology | DNA barcoding | freshwater ecology | biocontrol | environmental epigenomics | terrestrial ecology | invasive species | plant evolution and extinction | life history | genomic imprinting

Requirements completion of the third (junior) year of an undergraduate biosciences degree | ability to work independently | strong interest in the project of choice | career goals in organismal biology

Full funding for the 10-week programme will be provided for 10 successful candidates, including assistance with air transportation to and from Dublin, accommodation in Dublin, and a small weekly allowance, as well as project expenses. Prior experience with museum collections is not required $i_{\frac{1}{2}}V$ one of the goals of the

programme is to expose students to new research skills. The programme is open to all international as well as Irish and EU students.

Term dates: June 16th to August 22nd 2008

For application instructions and more information:

<http://www.ucd.ie/ureka/> Applications must be received by 30 March 2008

Kind regards,

The UREKA Team

Collections-based Biology in Dublin Undergraduate Research Experience & Knowledge Award www.ucd.ie/ureka ureka@ucd.ie

EmoryU LabTech HostParasite

Lab Technician Emory University, Atlanta, Georgia Department of Biology

Lab tech position available in the laboratory of Dr. Nicole Gerardo. The lab focuses on the evolutionary ecology of host-parasite interactions in insect systems. Primary research will focus on aphid- pathogen interactions, though other research projects are planned. For more information, go to: <http://www.biology.emory.edu/research/Gerard/-Gerardohome.html> .

The lab tech will be responsible for lab maintenance, organization and ordering, and will also conduct both molecular and experimental research.

Candidates should have a minimum of a bachelors, previous experience in biological research, and strong personal communication skills. It is critical that the candidate be organized, able to pay attention to detail and good at working with others. Experience with molecular techniques and in insect/plant rearing are strongly preferred, though not necessary. Both part time and full time applicants will be considered. Applicants needs to be able to start no later than May 2008, and an immediate start date is preferred.

For more information on how to apply, contact Nicole at nicole.gerardo@emory.edu . Send a CV and a brief statement of your interests.

Dr. Nicole Gerardo Emory University Department of Biology nicole.gerardo@emory.edu

FortHood Texas FieldTech Mar-Jun ConsGenet

Field technicians needed from approximately mid-March to late June 2008 (dates somewhat flexible; total position duration about 16 weeks) to participate in a stress ecophysiology project on two federally endangered species, the Black-capped Vireo and the Golden-Cheeked Warbler. The research is a collaboration among investigators at Princeton University, Tufts University, and University of Illinois. The Princeton group uses heart rate telemetry to study the metabolic demands of stress induced by human and military activity. The Tufts group studies the hormonal response to short- and long-term exposure to disturbance. Work takes place at Fort Hood, a beautiful 88,000-ha military installation adjacent to the city of Killeen, Texas. And, yes! It is beautiful! The base is home to many endemic insects, and also to bobcats and mountain lions not to mention tons of birds. Primary tasks of crew members will be to locate adult birds on their territories, map territories, find nests, and assist in targeted mist-netting, transmitter mounting, blood sampling, nest monitoring, behavioral observations, and various other activities related to field experiments on birds. Crew members will be responsible for keeping extensive, detailed field notes. Pay is approximately \$2,100/month and workers must provide their own housing and transportation to work (vehicle provided for field work). Applicants must be at least 21 years old by date of hire, have a valid driver's license, and a good driving record. Applicants must have good hearing, be able to see the full spectrum of colors, and be in sufficient physical condition to carry gear long-distances, cross-country, in hot and humid weather. Although Fort Hood offers a great wildlife experience, crews will start work before sunrise, walk many kilometers, and endure harsh field conditions including exposure to intense sun, heat, chiggers, fire ants, cactus, snakes, and abundant poison ivy. Preferred qualifications are: (1) a 4-year degree in a life science, or equivalent experience (2) field experience in finding nests, determining color band combinations from a distance, identifying birds by sight and sound, and mist-netting (experience with our study species not especially important) (3) self-motivation and ability to work independently and a willingness to learn new skills (4) flexibility to daily changes in activities and assignments as experiments progress (5) ability to navigate

alone in the field using map, compass, and GPS (6) excellent attention to detail.

To apply please send a letter of intent, CV, and the names of three referees to Isabelle-Anne Bisson at ibisson@princeton.edu with "Fort Hood Crew" in the subject line. E-mail applications are preferred but materials can also be sent to: Dr. Isabelle-Anne Bisson, Dept. Ecology and Evolutionary Biology, Princeton University, Princeton NJ 08544.

Isabelle-Anne Bisson, Research Associate

Dept. Ecology and Evolutionary Biology

Princeton University, Princeton NJ 08544

Phone: (609) 258-7925

ibisson@Princeton.EDU ibisson@Princeton.EDU

France FieldAssist BehaviouralEvolution

Field assistants in Behavioural Evolution

Four field assistant positions are available in an international research project on communication and behavioural evolution in nightingales (*Luscinia megarhynchos*).

Fieldwork will be done in April and May 2008 at the Research Station Petite Camargue Alsacienne in France (www.camargue.unibas.ch). The project is run by Dr. Valentin Amrhein (University of Basel, Switzerland) and Prof. Dr. Marc Naguib (Centre for Terrestrial Evolution, Heteren, Netherlands).

To investigate vocal communication strategies of nightingales, we record songs (including nocturnal song) and conduct playback experiments. The field assistants will also participate in systematic surveys of territory settlement and singing activity, and assist in capturing and banding the birds.

The field site is situated at the Petite Camargue Alsacienne in France, about 10 km north of Basel (Switzerland). We cannot cover travel expenses, but we offer free accommodation and use of the infrastructure at the research station. Field assistants will receive 400 Euros to cover living expenses.

Field assistants are expected to stay for the entire field season from 7 April to the end of May 2008. Field work will be demanding, and we will use bicycles to visit every nightingale territory on two extensive census rounds

per day at midnight and at dawn, respectively. Field assistants are expected to work on their own at night and thus should love working in dark and lonesome places only accompanied by singing nightingales.

The language at the research station will be English. Please send applications by email to the following address:

pca.recherche@orange.fr

Applications should be in English and should include, in one single pdf or word file, a curriculum vitae and a letter of motivation. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 15 February 2008 will be given full consideration.

valentin amrhein <v.amrhein@wanadoo.fr>

GeorgiaInstTech 12Month IntroEvolBiol

Instructor in BIOLOGY

The School of Biology in the College of Sciences is seeking a full-time, non-tenure track general faculty member at the rank of Instructor. Preference will be given to candidates with experience teaching quantitative Ecology, Evolution and Introductory Biology. In addition to teaching 2-3 courses/semester and contributing to curriculum innovation, the incumbent must be committed to student success and will be responsible for the academic advisement of undergraduate biology majors. This is a 12-month appointment. A Ph.D. and teaching experience in biological sciences are required. Salary is commensurate with experience. Starting date is August 2008. Please send a CV, statement of teaching philosophy and three letters of recommendation to: INSTRUCTOR Search Committee, Georgia Institute of Technology, School of Biology, 310 Ferst Drive, Atlanta GA 30332-0230 barbara.walker@biology.gatech.edu. Review of applications will begin immediately and continue until the position is filled. Georgia Tech is a unit of the University System of Georgia and an Affirmative Action/Equal Opportunity Employer and requires compliance with Immigration Control Reform Act of 1986.

Barbara E. Walker Administrative Manager II Georgia Institute of Technology School of Biology 310 Ferst Drive - Rm 201 Atlanta, GA 30332-0230 Phone - 404-894-3747 Fax - 404-894-0519 bar-

bara.walker@biology.gatech.edu

Barbara Walker <barbara.walker@biology.gatech.edu>

GettysburgCollege OneYear StatisticalGenetics

Gettysburg College invites applications for a one-year sabbatical replacement position (with the possibility of renewal for a second year) at the rank of assistant professor in the Biology Department to begin in Fall 2008. Ph.D. in a Biological Sciences discipline, commitment to teaching in the liberal arts tradition, and research that can involve undergraduates are essential. Must be able to teach genetics, biostatistics, and possibly in the second year a course in area of specialization.

Gettysburg College is a highly selective liberal arts college located within 90 minutes of the Washington/Baltimore metropolitan area. Established in 1832, the College has a rich history and is situated on a 220-acre campus with an enrollment of over 2,600 students. Gettysburg College celebrates diversity and welcomes applications from members of any group that has been historically underrepresented in the American academy. The College assures equal employment opportunity and prohibits discrimination on the basis of race, color, national origin, gender, religion, sexual orientation, age, and disability.

Send by post (no electronic applications) curriculum vitae and statement of teaching and research goals and have three letters of reference (at least one of which can speak to the candidate's teaching effectiveness) sent to: Dr. Véronique A. Delesalle, Biology Search, Biology Department, Box 392, Gettysburg College, Gettysburg, PA 17325. Review of applications will begin January 15th, 2008, and will continue until a successful candidate is found.

Veronique A. Delesalle Professor of Biology Chair of the Biology Department Box 392 Gettysburg College Gettysburg, PA 17325

Tel: 717-337-6153 fax: 717-337-6157

delesall@gettysburg.edu delesall@gettysburg.edu

GrinnellCollege 1year EvoBiol

GRINNELL COLLEGE invites applications for a one-year Assistant-Professor position (starting Fall, 2008) in the Department of Biology in the area of Evolutionary Biology. A Ph.D. is required and a post-doc preferred. Grinnell College is a highly selective undergraduate liberal arts college with a teaching schedule of five courses per year, with science lab sections counted as $\frac{1}{2}$ courses. Successful candidates will teach in Grinnell's innovative, research-centered undergraduate biology curriculum. Teaching for this position will include Organisms, Evolution, & Ecology with lab (Bio 252) and an advanced course with lab in the candidate's specialty, with the remaining teaching to be determined. Grinnell College's curriculum is founded on a strong advising system and close student-faculty interaction, with few college-wide requirements beyond the completion of a major. For more departmental information see <http://www.grinnell.edu/academic/biology/>. In their letters of application, candidates should discuss their interest in developing as a teacher and scholar in an undergraduate, liberal-arts college that emphasizes close student-faculty interaction. They also should discuss what they can contribute to efforts to cultivate a wide diversity of people and perspectives, a core value of Grinnell College. To be assured of full consideration, all application materials (pdfs preferred) should be received by February 15, 2008. Send a cover letter, statements of teaching and research interests, CV, undergraduate and graduate transcripts, and three letters of reference to BiologySearch@grinnell.edu, Jonathan Brown, Evolutionary Biologist Search Committee, Department of Biology, 1116 Eighth Avenue, Grinnell College, Grinnell, IA 50112-1690 Phone: 641-269-3172; Fax 641-269-4285.

Please feel free to contact me if you have any questions about this position.

Cheers,

Jackie

Jonathan Brown brownj@grinnell.edu

ImperialCollegeLondon AdaptationToClimateChange

Lectureships/Readerships Grantham Institute for Climate Change Imperial College London

Salary Range: £38,880 - £43,420 for Lecturers, £47,960 minimum for Readers

The Grantham Institute for Climate Change was established in February 2007 with a multi-year, multi-million donation from the Grantham Foundation for the Protection of the Environment. Its vision is to become a world-leading Institute generating and communicating the highest quality research on climate-driven change, how it affects ecosystems and human welfare and on developing the technological, market and policy solutions needed to mitigate and adapt to change at both global and local level.

Applications are invited for lectureships and readerships in any of the areas of fundamental earth systems science, climate change impacts on ecosystems and human welfare, mitigation, adaptation and climate policy research. There are several appointments to be made across all three Faculties of Engineering, Medicine and Natural Sciences, and the Tanaka Business School. Fixed term 3 year Fellowships will be advertised separately. The precise number and type of appointments will depend on the quality and experience of the applicants.

You must have an exceptional research record and are expected actively to contribute to the dynamic multi-disciplinary research environment within the Institute. Candidates would be expected to have a PhD or equivalent in a relevant research field.

Research areas should complement or strengthen existing activities which can be found on the following website: <http://www3.imperial.ac.uk/climatechange/research>.

A strong partnership in this area is envisaged with the University of Reading.

Further particulars and an application form (which must be completed) can be obtained from the following links: <http://www3.imperial.ac.uk/employment/-academic/grantham> Closing date: 21 February 2008

– Prof. Ian P.F.Owens Division of Biology & NERC Centre for Population Biology Imperial College London

Silwood Park Ascot, Berkshire SL5 7PY, UK

<http://www.imperial.ac.uk/biology> <http://www.imperial.ac.uk/cpb> <http://www.imperial.ac.uk/people/i.owens> Ian Owens <i.owens@imperial.ac.uk>

LaJolla FishEvolution

The Southwest Fisheries Science Center (SWFSC) in La Jolla, CA, seeks a lab manager for its Molecular Ecology Laboratory. Responsibilities include production of high quality genetic data for phylogenetic and population structure studies primarily of marine mammals and sea turtles by: overseeing daily operations of the genetics laboratory and its systems,

training laboratory personnel and students in basic laboratory techniques,

serving as liaison between project investigators and laboratory staff,

supervising laboratory technicians,

tracking status of all projects moving through the lab,

providing technical guidance, problem solving, and troubleshooting of laboratory methods

procurement of laboratory supplies and equipment,

ensuring maintenance of laboratory equipment and environment

providing fiscal oversight of laboratory budget and maintenance of a cost effective research environment

He/she must communicate with and report to principle investigators and collaborators on a regular basis, and be familiar with relational databases for laboratory data input, quality control, and tracking of projects. Additionally, she/he will: Oversee development and testing of new technologies and protocols to improve our data quality and efficiency; Introduce and evaluate new technology to improve our research capacity; Track and manage the laboratory budget using MS Access and Oracle databases; Assist in the development, monitoring, and maintenance of project budget and schedules; Produce and provide data to other laboratories within NMFS, to international organizations such as the International Whaling Commission, and to collaborators; Coordinate lab activities with members of other programs and divisions within the SWFSC

Required Qualifications: Ability to effectively communicate and interact with staff in a team-based environ-

ment. Requires a high degree of autonomy, flexibility, independent judgment, and leadership skills. Bachelor's degree or higher in biology or related field, at least 3 years experience with molecular genetics research methods including DNA extraction, microsatellite genotyping, SNP genotyping, and DNA sequencing, and experience with overseeing the operation of a lab, including procurement, training of new personnel, data quality control and assurance, and project management. Preferred Qualifications: Preference will be given to candidates who pay attention to detail, have good organizational skills, and can work collaboratively with others.

This is a full-time position with a two year term limit, but with potential for extension. Salary commensurate with experience and will include benefits. Candidates must be U.S. Citizens. This job is now available for applications through January 23rd, through the web site www.usajobs.com.

Announcement Number: NMF-SWC-2008-0008 Position: Supervisory Research Biologist (Lab Manager), ZP-401-III Location: La Jolla, CA Open: January 2, 2008 Close: January 23, 2008

– Phillip A. Morin, Ph.D. Southwest Fisheries Science Center 8604 La Jolla Shores Drive La Jolla, CA 92037, USA Phone: 858-546-7165 Fax: 858-546-7003
phillip.morin@noaa.gov <http://swfsc.noaa.gov/prd-popid.aspx>
phillip.morin@noaa.gov

Mexico Bee PopGenet and MolPhylogeny

Dear colleagues, A call is open until March 20th, for a position of researcher in Ecosur, southern Mexico. The research topics are the *population genetics and molecular phylogeny of tropical bees*. Please find a short description below, and for the complete call, refer to the following web page: - in English: <http://www.ecosur.mx/convocatorias/bees.html> - in Spanish: <http://www.ecosur.mx/convocatorias/abejas.html>
 I would appreciate your help in forwarding this information to potentially interested persons - and I am sorry if you receive this information through different distribution lists. Best to all, Remy Vandame (rvandame@ecosur.mx) Bee research line El Colegio de la Frontera Sur

—
 Southern Mexico and Central America is a particularly interesting region for tropical bee research. This region has been invaded by Africanized bees and possesses a great natural diversity of bees, in particular stingless and bumble bees. Despite this high diversity, few studies have been conducted to determine the existing genetic diversity, the evolutionary pathways followed by bees and the development of sociality. The conservation biology of endemic species also remains poorly studied. The present call is published with the aim of hiring a researcher with a strong background in population genetics and social insects biology, who will seek among other objectives, to: - describe and explain the biodiversity of tropical bees, with field based methodology as well as laboratory methods, in particular based on population genetic approaches; - conduct research on the phylogeny of bees, in particular of groups like stingless and bumble bees; - use such data to explain the evolution of sociality and behavior such as communication; - establish and participate in the implementation of protection strategies for endemic species threatened with extinction, possibly based on an agroecological approaches.

Remy Vandame <rvandame@ecosur.mx>

UBath PopBioLectureship

POPULATION BIOLOGY LECTURESHIP, UNIVERSITY OF BATH

Ref: 08H025A

Title: Lecturer in Population Biology - 08H025A

Department: Biology and Biochemistry

Description: Applications are invited from outstanding and highly motivated individuals for a Lectureship in population biology. The subject area is defined broadly and can include, but is not limited to, experimental evolution/ecology, comparative and ecological genomics, behavioural ecology, evolutionary ecology and conservation biology. You should have demonstrated excellence in original research and achievement in a relevant area, and the potential to develop and sustain a productive research programme at Bath. You will be expected to contribute to undergraduate and postgraduate teaching in the department. The appointment will be held in the Department of Biology and Biochemistry which is RAE grade 5 and very well equipped for molecu-

lar life science research. Further information about the Department is available at <http://www.bath.ac.uk/bio-sci/> Informal enquiries are welcome and should be directed to the Head of Department, Dr Richard Hooley on bssrah@bath.ac.uk

Salary: In the range £33,779 - £40,335

Contact: please email jobs@bath.ac.uk or call 01225 386924 quoting ref number 08H025A

Closing Date: 28th February 2008

Professor Tamas Szekely Professor of Biodiversity Dept of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK 01225 383676 (phone), 01225 386779 (fax), T.Szekely@bath.ac.uk (email) <http://www.bath.ac.uk/bio-sci/biodiversity-lab/index.htm>
SEX, SIZE AND GENDER ROLES: evolutionary studies of sexual size dimorphism <http://www.oup.com/uk/catalogue/?ci=9780199208784> bssts@bath.ac.uk

UBern VolunteerFieldAssist BirdPredation

I am seeking enthusiastic volunteers interested in assisting a field study in Bern, Switzerland. The research aims to study the effects of different avian predators on life-history traits of Great tits, and the interactions they might have with ectoparasites of the tits. The tits are a good system to examine the effects of different predators and ectoparasites since, being hole nesting birds, the risks the birds face as nestlings are different than those they face once they fledge. I will require 2 field assistants that will help with all the aspects of the work, including ringing the birds, simulating predators, conducting behavioral observations and recordings, and more. The study will take place in the forest near Bern starting roughly at the end of March 2008 and running until about the end of May 2008. Applicants with a BSc/Msc in Biology/Ecology and with bird handling experience would have an advantage. However, motivation will play a key role: the work is hard and demanding, may take place in changing weather and requires long hours at times. Motivated applicants could develop their own individual research on a topic related to the program and their own interests, and if particularly motivated could be involved in the publications. Accommodation and transportation within Europe may be provided. Some financial assistance may also be available to cover living expenses on a case by case basis and according to educational status.

Candidates must hold a valid European driving license. For further details please contact Michael Coslovsky at m.coslovsky@students.unibe.ch or at + 41 31 631 3019. m.coslovsky@students.unibe.ch

UCaliforniaBerkeley EvolutionOfDisease

Job Announcement:

Full time research associate

Ecology and Molecular biology of disease

Full time, permanent research associate position open January 2008. Disease ecology research program at the University of California, Berkeley seeks research associate to support Lyme disease ecology project. This research program is in the laboratories of Dr. Cheryl Briggs (UCSB) and Wayne Sousa (UCB) and focuses on the relationship between habitat and Lyme disease dynamics. Specifically, we investigate the influence of habitat characteristics on the population ecology of small mammals and lizards and their interactions with the disease vector, the western black-legged tick.

Position is primarily laboratory-based and will assist with molecular work and processing of field-collected samples. Duties include animal tissue extraction (primarily small mammal and tick samples), real-time PCR, nested PCR, and sequencing. In addition to laboratory duties, the successful applicant will be required to maintain a database of samples both from the field and the laboratory. There may be some opportunities for fieldwork in Marin and Monterey Counties as well.

Requirements include a bachelors degree in biology or related field and prior laboratory experience, particularly with nested PCR, real-time PCR, and sequencing. Other desirable qualities include attention to detail, organizational skills, strong self-motivation, and the ability to work independently.

Consideration of applications will begin immediately. Please submit a letter of interest, a resume, and the names, phone numbers, and email addresses of three professional references to:

Andrea Swei

swei@berkeley.edu

The job announcement can also be found at the website: jobs.berkeley.edu under the requisition number 7712

swei@calmail.berkeley.edu swei@calmail.berkeley.edu

UCaliforniaIrvine Specialist Position DrosEvolGenomics

UCaliforniaIrvine.Specialist_Position.DrosEvolGenomics

Applications are invited for a full time Specialist position at the laboratory of Dr. José M. Ranz. Funds for this post are available for at least two years and may, subject to the availability of funding, be renewed. The successful applicant will be expected to use molecular biology techniques including, but not restricted to, DNA and RNA extraction, cloning, PCR, and analysis of DNA sequence data. Additional tasks include day-to-day running of the lab and the maintenance of *Drosophila* (fruit fly) stocks. The ideal candidate should be highly motivated and possess at minimum an MSc or BSc's degree in life sciences.

Informal enquiries should be addressed to Dr. José M. Ranz. Applications should include a covering letter (with a brief research statement), a CV, and the name and address of three references. Applications should be sent to the email address below:

Dr. Jose M. Ranz jranz@uci.edu

The University of California, Irvine is an equal opportunity employer committed to excellence through diversity, has an active career partner program and a National Science Foundation Advance Gender Equity Program.

Jose M. Ranz, Ph.D. Department of Ecology and Evolutionary Biology 321 Steinhaus Hall University of California, Irvine Irvine, CA 92697 USA

E-mail: jranz@uci.edu Telf: +1 949 824 9071 Fax: +1 949 824 2181

Jose M Ranz <jranz@uci.edu>

UNebraska LabTech PlantViralEvolution

Lab Tech Position, University of Nebraska-Lincoln.

We are currently in search of a research technician to

evaluate the effects of virus infection on wild squash populations in both field and laboratory environments. Duties include extracting plant DNA and virus RNA from plant tissue to detect genetic resistance to viral infection and identify virus-infected plants, general lab maintenance, data entry, and database management. During the field season (4 months each year), work at a field site, establishing field experiments and collecting field data. Additional information about this position is listed at employment.unl.edu requisition number 070792.

If you know of anyone who may be interested in the full time position please have them submit an application to employment.unl.edu requisition number 070792.

Please send this information to anyone who you think is qualified and interested in such a position.

Sincerely,

Holly Prendeville hrp@unlserve.unl.edu

hrp@unlserve.unl.edu

UOxford AvianMalariaEvolution

Graduate Research Assistant Edward Grey Institute
Department of Zoology University of Oxford United Kingdom

Dispersal, individual variation and spatial heterogeneity: evolution of avian malaria in tits *Parus* spp.

Fixed term: 31 months Start date: 1 April 2008 Salary: £23,692 p.a. (Grade 06S-01)

Applications are invited to join a NERC funded project investigating the role of avian malaria infection in the dispersal and survival and evolution of blue and great tits; a collaboration between the EGI, the University of Sheffield and CEH Edinburgh.

Job description:

The primary role will involve the molecular diagnosis of avian malaria infection in breeding tits from the long-term study population in Wytham Woods, near Oxford. Lab techniques will include DNA extraction, PCR and qPCR diagnosis of infection and the cloning of mixed infections, with extensive opportunities for fieldwork involving both birds and the potential vectors of avian malaria.

The successful applicant will have: (i) proven laboratory skills in molecular ecology, (ii) the ability to work

effectively both individually and as part of a team, (iii) the ability to work long hours during the field season, and (iv) meticulous attention to detail, and the ability to manage large quantities of data and large numbers of samples. Experience of ornithological fieldwork, or entomological identification is desirable, but not essential, as training will be provided. A driving licence is desirable.

The Edward Grey Institute is an active research group within the Department of Zoology, working on the evolution, ecology and behaviour of birds, composed of senior scientists, research fellows, postdoctoral researchers and graduate students. This presents an excellent opportunity to develop a career in evolutionary ecology.

Informal enquiries may be sent to Dr. Matt Wood, email: matt.wood@zoo.ox.ac.uk, telephone +44 (0)1865 281999 or Prof. Ben Sheldon, email: ben.sheldon@zoo.ox.ac.uk. Website: www.zoo.ox.ac.uk/egi Details on how to apply will appear soon on the Department of Zoology's Current Vacancies website (<http://www.zoo.ox.ac.uk/jobs>).

Closing date for applications: 14 February 2008

Dr. Matthew J. Wood Edward Grey Institute Department of Zoology University of Oxford Oxford OX1 3PS U.K.

matt.wood@zoo.ox.ac.uk matt.wood@zoo.ox.ac.uk

UPennsylvania LabManager HumanEvolGenomics

University of Pennsylvania: Research Technician/Lab Manager Positions in Human Population Genetics

Lab manager and technician positions are available in a human population genetics laboratory affiliated with the Departments of Genetics and Biology at the University of Pennsylvania. Research foci in the lab include the study of African genetic diversity and population structure, human evolutionary history, the genetic basis of adaptation and disease, pharmacogenetics, and the genetic basis of resistance against infectious disease and evolutionary history of immune function genes. Additional information about the Tishkoff lab can be found at <http://www.med.upenn.edu/tishkoff/>. The Department of Genetics (<http://www.med.upenn.edu/genetics/>) is centrally located within the U Penn campus and is a short walk from the

Children's Hospital of Pennsylvania, the Biology Department (<http://www.bio.upenn.edu/>) and the Anthropology Department (<http://www.sas.upenn.edu/anthro/>). Outstanding core facilities are available for high throughput sequencing, genotyping, and gene expression studies (<http://www.med.upenn.edu/genetics/core.shtml>), and for bioinformatics and computational biology (<http://www.pcbi.upenn.edu/>). U Penn has a vibrant community of researchers with interests in evolutionary biology and genomics (<http://www.genomics.upenn.edu/default.jsp>), the genetics of complex traits (<http://www.cceb.upenn.edu/pages/cgact/>), and translational medicine (<http://www.itmat.upenn.edu/>).

The level of the position will vary depending on research experience and training but all candidates must have a B.S. degree or higher in a biological sciences field and a minimum of one year of laboratory research experience with knowledge of basic molecular biology and genetic analysis techniques. Job duties include assistance in research projects in the lab as well as laboratory management, training, and organization. Research may include a number of molecular methodologies such as DNA/RNA extraction and quantification, PCR amplification (both standard and quantitative PCR), SNP and STRP genotyping, DNA sequencing, molecular cloning, gene expression assays, cell culture, as well as data analysis using assorted sequencing, population genetics, and evolutionary genetics software. The successful candidates will have strong organizational and communication skills, the capability to work with minimal supervision, and excellent interpersonal skills. Motivated candidates will have opportunities to present and publish research results. Salary for these positions is commensurate with qualifications and experience.

Please send curriculum vitae, a brief description of research experience, and contact information for three references via e-mail to Dr. Sarah Tishkoff, Departments of Genetics and Biology, University of Pennsylvania, tishkoff@mail.med.upenn.edu.

tishkoff@mail.med.upenn.edu

tishkoff@mail.med.upenn.edu

UPennsylvania Programmer HumanEvolGenomics

University of Pennsylvania: Programmer Analyst Posi-

tion in Human Population Genetics

A programmer analyst position is available in a human population genetics laboratory affiliated with the Departments of Genetics and Biology at the University of Pennsylvania. Projects in the lab focus on a unique resource of DNA samples and phenotype data from 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, CNV analyses, and whole genome SNP genotyping). For many of these samples we also have phenotype data for a number of traits that are likely important in adaptation and disease. We are using these data (1) to infer population structure and demographic history and to test models of modern human evolution (2) to identify regions of the genome that are targets of selection (3) to identify functionally significant variants using genotype/phenotype association studies as well as gene expression analyses (4) to study genetic and phenotypic variation at loci that influence drug metabolism and (5) 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 Philip Awadalla, Carlos Bustamante, Junhyong Kim, Gil McVean, Joshua Plotkin, Jonathan Pritchard, Anna Tramontano, and Greg Wray. Additional information about the Tishkoff lab can be found at <http://www.med.upenn.edu/tishkoff/>. The Department of Genetics (<http://www.med.upenn.edu/genetics/>) is centrally located within the U Penn campus and is a short walk from the Children's Hospital of Pennsylvania, the Biology Department (<http://www.bio.upenn.edu/>) and the Anthropology Department (<http://www.sas.upenn.edu/anthro/>). Outstanding core facilities are available for high throughput sequencing, genotyping, and gene expression studies (<http://www.med.upenn.edu/genetics/core.shtml>), and for bioinformatics and computational biology (<http://www.pcbi.upenn.edu/>). U Penn has a vibrant community of researchers with interests in evolutionary biology and genomics (<http://www.genomics.upenn.edu/default.jsp>), the genetics of complex traits (<http://www.cceb.upenn.edu/pages/cgact/>), and translational medicine (<http://www.itmat.upenn.edu/>).

Candidates must have a B.S. degree or higher, strong computational and statistical skills, ability to program in Perl and C/C++, familiarity with database design and management, and a minimum of one year prior experience. Job duties include designing and implementing software for population genetics and bioinformatic analyses of genome-scale datasets of human ge-

netic variation, testing software, validating data, and providing quality assurance, and database design and maintenance. Familiarity with population genetic and association mapping methodology is a plus. Motivated candidates will have opportunities to present and publish research results. Salary for these positions is commensurate with qualifications and experience.

Please send curriculum vitae, a brief description of research experience, and contact information for three references via e-mail to Dr. Sarah Tishkoff, Departments of Genetics and Biology, University of Pennsylvania, tishkoff@mail.med.upenn.edu. The starting date is flexible.

tishkoff@mail.med.upenn.edu

tishkoff@mail.med.upenn.edu

US EPA ResTechnician QuantPopGenetics

Several full and part-time contract positions are available in the Molecular Ecology Research Branch, United States Environmental Protection Agency, in Cincinnati, Ohio. Selected individuals will provide technical laboratory support for research projects focusing on any of the following projects: (1) colonization of Pacific coast estuaries and the Great Lakes by aquatic invasive species; (2) quantitative and population genetic assessment of pest beetles controlled by Bt-corn; (3) quantitative and population genetic assessment of fish and aquatic invertebrates; (4) assessment of non-target effects on insect communities near conventional and genetically-modified corn fields; and (5) development of molecular techniques to inventory and quantify organisms collected from stream, lake, and ballast samples. Work involved with the tasks may include, but is not limited to: (1) tissue and sample collection and organization; (2) DNA extractions; (3) PCR amplification and purification; (4) molecular cloning; (5) microsatellite genotyping; (6) DNA sequencing; (7) analysis of genotype and DNA sequence data; and (8) other general laboratory and field duties necessary to carry out research (e.g., sample collection and transport, routine equipment maintenance).

Applicants should possess skills/experience in molecular biology laboratory work, such as DNA extraction and PCR chemistry and also general laboratory practices, including health and safety, as well as having completed a minimum of a B.S. degree in Biology,

or a related sub-discipline such as Genetics, Molecular Biology, Biochemistry, Evolution, Environmental Sciences, Zoology or Botany. Applicants must be recent graduates of a college or university (within the last 24 months) or students pursuing a college degree in order to qualify under this contracting authority.

Pay will be \$15.80 per hour. It is anticipated that research technicians shall work between 20 and 40 hours per week, to be negotiated prior to the start date. The closing date for applications is January 18, 2008.

For more information on the research environment, location, and facilities, please contact Dr. Mark Bagley (513-569-7455, bagley.mark@epa.gov). Applications must be sent to EPA's contracts office. Please visit <http://www.epa.gov/oamrtpsc/q0800027/index.htm> for detailed instructions on the application process.

mark.bagley@fuse.net

USydney Marine Animal Evolutionary Biology

Lecturer/Senior Lecturer in Marine Animal Evolutionary Biology

School of Biological Sciences Ref # 107947

The School of Biological Sciences is a leading centre for biological research in an organismal, ecological and evolutionary context. It now invites applicants for a full-time continuing position s Lesturer/Senior Lecturer in Marine Animal Evolutionary Biology from outstanding candidates working on the evolution of any marine animal system. This is a solid career opportunity to work with an internationally reputed group and to build a significant research profile.

For more information or to apply online, please visit

<http://positions.usyd.edu.au> and search by reference number 107947.

Specific enquiries about the role can be directed to Associate Professor Ross Coleman on (02) 9351 2039 or e-mail: ross.coleman@bio.usyd.edu.au Alternatively, general enquiries can be directed to Fabrice Noi; $\frac{1}{2}$ l on (02) 9036 7295.

Closing Date 10 February 2008

– Dr Maria Byrne Professor Developmental and Marine Biology Director One Tree Island Research Sta-

tion Anatomy and Histology, F13 University of Sydney NSW 2006 Australia

Ph: 61-2-9351-5166 FAX: 61-2-9351-2813
 mbyrne@anatomy.usyd.edu.au>mbyrne@anatomy.usyd.edu.au
<http://www.anatomy.usyd.edu.au/research/groups/-byrne/index.html> <http://www.bio.usyd.edu.au/OTI/mbyrne@anatomy.usyd.edu.au>

UTexasElPaso Evolutionary Genetics

Assistant/Associate Professor

Evolutionary Geneticist

The Department of Biological Sciences at The University of Texas at El Paso (UTEP) seeks to fill a tenure-track Assistant/Associate level position in the area of EVOLUTIONARY GENETICS for fall 2008. The position requires the establishment of an extramurally funded genetics research program, and teaching and mentoring at both the undergraduate and graduate levels (M.S. and Ph.D.). Research resources at UTEP include core facilities for molecular and cell biology, DNA sequencing, tissue culture, and microscopy; curated biosystematic collections of vertebrates, invertebrates, and plants; a 39,000 acre research station located in a Chihuahuan Desert landscape; and a biostatistics consulting facility. Preference will be given to applicants whose research combines molecular and field-based techniques, have post-doctoral research experience and are able to collaborate with other members of the Department. Candidates should send an application that includes a cover letter, curriculum vitae, a statement of research interests, a brief description of teaching philosophy and professional experience, and 3 letters of recommendation to: Search Committee Chair (Genetics), Department of Biological Sciences, The University of Texas at El Paso, El Paso, TX 79968-0519. Review of complete applications will begin 15 February 2008.

UTEP does not discriminate on the basis of race, color, national origin, gender, religion, age, or disability in employment or the provision of services.

Elizabeth J. Walsh Chair, Evolutionary Geneticist
 Search Committee Associate Professor Department of Biological Sciences 500 W. University Ave. University of Texas at El Paso El Paso, TX 79968

Office: 915-747-5421 Lab: 915-747-6989 Fax: 915-747-6194

“Walsh, Elizabeth” <ewalsh@utep.edu>

UUtah HerbariumCurator

HERBARIUM CURATOR AND ASSISTANT PROFESSOR OF GEOGRAPHY

UNIVERSITY OF UTAH

The Utah Museum of Natural History and Department of Geography at the University of Utah invite applications for a tenure-track joint position as Herbarium Curator and Assistant Professor of Geography beginning 1 July 2008. The Garrett Herbarium includes more than 126,000 specimens with an emphasis on the intermountain region. The majority of this split appointment is funded by the Museum, and tenure is vested in the Department. The successful candidate must maintain a strong field- and collections-based research program involving students. In addition, duties include overseeing the curation and continued development of the herbarium, teaching one formal course per year in the Department of Geography, participating in Museum public programs and exhibit development, supervising graduate students in the Geography Department, and participating in departmental governance. The position is a 10-month appointment at a competitive salary level.

Candidates must have a completed Ph.D. with a strong record of research and publication in plant biogeography, with experience in one or more of the following areas: plant systematics, floristics, phylogeography, paleoecology, biodiversity, or conservation biology. Familiarity with the flora of the intermountain region is desirable. A demonstrated interest in museum curation and public programming is essential. Because this position is joint with the Geography Department, the successful applicant will develop a research connection with the Department of Geography and advise undergraduate, Master's, and Ph.D. Geography students. Applicants seeking additional information about this position may contact Sarah George in the Utah Museum of Natural History (sgeorge@umnh.utah.edu) or Harvey Miller in the Department of Geography (harvey.miller@geog.utah.edu).

Review of applications will begin* *February 15 and continue until the position is filled. Applicants should submit an application letter including research, teaching and programmatic interests and agenda, curriculum vitae, and names of exactly three references to:

Herbarium Curator/Biogeography Search Committee Chair University of Utah Utah Museum of Natural History 1390 E Presidents Circle Salt Lake City, UT 84112-0050

/The University of Utah is an equal opportunity/affirmative action employer, encourages applications from women and minorities, and provides reasonable accommodation to the known disabilities of applicants and employees. The University of Utah values candidates who have experience working in settings with students from diverse backgrounds, and possess a strong commitment to improving access to higher education for historically underrepresented students. /<http://www.umnh.utah.edu/pageview.aspx?menu=-4257&id=16046> < <http://www.umnh.utah.edu/pageview.aspx?menu=4257&id=16046> >

Lisa Clayton Administrative Assistant Department of Geography The University of Utah 260 S. Central Campus Dr. Rm. 270 Salt Lake City, UT 84112-9155 Phone: (801) 581-8218 Fax: (801) 581-8219 Email: lisa.clayton@geog.utah.edu

Lisa Clayton <lisa.clayton@geog.utah.edu>

WoodsHole ResAssist ComparativeEvolution

RESEARCH ASSISTANT I or II [RAI II PCR] The Marine Biological Laboratory is seeking applicants for a full-time, year round Research Assistant I/II position in the Josephine Bay Paul Center in Comparative Molecular Biology and Evolution to work on projects that use high throughput techniques to study microbial ecology. This position is available immediately.

Duties include but are not limited to: High throughput sequencing activities, extraction of nucleic acids from microbial cultures, Polymerase Chain Reaction, cloning of PCR amplicons, automated preparation of DNA sequencing reactions, phylogenetic analysis and molecular database searching and maintenance.

EDUCATION/EXPERIENCE: A B.A. or M.S. in molecular biology and training in molecular techniques. Familiarity with Mac OS, Windows, and Linux/Unix a plus. Actual position level will depend upon education and experience.

Please apply at mbl.simplehire.com.

Also,

RESEARCH ASSISTANT I/II [RA I II JWL] The MBL seeks a highly motivated individual to join the Jennifer Wernegreen lab as a full time research assistant beginning mid summer 2008. The successful applicant will contribute to projects that employ high throughput molecular and computational approaches to study genomics of bacterial endosymbionts. Specific projects examine functional genomics and population dynamics of endosymbionts across ant castes and species, and explore the evolution of gene content and DNA sequence variation in host- associated bacteria.

Duties include but are not limited to: High throughput sequencing using ABI and pyrosequencing (454) technologies, DNA and RNA extractions, standard and quantitative PCR, in situ hybridization, microscopy, field collection of ants, and general lab organization and maintenance. Opportunities for data analysis will include DNA sequence alignment, phylogenetic analysis, design of PCR and sequencing primers, and use of molecular databases. Experience with any or all of the above is desirable.

Education/Experience: Applicants should have an interest in molecular biology, genomics, evolution, symbiosis and or microbiology, and possess a genuine drive to perform basic research. This position requires an independent, organized, and very motivated individual with molecular biology or a related field and prior experience in an active research lab. A working knowledge of UNIX and or LINUX operating systems, experience in computer programming (particularly PERL), and knowledge of microbiology are pluses.

Please visit mbl.simplehire.com to apply for further details and to apply for this position.

Marian Padenski Human Resources Assistant Marine Biological Laboratory 7 MBL St. Woods Hole, MA 02543 phone: 508.289.7422 mpadenski@mbl.edu

Human Resources <humanres@mbl.edu>

Research Assistant I/II Marine Microbe Ecology [RA I II MME]

The Marine Biological Laboratory in Woods Hole, Massachusetts seeks a highly motivated individual to join the Huber lab as a full time research assistant beginning in 2008. The successful applicant will contribute to projects that employ molecular and cultivation approaches to study the microbial ecology of hydrothermal vents and other marine environments. The Huber lab is housed within the MBL's Josephine Bay Paul Center, a collaborative research group entering on microbial diversity, molecular evolution, and comparative genomics.

Responsibilities will include but are not limited to: Cultivation of bacteria and archaea, high throughput sequencing using ABI and pyrosequencing (454) technologies, DNA and RNA extractions, standard and quantitative PCR, in situ hybridization, microscopy, and general lab organization and maintenance. Opportunities for field work may also be available.

Applicants should have an interest in microbiology, oceanography, molecular biology, and genomics and possess a genuine drive to perform basic research. This position requires an independent, organized, and very motivated individual with experience in microbiological techniques. Education requirements include a B.A., B.S., or M.S. in microbiology or a related field and prior experience in an active research lab. Excellent written, verbal, and interpersonal skills, attention to detail, and a superb work ethic are essential. Position level and salary will depend upon education and experience.

To apply online please go to mbl.simplehire.com.

Marian Padenski Human Resources Assistant Marine Biological Laboratory 7 MBL St. Woods Hole, MA 02543 phone: 508.289.7422 mpadenski@mbl.edu

Human Resources <humanres@mbl.edu>

**WoodsHole ResAssist
MarineGenomics**

Other

AlfredRusselWallace Birthday	41	lution	49
Bird Prolactin MaleInvestment	41	Social learning evolution tournament	49
Bovine semen DNA	42	Software FigTree v1 1	50
Clontech Smart RACE problems	42	Software FigTree v1 1 1	50
DNA extraction formol	42	Software MultiDivTime Helper	50
DNA from dry barnacles	43	Software Phobos TandemRepeatDetection	50
Drosophila MortalityProblems	43	Software RAxML-7 0	51
Fs Batch Software	43	Software TreeFinder-BugFixes	52
F statistic sample size answers	44	Software TreeSnatcher	52
IIASA Austria SummerStipends	45	SouthAfrica FieldAssistVolunteers	52
Nb estimation using linkage answers	45	SouthDakota FieldAssist AvianReproductionTiming	53
NTSYS analysis choice	47	SSE DobzhanskyPrize	54
PC equivalent of SeAl	47	Systematic Biology offer	54
PennState Astrobiology Summer	47	Tardigrade samples	55
Peru VolFieldAssist AmazonianBirdEvol	47	Tetraploid microsatellites software	55
Precast gels	48	UBern VolunteerFieldAssist BirdFertility	55
Question Fis vs Relatedness	48		
Smithsonian Panama SummerInternship TreefrogEvo-			

AlfredRusselWallace Birthday

Aloha,

I hope that everyone is off to a great start in this new year. I would like to acknowledge the birthday of Alfred Russel Wallace who, in my opinion, was the one with the deepest understanding of evolution by natural selection (though Darwin's political clout was certainly essential to the acceptance of their theory).

All the best. Cam

– I Hilo e ulu pono ai e literal transl: “In Hilo we can thrive” (Hilo = a strong rope made of wilted Ti leaves (used as an allegory for the benefit of working together) Hilo is also the capitol of Hawai'i Island

Cam <cmuir@big.uhh.hawaii.edu>

Bird Prolactin MaleInvestment

Hello Evoldir,

My name is Carlos Navarro (<http://www.eeza.csic.es/-eeza/personales/cnavarro.aspx> < <http://www.eeza.csic.es/eeza/personales/cnavarro.aspx> >), a PhD student at the Estación Experimental de Zonas Áridas (C.S.I.C.) in Almeria (Spain) under the supervision of Juan J. Soler (<http://www.eeza.csic.es/eeza/personales/jsoler.aspx> < <http://www.eeza.csic.es/eeza/personales/jsoler.aspx> >). My PhD project is related to the hypothesis that blue-green egg coloration is sexual signal of female's birds that influence male investment in reproduction (feeding) (Moreno and Osorno 2003. Ecol Letters).

For my PhD project, I am interested to analyse the prolactin plasma level in Starling (*Sturnus unicolor*). So, I would greatly appreciate any information and advice about the protocol needed.

Also, I could be happy to collaborate with anyone who is willing to help me with the prolactin analyse.

Sincerely yours,

Carlos

Carlos Navarro Puig Dept. Ecología Funcional y Evolutiva Estación Experimental de Zonas Áridas (CSIC) C/ General Segura, N^o 1, 04001-Almería, Spain

E-mail: cnavarro@eeza.csic.es Tel: +34 950 281 045 Ext. 208 +34 648 090 920 Fax: +34 950 277 100 <http://www.eeza.csic.es/eeza/personales/-cnavarro.aspx> < <http://www.eeza.csic.es/eeza/>

personales/cnavarro.aspx >

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Universita Cattolica del Sacro Cuore, Piacenza, Italy

davide.perini@unicatt.it

Bovine semen DNA

Dear EvolDir,

I am going to extract and purify DNA from Bovine semen (e.g sperm) preserved at -20C in a well-composed suspending medium (named mestruum). The number of samples I need for the experiments is more than 1800, so in order to save time, money and work, I'm looking for a DNA extraction kit in 96-wells plates instead of a single columns one. I have already tested the following commercial kit, but with NO appreciable results (none or very, very low amount of DNA!!!!):

-NucleoSpin Blood Quick Pure (manufacturer: Macherey Nagel).

-NucleoSpin Tissue (protocol modified for semen as suggested by the manufacturer: Macherey Nagel).

-BioFab research blood extraction kit.

I did not consider to use Qiagen, because the protocol requires the use of an expensive centrifuge from the manufacturer.

The minimum amount of DNA I need to get from any sample is 5 microgram in 50 or 100 microliters of elution buffer.

I guess the problem (low or none DNA yield) could be in the suspending medium (mestruum) in general a high concentrated solution of polysaccharides that could interfere with some steps in the extraction protocol (e.g. DNA binding to the column). I even tried to centrifuge the sample before starting the purification in order to separate the medium (surnatant) from the semen (pellet), but it didn't work!

Do anyone experienced the same problems?

Do anyone have any idea of a good commercial kit useful for my purposes (96-wells plates, minimum of 5 microgram, getting rid of suspending medium interference.)?

Any suggestion is appreciated!

Thanks a lot

Davide Perini

Davide.perini@unicatt.it

Clontech Smart RACE problems

Hello!

I have tried Clontech Smart 5' and 3' RACE with no success on the amplification of 5' and 3' cDNA, however GSPs work well as the GSP1 + GSP2 positive control gave good amplification, so cDNA is also ok. Anyone has a clue to go on..

Million thanks!

iruka_kin@yahoo.com

DNA extraction formol

Dear All,

I need to extract DNA from fish specimens that have been in formol for 3 years to less than six months. If anyone has had success extracting DNA in such circumstances, I would extremely appreciate if you could share the protocol used.

Thank you and best wishes,

Ella Vazquez Dominguez

Instituto de Ecologia, UNAM Tel. (5255) 5622 9015

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Ciudad Universitaria evazquez@ecologia.unam.mx

Mexico DF 04510

http://www.ecologia.unam.mx/-academicos/vazquez/ella_contacto.htm

evazquez@miranda.ecologia.unam.mx

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DNA from dry barnacles

Dear All,

I have some 15 year-old dried barnacle specimens and am exploring techniques to get DNA from them for amplification. If anyone has had success with such techniques in old crustacean material, I would be grateful to hear about them. The species involved all have membranous bases and very little soma (body tissue besides shell) is visible.

Thank you and best wishes, Anne Marie Power

Room 226, Martin Ryan Institute Department of Zoology National University of Ireland, Galway Ireland Tel: +353 91 493015 Fax: +353 91 525005 <http://www.nuigalway.ie/zoology/power> AnneMarie.Power@nuigalway.ie

Drosophila Mortality Problems

Dear all,

I'd like to call for advice or suggestions from people of the Evodir community who have encountered mortality issues in *Drosophila* lines.

Six months ago, the *Drosophila pseudoobscura* populations raised in my lab have suddenly shown high levels of mortality (80-90%), when the flies are 5-6 day old, particularly males. The flies that are still alive in the bottles look normal and have subsequent normal survival, although they seem to be a bit less productive. The problem has persisted despite trying several different procedures:

1) The room where the flies are handled was thoroughly cleaned (with dilute bleach and 90% ethanol) several days in succession and much of our equipment (plasticware, yeast etc.) was replaced.

2) An experiment was carried out to determine if the food was hosting some microorganism that could be the cause of the infection. This involved raising males and females separately on 3 different types of food medium; normal (cornmeal molasses medium), sugar agar or a potato based medium. Flies were transferred to fresh vials of the appropriate medium every day for around 10-14 days. The vials were then observed to see if anything grew on these substrates; it was assumed we could detect any microorganism present in the food. There was no obvious presence of a microorganism growing on any substrate and the survival of the flies did not differ according to which substrate they were kept on.

3) Finally, an antibiotic treatment (0.025% tetracycline) was introduced to the food. Flies cultured on this substrate were less productive and pupated faster than those on normal food. The offspring of the treated generation survived normally for one generation. Unfortunately, the following generation again displayed the same symptoms of mass mortality at 5 days old. I have contacted companies that can identify microorganisms and suggest treatments but they were not able to respond our queries.

I would be really grateful if anyone has any suggestions on other procedures that I could undertake or who to contact who would be able to suggest solutions to determine the problem. Thanks!

Nelly Gidaszewski Research associate Department of Animal and Plant Sciences University of Sheffield UK
email: n.gidaszewski@sheffield.ac.uk

Nelly <n.gidaszewski@sheffield.ac.uk>

Fs Batch Software

Dear Colleagues,

I am looking for software that will calculate Fu's Fs statistic, and that can be run in batch mode (making it possible to analyze many simulated data sets without need for user input). Ideally, I would like something that runs in UNIX and will accept Phylip, Nexus, or FASTA formatted data files. Any suggestions would be most appreciated.

Best regards,

Chris Smith.

Christopher Irwin Smith, Ph.D. Post-doctoral Research Fellow University of Idaho - Department of Biological Sciences Moscow, ID 83844 ph: 208 885 4229 fax: 208 885 7905

csmith@uidaho.edu chris.smith@post.harvard.edu
<http://www.webpages.uidaho.edu/~csmith/ChrisSmith.htm> Beginning Fall 2008:

Assistant Professor Department of Biology Willamette University Salem, OR 97301 503-370-6013

csmith@uidaho.edu

F statistic sample size answers

Thanks to everyone who responded to my question "Sample size calculation for 'F' statistics".

For your interest, I append the original question and copies of all responses.

***** original question *****

I want to look at parasites in a number of separate hosts to check for non-random breeding within hosts. Obviously there will be differences in genotypes between hosts (Fst) and non-random mating would show up as a significant Fis value. The problem is what sample size would I need to detect a given value of Fis? It looks like most people avoid the issue of sample size or power calculations when doing F statistics. The best recent one I could come up with is

N. Patterson, A. L. Price, and D. Reich. Population structure and eigenanalysis. *Plos Genetics* 2 (12):2074-2093, 2006.

They present calculations for Fst between two populations and state that the minimum Fst that can be reasonable detected is $1/\sqrt{nm}$ where n is no of individuals and m is no. of molecular markers. Would it be outrageous to extrapolate this to Fis so that, for example, examining parasites from 100 animals would have power to detect a minimum Fis of $1/\sqrt{100}=0.1$?

Responses (in chronological order of receipt) were as follows:

>From Adam Porter

The thing about power in F-statistical analyses is that the error variance depends on allele frequencies, in addition to the number of loci and populations (& scoring error). Frequencies near 1/2 give the highest power; if you're dealing with rare alleles, you need a lot more individuals to get the same insight. So, you have to make assumptions about the distribution of allele frequencies, which entails accounting for multiple and varying numbers of alleles at different loci. Another potential source of variation, in host-parasite cases with few founders and very high rates of increase: you might get stochasticity in mating patterns that could produce transient inbreeding or outbreeding patterns within a single host;

this would be problematic only if you measure the offspring from the first generation, but it would require sampling from more hosts regardless of numbers of individuals or loci.

Given the array of variance sources, personally I would try to simulate the process, varying the true inbreeding parameter and sampling regime, to see what variance I got. The simulation is pretty straightforward, since you can calculate the expected genotype frequencies as deviations from Hardy-Weinberg, then sample from those and recalculate the statistic. It should be possible to get a decent idea using a spreadsheet.

>From Peter Smouse, (I can forward the pdfs on request- Ian)

this is the sort of question people asked of breeding designs in Quantitative Genetics. I am attaching two *.pdf of our own papers. The equation (in the first TwoGener paper) you want to look at is # (10), and the translation would be Phi-ft becomes Fst. In the second paper, we pick the argument apart a bit more, because there are design issues. You should look at Falconer, re the variance of an intra-class correlation, and you should track it back to its original source. Try Falconer and Mackay (the most up to date version of the book), and in a pinch, get in touch with Trudy Mackay. She'll be able to guide your efforts. Note that the number of loci does not (for that treatment) come into the argument, but then Falconer was talking about pedigree relationships and groupings, where we are averaging over a very large number of loci, not assaying particular groups of convenient genetic marker loci. Fst and Fis are going to be a little trickier, because there is extra replication involved. Good luck with it. PS, John Nason recently asked me a similar question, so he is probably working on it as well.

***** >From Rodney J. Dyer.

In a perfect world the assumptions behind the $1/\sqrt{nm}$ would hold up, but unfortunately, we do not live in such a world. As a result, IMHO the best approach would be to subsample your data set as you go to find out when the variance of your estimator stabilizes. We did this in Dyer, RJ and VL Sork. 2001. Pollen Pool Heterogeneity in Shortleaf Pine, /Pinus echinata/ Mill. /Molecular Ecology/ 10: 859-866. It will work the same for you for Fis. You may also want to think about the Ayers&Balding estimators for the distribution of inbreeding rather than point estimates (Fis is in general non-symmetric).

>From Bruce Weir:

If it is Fis you want, then the easiest thing is to recognize that the chi-square goodness-of-fit test for Hardy-Weinberg is $n(m-1)f^2$ where n is the sample size, m is the number of alleles at the locus and f is the sample value of Fis. If f is replaced by the parametric value then $n(m-1)f^2$ is the noncentrality parameter for the noncentral chi-square distribution.

e.g. For a two-allele locus, the noncentrality is nf^2 and this should

— / —

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>

IIASA Austria SummerStipends

Summer Fellowships for Young Scientists at the International Institute for Applied Systems Analysis

Funding is available for PhD students interested in three months of collaborative research on

Evolutionary and Ecological Modeling

in population ecology, evolutionary ecology, community ecology, spatial ecology, and fishery ecology.

Young scientists from all countries are eligible for stipends, provided by IIASA's Evolution and Ecology Program, contributing to travel and accommodation costs. Students from Austria, China, Egypt, Estonia, Finland, Germany, India, Japan, Korea, the Netherlands, Norway, Pakistan, Poland, Russia, South Africa, Sweden, and the USA are eligible for fellowships providing travel, accommodation, and living expenses.

Summer research projects are invited in any of the following areas

Fisheries-induced Evolution Adaptive Speciation Adaptive Dynamics Food Web Evolution Evolution of Cooperation Evolutionary Conservation Biology Spatially Explicit Evolutionary Models Moment-based Spatial Models Artificial Evolution

Previous experience with implementing and studying evolutionary or ecological models will be an important asset. Informal inquiries about specific research interests and plans can be directed to Ulf Dieckmann (dieckmann@iiasa.ac.at).

Online applications have to be submitted before January 15, 2008.

Since 1977, the annual Young Scientists Summer Program (YSSP) of the International Institute for Applied Systems Analysis (IIASA) in Laxenburg, Austria, has attracted 1400+ students from 70+ countries. The YSSP 2008 will take place from June 2 to August 29, 2007. IIASA is located in the former summer palace of Austria's royal family, ca. 15 km south of Vienna. IIASA's summer program offers exceptional opportunities for acquiring experience in an international and interdisciplinary research environment. Research training is based on regular personal interaction with advising senior scientists, and typically leads to a publication in an international journal (as well as to a chapter in a candidate's PhD thesis).

Some useful links:

+ http://www.iiasa.ac.at/Admin/YSPP/reg-info-more_about_the_program.html Details about the summer program, and online application

+ www.iiasa.ac.at/Research/EEP Information about IIASA's Evolution and Ecology Program

+ www.iiasa.ac.at/Research/EEP/Students.html Examples of successful YSSP projects

+ www.iiasa.ac.at/docs/IIASA_Info.html General information about IIASA

Ulf Dieckmann Program Leader Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

Email dieckmann@iiasa.ac.at Phone +43 2236 807 386 Phone secretary +43 2236 807 231 Fax +43 2236 807 466 or +43 2236 71313 Web www.iiasa.ac.at/Research/EEP Online reprints www.iiasa.ac.at/~dieckman FishACE Network www.iiasa.ac.at/Research/EEP/FishACE FinE Network www.iiasa.ac.at/Research/EEP/FinE dieckman@iiasa.ac.at dieckman@iiasa.ac.at

Nb estimation using linkage answers

Here is my original question:

Dear EvolDir folks,

I have a sample from a single cohort of juvenile frogs and am wondering if I can apply the linkage disequilibrium method (as implemented in the NeEstimator

program) to this sample to get an estimate of the effective number of the parents (N_b) that produced the juvenile cohort. Can anyone verify or refute this? I have microsatellite genotype data for the juveniles as well as the adults, so I will have an N_b estimate from the temporal method as well. I am hoping to use the LD method to get an additional estimate of N_b .

Any of your comments on this issue will be greatly appreciated!

Thank you,

Ivan

And here are the answers I received:

Yes, you certainly can get an estimate of parental N_b from your samples of juvenile frogs (you can also get another estimate from your sample of adults). You can get such an estimate from NeEstimator, but you might want to consider as an alternative a program (LDNe) we wrote and have described in a paper in press at Mol. Ecol. Notes. LDNe has a couple of advantages over other methods based on linkage disequilibrium: * it implements the bias correction described in Waples 2006 (Con. Genetics 7:167-184.) * It provides separate estimates based on different user-specified criteria for excluding rare alleles. this facilitates evaluation of potential biases from use of microsat data.

it is easy to use and reads standard input files (FSTAT, GenePop). you can access the program, user's manual, and related files at <http://fish.washington.edu/xfer/-LDNE/> you might also consider using OneSamp (recently described in an online early paper by Tallmon et al. in Mol. Ecol. Notes). this program uses approximate Bayesian computation methods to derive an estimate of effective size based on a single sample.

for your temporal estimate, if you have sampled the adults non-lethally you have Plan I samples and you should make sure you use an estimator that accounts for the correlation in allele frequencies between parents and offspring. this requires an estimate of N , the total number of adults your initial sample was (presumably randomly) sampled from.

best wishes, and let me know if you have any questions.

Robin Waples

Regarding your question posted on EvolDir:

First of all I suspect you already have the references on this method? Here are some - there may be more:

Bartely D, Bagley M, Gall G, Bentley B (1992). Use of linkage disequilibrium data to estimate effective size

of hatchery and natural fish populations. Conservation Biology, 6, 365-375.

England PR., Cornuet J-M, Berthier P, Tallmon DA, Luikart G (2006). Estimating effective population size from linkage disequilibrium: severe bias in small samples. Conservation Genetics, 7, 303-308.

Hill WG (1981). Estimation of effective population size from data on linkage disequilibrium. Genetical Research, Cambridge, 38, 209-216.

Waples RS (1991). Genetic methods for estimating the effective size of cetacean populations. Report of the International Whaling Commission (special issue 13), 279-300.

Waples RS (2005). Genetic estimates of contemporary effective population size: To what time periods do the estimates apply? Molecular Ecology, 14, 3335-3352.

Weir BS, Hill WG (1980). Effect of mating structure on variation in linkage disequilibrium. Genetics, 95, 477-488.

I've used Ne estimator to estimate the number of breeders from a single cohort of amphibian progeny as you outline. With my dataset (40 tadpoles per population and 9 microsatellite markers), I definitely received estimates within a plausible range, when applying this method. Not knowing the actual number of breeders in the various populations, I had no way of testing the reliability however. I can only say that in general the results appeared in the range we expected, and that large populations yielded a larger Ne-estimate than small populations.

Nonetheless, I think you should be very careful to use any of the Ne methods isolated, and the results should always be interpreted with caution. To employ several methods in combination and use a large number of polymorphic markers would of course be preferable.

I would be very keen to see the answers you get, so please post them, if you receive anything useful. Also, I would appreciate to learn your opinion and experiences with the method once/if you chose to apply it to your data.

Cheers,

Morten

Morten E. Allentoft

M.Sc., Ph.D. candidate

School of Biological Sciences

University of Canterbury

Private Bag 4800

Christchurch New Zealand

Ivan C. Phillipsen Department of Zoology Oregon State University Corvallis, OR 97331-2914 philliv@science.oregonstate.edu

NTSYS analysis choice

Hi,

I am currently working on a population genetics project, trying to find out within and among population dis/similarities. We amplified the ISSR region, scored bands, and generated a band present/absent table for each individual. We have 8 populations and an average of 30 individuals per population and we have data from 9 primers for each of these individuals. We have scored around 1200 plus across individuals and across loci.

Our first choice was to use NTSYS to calculate distances and further generate a dendrogram. I am sure many out there have experience working with NTSYS. Here are my questions:

1. First of all is this the correct choice for my kind of data? If not then what?
2. If using NTSYS, what will be the sequence of operations that I should perform? Ultimately I need within and among population comparisons. What is the way of arranging data in order to obtain among population comparisons? Or do I have to first carry out within population comparisons and then is there some way of averaging out distances obtained from such comparisons to further use for among population comparisons?
3. Is it relevant to obtain comparisons across populations for each primer?

Thanks,

Sheeja George Biological Scientist UF
sheejageorge@ufl.edu sheejageorge@ufl.edu

PC equivalent of SeAl

Dear All, does anyone know of a PC equivalent of SeAl,

a program which basically allows manual alignments of sequences?

Thanks for your help

Dr. Sarah Helyar Marine Biodiversity, Ecology & Evolution (MARBEE) Science Centre West University College Dublin Belfield, Dublin 4 Republic of Ireland

email: sarah.helyar@ucd.ie tel. +353 1 7162013/2262 fax. +353 1 7161152 <http://www.ucd.ie/zoology/-marbee/sarah-helyar.html> sarah.helyar@ucd.ie

PennState Astrobiology Summer

Please announce to your undergraduates:

Penn State's Astrobiology Summer Program - 2008 (An NSF-REU Site)

Each summer the program supports 10 students from universities and colleges across the U.S., between their freshman and senior years, to conduct research with astrobiologists (including evolutionary biologists) for 10 weeks at Penn State (8 June to 16 August, 2008). Activities also include a behind-the-scenes field trip to NASA-Goddard Space Flight Center, NASA Headquarters, the Smithsonian Air and Space Museum, as well as weekly seminars, discussion groups and a research symposium. The program covers the cost of travel (up to \$500), room, and meals and provides a \$4,000 stipend. For further information see <http://evo.bio.psu.edu/asp/>. Review of applications begins February 15th.

sbh1@psu.edu sbh1@psu.edu

Peru VolFieldAssist AmazonianBirdEvol

VOLUNTEER FIELD ASSISTANTS

Volunteer field assistant(s) sought for an ornithological research project at Los Amigos Research Station, SE Peru for at least three months, any time from Mar 2008 onwards.

Assistant(s) will be required to carry out behavioural observations on color-banded birds, mist-netting, nest-

searching, nest-monitoring, trail cutting, and data entry. Work forms part of a long-term research project into the mechanisms of species co-existence in Amazonian birds. Work will be carried out mainly alone at 04:30 to 11:00 am and 14:00 to 18:00, six days a week. Field conditions are hot and humid, encounters with snakes are fairly common, and wasp and bee stings are frequent. This work is suitable for those with a love of birds and the tropics, who are interested in pursuing a career in behavioral ecology or evolutionary biology, and who have previous field experience. Strong preference will be given to those who speak Spanish and have experience in mist-netting and reading color bands on small birds. No salary offered, and assistants from outside Peru must cover international travel. All other expenses (i.e. station fees and local travel) will be covered.

Applications should be made via email to Claire Salisbury (claire.salisbury@zoo.ox.ac.uk) with: (1) a cover letter explaining why you want this challenging job (2) a 2-page CV (3) the names and email addresses of three researchers familiar with your field skills.

claire.salisbury@zoo.ox.ac.uk
claire.salisbury@zoo.ox.ac.uk

Precast gels

Dear all

I would like to hear someone that it has used the Genephor electrophoresis unit (Amersham Bioscience) to analyse microsatellites about the success and the possible alternatives more cheaper than the original precast gels.

With very best wishes and thanks

Paulo

Paulo António Russo Almeida Departamento de Zootecnia Univ. Trás-os-Montes e Alto Douro Apartado 1013 5001-801 Vila Real PORTUGAL e-mail: prusso@utad.pt tel: +351-259350432 fax:+351-259350482

Paulo Russo Almeida <prusso@utad.pt>

Question Fis vs Relatedness

Dear All,

We are struggling with FIS and Relatedness results obtained for several populations of tilapia - a cichlid fish with complex mating behaviors.

We have found 2 different cases: - 3 population FIS >0 ***=> Relatedness(non-significant) - 4 population FIS >0*** => Relatedness*** Just by curiosity we have run Relatedness as well on populations showing FIS=0 and found X population with FIS=0 => Relatedness***(?).

Positive Fis values are generally regarded as departure to HWE due to heterozygote deficit. Among the different factors that may explain we find: 1. Technical artefacts (null alleles, allele stutter => most of the time, tested using Microchecker or a similar method) 2. Sub-structure (tested with Structure, PartitionML or AMOVA approach) 3. Inbreeding - due to potential mating among relatives (tested using Relatedness or Identix for instance).

The impact of the two first ones have been tested and ruled out as potential factors causing Fis>0 on our populations. Identix and relatedness have been run to check whether the presence of related individuals in our samples may explain these results.

Question: Would it be possible that heterozygotes deficits -revealed by FIS- do not reflect exactly the same thing than the results of Relatedness (excluding cases of technical artifact & sub-structure) => for instance different degree of kinship (recent and remote common ancestors)? Or could it be just an effect due to the calculation method of associated probabilities for these different estimators (Fis & R), eventually affected differently by the stochasticity of sampling (e.g. more sensitivity to detect departure from H0 for Fis than R estimators)? Does anybody know a paper about this subject?

Any help would be greatly appreciated. Thanks a lot for your time and expertise.

Best wishes,

Etienne & Pat

Etienne Bezault, PhD Aquatic Ecology & Evolution Institute of Zoology, University of Bern & Centre of Ecology, Evolution & Biogeochemistry, EAWAG

Seestrasse 79, CH-6047 Kastanienbaum SWITZERLAND Phone/Fax: +41 (0)41 349 21 69/68 e-mails: etienne.bezault@eawag.ch or ebezault@yahoo.fr Web: <http://www.fishecolgy.ch/> etienne.bezault@yahoo.fr

Smithsonian Panama Summer Internship Treefrog Evolution

Dear Colleagues,

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

<http://people.bu.edu/kwarken/KWLabREU.html>

Please encourage any students whom you believe would benefit from this experience to apply. Applications are due February 10, 2008.

Thank you, Karen Warkentin

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

Karen Warkentin <kwarken@bu.edu>

Social learning evolution tournament

Tournament: The evolution of social learning strategies: 10,000 euro prize

Dear all,

This email is to provide information about a tournament that might be of interest to evolution researchers. The tournament has a cash prize of 10,000 euro:

We have received funding from the European Commission to organize a major international multi-disciplinary tournament on the evolution of social learn-

ing, inspired by Robert Axelrod's famous Prisoner's Dilemma tournaments on the evolution of cooperation. In recent years there has been a lot of interest (spanning several research fields, but especially economics, anthropology, and biology) in the problem of how best to acquire valuable information from others. Mathematical and computational solutions to this problem are starting to emerge, often using game-theoretical approaches. We feel the time is right for such a tournament, a sentiment shared by leading researchers in the field who are enthusiastic about this project. We have set up a committee of world-leading scientists as experts to help us design the tournament (Rob Boyd, Marc Feldman, Magnus Enquist, Kimmo Eriksson) and other leading authorities in this area of science, including Axelrod, have been advising us.

In the competition, entrants will submit behavioural strategies detailing how to respond to the problem of resource gain in a complex, variable environment in terms of combinations of individual and social learning. Where social learning is involved, entrants will be required to specify effective rules (e.g. conform, imitate the most successful individual, copy in proportion to each demonstrator's payoff, copy when dissatisfied, etc). Entered strategies will be evaluated in two stages, with good performers in pair-wise contests going forward to an all-against-all melee. The author(s) of the strategy that performs best overall will be presented with a cash prize of 10,000 euros at the European Human Behaviour and Evolution Society meeting, in St. Andrews, U.K. in April 2009.

The competition is now running, and has a closing date of June 30 2008 and active website: <http://www.intercult.su.se/cultaptation/tournament.php>.

On behalf of ourselves and the committee we would like to encourage you, the members of your laboratories, and your colleagues and collaborators, to participate in this competition. Please forward this message to anyone you think might be interested. We hope that the social learning strategies tournament will increase understanding of, and stimulate research on, the evolution of learning, as Axelrod's tournament did for the evolution of cooperation.

Luke Rendell Kevin N. Laland University of St Andrews – Dr. Luke Rendell Post-Doctoral Research Fellow Tel: (44)(0)1334 463499 E-mail: ler4@st-andrews.ac.uk WWW: <http://bio.st-andrews.ac.uk/~staff/ler4.htm> School of Biology, University of St. Andrews Bute Medical Building, Queen's Terrace St. Andrews, Fife KY16 9TS U.K.

Social Learning Strategies Tournament - 10,000 Euro

prize: <http://www.intercult.su.se/cultaptation/-tournament.php>
 Luke Rendell <ler4@st-andrews.ac.uk>

+44 131 6508624
 a.rambaut@ed.ac.uk a.rambaut@ed.ac.uk

Software FigTree v1 1

I have posted a new version of FigTree (v1.1):

<http://tree.bio.ed.ac.uk/software/figtree/> Despite the small increment in version number, it is a fairly major update. It can now re-root the tree, rotate nodes and collapse clades (or draw them as a big 'cartoon' triangle).

It is cross platform and binaries are available for Mac, Windows and UNIX/Linux.

I have also now made the source code available:

<http://http://figtree.googlecode.com/> Andrew

Andrew Rambaut Institute of Evolutionary Biology
 University of Edinburgh Ashworth Laboratories Edinburgh
 EH9 3JT EMAIL - a.rambaut@ed.ac.uk TEL -
 +44 131 6508624

Software FigTree v1 1 1

I have posted an updated version of FigTree (v1.1.1):

<http://tree.bio.ed.ac.uk/software/figtree/> This fixes a number of bugs that were kindly reported since v1.1 was released. It also adds a couple of features.

As over 600 people have downloaded the last version since my announcement on EvolDir, I have created a mailing list for announcements of new versions of FigTree (there will be no other messages on this list - it is not a general discussion list - only I can post):

<http://groups.google.com/group/figtree-announce> Or use the form on the FigTree page, above.

If you use FigTree I urge you to join this as I will not announce other minor updates on EvolDir.

Thanks, Andrew

Andrew Rambaut Institute of Evolutionary Biology
 University of Edinburgh Ashworth Laboratories Edinburgh
 EH9 3JT EMAIL - a.rambaut@ed.ac.uk TEL -

Software MultiDivTime Helper

Dear EvolDir folks,

We would like to thank all users for the feedback we have received. Based on these suggestions we have developed a new version of the script, which incorporates most of the requests made. The two most important improvements are:

1.- The alignment file must be in FASTA format, the script will now take care of the format conversion automatically.

2.- The script now creates a file containing tree(s) with branch lengths that can be used to estimate the root to tip distances in TreeStat (<http://tree.bio.ed.ac.uk/software/treestat/>). There is a tree per partition, and it should be ready to be loaded into TreeStat for the root to tip calculations.

This script can be obtained at www.biokubuntu.com (click in enclases). If you find any problems please let us know.

Federico G. Hoffmann (federico@biokubuntu.com)
 Juan C. Opazo (jopazo@biokubuntu.com)

jopazo2@unlnotes.unl.edu jopazo2@unlnotes.unl.edu

Software Phobos TandemRepeatDetection

Dear Community,

Phobos is a new and highly accurate search tool for tandem repeats (microsatellites, minisatellites, and satellites) in complete genomes.

Some of the most important features are:

- search modes for perfect and imperfect tandem repeats.

- perfect repeats can be detected in the pattern size range from 1 to 5000 bp (and more) in complete genomes

- imperfect repeats for which two successive units are identical can be detected in the pattern size range from 1 to 5000 bp (and more) in complete genomes
- imperfect repeats for which no two units must be identical can be detected in the pattern size range from 1 to 50 bp (and more) in complete genomes.
- Phobos searches for overlapping repeats and for repeats hidden within other repeats.
- Phobos searches for alternative alignments.

Example: Let us consider the following simple target sequence AT(ATATAG)_{x10} with 10 repetitions of the main pattern. Using a mismatch penalty of -4, most microsatellite search tools detect in this sequence only the imperfect repeat with repeat pattern (AT). In contrast, Phobos detects the perfect repeat with pattern (ATATAG) and (if requested by the user) also the imperfect repeat with lower score and pattern (AT).

- Phobos uses an exact, in particular non-probabilistic search algorithm.
- Phobos is fast. Detecting imperfect microsatellites (1-6bp) takes, with a mismatch and gap penalty of -6, about 30 minutes on a modern computer.
- The main feature of Phobos is the high precision with which it finds tandem repeats. This makes Phobos an ideal tool also for a statistical analysis of tandem repeats in genomic libraries and complete genomes.
- Phobos comes as a version with GUI and a command-line version.

Download: http://www.ruhr-uni-bochum.de/spezzoo/cm/cm_phobos.htm Project status: (current Phobos version 3.2.6) ————— Phobos is still in development. It has been released for public use a while ago since we believe that in its current state it is already one of the leading tools in its discipline. Its high accuracy is a major advantage over all other tandem repeat detection tools that are currently available.

The following features are currently under development and should become available this year:

- More filter options shall be given to the user concerning which and how many alternative alignments should be reported. (Currently: Report only best alignment or report all alternative alignments Phobos has found.)
- Detection of compound tandem repeats
- A statistical analysis tool (finished except for the GUI).
- I still see the potential of significantly reducing the run time of Phobos especially for long repeat patterns.

Comments and suggestions are always welcome.

Best regards,

Dr. Christoph Mayer Department of Animal Ecology, Evolution and Biodiversity, NDEF 05/751 Ruhr-Universitaet Bochum 44780 Bochum Germany

Email: cm@tp4.rub.de Web.: www.ruhr-uni-bochum.de/spezzoo/cm Tel.: 0234 32 25072

Christoph Mayer <cm@tp4.ruhr-uni-bochum.de>

Software RAxML-7 0

Dear Community,

RAxML has recently been updated and is now available for download as RAxML-7.0.0 at icwww.epfl.ch/~stamatak/ (software frame) together with the Manual (v7.0.0).

Some of the most important new features are:

- A rapid Bootstrapping algorithm, that is on average 15 times faster than the current RAxML Bootstrapping algorithm, while yielding qualitatively comparable results.
- A novel, more efficient, fine-grained parallelization that is based on Pthreads instead of OpenMP. It is also easier to compile and intended for use on shared-memory machines and multi-core architectures.
- RAxML can now analyze heterogeneous datasets that comprise concatenated sequences of DNA and AA data.
- Option to perform a per-partition optimization of branch lengths.

In addition, there are many more less important new options that are listed at <http://icwww.epfl.ch/~stamatak/index-Dateien/Page443.htm> and on the first page of the Manual.

Comments and suggestions are always welcome.

Best regards,

Alexis

– Dr. Alexandros Stamatakis

Postdoctoral Researcher High Performance Computing Bioinformatics

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Alexandros.Stamatakis@epfl.ch
Alexandros.Stamatakis@epfl.ch

Alexan-

Software TreeFinder-BugFixes

Sorry folks,

the November 2007 TREEFINDER was unstable in some cases and should no longer be used. There is now a repaired version available at:

www.treefinder.de The good news is that the instabilities all produced error messages, so if you have not seen any message, your results are OK. The new TREEFINDER is now more stable, more accurate, more efficient, more thoroughly tested than ever before. TREEFINDER is a software to compute phylogenetic trees from molecular sequences.

New features are:

- model proposer for DNA, Proteins, RNA - sequence simulation dialog - improved tree search algorithm - several bugfixes

The model proposer can generate partitioned models.

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

Gangolf Jobb

Gangolf Jobb <gangolf@treefinder.de>

Software TreeSnatcher

we have developed a JAVA application, "TreeSnatcher", that might be of interest for researchers in the field of Phylogenetics. Please kindly refer to our website: <http://www.cibiv.at/software/treesnatcher/> Abstract: "TreeSnatcher is a GUI-driven Java application for the semi-automatic recognition of multifurcating phylogenetic trees in pixel images. The program accepts an image file as input and analyzes

the topology and the metrics of a tree depicted with user assistance. The analysis is carried out in a multiple-stage process using basic algorithms from the field of image analysis. It yields a Newick expression that represents the tree structure optionally including branch lengths. TreeSnatcher can process trees with more than 100 leaves or more in a few seconds."

The JAVA source code will be made available upon request. It is our hope that someone will build a better user interface, improve the concept or write a similar program.

We welcome any suggestions

Best regards,

Thomas Laubach B. Sc. Dept. of Bioinformatics
Heinrich-Heine-University Duesseldorf

Thomas Laubach <tlaubach@gmx.de>

SouthAfrica FieldAssistVolunteers

Volunteer needed as field assistants for the project:

Socio-Evolution of small Mammals in the Succulent Karoo of South Africa

>From April 2008 onwards

Project: We study the reasons of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students with a BSC/Vordiplom or equivalent are preferred as candidates. Applicants must have an interest in working in the field and with animals. Whereas the research is mainly non-invasive, this is no job for extreme animal right persons (we take tissue and blood samples). Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o' clock), and stops its activity with dusk (19 o' clock). Work during nights might also be necessary. Work in the field will be done for 5-6 days a week. Applicants must be able to manage extreme temperatures (below 0 at night, sometimes over 40C during days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small group.

Work of field assistants: Trapping and marking of mice

and rats; radio-tracking to determine home ranges and nest sites; direct behavioral observations in the field; experiments and observations with captive specimen under natural weather conditions; maintenance and cleaning of the research station.

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 750 (around 80 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 2000 or 200 Euro/month). Including extras, you should expect costs of about 350 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: Currently we are looking for a volunteer from April 2008. Field assistants are expected to stay at least 2 months, but longer periods of up to 6 months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to carsten.schradin@zool.uzh.ch.

More information under www.strippedmouse.com Contact via e-mail: carsten.schradin@zool.uzh.ch

Best regards, Carsten

Dr. Carsten Schradin Research Associate, Zoological Institute, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel; +41 - (0)44 635 5486 Fax: +41 - (0)44 635 5490

(Tel. secretary: +41 - (0)44 635 5271)

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

Succulent Karoo Research Station, Goegap Nature Reserve, Private Bag X1, 8240 Springbok, South Africa.

visit <http://www.strippedmouse.com> Carsten Schradin <carsten.schradin@zool.uzh.ch>

SouthDakota FieldAssist AvianReproductionTiming

FIELD ASSISTANTS needed for a field study in the Black Hills National Forest of South Dakota starting roughly at the beginning of April and running through the end of July 2008 (dates somewhat flexible). The research aims to study the effects of environmental cues on the endocrinology and reproductive timing of Dark-eyed juncos. I will require three field assistants that will help with all the aspects of the work, including locating birds on their territories, finding nests, targeted and passive mist-netting, bird measuring and blood sampling, nest monitoring, behavioral observations, and various other activities related to field experiments on birds. Crew members will be also be responsible for keeping detailed field notes, as well as completing some lab work and data entry associated with progress in the field. Applicants with a degree or progress toward a degree in the life sciences will have an advantage, as well as those with field experience in finding nests, mist-netting, and bird handling. However, motivation is a primary consideration: the work is hard and demanding, may take place in changing weather and requires long hours at times. Field assistants will be expected to work 6 days per week, have the ability to work both independently and cooperatively, be self-motivated and demonstrate a willingness to learn new skills, and be willing to do minor manipulative research with animals. The work is very rewarding if you are interested in animal behavior and like to be outdoors. Housing will be provided, and financial assistance will be available to cover some living expenses as well as transportation to the study site. Write to Christy Bergeon, Department of Biology, Indiana University, 1001 E. 3rd St., Bloomington, IN, 47405 or email (preferred) cbergeon@indiana.edu. Please include a summary of your background and your reasons for applying for this position, as well as the names and email addresses of 3 people who might evaluate your work or potential. REVIEW OF APPLICATIONS WILL BEGIN 15 FEB 2008, but applications will be accepted until positions are filled.

cbergeon@indiana.edu cbergeon@indiana.edu

SSE Dobzhansky Prize

2008 Theodosius Dobzhansky Prize The Dobzhansky Prize is awarded annually by the Society for the Study of Evolution to recognize the accomplishments and future promise of an outstanding young evolutionary biologist. The prize was established in memory of Professor Dobzhansky by his friends and colleagues, and reflects his lifelong commitment to fostering the research careers of young scientists.

Eligibility The candidate must have a Ph.D. (or equivalent) awarded no earlier than May 2004 and no later than 1st February 2008, and must be actively involved in research in the field of evolutionary biology. There are no other restrictions. Applicants do not have to be members of the Society for the Study of Evolution, but such membership is encouraged.

Nomination/Application.- Candidates may apply directly or may be nominated. Established researchers are encouraged to nominate outstanding young scientists who may be unaware of the existence and prestige of this prize. Each candidacy must be supported by the following materials detailing the candidates career to date: (1) a curriculum vitae, (2) a summary of research accomplishments, (3) a 3-5 page statement of research plans for the next 5 years (note length limitation), (4) pdf copies of three recent publications, (5) names and addresses of the three referees (including the nominating scientist where applicable) who have sent supporting letters. N.B.: THE THREE LETTERS OF REFERENCE ARE SENT SEPARATELY, but no application will be considered without these letters. All application/nomination materials and letters of reference must be sent as PDF e-mail attachments. No file type other than PDF will be accepted. The deadline for receipt of all materials, including letters of reference, is 15 February 2008. All materials should be sent to the secretary of SSE (Dale H. Clayton) at the following email address: careymadsen@bioscience.utah.edu

Award.- The Dobzhansky Prize is accompanied by a check for U.S. \$5000, and will be awarded at the annual meeting of the Society for the Study of Evolution, June 20-24 2008, at the University of Minnesota, Minneapolis. The recipient is expected to be present to receive the award and to give an oral presentation about his/her research. To facilitate attendance, the SSE provides funds to cover the costs of conference registration,

accommodation during the conference, and expenses for travel to and from the conference. The recipient will be notified of the award by late March 2008.

Notice: 2008 R. A. Fisher Prize The R. A. Fisher Prize is awarded annually by the Society for the Study of Evolution for the ³best² Ph.D. dissertation paper published in the journal *Evolution* during a given calendar year. The award comes with a \$1000 honorarium.

Eligibility. To be eligible for consideration, a manuscript must be from a dissertation completed in the year of publication or in the two previous years. Membership in SSE is not a prerequisite; however, the author must have completed the Ph.D.

Nominations/Application. Authors of eligible manuscripts may initiate a nomination upon acceptance of their manuscripts for publication. Nominations must include the final version of the manuscript, dissertation completion date, and a supporting letter from the Ph.D. supervisor or other individual familiar with the work. If the candidate is not the sole author of the paper, the supporting letter should identify the candidate's role in completing the research and writing the paper. Nominations for manuscripts published in 2007 will be accepted throughout the year but must arrive no later than January 31, 2008. The complete nomination should be submitted electronically to: the secretary of SSE (Dale H. Clayton) at the following address: careymadsen@bioscience.utah.edu

Carey Madsen <careymadsen@biology.utah.edu>

Systematic Biology offer

Other: Open Access Systematic Biology Introductory Offer 2008

The publisher of Systematic Biology, Taylor & Francis, is offering a special introductory rate for open access of \$500 per article. Articles accepted for publication during 2008 are eligible for this discounted rate and will remain open access in perpetuity.

Systematic Biology, the journal of the Society of Systematic Biologists, is the most highly cited primary research journal in the field of Evolutionary Biology (third most highly cited if review journals TREE & AREES are included). Systematic Biology's 2006 Web of Science most recent "5-year impact factor" was 10.466.

Tardigrade samples

Hello members of Evoldir.

My name is Søren Faurby I am a danish Ph.D. student working on the biogeography of tidal tardigrades, which usually are found in rather high densities associated with barnacles and occasionally other substrates.

My traveling funds are unfortunately extremely limited and I would therefore greatly appreciate if some of you could send samples of dried barnacles (50-100 individuals).

Samples from the southern hemisphere are especially interesting but collections from almost everywhere would be greatly appreciated. I would be happy to collect material for you in Denmark in exchange if you are interested.

Kind regards, Søren

Ph. D. student Søren Faurby Ecology and Genetics Institute of Biology University of Aarhus Ny Munkegade - Building 1540 8000 Århus C Denmark

soren.faurby@biology.au.dk
soren.faurby@biology.au.dk

Tetraploid microsatellites software

Dear Evoldir I have a question about tetraploid microsatellites from plants: How to build a Minimum Spanning Network of haplotypes? or other kind of graphic representation that give me an idea of genetic relatedness

1)The topic was already discussed in 2004 at least but I can not now get the complete answers (these were truncated in the month review of September and July 2004). If you could provide me the complete replies to Madhav Pandey who posted the question in July 2004 that could help also.

2) Anyway that was in 2004, we are in 2008 is there now any way to treat tetraploid microsatellites without knowing the allele dosage. I understood in 2004 Ruzica used Arlequin to make a MSN with different ploidy

levels including tetraploids so that should be possible (paper in Molecular Ecology 2004, 13:2101-2103). Do anyone knows how to put the data into Arlequin? : as Haplotypic or Genotypic data? If haplotypic data, how will be the 2 or 3 allele samples interpreted by Arlequin (as missing data or what)?

EXAMPLE OF MY DATA: Locus 1

Plant 1 112

Plant 2 112 114 118 120

Plant 3 114 118

Plant 4 118

Plant 5 114 118 120

3) Is there NOW any other better program to treat tetraploid microsatellites?

Thank You very much for your help

Cheers

Helena

Helena Cotrim <hmcotrim@fc.ul.pt>

UBern VolunteerFieldAssist BirdFertility

Ubern: field assistance bird fertility

I am seeking an enthusiastic volunteer interested in assisting a field study in Bern, Switzerland. The research aims to study the effects of carotenoids and oxidative stress on sperm quality in a passerine bird, the great tit. The tits are a good system to examine such questions as they are hole nesting birds and can then be easily manipulated. I am part of a 5 people lab team, all working with great tits in natural conditions. We work with about 300 nestboxes for each, disposed in several forest around Bern. I will require 1 field assistant that will help with all the aspects of the work, including checking nests, ringing the birds, catching adults, making treatments, and more. Applicants with a Msc in Biology/Ecology and with bird handling experience would have an advantage. Supervising for potential Msc analysis and report would be assured by PhD and post-doc people from the lab. Motivation will play a key role: the work is hard and demanding, may take place in changing weather and requires long hours at times. The study will start at the end of March 2008 until the end of May 2008. Fluent English or French speaking is

required as well as a valid European driving license.

Applicants can send me a letter + CV and ask for further details or questions on the following email address:

/

sylvain.losdat@esh.unibe.ch/

Sylvain Losdat Evolutionary Ecology Group, Zoological Institute University of Berne Baltzerstr. 6 3012 Bern Switzerland

email: sylvain.losdat@esh.unibe.ch phone: +41316313020 mobile: +33684614383/

Sylvain Losdat <sylvain.losdat@esh.unibe.ch>

PostDocs

BrandomU AscomyceteSystematics	56	UArizona EvolutionaryBiology	65
CornellU ComputationalGenomics	57	UAzores SubterraneanBioDiversity	66
EAWAG Switzerland PlanktonCommunityEvolution	57	UCBerkeley ComparativeBiodiversity	67
France FloralEvoDevo	58	UCollegeCork PlantApomixisGenetics	67
InstGulbenkian Portugal EvolutionaryCellBiology .	58	UCollegeLondon EvoDevo	68
IowaStateU SexGenomics	59	UCopenhagen PlantMitochondrialEvolution	69
Leiden AmphibianEvoDevo	59	UdeBourgogne ZebraFinchLifeHistory	69
Montpellier Forest Genetic Diversity	60	UHawaii InsectEvolFunctionalMorphology	70
Montpellier MolEvol	61	UNorthCarolinaWilmington Evolution marine inverts	71
NCI-Frederick Maryland ComparativeGenomics ...	61	UParis-Sud11 Phylogenetic trees	71
QueensU EvolutionaryTheory	62	UPennsylvania HumanEvolGenomics	72
RanchoSantaAna Botanic Garden SystEvolPlantBio	62	UPittsburgh EvolutionaryBiology	72
Russia SalmonParasite EvolutionaryGenetics	63	Uppsala ComputationalGenetics	73
Townsville Australia MolecularPhylogeneticist	63	UTexasAustin NicheVariation	73
TromsoNorway SkuaLifeHistoryChange	64	UZurich Post-copulatory sexual selection	74
UAlaska Evolution	64		

BrandomU AscomyceteSystematics

Postdoctoral position in ascomycete systematics

A full-time postdoctoral position in ascomycete systematics is available immediately in the Department of Biology at Brandon University. The focus of this research is the investigation of the Chaetomiaceae (Sordariales, Ascomycota). Candidates should have a Ph.D. in mycology, plant pathology, or a related discipline, previous experience in the cultivation and molecular characterization of ascomycetes, training in phylogenetic analy-

sis, and a strong interest in systematics and revisionary taxonomy.

This position has guaranteed funding for one year with a possibility of extension. Salary is commensurate with experience and qualifications, with a minimum of \$32,000 per year.

The City of Brandon is a small community (pop. 42,000) with a lively cultural life and vibrant economy. It offers a high quality of life and many, all-seasons recreational opportunities. Brandon is located 100 km from Riding Mountain National Park and is 200 km from the City of Winnipeg (pop. 634,000).

All qualified candidates are encouraged to apply. However, Canadian citizens and Permanent Residents will

be given priority. Interested individuals should send a curriculum vitae, contact information for three references, and a cover letter describing their interest in the position to <untereiner@brandonu.ca>. Please place the words postdoc in the subject line of your email.

Wendy A. Untereiner, Ph.D. Professor, Department of Biology and Tier II CRC Brandon University 270-18th Street Brandon, MB Canada R7A 6A9 Tel.: 204-727-9603 (office), 204-724-5482 (lab) Fax.: 204-728-7346 Email: untereiner@brandonu.ca

Wendy Untereiner <untereiner@brandonu.ca>

CornellU ComputationalGenomics

Postdoctoral Position in Computational Genomics at Cornell University

A POSTDOCTORAL POSITION is available in the laboratory of Dr. Adam Siepel in the Department of Biological Statistics and Computational Biology at Cornell University (Ithaca, NY). The research focus will be in the general areas of comparative/evolutionary genomics, population genetics, phylogenetics, and/or functional element identification, with specific topics to be determined in consultation with the candidate. The candidate will be expected to participate in both methods development and data analysis, to work cooperatively with other lab members and outside collaborators, to help maintain and improve the laboratory infrastructure (software, databases, etc.), and to actively publish and present results. The position involves no mandatory teaching, but interested candidates will be given opportunities to deliver guest lectures and mentor undergraduates. The ideal candidate will be enthusiastic, highly motivated, and independent, will have a strong background in one or more of the areas of focus, a serious interest in molecular biology and genetics combined with good skills in mathematics and computer science, and a strong record of accomplishment in research.

Required qualifications:

- Ph.D. in bioinformatics, computer science, statistics, genetics, molecular biology, applied mathematics, or a related field.
- Research experience (with first-author publications) in computational genomics
- Fluency in probabilistic modeling and computational statistics
- Proficiency in programming, ideally in C or C++ as well as in scripting languages such as perl, matlab, or

R. Should be comfortable in a linux environment, with large data sets, computer clusters, and database software.

Term:

The term is flexible but most likely will be 2 or 3 years. The proposed start date is Spring or Summer of 2008. Applications will be accepted until the position is filled.

To Apply

Submit a CV, a short (roughly two-page) description of research interests and experience, and contact information for three references by e-mail to acs4 at cornell dot edu. Informal inquiries are welcome.

For complete information, see <http://-compngen.bsccb.cornell.edu/~acs/postdoc-ad.html>

Adam Siepel 101 Biotechnology Building Cornell University Ithaca, NY 14853 phone: 607-254-1157

Cornell University is an affirmative action/equal opportunity employer.

Adam Siepel <acs4@cornell.edu>

EAWAG Switzerland PlanktonCommunityEvolution

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

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

Postdoc in plankton community evolution

The Postdoc will work on a 3 year project in which long term continuous data on phytoplankton abundance and diversity are collected in lake ecosystems (using in situ scanning flowcytometry) and studied for patterns in community assembly. The role of ecological assortment and trait evolution on phylogenetic clustering / overdispersion will be studied. The study forms a basis for better understanding the impact of climate change on lakes in (pre)Alpine regions.

For this, directly from Eawag financed project, we are looking for a highly motivated candidate. The ideal candidate has modeling and good statistical skills and a demonstrable interest in plankton ecology and evolution.

We offer a stimulating research environment in a lively and social institute in Kastanienbaum (near Luzern), where several other evolutionary and ecologically oriented aquatic research groups are based. The position will be for a period of three years, and may start from May 2008 onwards. A PhD degree in biology or related subject is necessary for admission. The working language in the group is English.

The project is a collaborative effort between different departments in Eawag. Amongst others a close collaboration with the group of Prof. Reichert (Department of System Analysis, Integrated Assessment and Modeling) on further development of biogeochemical lake models is foreseen. Part of the work will be done in the Netherlands (Group of Prof. Jef Huisman) where the phytoplankton field dataset will be analyzed for chaotic patterns. Transfer of the knowledge (e.g. on innovative monitoring techniques) to stakeholders like the Swiss Cantons is a relevant part of the final stages of the project.

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

Please submit your application by 1 March 2008 as one PDF file to Sandra Isenring, Eawag, Human Resources Department: recruiting@eawag.ch, indicating reference number 084402 For further information, consult <http://www.eawag.ch> or contact Bas Ibelings (Tel + 41 41 349 2174), bas.ibelings@eawag.ch

Bas.Ibelings@eawag.ch

France FloralEvoDevo

< <http://moulon.inra.fr/SGV/GEAR/geargb.html> >

Postdoctoral Position:

*Evolutionary developmental genetics of floral symmetry in Basal Eudicots

*A postdoctoral position is available for 18 months at UMR Genetique Vegetale - France. The objective is to characterize diversity and evolutionary patterns of TCP transcription factor genes (/Cycloidea/-like genes) in Basal Eudicots. The research is designed to better understand the patterns of duplication and evolution of paralogues in this gene family, and the possible connec-

tions with the evolution of floral symmetry.

The successful applicant must have a background in molecular evolution concepts (phylogeny, tests for adaptive evolution), with strong lab experience in molecular methods (e.g., PCR, race-PCR and cloning). Candidates with less optimal profiles will be considered providing that their motivation and past experience allow them to adapt rapidly to the project. Applications will be reviewed from January 2008 until the position is filled. Postdoc annual salary is approximately 28.000 euros and includes medical benefits.

Applicants should submit their CV, a short summary of research interests and contact information of two references (either electronically or via post) to:

Dr. Catherine Damerval, UMR Genetique Vegetale, Ferme du Moulon, 91190 Gif-sur-Yvette, France - damerval@moulon.inra.fr <<mailto:damerval@moulon.inra.fr>>

For more information, please visit our web site at

<http://moulon.inra.fr/SGV/GEAR/geargb.html> <
<http://moulon.inra.fr/SGV/GEAR/geargb.html> >

–
 Catherine DAMERVAL UMR Genetique Vegetale
 INRA/INA PG/UPS/CNRS La Ferme du Moulon 91
 190 Gif-sur-Yvette FRANCE Tel : 33 (0)1 69 33 23 66
 Fax : 33 (0)1 69 33 23 40

damerval@moulon.inra.fr damerval@moulon.inra.fr

InstGulbenkian Portugal EvolutionaryCellBiology

Instituto Gulbenkian de Ciencia, Portugal - Post doc position in evolutionary cell biology

The Computational Genomics Laboratory (www.evocell.org) is looking for a post-doctoral fellow to work on the origins and evolution of intracellular compartmentalization and protein trafficking pathways. This involves a mixture of small-scale sequence and structural analysis as well as global genomic analyses, combined with the design and implementation of databases, visualization and querying systems. Unicellular pathogens such as Trypanosoma and Plasmodia are of special interest to us, as well as Fungi and Metazoa. This post would suit someone with prior experience in Bioinformatics and/or computer science, with an interest in evolution, genomics and

cell biology. We favor experience with scripting (Perl and/or Python), databases (SQL), familiarity with molecular evolution and protein structure. Extremely motivated applicants with any combination of the above skills will be considered.

The fellowship would be initially for two years. The successful candidate would be encouraged to apply for independent funding from international funding bodies.

The Institute "Instituto Gulbenkian de Ciencia" (www.igc.gulbenkian.pt) is located in Oeiras, a small sea-side town 12 Km away from Lisbon, next to several other research institutions. We are a private research institute with roughly 30 research groups, pursuing fundamental questions in biomedical sciences using interdisciplinary approaches. We are part of a research consortium with two other research institutes, and within this there is wide interest in computational and theoretical biology (<http://compbio.igc.gulbenkian.pt>). The institute promotes the organization of workshops, courses and various types of meetings or visitors programs (e.g. EMBO workshop on Light Microscopy on Living Cells, PhD program in Computational Biology and regular Bioinformatics Training program both taught mostly by international faculty) and it has a generous budget for inviting international speakers. All communications are done in English (even within teams that only have Portuguese members). And the quality of life is great in Portugal (the Institute is 5 min walking distance from beach), and the cost of living is still lower than in most other places in the European Union.

Applications in PDF format will be accepted by email only (to jleal@igc.gulbenkian.pt) until February 15th, 2008, and will include a short CV, a motivation letter, two recommendation letters or contacts of two references

jleal@igc.gulbenkian.pt

IowaStateU SexGenomics

POSTDOCTORAL POSITION in Genomics at Iowa State University.

A postdoctoral position is available to study the gene expression response to naturally fluctuating temperature in turtles with alternative sex determining mechanisms. The position is part of an NSF-funded project in the laboratory of Dr. Nicole Valenzuela, Department of Ecology, Evolution, and Organismal Biology,

Iowa State University. The position calls for field and laboratory developmental experiments to help elucidate the effect that naturally-fluctuating temperature has on the expression of genes involved in gonadal formation in turtles with temperature-dependent and genotypic sex determination, and how males and females are produced in nature. Explicit hypotheses derived from previous gene expression and ecological research will be tested to help reveal how TSD species may respond to short- and long-term climate change. Primary responsibilities for this position include: 1) conducting field and laboratory research in developmental biology and gene expression analyses; 2) molecular evolution analyses; 3) maintaining laboratory databases and requesting/retrieving specimens from multiple sources; 4) analyzing data and writing manuscripts, and 5) helping to coordinate projects of graduate and undergraduate students involved in the project. For additional information concerning this and other research projects, please refer to the laboratory web site (<http://www.public.iastate.edu/~nvalenzu>).

Successful applicants should have a Ph.D. in developmental biology, ecology, evolution, or a related field. Strong molecular skills are desirable. Salary is \$35,000 plus benefits, and funds are available for two years pending satisfactory progress. The position can begin as early as September 1 2008. Review of applications will begin immediately and continue until a candidate is selected.

To apply, please send a cover letter, CV, and names and e-mail addresses of three references to Nicole Valenzuela (nvalenzu@iastate.edu), Department of Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, IA 50011-3223, USA.

ISU is an equal opportunity/affirmative action employer.

Dr. Nicole Valenzuela Assistant Professor Dept. of Ecology, Evolution, and Organismal Biology Iowa State University 239 Bessey Hall Ames, IA 50011 (515) 294-1285 <http://www.public.iastate.edu/~nvalenzu/> nvalenzu@iastate.edu nvalenzu@iastate.edu

Leiden AmphibianEvoDevo

Postdoctoral Research Assistant (3 years) in amphibian evo-devo, Leiden, The Netherlands

A postdoc with molecular biology experience is required

for a joint position between the Institute of Biology, Leiden and the National Museum of Natural History - Naturalis, Leiden. The project will involve a comparative study of Hox gene expression in the embryos and larvae of European salamanders with a view to understanding body plan evolution. The project is funded by the Netherlands Organisation for Scientific Research. Please send your application to MR or PA by e-mail or postal mail before January 18, 2008.

Enquiries to Prof. Michael Richardson (m.k.richardson@biology.leidenuniv.nl) or Dr. Pim Arntzen (arntzen@naturalis.nl).

Michael Richardson, Institute of Biology, Leiden University, Kaiserstraat 63, 2311 GP, Leiden, The Netherlands. Phone: (international: 31) (0) 71 527 5215; fax: 71 527 4900.

Pim Arntzen, National Museum of Natural History | Naturalis, P. O. Box 9517, 2300 RA Leiden, The Netherlands. Phone: (international: 31) (0) 71 568 7618; fax: 71 568 7666.

Montpellier Forest Genetic Diversity

Postdoc

Projet post-doctoral 2007 Reference P-EFPA-4 Axe de recherche INRA : Environnement et espace rural
 Departement de recherche : Ecologie des forests, prairies et milieux aquatiques (EFPA)
 Champ thematique du departement : Adaptation des organismes et des populations e leurs milieux
 Nom de l' unite de recherche : UMR Biodiversite, genes et communautes (BIOGECO)
 Responsable de l' unite : A Kremer
 Responsable scientifique : C Plomion (Christophe.Plomion@pierroton.inra.fr) (INRA), JM Bouvet (CIRAD)
 Titre : Etude de la diversite nucleotidique de genes candidats impliquees dans la composition chimique du bois chez l' eucalyptus et le pin /
 Pattern of nucleotide diversity in candidate genes for wood chemical properties in eucalyptus and pine

Discipline(s) scientifique(s) : Genetique des populations, genetique moleculaire, Genomique / Population genetics, Molecular genetics, Genomics
 This project is driven by our desire to understand the genetic basis of wood formation, a unique feature of trees, and by our ambition to exploit this knowledge to accelerate and improve tree breeding for wood and end-use properties. There is a great need to accelerate breeding in

forest trees because of their long generation times and the projected demand for increased production of good quality fibres. However, ecological concerns and market acceptability require knowledge-based, non-GMO tree improvement. In this context, our goal will be to identify genes and nucleotide polymorphisms that govern naturally occurring phenotypic variation of wood and end-use properties in breeding populations of *Pinus pinaster* and *Eucalyptus urophylla*, two species belonging to the main forest tree genera used in industrial plantations.

Rational/Background : During the past 40 years, optimisation of silvicultural practices combined with the introduction of improved varieties have contributed to increase the productivity of our forest in temperate and tropical regions. Gains in productivity have often been followed by a reduction in harvest age which has led to a greater proportion of lower quality juvenile wood being harvested. In order to maintain the utility of plantation grown wood, there is now a critical need to focus breeding efforts on the improvement of wood quality. INRA and CIRAD have developed multidisciplinary researches in order to study whether these traits are variable and heritable and whether simple and early selection criteria can be defined. In addition, QTL analysis and the tool kits of genomics have been used in concert in order to identify the genes putatively involved in wood properties.

Objectives : The main objective of this project is to study the landscape of nucleotide variation of candidate genes for wood chemical composition, as a prerequisite toward the application of gene assisted selection. First, the level and structuration of the diversity will be described in the genetic pool from which the breeding populations were derived. Second and keeping in mind the potential adaptive value of wood, we will test whether the pattern of nucleotide diversity is compatible or not with the effect of natural selection.

Methodology, Partner, and Schedule: Re-sequencing and cloning will be used to describe nucleotide diversity in a discovery panel of 20-40 genotypes. In *Eucalyptus*, emphasis will be made on cellulose biosynthesis related genes. The study will be carried out in Montpellier for one year, within the forest genetics unit of CIRAD (http://www.cirad.fr/ur/genetique_forestiere). In pine, 2000 amplicons are being re-sequenced in USA (NSF project coordinated by D Neale), and will be used in association study for several wood properties including chemical composition. Genes for which SNPs will be significantly associated with trait variation will be selected for full length resequencing. The study will be carried out in Bordeaux for one year, within the BIOGECO research unit (<http://www.pierroton.inra.fr/>-

biogeco/). Nucleotide and haplotype diversity, extent of linkage disequilibrium, departure from the neutral model of evolution will be the main outputs of this study. In perspectives, relevant polymorphisms will be selected for association mapping in both species.

Jean-Marc Bouvet CIRAD, Biological System Department Head of Research Unit 39: "Genetic Diversity and Breeding of Forest Tree Species" Campus international de Baillarguet TA A-39/C 34398 Montpellier Cedex 5 FRANCE Tel: 33 (0)4 6759 3728 Fax: 33 (0)4 6759 3732 Web site : http://www.cirad.fr/-ur/genetique_forestiere Personal web site : <http://agents.cirad.fr/index.php/jean-marc.bouvet@cirad.fr> jean-marc.bouvet@cirad.fr

Montpellier MolEvol

A 18-month post-doc position is available in Montpellier, France, to be started before May 2008.

Project: Molecular evolution of the mitochondrial mutation rate

The evolution of mitochondrial DNA is of particular interest given its importance as a marker of biodiversity, and its implication in fundamental processes of life. The mtDNA mutation rate is very high in animals, and varies by several orders of magnitude across lineages. These variations have been linked to species metabolic rate, body mass, and longevity. Taking mammals as a model taxon, and making use of the extensive genomic resources available in this group, this project aims at analysing the evolution of candidate genes potentially controlling the mutation rate of the mitochondrial genome.

Salary: 2500 euros per month

Requirements: This is in the first place a bioinformatic project, although switching to an experimental stage at some point is conceivable. Skills in molecular phylogeny, evolutionary/population genomics, bioinformatics, statistics and programming will be appreciated.

Context: Montpellier is a dynamic city of southern France hosting a strong community of evolutionary biologists. The post-doc will be part of the Molecular Phylogeny group (E. Douzery, N. Galtier, F. Delsuc, S. Glemin, V. Ranwez, F. Catzeflis, among others). We deal with a variety of questions about molecular phy-

logeny, systematics, and genome evolution.

Recent publications of ours relevant to the project:

- Nabholz et al 2008 Strong variations of mitochondrial mutation rate across mammals - the longevity hypothesis. *Mol Biol Evol* (ahead in pub) - Ranwez et al 2007 Orthomam: a database of orthologous genomic markers for placental mammal phylogenetics. *BMC Evol Biol* 7:241 - Bazin et al 2006 Population size does not influence mitochondrial genetic diversity in animals. *Science* 312: 570-571. - Galtier et al 2006 Mutation hot spots in mammalian mtDNA. *Genome Res* 16: 215-222.

To apply: send CV + references to Nicolas Galtier galtier@univ-montp2.fr galtier@univ-montp2.fr

NCI-Frederick Maryland Comparative Genomics

A Postdoctoral position is available in the Laboratory of Genomic Diversity of the National Cancer Institute-Frederick (Chief, Stephen J. O'Brien), in Frederick Maryland (<http://home.ncifcrf.gov/ccr/lgd/>). The position is in the comparative genomics and evolutionary biology group led by Jill Pecon-Slattery, to investigate aspects of genomics, genetics, and evolution of mammalian genomes.

We are interested in characterizing genome patterns of diversity, recombination, and mutation; conducting gene annotation; detecting endogenous retroviruses; and uncovering repetitive elements in ongoing whole genome projects of carnivores, primates, and ungulates. The successful candidate will have a PhD in genetics, genomics, or a related field.

A background in the application of bioinformatic methods to genome studies and/or host-pathogen genomics would be a competitive advantage. Please submit to Jill Pecon-Slattery by email (slattery@ncifcrf.gov) the following: (1) a complete curriculum vitae, (2) a 1-2 page research statement, (3) PDF files (no more than 2) of reprints, and (4) the name, address, and email of three references. Review will begin February 1, 2008, and will continue until the position is filled.

slattery@mail.ncifcrf.gov slattery@mail.ncifcrf.gov

QueensU EvolutionaryTheory

Postdoctoral Fellowship in Evolutionary Theory

Applications are sought from outstanding researchers for a 2-year postdoctoral position in evolutionary theory, working in the lab of Dr. Troy Day in the Departments of Mathematics and Statistics and the Department of Biology at Queen's University (www.mast.queensu.ca/~tday). The specific research topic is wide open, with current projects in the lab focusing on developing theory for kin selection and spatial models of evolution, host/parasite epidemiology and (co)evolution, evolutionary immunopathology, genomic imprinting and nongenetic inheritance, and coral bleaching. The successful applicant will be free to conduct research in any of these or other related areas of interest. Ideally the position will be taken up by Sept. 1, 2008 but there is some flexibility in start date. Salary will be C \$40,000 per year.

Information about the Department of Mathematics and Statistics, the Department of Biology, and Queen's University can be found at www.mast.queensu.ca, <http://biology.queensu.ca> and www.queensu.ca respectively.

To apply, send a current CV and a statement of research interest to Troy Day via email (tday@mast.queensu.ca). Please include the names of 2-3 potential referees, but applicants need not solicit reference letters at this stage. Review of applications will begin on February 15, 2008 and continue until the position is filled.

math122@mast.queensu.ca

RanchoSantaAna Botanic Garden SystEvolPlantBio

Please post the following on the EvolDir:

Postdoctoral Fellowship in Systematic & Evolutionary Plant Biology

Rancho Santa Ana Botanic Garden invites applications for the Fletcher Jones Foundation Postdoctoral Fellowship in Botany. Applications for this full-time position are solicited from individuals with a primary in-

terest in, and commitment to, active field-, lab- and/or collection-oriented research in the systematics, phylogenetics, or evolution of vascular plants using contemporary techniques. We seek an individual who will bring an exciting and innovative project that will complement and extend on-going research activities, and who will interact extensively with scientists, students, and professional staff.

The Garden's Research Department is home to staff scientists who are also faculty members at Claremont Graduate University; 14 graduate students; and facilities that include laboratories (molecular and structural, including SEM); an herbarium of more than 1.1 million plant specimens, almost entirely of vascular plants; an excellent research library; and extensive plant growth facilities. For additional information about Rancho Santa Ana Botanic Garden and its Research Department, please visit <http://www.rsabg.org> or communicate with any of the department's faculty.

Candidates must have their Ph.D. prior to beginning the position. This is a one year position with possible extension to two years based on performance. The position carries a competitive salary (\$39,000) and a budget of \$5,000 per year for research expenses.

Regular employment at Rancho Santa Ana Botanic Garden is for no specified period of time; conditions and status of employment (hours, pay, title, duties, etc.) are subject to change at any time. Employees, and likewise RSABG, are free to end the employment relationship at any time, for any reason, with or without notice or cause, unless otherwise prohibited by law.

To apply, send a letter of interest, a curriculum vitae, and a brief research proposal (no more than 10 pages all inclusive). The proposal should clearly indicate how the project both extends the applicant's dissertation research and fits into his/her long-term plans. Please also include the names, addresses (including e-mail), and telephone numbers of three references. Send applications to: Ms. Alex Charlap, Fletcher Jones Postdoc Search, Rancho Santa Ana Botanic Garden, 1500 N. College Ave., Claremont, CA 91711. Applications will be considered beginning Feb. 15, 2007 for a starting date in mid to late 2008.

j.travis.columbus@cgu.edu

Russia SalmonParasite EvolutionaryGenetics

Title- Russian speaking post-doctoral/PhD student position in salmon parasite evolutionary genetics

A position is available for up to 2.5 years to work as part of a collaborative project aimed at understanding the molecular and ecological mechanisms that have contributed to evolution of *Gyrodactylus* parasite resistance in Atlantic salmon populations of the Karelian republic in Russia. Our earlier research has demonstrated that a remarkable feature of this host-parasite system is that there is a gradient of parasite tolerance which mirrors the phylogeography of Atlantic salmon: The freshwater salmon of Karelia (in Lakes Onega and Ladoga) have the longest common history with the parasite and have evolved almost complete immunological resistance.

The project consortium includes research groups in Finland (Prof. Craig Primmer at the University of Turku: <http://users.utu.fi/primmer> ; Prof. Jaakko Lumme at the University of Oulu: <http://cc.oulu.fi/~jlumme/>) and Russia (Dr. Alexei Veselov at the Karelian Research Center: <http://ib.krc.karelia.ru/>).

The successful applicant should be able to communicate fluently in both English and Russian and have a strong background in evolutionary genetics and/or fish parasitology plus an interest in multi-disciplinary research on these topics.

The successful applicant would be expected to spend extended periods of time in each of the research groups as well as in the field in northwest Russia.

Informal inquiries and applications. Applications in BOTH English and Russian should be emailed as pdf attachments to Craig Primmer (craig.primmer@utu.fi) and should include a full CV and publication list, a free-form letter indicating current research interests and motivation for applying for the position and names and contact details of at least two referees. Prospective post docs should also include a statement of previous research and supervision experience and prospective PhD students should send a formal university document outlining courses taken during their degree.

Review of applications will commence on 15.2 with the preferred starting date being April 2008. The salary range is approximately 2350-2600 EUR per month for post-docs and 1730-2050 for PhD students, depending on the level of previous experience of the candidate.

Relevant project publications:

Kuusela, J. Zie; tara, M. S. and Lumme J (2007) Hybrid origin of Baltic salmon-specific parasite *Gyrodactylus salaris*: a model for speciation by host switch for hemichlone organisms *Molecular Ecology* 16: 5234-5245

Tonteri, A., Veselov, A.Je. Titov, S., I., Lumme, J. and Primmer, G.R. (2007) The effect of migratory behaviour on genetic diversity and population divergence: a comparison of anadromous and freshwater Atlantic salmon *Salmo salar*. *Journal of Fish Biology* 70: 381-398

Vasemägi A, Nilsson J and Primmer CR (2005) Expressed sequence tag (EST) linked microsatellites as a source of gene associated polymorphisms for detecting signatures of divergent selection in Atlantic salmon (*Salmo salar* L.). *Molecular Biology and Evolution* 22: 1067-1076

Zie; tara, M. S., Kuusela, J., Veselov, A. and J. Lumme (2008). Molecular faunistics of accidental infections of *Gyrodactylus Nordmann, 1832* (Monogenea) parasitic on salmon *Salmo salar* L. and brown trout *Salmo trutta* L. in NW Russia . *Systematic Parasitology* 69: 123-135.

Craig Primmer

Professor of Genetics Division of Genetics and Physiology Department of Biology (Vesilinnantie 5) 20014 University of Turku FINLAND

tel. +358 2 333 5571 fax. +358 2 333 6680 craig.primmer@utu.fi <http://users.utu.fi/primmer>
Craig Primmer <craig.primmer@utu.fi>

Townsville Australia Molecular Phylogeneticist

We are advertising for a postdoc in molecular phylogenetics on squat lobsters and temperate fishes.

The position will contribute to the Marine Biodiversity Hub, which is a collaboration among marine scientists from AIMS, CSIRO, Geoscience Australia, Museum Victoria, and the University of Tasmania, that is funded by the Commonwealth Environment Research Facilities (CERF) Programme. The outputs of the project will support the sustainable management of Australia's marine environment.

This position will use molecular phylogenetic methods to reconstruct biogeographic histories of selected taxa in the decapod families Chirostylidae and Galatheididae, and several fish groups identified as indicator groups in the National Marine Bioregionalisation of Australia.

All details are on our website www.aims.gov.au/-

employment Feel free to contact Madeleine van Oppen for more information about the position

Dr Madeleine van Oppen Principal Research Scientist
Australian Institute of Marine Science PMB No. 3,
Townsville MC Queensland 4810, Australia

Phone: +61-7-47534370 Fax: +61-7-47725852
E-mail: m.vanoppen@aims.gov.au Web address:
www.aims.gov.au

Phillip.England@csiro.au Phillip.England@csiro.au

TromsoNorway SkuaLifeHistoryChange

Postdoctoral Position (three years) - Norwegian Institute for Nature Research (NINA), Department of Arctic Ecology, Tromsø, Norway

Project: Impact of stress from pollutants and climate on the life history and immunocompetence in a seabird top predator, the great skua. Project leader Jan Ove Bustnes

Applications are invited for a three year postdoctoral research associate position (from ~15 March 2008) at the Department of Arctic Ecology, NINA, located in the Polar Environmental Centre in Tromsø, Norway. The position is funded by a grant from The Research Council of Norway.

The main theme of the project is to increase the understanding of how persistent organic pollutants (POPs) are transported through northern marine ecosystems, and how stress from such compounds, in addition to climate change, may affect reproductive costs in top marine predators at latitudes from temperate regions to the high Arctic. A high trophic level seabird, the great skua *Catharacta skua* will be the study species. The study will be undertaken at three main (Shetland, Iceland and Bear Island) and four auxiliary locations. The field studies will, by combining observational and experimental approaches, relate various life history traits (reproductive performance and survival) and other sensitive traits (immune system, stress hormones, blood parameters) to blood concentrations of various POPs.

The Postdoctor will be a member of a strong project group with members from among others NINA, Norwegian Institute for Water Research, the Norwegian Polar Institute, University of Glasgow, Icelandic Institute for Natural History and Great Lakes Institute for Environ-

mental Research University of Windsor, Canada. This exciting environment is ideally suited for research and researcher training. The candidate is expected to take an active part in planning and conducting the fieldwork during the project period.

Candidates must have a Ph.D. in Ecology, Evolutionary Biology or Ecotoxicology. We are looking for a candidate with independent fieldwork experience and with good understanding of laboratory techniques used in ecological and/or ecotoxicological studies.

As NINA would like to increase the percentage of women in research positions, women are encouraged to apply.

The position is remunerated at salary level 54 - 58 on the Norwegian State Salary scale, amounting to an annual gross salary (level 54) of NOK 394.700. NINA offers good pension and insurance schemes.

For further information about the position please contact Senior Scientist Jan Ove Bustnes Jan.O.Bustnes@nina.no Tel. +47 77750407 or +47 93466790 or Research Director Sidsel Grønvik sidsel.gronvik@nina.no Tel. +47 77750408 or +47 92407626

Applications should contain a cover letter including a short summary of past accomplishments and future research interests, a CV, list of publications, PDFs of the most relevant publications, and contact information of two referees. Applications should be sent to NINA, Personalkontoret, 7485 Trondheim Norway, or preferably by e-mail to siri.svendsen@nina.no

Application deadline: 8 February 2008.

Sveinn Are Hanssen Research Scientist

Norwegian Institute for Nature Research - NINA
Postal address: Polar Environmental Centre, NO-9296 Tromsø, NORWAY Delivery/Visiting address: Hjalmar Johansens gate 14, NO-9007 Tromsø, NORWAY Phone: +47 77 75 04 16 * Cell: +47 926 35 455 * Fax: +47 77 75 04 01 * www.nina.no "Hanssen, Sveinn A." <sveinn.a.hanssen@nina.no>

UAlaska Evolution

Post-doctoral Fellowships in Biogeography, Ecology, and Evolution, University of Alaska

The University of Alaska (Anchorage-Fairbanks-Juneau) invites applications to post doctoral fellow-

ships in 2 integrative research foci of biology: Landscape Genetics and Plant-Microbe interactions. This fellowship program is part of the broader NSF-funded Alaska EPSCoR initiative to fund integrative science concerning socio-ecological sustainability in rapidly transforming northern regions. Please refer to < www.alaska.edu/epscor/bio.grad.postdoc.08-09.html > for additional information regarding potential faculty mentors and application procedures.

We anticipate awarding three, two-year fellowships beginning July 2008. Fellowships will provide competitive salaries of approximately \$42,000 plus benefits as well as \$24,000 for research. Fellowships will be offered to high quality candidates that hold a Ph.D. before July 2008 and that have experience conducting research in the subdisciplines of biogeography, landscape & spatial genetics, plant-microbial interactions, ecology & genetics of invasive species, and the influences of environmental change and species interactions on range expansions. In addition, priority will be given to applicants who: conduct research on Alaskan species and with relevance to Alaskan issues, demonstrate potential for collaborative projects that span multiple subdisciplines listed above, and can work with multiple faculty and > 1 campus in the University of Alaska system.

The University of Alaska offers an opportunity to conduct research and live in places of unparalleled beauty and untouched landscapes, as well as unique and cutting edge research opportunities and facilities. Research at UA includes topics such as adaptations to our extreme climate, plant-mycorrhizal biology, invasive species biology, climate change, how interactions among species influence community composition, the unique evolutionary history of organisms influenced by glacial cycles and migrations from both North America and Asia, and the interactions between ecosystems and the people living in them.

To apply:

Interested persons are strongly encouraged to first contact faculty listed below about potential projects prior to submission of an application. Participating faculty can be found at: < www.alaska.edu/epscor/bio.grad.postdoc.08-09.html >. Review of applications will begin on 15 February 2008; to ensure full consideration, applications should be submitted by this date. Applications should include the following:

- 1) Cover letter referencing the position number
- 2) Statement of research interests (up to 2 pages)
- 3) Curriculum vitae
- 4) Three letters of reference

5) UA Applicant Form at < www.uakjobs.com/-applicants/Central?quickFinda842 >

Applications must be received by mail to UAF Human Resources following the instructions provided at www.uakjobs.com/applicants/Central?quickFinda842 . Electronic copies of applications should also be sent to fyepscor@uaf.alaska.edu and the individual faculty member(s) you propose to work with.

Matt Olson <matt.olson@uaf.edu>

UArizona Evolutionary Biology

Positions Available: Research Associate Arizona Research Laboratories, University of Arizona NIH-IRACDA Program in Postdoctoral Excellence in Research and Teaching (PERT)

The Postdoctoral Excellence in Research and Teaching (PERT) Program is a comprehensive program which offers up to three years of support to outstanding candidates seeking advanced post doctorate research training, teacher training and student mentorship in preparation for an academic career. Another desired long-term outcome is to increase the number of well-qualified underrepresented minority students entering competitive careers in biomedical research.

PERT trainees may select from over forty-two faculty research mentors representing a broad range of disciplines in biomedicine, bioengineering, genetics, biochemistry, neurobiology, evolutionary biology, molecular/cellular biology, physiology and behavior. The program stresses the use of non-vertebrate models for Biomedical and Life Sciences research. The program is administered through the Arizona Research Laboratories Division of the Center for Insect Science and is partnered with a Minority Serving Institution, Pima Community College.

Starting salary, based on the NIH NRSA scale, will be \$36,996 for program participants with less than one year of postdoctoral experience, and includes an annual allowance for research supplies and travel. Positions are dependent upon continued funding. Additional information about the Center for Insect Science and the PERT program is available at <http://cis.arl.arizona.edu/PERT> . Qualifications: Applicants must have a Ph.D. in a related field and must be U.S. citizens or permanent residents. Applicants should have no more than two previous years of postdoctoral experience.

rience at the time of application.

Application: All applicants must apply electronically through the University of Arizona's Career Track website at: <https://www.uacareertrack.com>, citing job #40058. All applications are to include: –a letter of interest with a statement explaining how the PERT program will assist the applicant in his/her goals. –a CV –a three to six page research proposal developed with the intended PERT faculty research mentor describing the project to be undertaken during the training period –three letters of reference –a letter of support from the intended faculty research mentor

Original letters of reference and the letter from the proposed faculty research mentor should be mailed to: PERT, Center for Insect Science, 1007 E. Lowell Street, University of Arizona, Tucson, AZ 85721-0106. The letter of interest, CV and research proposal should be submitted online through the UA Career Track website listed above. Review of applications begins Monday, March 3 and will continue until all positions are filled. As an equal opportunity and affirmative action employer, the University of Arizona recognizes the power of a diverse community and encourages applications from individuals with varied experiences and backgrounds. Questions can be directed to: Teresa Kudrna, tkudrna@email.arizona.edu, 520-621-4923.

Teresa Kudrna <tkudrna@email.arizona.edu>

UAzores SubterraneanBioDiversity

Paulo Alexandre Vieira Borges E-Mail: pborges@uac.pt

POST-DOC POSITION

Post-Doctoral Grant Under the scope of the Project PTDC/AMB/70801/2006 A position will be available for a Post-Doctoral Grant holder under the scope of the project "Understanding Underground Biodiversity: Studies in Azorean Lava Tubes" (reference PTDC/AMB/70801/2006), funded by the Foundation for Science and Technology, Ministry of Science, Technology and Higher Education of Portugal (FCT). The research work will take place in the Centre for Agricultural Research and Technology of the Azores (University of The Azores), under the following conditions: 1. Duration, regime of activity and payment: 1.1 Duration: The grant is due to start on February, 2008 and will last for 12 months. It can be renewed for

a maximum of 36 months, depending on the periodic evaluation of the performance of the grant holder. Insufficient performance will lead to termination of the grant. 1.2 Regime of activity: The grant holder will perform the work required under the grant terms in exclusivity, according to the Regulation for Advanced Education of Human Resources of the funding institution (FCT) (<http://www.fct.mctes.pt/pt/apoios/-formacao/ambitoprojectos>). 1.3 Payment: Payment is in accordance to the values established by the funding institution (FCT): monthly payments of 1495,00 + 79,57 (voluntary social security payment). Payments are carried out by bank transfer to the account of the grant holder.

The grant holder will also have an insurance against work accidents. 2. Object of activity: 2.1 The objectives of the Project, as far as this grant is concerned, are: a. Study the biodiversity of microbial biofilms in lava tubes, identifying the microorganisms they contain by culture-dependent and culture-independent methods. b. Study the antimicrobial potential of microorganisms from caves against antibiotic resistant, pathogenic microbial strains. c. Understand the physical environment within the caves. d. Find biological indicators that serve as surrogates for evaluating the biodiversity of microbial biofilms. e. Provide information to various types of target groups (politicians, technicians, scientists, teachers, visitors, etc.) to spread the obtained knowledge and to promote a balanced exploitation of the caves. 2.2 Within this project, the grant holder will carry out work that requires employing: a) Molecular biology techniques; b) Techniques for the maintenance of microbial cultures; c) Chemical, instrumental analysis techniques, such as chromatographic techniques; d) Field work in the area of speleology. 3. Scientific supervision: Dr. Maria de Lurdes Enes Dapkevicius; Dr. Paulo Borges; Dr. Rosalina Gabriel; Dr. C lia Silva, Dr. Diana Northup. 4. Qualification and requirements: Candidates must have a PhD in Biological Sciences, Microbiology, Biochemistry, Molecular Biology or similar areas, with good classification. Candidates that have proved previous experience in microbiology, molecular biology techniques, systems for maintaining microbial cultures, instrumental chemistry and good language skills (both in writing and speaking) of Portuguese or English will be preferred. 5. Criteria for the evaluation of the applications: The evaluation of the applications will be based on the merit of the candidate, taking into account its academic education, its curriculum and previous experience in scientific research of relevance for the project. The curriculum evaluation may be completed with and interview, if judged necessary by the jury. 6. Doc-

uments for application: 6.1 Applications will be formalized by means of a motivation letter addressed to the president of the jury, to which the following documents must be attached: a) Copy of the document that proves the obtention of the academic degree(s), with a list of all marks obtained in each subject in the course; b) Copy of the legal identification document; c) Detailed Curriculum vitae (maximum 10 pages); d) Support letters (maximum 2). 6.2 If the documents required in a) to c) of the previous item are not presented by the candidate, the application is not valid. Note: The present announcement will be published in <http://www.angra.uac.pt/gba>. 7. Applications: Applications will take place within January 14th and January 28th, 2008 (date of the postal stamps). Applications must be sent by post to:

Dr. Maria de Lurdes Enes Dapkevicius Universidade dos Azores Departamento de Cincias Agrarias CITA-A Terra Ch 9701-851 Angra do Herosmo Portugal

Additional informations may be obtained from marienes@notes.angra.uac.pt or pborges@uac.pt, as well as by phone +351 295 402 200 (Prof. Dr. Maria de Lurdes Enes Dapkevicius or Prof. Dr. Paulo Borges).

Paulo Alexandre Vieira Borges <pborges@uac.pt>

UCBerkeley ComparativeBiodiversity

JOB TYPE Post Doctoral Scholar, 2.5 years (beginning March 1, 2008)

JOB AREA University of California, Museum of Vertebrate Zoology (MVZ)

JOB NOTES:

The Museum of Vertebrate Zoology at UC Berkeley is currently engaged in a long-term project to document changes in diversity and distributions of small mammals and birds in California through re-surveys of sites originally examined by Joseph Grinnell and colleagues in the early 20th Century. The intent is to use these data to test the performance of model-based predictions of species responses to changes in climate and land-cover, and thereby improve on predictions of future responses. There is considerable scope for creativity within the broad goals of the project. With support from the National Science Foundation, we seek to recruit two vertebrate ecologists V one at the postdoctoral level and

the other a field biologist. Further information can be found at <http://mvz.berkeley.edu/Grinnell/index.html> or by contacting the Director of the MVZ, Craig Moritz, at craigm@berkeley.edu.

DUTIES: The Post Doctoral vertebrate ecologist will document changes in diversity and distributions of small mammals and birds in California through re-surveys of sites originally examined by Joseph Grinnell and colleagues in the early 20th C. The intent is to use these data to test the performance of model-based predictions of species responses to changes in climate and land-cover, and thereby improve on predictions of future responses. The appointee is expected to lead a field team, analyze data and prepare papers for publication.

QUALIFICATIONS: The ability to lead field survey teams, often in remote locations requiring back-packing and camping, and to commit to extensive periods in the field. Experience with specimen preparation is required as well as strong analytical skills, field experience in small mammal survey, and the ability to communicate its goals and outcomes. Prior experience with spatial modeling or analyses would be an advantage. A PhD and experience in a relevant discipline is required.

Salary range is \$34,752 to \$41,496 commensurate with skills and experience.

To apply for the postdoctoral position: Please email the MVZ Director, Craig Moritz, craigm@berkeley.edu, with a two to four page statement of interest describing your personal and professional background, experience, interests and goals, your CV, transcripts of graduate coursework, and the names and addresses of three references. You may also apply via mail to the MVZ, Director Craig Moritz, University of California, 3101 VLSB, Berkeley, CA 94720-3160. The application deadline is February 22, 2008.

The University of California is an equal opportunity/affirmative action employer.

Chris Conroy

Chris Conroy <ondatra@berkeley.edu>

UCollegeCork PlantApomixisGenetics

UniCollegeCork.PlantApomixisGenetics

Our lab is seeking applications from highly motivated postdocs to work on genetics of reproduction

in *Arabidopsis thaliana*. The successful applicant will work within a small team of researchers investigating approaches for triggering of asexual reproduction (apomixis). We seek enthusiastic and highly motivated candidates with excellent and proven skills in plant genetics, molecular biology and reproduction (as demonstrated by their publication record). We particularly seek candidates with experience of DIC/fluorescence microscopy, in situ hybridisation, cytogenetics, chromatin analysis and/or association/QTL mapping in *Arabidopsis thaliana*. Prospective applicants should send an e-mail outlining your research interest and motivations, including; (a) your C.V. (please list publications and experimental skills) & (b) contact details and e-mail addresses for 3 referees to:

Dr. Charles Spillane, Genetics & Biotechnology Lab, Biochemistry Dept & Biosciences Institute, University College Cork, Cork, Ireland. E-mail: c.spillane@ucc.ie

Lab website: www.ucc.ie/spillane Deadline: 15th January 2008

UCC is an equal opportunities employer

“Spillane, Charles” <C.Spillane@ucc.ie>

UCollegeLondon EvoDevo

Repeat posting because this may have got lost in pre-Christmas emails.

Deadline extended to end of Jan.

Potential projects and duration very flexible so please contact me to discuss.

Apologies for cross posting.

Max

University College London, Dept Biology.

A postdoctoral position is available for 9 months from February 2008, funded by the Marie Curie Research Training Network “ZOONET” to study comparative animal development. Potential projects include:

- Expression of developmental genes in *Xenoturbella* and comparisons with other deuterostomes.
- Developmental genes in the platyhelminths and evidence for secondary simplification in the flatworms.

Applicants should have a doctorate and relevant experience of molecular biology and comparative developmental studies. Training will be given in the full range

of approaches relevant to Evolutionary Developmental Biology, and may require exchanges between laboratories in the ZOONET network, as well as participation in network meetings.

In the selection process, the sponsor stipulates that: - Candidates must have at least four and no more than ten years (full time equivalent) of graduate research experience; - At the start of their fellowship, researchers may not have resided or carried out their main activity (work, studies, etc) in the UK for more than 12 months in the 3 years immediately prior to the appointment.

The total annual salary will be approximately: 30,400 without Dependents, 32,767 with Dependents (for employees contributing to a pension scheme), including London Allowances and Marie Curie Allowances. For employees not contributing to a pension scheme, the salary will be approximately: 33,440 without Dependents or 36,043 with Dependents.

Researchers will be eligible for an annual travel allowance (distance dependent) as well as a monthly mobility allowance. Please note, the amounts quoted for salary, mobility and travel allowance will be dependent upon the EU exchange rate at the time of appointment.

Applicants should post their CV and publication list, together with a completed UCL application form, Equal Opportunities form to: Dr. Max Telford, Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. To download the UCL Application Form and Job Description, please go to:

<http://www.ucl.ac.uk/biology/academic-staff/-vacancies/postdoc.html> Closing date for applications: End January 2008

Dr Max Telford Reader in Zoology Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 Fax: +44 (0)20 7679 7096 <http://www.ucl.ac.uk/biology/academic-staff/telford/telford.html> Zoonet: Marie Curie Research Training Network <http://www.zoonet.eu.com> Xenoturbella You Tube video <http://uk.youtube.com/watch?v=3DyJXNcoXL2Xs>

m.telford@ucl.ac.uk

UCopenhagen PlantMitochondrialEvolution

Postdoc position in plant mitochondrial evolution

at Laboratory of Molecular Systematics, Natural History Museum of Denmark, University of Copenhagen

The post doc. position is associated with the project "Molecular Systematics - Limits and Challenges" financed by the Danish Natural Science Research Council. The post doc. project will be centered on aspects of mitochondrial gene evolution including occurrence and formation of processed paralogs, transfer of mitochondrial genes to the nucleus, and substitution rate changes. Research will have a phylogenetic focus and it will be centered on the monocots. For a more detailed project description, application requirements, and deadline; see <http://snm.ku.dk/opslag/evolution/oles@snm.ku.dk>

UdeBourgogne ZebraFinchLifeHistory

A postdoctoral research assistant is required, in 2008, for a project entitled "Oxidative stress, aging and longevity in birds", funded by an ANR grant to Bruno Faivre. The project aims to explore the association between age and (i) anti-oxidant defences, (ii) ROS production and (iii) oxidative damages, and finally life-history traits in zebra finches. Observational and experimental works to control endogenous production of ROS will be conducted. The candidate should have a good background in evolutionary biology and a skill for laboratory work (biochemical analyses). She/he will be involved both in biochemical analyses and in the experiments carried out on living birds. The post is available for one year, starting spring 2008, and will be based in the Universite de Bourgogne, Dijon (UMR CNRS Bio-Sciences). The candidate should not be French.

Further information can be asked to :

Bruno Faivre (bruno.faivre@u-bourgogne.fr <<mailto:bruno.faivre@u-bourgogne.fr>>)

Letters of application, including a CV, the names, postal and e-mail addresses and fax numbers of three academic referees, should be sent to: Bruno Faivre (bruno.faivre@u-bourgogne.fr <<mailto:bruno.faivre@u-bourgogne.fr>>).

Closing Date: *25 January 2008*.

Summary of the project

The study of patterns and processes underlying aging

depends on two crucial questions addressed at two different levels. The first one investigates how natural selection shapes the pattern of aging currently observed. The second one focuses on the proximal physiological and molecular mechanisms that determine the fitness reduction with age. Among the proximal factors, the deleterious effects of internal damages caused by free radicals have received much attention. This idea is based on the observation that mitochondrial respiration produces harmful molecules called oxygen free radicals, or reactive oxygen species. Free radicals are very unstable molecules that are prone to react with other molecules, resulting in an oxidative chain reaction. They can cause deleterious effects on cellular integrity by damaging cellular membranes, peroxidizing lipids, oxidizing proteins or damaging DNA. Because free radical-induced damages accumulate during the lifespan, they have been suggested to be one of the major proximate causes of the age-associated decline in fitness. Birds are particularly interesting species for the study of aging. Indeed, they show particularly low aging rates and extended lifespan compared to mammals of similar size. This is puzzling, because birds have higher metabolic rates, internal temperatures, energy expenditure and circulating plasmatic glucose levels than mammals of similar size. To temper the negative effects of ROS, aerobic organisms have evolved a sophisticated antioxidant system relying on an arsenal of compounds which scavenge and quench free radicals. Therefore, the particularly high longevity of birds may be due to a low production of free radicals or to a high level of antioxidant defences, or both. This proposal attempts to merge the expertise of two disciplines: evolutionary biology and energetic.

Recent publications of the group on the topic

Alonso-Alvarez C., Bertrand S., Devevey G., Prost J., Faivre B. & G. Sorci (2004). Increased susceptibility to oxidative stress as a proximate cost of reproduction. */Ecology Letters /7 : 363-368.*

Alonso-Alvarez C., Bertrand S., Devevey G., Gailard M., Prost J., Faivre B. & G. Sorci (2004). Are carotenoids limiting resources? An experimental test of dose-dependent effect of carotenoids and immune activation on sexual signals and antioxidant activity. */American Naturalist/ 164 : 651-659.*

Bertrand, S, Alonso-Alvarez, C, Devevey G., Prost J., Faivre B. & * Sorci G. (2006). Carotenoids modulate the trade-off between egg production and resistance to oxidative stress in zebra finches. */Oecologia/, 147 : 576-584.*

Alonso-Alvarez C., Bertrand S., Devevey G., Prost J., Faivre B., Chastel O. & Sorci G. (2006). An Exper-

imental Manipulation of Life History Trajectories and Resistance to Oxidative Stress. / *Evolution* /60 : 1913-1924*/. /*

Bertrand S., Faivre B. & Sorci G. / (2006). / Do carotenoid-based sexual traits signal the availability of non-pigmentary antioxidants? An experimental test in zebra finches. / *Journal of Experimental Biology* / 209 : 4414-4419.

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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>

UHawaii InsectEvolFunctionalMorphology

2 POSTDOCTORAL RESEARCHERS: VISUAL TARGET DETECTION IN HAWAIIAN DAMSELFLIES and WING VEIN EVOLUTION IN FLYING INSECTS

UNIVERSITY OF HAWAII. I am seeking two highly motivated postdocs to work on:

Visual target detection behavior, morphology, and visual performance in damselflies: The Hawaiian damselfly genus *Megalagrion* is an endemic adaptive radiation with extensive color variation and extreme ecological diversification in terms of breeding habitat (light environment). Vision is important for foraging (identifying insect prey), identifying sexual partners (females are often cryptic), as well as avoiding predators. Thus, learning the fundamental mechanisms by which these animals with simple visual systems accomplish very difficult visual tasks may have broad implications for their ecology and evolution, in addition to possible practical

applications.

Wing Vein Evolution in Flying Insects: The material properties of insect wings are widely believed to be conferred by the structure and organization of wing veins. We will conduct a broad-based comparative study to quantify wing vein diversity, model how the morphological features of the veins contribute to the material properties of the wing, and how this in turn affects the aerodynamic performance of the wing in flight. Data collected will include confocal microscopy, SEM, and estimates of fluid flow via light microscopy. Morphological data will be used to inform computational models using genetic algorithms to “evolve” wing vein patterns subject to “fitness” imposed by aerodynamics. Models will be validated by field tests of wing damage and flight performance.

Candidates should have the following: Drive and motivation to solve difficult scientific problems. Good communication/interpersonal skills, good experimental skills and experience in either animal behavior, visual or neurophysiology, or kinematic analysis using high-speed video for postdoc 1 and candidates for postdoc 2 should have good experimental skills and experience with microscopy, kinematic analysis using high-speed video, or morphometrics with experience with image analysis. Demonstrated ability to do field and lab work. Self-starter and creative problem-solver. Both postdocs must have some familiarity with scientific computer programming and excellent quantitative skills.

Desirable qualifications: Candidates experienced in the R programming language and with solid data analysis skills are preferred. Candidates interested in extending the project to address major questions in behavior, sensory physiology, or evolutionary ecology are particularly welcome. Fabrication skills. Experience with insects a plus.

Candidates interested in extending the project to address major questions in behavior, sensory physiology, or evolutionary ecology are particularly welcome.

The Butler lab is in the Department of Zoology at the University of Hawaii, studies the evolution of morphology from functional, structural, and adaptive (evolutionary) perspectives. Other projects in the lab include: the evolution of sexual dimorphism in lizards and damselflies, locomotor biomechanics and the physical effects of pregnancy in lizards, opsin evolution in damselflies, and direct modeling approaches to phylogenetic comparative methods.

We have a dynamic network of colleagues and resources available via: the Bishop Museum, Pacific Biomedical Research Center, Hawaii Institute of Marine Biology,

Kewalo Marine Laboratory, Pacific Center for Emerging Infectious Diseases Research, as well as the Bekey Laboratory of Neurobiology.

Appointment is initially for one year, renewable for second year based on satisfactory performance. Competitive stipend. Start date flexible. Positions subject to availability of funds.

E-mail inquiries are welcome to mbutler@hawaii.edu. Applications (preferably by e-mail) should include cover letter, CV, names and contact info for 3 references, pdf's of two most significant publications or manuscripts.

Review of applications begins February 1, 2008 and will continue until filled.

Marguerite Butler <http://www2.hawaii.edu/~mbutler> <http://www.hawaii.edu/zoology/> Marguerite A. Butler Department of Zoology University of Hawaii 2538 McCarthy Mall, Edmondson 259 Honolulu, HI 96822

Phone: 808-956-4713 Lab: 808-956-5867 FAX: 808-956-9812 Dept: 808-956-8617 <http://www.hawaii.edu/zoology/faculty/butler.html> <http://www2.hawaii.edu/~mbutler> <http://www.hawaii.edu/zoology/> mbutler@hawaii.edu mbutler@hawaii.edu

UNorthCarolinaWilmington Evolution marine inverts

Post-doctoral Research Associate

We seek a post-doctoral researcher interested in applying molecular techniques to a variety of questions in the general area of the evolutionary reproductive biology of free-spawning marine invertebrates. Possible projects include:

- 1) Assessing the contribution of genotype at the sea urchin sperm binding locus to fertilization in different flow regimes, in laboratory flumes, using microsatellites for paternity analysis and sequencing of cloned binding alleles.
- 2) Exploring introgression and gamete recognition in hybridizing blue mussels using a combination of molecular markers for species and hybrid ID, assays for gamete interactions, and characterization of multiple sperm lysin loci.
- 3) Evaluating the causes and consequences of multiple paternity in a colonial ascidian via microsatellite-based

paternity analysis.

A Ph.D. degree and prior experience with molecular methods is required. Support is initially available for one year, with continuation subject to future funding.

Consideration of applications will begin immediately and continue until the position is filled. Please send a CV and a cover letter to Phil Yund, Marine Science Center, University of New England, 11 Hills Beach Road, Biddeford, ME 04005. Electronic applications may be submitted to pyund@une.edu

The University of New England is an Equal Opportunity/Affirmative Action employer and strongly encourages the application of candidates of diverse backgrounds. Please see our website (<http://www.une.edu>) for additional information.

Michael A. McCartney Associate Professor Dept. of Biology and Marine Biology Center for Marine Science UNC Wilmington 5600 Marvin Moss Lane Wilmington, NC 28409 Phone 910-962-2391 Fax 910-962-2410

“Michael A. McCartney” <mccartneym@uncw.edu>

UParis-Sud11 Phylogenetic trees

A one year postdoctoral position is immediately available in the group of Pr. Christine Froidevaux “Bioinformatic Team”, (see complete address below) on the following theme: “Phylogenetic trees classification”.

The main objective of the postdoc will be the clustering of phylogenetic trees. A good distance measure should be found to allow the comparison of two different phylogenetic trees. Research work has been done in this domain. The different approaches proposed in the literature should be analysed to determine which one could be used for the purpose of the work.

The analysis of these clusters will be the major work of the postdoc. This analysis should be done using all the information collected in the datawarehouse of the Microbiogenomics project.

The candidate (under 35) must have a good experience in Microbiology and a solid knowledge of the informatic tools used for sequence analysis. Position is for exactly 12 months. It is part of the ANR Microbiogenomics project, special program provided by the French Ministry of Research, and accordingly any visa procedure will be accelerated. The salary will be 2038 euros per month. A Social Security cover will be provided by the

University of Paris-Sud 11. There will be no funding for travel expenses. Knowledge of the French language is not required.

Contact : Jérôme Azé, jerome.aze@lri.fr, 33 1 69 15 64 09 Laboratoire de Recherche en Informatique, Université de Paris-Sud 11, Bâtiment 490, 91405 Orsay Cedex, France <http://www.lri.fr/~aze/> Jérôme Azé <Jerome.Aze@lri.fr>

UPennsylvania HumanEvolGenomics

University of Pennsylvania: Postdoctoral Positions in Human Evolutionary Genomics

Postdoctoral positions are available in a human population genetics laboratory affiliated with the Departments of Genetics and Biology at the University of Pennsylvania. Projects in the lab focus on a unique resource of DNA samples and phenotype data from 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, CNV analyses, and whole genome SNP genotyping). For many of these samples we also have phenotype data for a number of traits that are likely important in adaptation and disease. We are using these data (1) to infer population structure and demographic history and to test models of modern human evolution (2) to identify regions of the genome that are targets of selection (3) to identify functionally significant variants using genotype/phenotype association studies as well as gene expression analyses (4) to study genetic and phenotypic variation at loci that influence drug metabolism and (5) 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 Philip Awadalla, Carlos Bustamante, Junhyong Kim, Gil McVean, Joshua Plotkin, Jonathan Pritchard, Anna Tramontano, and Greg Wray. Independent and creative postdoctoral research projects will be encouraged. Additional information about the Tishkoff lab can be found at <http://www.med.upenn.edu/-tishkoff/>. The Department of Genetics (<http://www.med.upenn.edu/genetics/>) is centrally located within the U Penn campus and is a short walk from the Children's Hospital of Pennsylvania, the Biology Department (<http://www.bio.upenn.edu/>) and the An-

thropology Department (<http://www.sas.upenn.edu/-anthro/>). Outstanding core facilities are available for high throughput sequencing, genotyping, and gene expression studies (<http://www.med.upenn.edu/-genetics/core.shtml>), and for bioinformatics and computational biology (<http://www.pcbi.upenn.edu/>). U Penn has a vibrant community of researchers with interests in evolutionary biology and genomics (<http://www.genomics.upenn.edu/default.jsp>), the genetics of complex traits (<http://www.cceb.upenn.edu/-pages/cgact/>), and translational medicine (<http://www.itmat.upenn.edu/>).

Candidates with either a strong molecular and/or statistical genetics background are encouraged to apply. Both computational and laboratory positions are available and individuals interested in theory/statistical methods development are encouraged to apply (possibilities exist for joint supervision with statistical geneticists). Familiarity with population genetics theory and/or computer programming is a plus. Salaries are commensurate with qualifications and experience.

Please send curriculum vitae, a brief statement of interests, and contact information for three references via e-mail to Dr. Sarah Tishkoff, Departments of Genetics and Biology, University of Pennsylvania, tishkoff@mail.med.upenn.edu. The starting dates of positions are flexible.

tishkoff@mail.med.upenn.edu
tishkoff@mail.med.upenn.edu

UPittsburgh EvolutionaryBiology

POST-DOCTORAL POSITION

AQUATIC ECOLOGY, EVOLUTION, BEHAVIOR,
OR ECOTOXICOLOGY

Applications are invited for a post-doctoral position at the University of Pittsburgh in any area of aquatic ecology or evolution under the direction of Dr. Rick Relyea. Current areas of research in the Relyea Lab include inducible defenses (and other forms of phenotypic plasticity), predator-prey communication, animal mating systems, disease ecology, and community ecotoxicology in aquatic communities. Interested applicants should propose potential research ideas that either build upon our existing work or add interesting new dimensions to areas currently being pursued.

The post-doc will reside on the main campus in Pitts-

burgh from September to March each year and reside at the University's biological field station from April to August (www.pitt.edu/~biology/pymatuning.htm). For more information about the field station's aquatic facility, go to www.pitt.edu/~relyea/facilities.html. The starting salary is \$34,000 plus excellent health benefits. To ensure a productive field season in 2008, the latest start date is 1 April 2008 (a completed Ph.D. is required prior to the start date).

Applicants should send a cover letter, cv, a research statement (including potential research projects), and letters of reference to Dr. Rick Relyea (relyea@pitt.edu) by 15 February 2008 (all in pdf format).

relyea+@pitt.edu

Uppsala ComputationalGenetics

We are seeking researchers interested in joining our Computational Genetics program in Uppsala, Sweden.

We are interested in understanding the genetics underlying complex traits using a computational approach. Projects are often, but do not necessarily have to be, inspired by problems or opportunities that advent from experimental data. We encourage scientists to form and develop their projects to suit their interests and abilities within the framework of existing funding. We also support grant proposals from individuals that wish to pursue individual projects. The project portfolio in the group will thus vary, but we usually have ongoing projects in the field of statistical and computational methods in genetics, genetic modeling, exploratory analyses of experimental datasets and experiments to validate interesting biological findings.

A common theme in our research is epistasis. We are actively developing models, algorithms and tools for large scale screening and interpretation of the genetic effects of epistatic QTL in regulating complex trait expression. Our tools have mostly been used to study the importance of epistasis in phenotypic evolution using data from divergent crosses between domesticated animals. If you have an interest in or ideas for projects in this field or an interest in working with i) explorations of the role of of epistasis in ecological and population genetics, ii) how data from large-scale genome resequencing can be utilized in genetic mapping or iii) development of new methods for genetic mapping of complex traits, we look forward to hear from you!

We aim to integrate researchers with different backgrounds both within and across traditional scientific disciplines. We do, however, foresee that you have a relevant scientific education (Ph.D. degree or similar) and an interest in Quantitative-, Population- and Evolutionary Genetics. A strong mathematical / statistical background and programming experience is an advantage

If you want to learn more about us, please visit <http://www.computationalgenetics.se> or contact Örjan Carlborg (orjan.carlborg@hgen.slu.se). If you are interested in working with us, please send us a CV, list of publications and a short description of what interests you in the field of complex trait genetics and what you can contribute to in an interdisciplinary group working on this topic. We look forward to hear from you!

Salary and conditions of future employment(s) are under the terms of the current agreement for academic scientists employed in the public sector. We are looking for several candidates and positions will remain open until suitable candidates have been found. Positions can start 1 Feb, 2008 at the earliest.

Please feel free to spread this advert to others that might be interested!

Örjan Carlborg Department of Animal Breeding and Genetics Swedish University of Agricultural Sciences Box 7023 SE-75007 Uppsala Sweden
Email: orjan.carlborg@hgen.slu.se Phone: +46-18-672001 Mobile: +46-76-2109114 Fax: +46-18-672848 Web: <http://www.orjancarlborg.com> ; <http://www.computationalgenetics.se>

Orjan.Carlborg@hgen.slu.se
jan.Carlborg@hgen.slu.se

Or-

UTexasAustin NicheVariation

A postdoctoral position is available in the laboratory of Daniel Bolnick, in the Section of Integrative Biology at the University of Texas at Austin. The lab's research focuses on the evolutionary and ecological consequences of among-individual variation in resource use within populations. More information on research in the lab can be found at < <https://webspace.utexas.edu/~dib73/Bolnicklab/Bolnicklab.htm?uniq=5ptsas> > <https://webspace.utexas.edu/dib73/Bolnicklab/-Bolnicklab.htm?uniq=5ptsas> . More information on the Section of Integrative Biology can

be found at < <http://www.biosci.utexas.edu/ib/> ><http://www.biosci.utexas.edu/ib/> .

The goal of this postdoctoral position is to bring in a creative and innovative researcher to work on any topic closely related to the focus of the Bolnick lab. The postdoctoral researcher will be expected to contribute to collaborative field and lab projects on niche variation within populations of three-spine stickleback. The postdoc will also be encouraged to develop an independent research program related to the general topic of within-population niche variation. Such research could entail lab or field work on three-spine stickleback or on another study organism, or theoretical modeling.

The postdoctoral researcher should have a PhD in evolution, ecology, behavior, or a closely related field. He/She should have a record of successful publications. The specific skills required for this postdoctoral position depend on the research topics the applicant wishes to pursue, but might include some combination of experimental ecology in aquatic systems, geometric morphometrics, biomechanics, theoretical modeling, or quantitative genetics. Excellent analytical and communication skills are essential. Please contact Dr. Daniel Bolnick (danbolnick@mail.utexas.edu) for inquiries.

To apply for the postdoctoral position, please send a cv, two letters of recommendation, and pdfs of relevant papers, to Dr. Bolnick (contact information below). Applicants are also encouraged to write a 2 page proposal regarding the research topic(s) they wish to pursue during their postdoc, and how this would fit into the overall focus of the lab. Review of applications will begin on Jan 25, and the position will remain open until filled (later applications will be accepted).

Preferably, the postdoc would be available to start work prior to the beginning of the lab's field season in late May, but this may be flexible. It is expected that the postdoctoral position will last three years, on condition of satisfactory progress, to be assessed annually. There is the potential for further extension beyond three years, subject to funding availability. Salary and benefits are competitive.

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

Dr. Daniel Bolnick Section of Integrative Biology University of Texas at Austin Austin, TX 78712 USA <<mailto:danbolnick@mail.utexas.edu>> danbolnick@mail.utexas.edu 512-471-2824 (work) 512-471-3878 (fax)

danbolnick@mail.utexas.edu
danbolnick@mail.utexas.edu

danbol-

UZurich Post-copulatory sexual selection

A postdoctoral position is available from 1st April, or as arranged, in the Zoological Museum of the University of Zurich, Switzerland. The successful applicant will join an active research group, headed by Prof. Paul Ward, working on post-copulatory sexual selection in the yellow dung fly, *Scathophaga stercoraria*. The biology of the species is well known and methods for a number of research directions well-developed.

The precise research topic(s) within the broad theme will substantially depend on the interests and background of the applicant. However, preference will be given to candidates with backgrounds in evolutionary biology or insect immunology or physiology.

Applicants must have a completed Ph.D. Postdoctoral experience would be advantageous. A knowledge of, or a willingness to learn, German would also be advantageous. A small amount of teaching, in either English or German, will be required. The position will be offered for two years in the first instance, with the possibility of annual renewal to a maximum of six years.

Please send a curriculum vitae, publication list and a one-page statement of research interests to zmdirektion@zm.uzh.ch. Applications should be sent by the 3rd March 2008.

Applicants for a previous similar position need not re-apply

Enquiries to Prof. Paul Ward, Zoological Museum of the University of Zurich, Winterthurerstr. 190, CH-8057 Zurich, Switzerland. Email: pward@zm.uzh.ch.

Prof Paul I Ward Direktor Zoologisches Museum der Universität Zürich Winterthurerstrasse 190 CH 8057 Zürich Switzerland Phone +41 44 635 4760 Fax +41 44 635 4780 email: pward@zm.uzh.ch

Administration: Sabine Marty Mail: zmdirektion@zm.uzh.ch Phone +41 44 635 4761

Paul Ward <pward@zm.uzh.ch>

WorkshopsCourses

BodegaMarineLab AppliedPhylogenetics Mar8-15 . 75	UManchester EvolGenomics 2 80
CosatRica BiodiversityGenetics May18-31 76	Uppsala QTL-MAS May15-16 registration 80
France AnimalGenomics Mar25-28 76	UWashington InstStatGenetics Jun16-July2 80
MLBS Virginia FieldBasedEvolution Summer 77	UWyoming CompBiology Summer 81
Montreal PopulationGenomics May20-23 78	WoodsHole MolEvol Jul27-Aug15 81
UBologna 9thWinterBioinformaticsSchool Feb11-15 78	
UEdinburgh PlantTaxonomy 79	

BodegaMarineLab AppliedPhylogenetics Mar8-15

UC Davis WORKSHOP IN APPLIED PHYLOGENETICS at Bodega Marine Laboratory, Bodega Bay, California

March 8-15, 2008

sponsored by the

University of California, Davis and Bodega Marine Laboratory (additional financial support provided by the University of Rochester, Yale University, and NESCent)

Introduction. Phylogenetic methods have revolutionized modern systematics and become indispensable tools in evolution, ecology and comparative biology, playing an increasingly important role in analyses of biological data at levels of organization ranging from molecules to ecological communities. The construction of phylogenetic trees is becoming a methodology that is well-defined, with broad agreement on the central issues and questions. A nearly standard set of topics is now taught as part of the curriculum at many colleges and universities. On the other hand, application of phylogenetic methods to interesting problems outside of systematics is an area of special excitement, innovation, and controversy, and perspectives vary widely.

In March, 2008, for the ninth year, we will teach a workshop for graduate students interested in applying phylogenetic methods to diverse topics in biology. The one-week course will be an intensive exploration of problems to which modern phylogenetic tools are being applied. We cover a range of topics in biogeography, ecology, conservation biology, phylogenomics, functional mor-

phology, macroevolution, speciation, and character evolution. The course starts with recent advances in phylogenetic methodology, and then focuses on methods and tools that can be brought to bear on these “applied” issues in the context of a given phylogeny.

The course will be held entirely at the Bodega Marine Lab on the Northern California coast, which has extensive computing resources and on-site housing. The course format will involve equal parts of lecture, discussion, and training in software and internet tools. One afternoon during the week will be left free for field trips to local natural areas.

Specific Topics to be Covered

* Finding, evaluating and interpreting phylogenetic trees; phylogenetic databases * Recent advances in tree reconstruction: Bayesian inference; stochastic optimization strategies; divide-and-conquer methods; Garli & other approaches * Analysis of character evolution—theory: parsimony, likelihood and Bayesian approaches; null models and statistical testing * Analysis of character evolution—form and function of complex character systems * Phylogeography; coalescent methods for inferring migration rates and patterns * Phylogenetic comparative methods * Phylogenetic perspectives on biodiversity and conservation biology * Data mining of sequence databases for phylogenetic analysis * Estimation of divergence times from sequence data * Species delimitation and phylogenetic taxonomy

Instructors for the main workshop.

* H. Bradley Shaffer * Peter Wainwright * Kevin de Queiroz * Tom Near * Rich Glor * Phil Spinks * Justen Whittall * Brian O’Meara * Alan Lemmon * Emily Moriarty Lemmon * Robert Thomson * Bruce Rannala

plus guest lecturers!!

Prerequisites. Students should have some familiarity

with phylogenetic methods through previous coursework. Some experience with PAUP, PHYLIP, or other programs for phylogeny reconstruction will be assumed.

Admission and Fees. Students will be admitted based on academic qualifications and appropriateness of research interests. The course fee is \$450. This includes room and board at BML for duration of the course (arriving March 8, leaving March 15) and transportation from Davis to BML.

Application Deadline. Applications are due by January 15, 2008. Please send a completed application form (available at <http://www.eve.ucdavis.edu/-bodega/bodega08app.doc>) and one letter of recommendation from your major advisor. Applications should be sent via email as PDFs to pqspinks@ucdavis.edu. Sorry, but due to the limited size of the class, postdocs and faculty are discouraged from applying. Students will be notified via e-mail by 20 January of acceptance.

Send all application materials to

Dr. Phillip Q. Spinks Section of Evolution and Ecology
2320 Storer Hall University of California Davis Davis,
CA 95616 email:pqspinks@ucdavis.edu

grate a workshop component into each topic, where we will discuss and present pertinent computer software and will critique the advantages and disadvantages of the available software packages. Students will be given an opportunity to present and discuss their own conservation research projects.

When: 18-31 May 2008 **Where:** Costa Rica, Palo Verde Biological Station **Participants:** Graduate students in biology, ecology, genetics and related disciplines **Application deadline:** February 15, 2008 for priority consideration, followed by rolling admission until fully enrolled (22 students)

Tuition: \$1500 OTS consortium applicants \$2000 non-consortium applicants Partial scholarships of \$500 may be requested. Awards will be based on academic merit and proven financial need, with priority given to students from consortium institutions.

For further information: for registration information contact Barbara Lewis (blewis@ots.ac.cr) or the OTS website at www.ots.duke.edu for course content, contact Jim Hamrick (hamrick@plantbio@uga.edu) or John Wares (jpwares@uga.edu)

jpwares@uga.edu

CosatRica BiodiversityGenetics May18-31

OTS Specialty Course: Conservation and Biodiversity Genetics taught by Jim Hamrick, Erich Fuchs, and John Wares

This is an intensive, two-week course aimed at providing ecologists, biologists, geneticists, and students from similar disciplines with an overview of conservation genetics and related issues in neotropical biodiversity. The course is supported by a grant from the American Genetics Association. Course topics include: measurement of genetic diversity, phylogeography, application of molecular data to taxonomic questions, gene flow, mating systems and effective population size estimates, habitat fragmentation and restoration. We will also discuss the cost-effectiveness of different approaches, the underlying theory as it applies to conservation questions, and the best ways to integrate experimental and field-based data with these analytical results. Local conservation experts will present invited lectures on conservation issues in Costa Rica.

Topics will be covered through lectures, discussions, and readings in the primary literature. We will inte-

France AnimalGenomics Mar25-28

European Research School

Post-genomics in Animal Science Research and career prospects

Les Loges En Josas (78) , France, 25TH - 28TH March 2008

Advisory committee J. van Arendonk, P. Debey, A.M. Neeteson, E. Verrier, J. Williams

Organising committee S. Arrault, F. Hospital, M. Mambri, N. Roger, L. Silveri, A. Trubuil, C. Tournu, X. Vignon, S. Vincent-Naulleau

This research school is organised by RIVAGE, Marie Curie Early Stage Research Training action of the European Community's Sixth Framework Programme (contract MEST-CT-2004-504854) and Formasciences INRA. RIVAGE gratefully acknowledges the financial support of the Conseil Regional Ile de France and INRA for this event.

In a completely innovative form, this event will bring together top scientists and young researchers to address

cutting-edge scientific topics, and use it as case-studies for transdisciplinary analysis, practice project building, and work out their careers plan.

Context and issues Facing the challenges of the post-genomic era implies a change of scale for which researchers have to be prepared. In response to these major scientific and economical issues, initiatives in system biology and epigenomics are teeming. The programme of this research school aims to facilitate the identification of coherent strategies for research prospects as well as training (initial and life-long) and careers. This change of scale implies the defragmentation of research activities, disciplinary barriers, applied and fundamental frontiers. Consequently, the programme is built around three main sequences: a science update, project building and trans-disciplinary processes. We mix in a very innovative way scientific conferences on key topics, technical lectures on project building, interdisciplinarity and careers, and workshops where attendees will practice project building in transdisciplinary interactions. This training should guide each participant to define his(her) role in creating the best research environment (institutional and business) to tackle the complexity of the post-genomic challenges.

Public Senior, experienced and young researchers (PhDs) from the public or private sectors working in animal genetics & physiology or mathematics, particularly those who use generic data, and who wish to clarify their position, and career prospects through a coherent strategy regarding the development of animal post-genomics. In particular, we hope to have the joint participation of supervisors with trainees.

Participation to the school (registration, accomodation) is free, only the travel is at the expense of the participant (though support for travel might also be considered depending on particular situations, please contact us). However, for best efficiency and success, the number of participants is limited to 60. Candidates must fill in a questionnaire, and might be selected by the advisory and organising committees according to the field of experience, interest and motivation to participate to the training. The twin participation of a young researcher with his(her) supervisor will be a plus. The questionnaire is to be asked/sent to: Nadine.roger@jouy.inra.fr Tel: +33 (0)1 34 65 27 00 Fax: +33 (0)1 34 65 21 46

The school website (to be updated regularly, please check): https://colloque.inra.fr/european_research_school Download the flyer at: https://colloque.inra.fr/european_research_school/content/download/447/4079/version/1/file/RIVAGE_european_research_school_flyer.pdf Looking forward to see you in Les Loges, The organizers.

– Frédéric Hospital UMR Génétique et Diversité Animales - Bâtiment 211 INRA - Domaine de Vilvert - 78352 JOUY-EN-JOSAS cedex - FRANCE Tel. +33-1-3465-2169 Fax. +33-1-3465-2210 <http://fhospital.free.fr/fred/-work/> Frederic.Hospital@jouy.inra.fr Fred-eric.Hospital@jouy.inra.fr

MLBS Virginia FieldBasedEvolution Summer

ANNOUNCING: MLBS Summer 2008 Field Course and REU Opportunities Mountain Lake Biological Station MLBS.org Dear Colleagues and Friends, Mountain Lake Biological Station (University of Virginia) is pleased to announce its 13-week summer program of field-based undergraduate and graduate-level credit courses and workshops offered by nationally recruited faculty, and its 10-week NSF REU undergraduate research internship program, now in its 16th year. Work at MLBS focuses on field-based ecology, evolution, physiology, and behavior. Learn more about the programs, complete an on-line applications, or download a flier to post: Courses web page -

<http://mlbs.org/courses.html> REU web page - <http://mlbs.org/REU.html> Fliers to Post -

http://mlbs.org/download/MLBS_Poster.pdf (and attached)

http://mlbs.org/download/MLBS_REU_Poster.pdf

Please forward this information to colleagues or students you think might be interested. Thanks for your help! Best wishes and Happy New Year, Butch Brodie, Director Eric Nagy, Associate Director MLBS.org

Eric S. Nagy, Ph.D. Associate Director, Mountain Lake Biological Station Research Assistant Professor, Department of Biology University of Virginia / P.O. Box 400327 Charlottesville, VA 22904-4327 USA street address: 485 McCormick Road / 219 Gilmer Hall tel: +1-434-243-4989 (+1-540-626-5227 summer) fax: +1-434-982-5626 (+1-540-626-5229 summer) cel: +1-434-906-3122 eml: enagy@virginia.edu

skype: flightofthesandor web: faculty.virginia.edu/nagy

MLBS web page: mlbs.org

enagy@virginia.edu

Montreal Population Genomics May 20-23

Montreal Spring School of Population Genomics and Genetic Epidemiology May 20 - 23, 2008 Montreal, Quebec, Canada

General Information www.montrealspringschool.ca

The main objective of the School is to provide training in rapidly developing disciplines that are becoming increasingly important in health sciences. It includes genetic epidemiology and human evolutionary genetics, population genomics and bioinformatics, integrating tools of formal analysis with data retrieval and extensive use of internet resources. The training will be based on real-data examples from the research of the instructors' laboratories. In one module we will also present genealogical resources specific to Quebec and introduce informatics methods for their use in population analysis and epidemiology. The School consists of four days of workshops: genetic epidemiology including biostatistics (2 days), population genomics (1.5 days), and Quebec population resources (0.5 days).

The School, organized by Dr Damian Labuda from CHU Sainte-Justine, will be held at the Universite de Montreal, Pavillon Lionel-Groulx, 3150 Jean-Brillant Street, Room C3001, in Montreal, Quebec, Canada.

Faculty

Alexandre Alcaes Laboratory of Human Genetics of Infectious Diseases Institut National de la Sante et de la Recherche Medicale University Paris Rene Descartes, Necker Medical School Paris, France

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Marc Tremblay Department of Human Sciences Universite du Quebec e Chicoutimi Chicoutimi, Canada

Helene Vezina Department of Human Sciences Universite du Quebec e Chicoutimi Chicoutimi, Canada

Application Procedures

If you wish to participate in the workshop, please submit (i) the completed application form, including a statement explaining your interest in the School, accompanied by one-page CV and (ii), if a travel award is requested (see below), a short letter explaining your financial needs, accompanied by a letter of support from your academic advisor (if applicable). Please submit these documents by e-mail to Ms. Dominika Kozub-ska (info@montrealspringschool.ca) no later than Friday, February 24, 2008.

damian.labuda@umontreal.ca

UBologna 9th Winter Bioinformatics School Feb 11-15

9th Bologna Winter School on Bioinformatics

GRAND CHALLENGES IN COMPUTATIONAL BIOLOGY New developments for solving the unsolved problems of Computational Biology

University of Bologna, Giorgio Prodi Hall, Piazza San Giovanni in Monte Bologna (Italy)

Feb 11-15, 2008

In our century grand challenges are at hand in Science. Great expectations have been generated in different fields by the increasing role and impact of computing and computer science in processing terabytes of data. In our era the 'computational thinking' of computer science meets the empirical and theoretical methods of Natural Sciences, from Physics to Biology with an un-precedent effort of accelerating breakthroughs and benefits to society. Ongoing projects aim at understanding the universe and the origin of life for better helping to preserve and protect our planet. Simulation and modeling go global and the novelty is that this is so also in Biology, where Bioinformatics and Computa-

tional Biology help in understanding basic mechanisms from molecular biology to systems/organismic biology in order to revolutionizing medicine and healthcare. Data acquired at molecular level from different species and/or individuals need to be analyzed at large and integrated in order to investigate our common origins and how we differentiated from each others, also in relation to environmental factors. Worldwide-integrated platforms for scientific computing, implementing also new mathematical and statistical approaches, and based on new computing paradigms need to be implemented for real time processing of the enormous amount of experimental data, produced at hyperbolic rate by genomics and proteomics efforts. New ideas and/or reorganization of scientific efforts with a better collaboration among researchers in theoretical, computational, experimental areas of investigation are urgently needed.

In the 9th edition of the Bologna Winter School in Bioinformatics, we will then ask the question of what grand challenges Computational Biology and Bioinformatics will explore in the next decade. Different subjects focusing as a test case on the human genome, including genome annotation, biodiversity, alternative splicing and its regulation, epigenetics, information transfer from 1D to 3D genetic code, cellular function and simulation, genomic medicine, SNPs and maladies will be reviewed to highlight present results and future perspectives to cope with the requirement of integrating computation with molecular description to understand basic principles of Biology.

LECTIO MAGISTRALIS

Complexity at the fundamental level - Antonino Zichichi, CERN, Geneva, CH

TEACHERS - Giovanni Aloisio, University of Lecce, IT - Patrick Aloy, Institute for Research in Biomedicine, Barcelona, ES - Francesco Beltrame, University of Genova, IT - Jaume Bertranpetit, University "Pompeu Fabra", Barcelona, ES - Alvis Brazma, European Bioinformatics Institute, Hinxton, UK - Joaquin Dopazo, Centro de Investigacion "Principe Felipe", Valencia, ES - Arne Elofsson, Stockholm University, SE - Roderic Guig \ddot{u} , University "Pompeu Fabra", Barcelona, ES - David T. Jones, University College, London, UK - Arthur Lesk, PennState University, USA - Giuseppe Martini, National Research Council, Roma, IT - Christine Orengo, University College, London, UK - Modesto Orozco, Institute for Research in Biomedicine, Barcelona, ES - Graziano Pesole, University of Bari, IT - Bernhard Schelkopf, Max Planck Institute, Tuebingen, DE - Aldo Tagliabue, ALTA srl, Siena, IT - Willie Taylor, National Institute for Medical Research, London, UK - Anna Tramontano, University

"La Sapienza", Roma, IT - Alfonso Valencia, Centro Nacional de Investigaciones Oncologicas, Madrid, ES

Additional Information: <http://www.biocomp.unibo.it/~school2008/> Contact: school2008@biocomp.unibo.it

For Application send a short C.V. to school2008@biocomp.unibo.it You will be notified by e-mail of acceptance. Deadline for application: January 29, 2008

gigi@biocomp.unibo.it

UEdinburgh PlantTaxonomy

Royal Botanic Garden Edinburgh and University of Edinburgh

The Biodiversity and Taxonomy of Plants

MSc (12 months Full Time)/Diploma (nine months Full Time)

Applications are invited for the MSc course in the Biodiversity and Taxonomy of plants before 31 March 2008.

The course aims to bridge traditional and modern approaches and equip evolutionary biologists, conservationists and ecologists with a high level of skill in pure and applied taxonomy and a wide knowledge of biodiversity and its investigation. The course combines formal instruction, practical work, workshops, essays, field work and conservation initiatives, research projects and tutorials covering all major areas of botanical endeavour and including the function, management and funding of taxonomic collections and institutes. Currently it comprises work with plants and fungi and benefits from a close partnership with the Royal Botanic Garden Edinburgh.

There is a growing need for individuals with specialized knowledge of plant biodiversity and their evolution. The course is also an excellent platform for doctoral studies.

More information on the course can be found at:

<http://www.rbge.org.uk/education/professional-courses/msc-in-biodiversity-and-taxonomy-of-plants>

The course is supported by six NERC studentships (open to EU students only: www.nerc.ac.uk/funding-students/students-faq.shtml). Studentships will be allocated on a competitive basis.

Contact: Graduate School of Biology, King's Buildings, Mayfield Road, Edinburgh EH9 3JR, United Kingdom-
Tel: +44 (0) 131 650 5522; - Email:gradlife@ed.ac.uk

application forms can be downloaded from the Postgraduate Office web pages at: <http://www.postgrad.ed.ac.uk/applicat/form.htm> Informal enquiries and requests for further information can be obtained from Dr Louis Ronse De Craene, course director email: l.ronsedecraene@rbge.ac.uk tel. +44 (0)131 248 2804

Dr Louis P. Ronse De Craene Director of the MSC-course

Royal Botanic Garden Edinburgh 20A Inverleith Row, Edinburgh EH3 5 LR Scotland, U.K.

tel. +44 (0)131 248 2804 fax +44 (0)131 248 2901
Email: l.ronsedecraene@rbge.ac.uk

URL: <http://www.rbge.org.uk/education/professional-courses/msc-in-biodiversity-and-taxonomy-of-plants>
<http://www.rbge.org.uk/science/tropical-diversity-evolutionary-development/early-diverging-eudicots>

Louis Ronse De Craene <l.ronsedecraene@rbge.ac.uk>

UManchester EvolGenomics 2

Apologies, the url for further information in the previous announcement for this course had a typo. This has now been corrected below.

Please bring this new MSc course to the attention of potentially interested students.

This course is aimed largely at students with an interest in evolution who are thinking about going on to do a PhD in some aspect of evolutionary biology e.g. conservation, molecular evolution, speciation, population genetics, ecological genomics, bioinformatics. The taught component of the course (~one third) covers the principles of evolutionary genetics and genomics and some of the statistical approaches used. Engaging in full-time research in active laboratories is a key part of this programme and each student will undertake two full-time research projects (~two thirds of the course). Projects, which can be lab-based, field-based, bioinformatics or theoretical, will be on offer from a large number of academic staff with a wide range of research interests.

Several fully, or partially, funded BBSRC studentships are available for UK and EU students and will be awarded on merit. Timely applications are encouraged

as studentships will be awarded as suitable candidates apply.

Apply online: www.manchester.ac.uk/lifesciences/postgraduate/apply Further information: www.manchester.ac.uk/lifesciences/evolutionarygeneticsmsc Enquiries for applications: Tel: 0161 275 5608 Fax: 0161 275 5657 Email: pg.lifesciences@manchester.ac.uk

Enquiries for further information on the course: Tel: 0161 275 1533 Email: Cathy Walton (Catherine.walton@manchester.ac.uk) or Richard Preziosi (Richard.Preziosi@manchester.ac.uk)

Catherine.Walton@manchester.ac.uk Catherine.Walton@manchester.ac.uk

Uppsala QTL-MAS May15-16 registration

Registration for the 12th QTL-MAS workshop in Uppsala, Sweden on 15th-16th of May is now open.

The main themes of the meeting will be fine mapping, genome-wide association studies and genomic selection. Talks are invited on these or other topics.

A simulated data set is now available for analysis as part of the workshop. We invite both talks and papers based on this data set. The data are designed for association, linkage and genomic selection methods. Papers will be considered for publication in BMC Proceedings. Ph. D. students and postdocs whose papers are accepted may qualify for a reduced conference fee.

Deadline for early registration is 20th March.

For more details, registration form and to download the data set, please visit our website: www.computationalgenetics.se/QTLMAS08 Lucy Crooks, organising committee, QTL-MAS XII.

Lucy Crooks <qtlmas12@computationalgenetics.se>

UWashington InstStatGenetics Jun16-July2

The modules and dates for the 2008 Summer Institute

in Statistical Genetics have been set. Details on registration procedures, scholarships and housing will soon be available at <http://www.biostat.washington.edu> Enquiries may be sent to sisg08@u.washington.edu Brochures will be mailed on request (and will be sent to 2007 participants).

Bruce Weir

Module Dates and Name Instructors * *

June 16,17,18 (8:30 am Monday V noon Wednesday)
1 Probability and Statistical Inference Jim Hughes, David Yanez 2 Molecular Genetics Josh Akey, Greg Gibson 3 Computing for Statistical Genetics Thomas Lumley, Ken Rice 4 Interpreting DNA Evidence John Buckleton, Bruce Weir

June 18,19,20 (1:30 pm Wednesday V 5 pm Friday) 5 Regression and Analysis of Variance Bill Barlow, Lurdes Inoue 6 Natural Population Genetic Data Analysis Kent Holsinger, Bruce Weir 7 MCMC for Genetics Eric Anderson, Matthew Stephens

June 23,24,25 (8:30 am Monday V noon Wednesday) 8 Quantitative Genetics Bill Muir, Bruce Walsh 9 Human Population Genetic Data Analysis Katie Kerr, Bruce Weir 10 Analysis of Genetic Data on Related Individuals Shili Lin, Elizabeth Thompson 11 Comparative Genomics \ Molecular Evolution Spencer Muse, Adam Siepel

June 25,26,27 (1:30 pm Wednesday V 5 pm Friday)
12 QTL Mapping Rebecca Doerge, Zhao-Bang Zeng 13 Functional Genomics and Proteomic Data Martin McIntosh, TBN 14 Human Association Mapping Lon Cardon, Dahlia Nielsen 15 Coalescent Theory Philip Awadalla, Mary Kuhner

June 30, July 1,2 (8:30 am Monday V noon Wednesday)
16 Advanced QTL Mapping Brian Yandell, Zhao-Bang Zeng 17 Plant and Animal Association Mapping TBN, Michel Georges 18 Genetic Epidemiology and Clinical Trials Jared Lunceford, Barbara McKnight

Bruce Weir <bsweir@u.washington.edu>

UWyoming CompBiology Summer

Hi,

University of Wyoming will again host a summer research program for students interested in computational biology. Details can be found at [http://](http://www.wyomingbioinformatics.org/SummerSchool/)

www.wyomingbioinformatics.org/SummerSchool/.

The program will carry a stipend of \$3500 to cover travel and living expenses for the summer and enable the student to spend the summer in Laramie, WY working in one of several laboratories on a problem in computational molecular biology. Please forward this email to any students who might be interested in attending. The program is open to undergraduates at North American universities regardless of nationality (but dependent upon visa constraints). If there are any questions, please do not hesitate to contact me. I look forward to hearing from you or your top students... Thanks and best wishes,

David Liberles

David Liberles <liberles@uwyo.edu>

WoodsHole MolEvol Jul27-Aug15

Workshop on Molecular Evolution, Woods Hole, 2008

27 July - 8 August 2008, and extended topics session 8 August - 15 August 2008

Application Deadline 3 March 2008

Michael P. Cummings, Director

The Workshop on Molecular Evolution has been the finest course in the subject 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 Apple Macintosh computers and servers for comparative analysis of molecular data. Authors and experts in the use of computer programs and packages such as BEAST, Clustal W and Clustal X, FASTA, GARLI, LAMARC, MAFFT, 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 * Maximum likelihood theory and practice in phylogenetics and population genetics: coalescent theory; maximum likelihood estimation of population genetic parameters * Molecular evolution integrated at organism and higher levels: population biology; biogeography; ecology; systematics and conservation * Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution * Comparative ge-

nomics: genome content; genome structure; genome evolution * Molecular evolution integrated at lower levels: biochemistry; cell biology; physiology; relationship of genotype to phenotype

2008 Fees: \$2400 (room and board at no additional charge), plus an additional \$850 for the extended topics session.

More information is available on the Workshop web site -

<http://workshop.molecularevolution.org/> Application instructions are provided on the following link -

<http://gosnold.mbl.edu/StudentApp/-StudentApp.asp?CourseID=MOLE>

mike@umiacs.umd.edu mike@umiacs.umd.edu

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.