
E v o l D i r

January 1, 2006

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

Forward

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

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

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Conferences

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Anney France Bioinformatics Jun27-30

Special Session on Bioinformatics at the IEA/AIE 2006 Conference Anney (FRANCE) 27-30 June 2006

You are invited to submit a paper to the Bioinformatics track of the IEA/AIE 2006 conference. The goal of the special track is to facilitate collaboration between AI researchers and biologists by presenting cutting edge algorithms, ideas and the applications of AI technology to solve interesting problems in computational biology. We plan to accept up to 10 papers for presentation (after a formal peer review process) and these will be included in the IEA/AIE 2006 conference proceedings, which is published in a bound volume by Springer-Verlag in their 'Lecture Notes in Artificial Intelligence' series. All the accepted papers will be considered for a special issue of the Journal of Applied Intelligence. The topics of interests include, but not limited to: Sequence Alignment Evolution and Phylogenetics Gene Discovery Molecular Structures Protein /RNA structure Prediction and Modeling Protein protein or protein dna interactions Comparative Genomics Microarray data analysis Regulatory modules and Pathway analysis Application of machine learning to molecular biology

Session Organizer: Dr. Raja Loganantharaj Bioinformatics Research Laboratory at University of Louisiana
Phone: (337) 482-5345 Fax: (337) 482-5791 logan@cacs.louisiana.edu, raja@louisiana.edu
The organizing and the program committee members are: John

Clifford, LSU Health Sciences Center, Shreveport, USA
David Gilbert, Bioinformatics Research Center, University of Glasgow, UK
Steven Jennings, Bioinformatics, University of Arkansas, USA
Jugal Kalita, University of Colorado, Colorado Springs, USA
B. Franz Lang, University of Montréal, Canada
Raja Loganantharaj, Bioinformatics Research Lab, University of Louisiana, USA
Debasis Mitra, Florida Institute of Technology, USA
Important Dates for Papers Electronic Paper Submission Deadline Author(s) Notification Camera-Ready Copy Deadline December 9 , 2005 January 23, 2006 February 24, 2006

To submit paper, go to author access at the main conference site and register yourself before you submit your complete paper up to 12 pages for full presentation or up to 6 pages for short presentation. Please follow the formatting instruction given at the conference site at

<http://esia2.univ-savoie.fr/conf-iea-aie/> Franz Lang <Franz.Lang@Umontreal.ca>

Barcelona Bivalvia2006 July22-27

We are happy to announce the following conference:

International Congress on Bivalvia Bellaterra (Barcelona), Spain 22-27 July 2006

The congress with venue at the Universitat Autònoma de Barcelona calls together neontologists and palaeontologists with a research focus on bivalve molluscs. Plenary talks include ecology and life history, population

genetics and phylogenetics, evolution of ontogeny, evolutionary paleontology, biomineralisation and freshwater conservational biology, but contributions need not be restricted to these topics. In addition, there will be a planning session for a new bivalve treatise. Two one-day excursions - one on recent one on fossil bivalves - will be organised.

Interested persons are asked to register and submit abstracts via the congress webpage

<http://bivalvia2006.uab.es> Further inquiries may be directed to Niko Malchus (n.malchus@gmx.net). Please include in the subject line "Bivalvia 2006".

– Dr. Carlos Saavedra

Instituto de Acuicultura de Torre la Sal (IATS) Consejo Superior de Investigaciones Cientificas (CSIC) 12595 Ribera de Cabanes Castellon - SPAIN

Tel.: ++34 964 319 500 Fax.: ++34 964 319 509 Email: saavedra@iats.csic.es

<http://www.iats.csic.es/> ~ moluscos saavedra@iats.csic.es

BuenosAires PhthirapteraEvol Oct16-20

ICP3: Third International Congress on Phthiraptera (Lice), call for papers

Date: 16 - 20 October 2006 Location: Hotel Pestana, Buenos Aires, Argentina Website: <http://icp3.phthiraptera.org/> Host: Centro de Investigaciones en Plagas e Insecticidas (CITEFA - CONICET)

This interdisciplinary conference will bring together leading authorities working on parasitic lice (Insecta: Phthiraptera) and louse-borne disease. Slots are available for talks in seven symposia focusing on all aspects louse biology, evolution and control. As in prior meetings the medical, veterinary, and non-applied research talks will be integrated. The official conference languages are English and Spanish, with simultaneous interpretation provided at plenary and scientific sessions. Posters will be in English. Abstracts of no more than 200 words can be submitted by e-mail to Kostas Mumcuoglu (kostam@cc.huji.ac.il) concerning human lice, and Lajos Rózsa (lice@nhmus.hu) on animal lice. Early registration closes 31 December 2005, and is heavily discounted for students. Further details are available on the conference website at [\[icp3.phthiraptera.org/\]\(http://icp3.phthiraptera.org/\)](http://</p>
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Sent on behalf of the ICP3 organizing committee by Vince Smith Web: <http://darwin.zoology.gla.ac.uk/~vsmith/> Apologies for cross postings

vsmithuk@yahoo.co.uk

Edinburgh PopGenetics Dec2005 5

An updated programme is available. I hope everyone's need have been met. Below are some final updates on arrival etc. Other information is unchanged on the web site.

Arrival Please see the information on the web site for how to get to Heriot-Watt's Edinburgh campus and the James Watt Centre. A registration desk will be open on Tuesday December 13th, from 2pm until 9pm. For instructions about later arrival, see the document available from the web site. A buffet dinner will be served from 6.30 pm. For those not staying at Heriot-Watt, the registration desk will be open on Wednesday December 14th from 8am. The first talk is at 9am.

Paying on arrival Please NOTE that payments must either be by cheque to the University of Edinburgh, or in cash. There are no facilities to pay by credit card at that point. There are cash points at the James Watt Centre.

Receipts: After you paid, you should have received an email from the University of Edinburgh finance office, stating that your payment had been received. I hope that this can serve as a receipt for reimbursement, but if anyone has particularly pernicky administrators at their own university, a receipt can be given on registration at the meeting. Please ask if you need one.

– Professor Deborah Charlesworth Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Ashworth Lab., King's Buildings, West Mains Rd., Edinburgh EH9 3JT, UK

phone 131-650-5751 Fax: 131-650-6564

deborah.charlesworth@ed.ac.uk

zeng@statgen.ncsu.edu

Hangzhou Quantitative Genetics Aug18-24

Preliminary Announcement The 3rd International Conference of Quantitative Genetics

Zhejiang University, Hangzhou, China August 18-24, 2007

The 3rd International Conference on Quantitative Genetics (ICQG) will be held during August 18-24, 2007 at Zhejiang University in Hangzhou, China. As with the 1st ICQG in Ames, Iowa in 1976 and the 2nd ICQG in Raleigh, North Carolina in 1987, the 3rd Conference will be a comprehensive survey of the current status of quantitative genetics. New technologies in areas ranging from genomics and molecular genetics to statistics are providing both opportunities and challenges for our understanding of the genetic basis of quantitative traits in natural populations, the evolution of characters, and use for plant and animal breeding. Program suggestions will be welcomed by the Conference Organizers listed below.

Zhejiang University is one of the few top-rank research institutions in China. It is a comprehensive institute with a full range of disciplines. With a faculty capable of top-level and large-scale research and a high proportion of graduate students, the university has been undertaking projects, both basic and applied, to address pressing issues and challenges of today and of the future.

The City of Hangzhou is one of the seven ancient capital cities of China. It has a population of 3.72 million and has a recorded history spanning 2100 years. Marco Polo described Hangzhou as the "Most beautiful, magnificent, and heavenly city in the world." Located in China's most developed southeast coastal area, Hangzhou is renowned for its thriving economy, colorful culture and beautiful landscape, especially its famed West Lake and Tea House.

Academic Chairs: Bruce Weir
(bsweir@u.washington.edu) and Bill Hill
(w.g.hill@ed.ac.uk)

Academic Co-chairs: Junyi Gai (sri@njau.edu.cn) and Changqin Wu (chxwu@public.bta.net.cn)

Conference Organizers: Jun Zhu (jzhu@zju.edu.cn) and Zhao-Bang Zeng (zeng@stat.ncsu.edu)

Marseilles 10thEvolBiol Sept20-22 2

The 10th evolutionary biology meeting at marseilles will take place the 20th, 21st, 22nd of September 2006. for more info

<http://www.up.univ-mrs.fr/evol-cgr/> abstract submission and early registration will be possible after the 12/10/2005 best regards Pierre

– Pierre Pontarotti EA 3781 Evolution Biologique
Université d'Aix Marseille I Centre St Charles
3 Place Victor Hugo 13331 Marseille Cedex 3
33491106489 <http://www.up.univ-mrs.fr/evol> We are organizing the 10th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/>
Pierre.Pontarotti@up.univ-mrs.fr

McGillU CSEE Apr3-4

SOCIÉTÉ CANADIENNE D'ÉCOLOGIE ET D'ÉVOLUTION

CONGRÈS INAUGURAL

Première annonce et appel de conférences affichées

Le Congrès inaugural de la Société Canadienne d'Écologie et d'Évolution aura lieu les 3 et 4 avril 2006, à Montréal, co-organisé par l'UQÀM et l'Université McGill. Le programme comprend une assemblée générale pour ratifier la constitution et élire les membres du comité exécutif et du conseil, un symposium regroupant des conférences invitées sur le thème de "l'importance de l'écologie et de l'évolution pour le Canada", ainsi qu'une réunion d'information sur les programmes de financement CRSNG Découverte et autres. Nous aurons également une session permettant aux participants de présenter des affiches.

Nous invitons toutes les personnes intéressées à participer à ce congrès. Merci de nous envoyer un message courriel à ecoevo@gmail.ca, incluant votre nom et affiliation. Le titre du courriel doit comprendre les informations suivantes: nom de famille-initiales-inscription. La date limite pour les inscriptions est le 1er février 2006.

Les frais d'inscription seront de \$20 (membres-étudiant(e)s) ou de \$40 (membres) ou de \$80 (non-membres). Merci de faire parvenir votre chèque au nom d' "Aquasalmo R&D Inc" à Louis Bernatchez, Département de biologie, Pavillon Charles-Eugène Marchand, Université Laval, Québec QC, G1K 7P4, Canada. Ces chèques sont déposés dans un compte que nous utilisons temporairement, en attendant que la Société soit officiellement constituée.

Nous encourageons tous les participants à présenter une affiche et espérons que ce premier congrès constituera une vitrine pour la recherche canadienne en écologie et évolution. Si vous souhaitez présenter une affiche, merci de suivre la procédure ci-dessous. La société est bilingue et toutes les présentations peuvent être faites en français ou en anglais.

Des informations sur la Société et les modalités d'inscription sont disponibles sur notre site web www.ecoevo.ca. Nous vous enverrons en janvier un programme détaillé du congrès incluant le projet de constitution et la liste de candidats pour le comité et le conseil.

Instructions pour les affiches

Les affiches doivent présenter des travaux dans les domaines de l'écologie et de l'évolution. Nous encourageons également les projets interdisciplinaires, destinés à une plus large audience, ou qui explorent l'enseignement de l'écologie et de l'évolution en général. Merci de suivre les instructions suivantes pour la soumission de votre résumé :

* Les affiches doivent être d'un maximum de 2.35 m de large x 1.15 m de haut (7.7 x 3.77 pieds). Des punaises seront disponibles pour installer votre affiche et seront le seul moyen de l'attacher.

Evaluation et acceptation des résumés * Les auteurs sont responsables de l'exactitude et de l'apparence de leur résumé. * Le résumé doit être basé sur des résultats nouveaux et non publiés. * Le résumé peut être soumis avant que toutes les analyses et conclusions de l'étude soient finalisées. Dans ce cas, il est important d'indiquer au moins les résultats préliminaires.

Soumission du résumé * Merci d'envoyer votre résumé par courriel à ecoevo@gmail.com, avant le 1er février 2006. Le titre du courriel doit comprendre les informations suivantes: nom de famille-initiales-inscription&résumé. * Un accusé de réception vous sera envoyé à l'adresse courriel indiquée dans votre message d'inscription. Si cette adresse est erronée vous ne recevrez pas d'accusé de réception. Un numéro de référence sera attribué à votre résumé. **MERCI DE NE PAS PERDRE CE NUMÉRO QUI VOUS**

SERA DEMANDÉ LORS DE COMMUNICATIONS ULTÉRIEURES. * Vous serez informé par courriel si votre affiche a été sélectionnée pour présentation, avant le 1er mars 2006. NOTE: les personnes qui soumettent leur résumé le plus tôt possible, seront informées les premières. * Si vous rencontrez des difficultés durant la soumission de votre résumé, merci de nous contacter à ecoevo@gmail.com. Le titre du courriel devra faire mention de: nom de famille-initiales-problèmesoumission.

Préparation des résumés Les résumés doivent être soumis en document attaché (.txt) ou rich text (.rtf). Utilisez le format suivant pour préparer votre résumé: 1. Auteurs et Affiliations. 2. Adresse complète, incluant courriel valide, du premier auteur. 3. Titre et résumé: le titre ne doit pas dépasser 255 caractères (environ 15 mots). Ne pas taper le titre en lettres capitales ou en gras. 4. Texte du résumé: le texte ne doit pas dépasser 1000 caractères (environ 150 mots). Le résumé dot

— / —

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>

Oeiras Portugal CaenorhabditisEvol May24-26

EMBO WORKSHOP ON THE STUDY OF EVOLUTIONARY BIOLOGY WITH CAENORHABDITIS ELEGANS AND CLOSELY RELATED SPECIES

24-26 MAY 2006, INSTITUTO GULBENKIAN DE CIÊNCIA, OEIRAS, PORTUGAL SECOND CALL FOR PARTICIPANTS (DEADLINE 15 JANUARY 2006)

This is the second call for the first international workshop dedicated to the study of evolution with Caenorhabditis species. The workshop will be held for three days from 24 to 26 of May 2006, at the Instituto Gulbenkian de Ciencia in Oeiras, 20km from Lisbon, in Portugal. Reception will take place on the 23rd.

The program will encompass several sessions on diverse topics such as: - breeding system evolution and male function; - genotypic distributions during inbreeding and adaptation to novel environments; - genetics of

complex characters; - intra and inter-specific developmental genetics of vulval differentiation, sex determination, behaviour and host-parasite interactions;

A session will also be dedicated to *Caenorhabditis* spp. evolutionary biology resources.

If you would like to participate, please send a brief description of your research together with a title and abstract of a 30min talk or poster to Henrique Teotónio (teotonio@igc.gulbenkian.pt), until the 15th of January 2006.

There is no registration fee and accommodation and subsistence costs will be covered for all participants. Commercial participants will however have to pay 450? for registration. We will also be able to give 20 travel aid grants for European researchers (350? each) and 5 travel grants for non-European researchers (700? each), with preference given to early-stage researchers (PhDs and PostDocs).

Further details about the workshop will be posted at <http://cwp.embo.org/w06-31>. Organizing Committee: Henrique Teotónio (IGC, Portugal) Marie-Anne Felix (Institut Jacques Monod, France) Patrick Phillips (University of Oregon Eugene, USA) Ricardo Azevedo (University of Houston, USA)

Funding by: European Molecular Biology Organization Fundação Calouste Gulbenkian

henrique teotonio <teotonio@igc.gulbenkian.pt>

RoyalSocietyLondon Speciation Mar13-14

Announcement of a two day Discussion Meeting on 'Species and Speciation in Micro-organisms'

Venue: The Royal Society in London, UK, on 13th and 14th March 2006.

The meeting will focus on the evolutionary processes that generate the vast array of species that we see in prokaryotes and microbial eukaryotes.

"After three billion years of evolution only 5,000 bacterial species are known compared to over a million animal species that have evolved in only 600 million years. Bacterial species have been defined without any coherent concept of species, but advances in bacterial population biology, and increasing interest in the vast diversity of microbial life, is leading to new insights into

microbial speciation."

Details of how to register for the meeting (which is free) can be found at the following webpage, along with the meeting program.

<http://www.royalsoc.ac.uk/event.asp?id=-3146&month=3,2006>

With best wishes

Dr. Matthew Fisher Imperial College Faculty of Medicine Dpt of Infectious Disease Epidemiology

matthew.fisher@imperial.ac.uk

matthew.fisher@imperial.ac.uk

Tucson Genomics Jan12-14

GENOMICS OF CLOSELY RELATED ORGANISMS

January 12-14, 2006 Marriott University Park Hotel, Tucson, Arizona

The University of Arizona IGERT Program in Genomics is sponsoring an international meeting on the genomics of closely related organisms. It will bring together leading researchers on genome evolution of both prokaryotes and eukaryotes, including empirical, theoretical, and computational approaches. The meeting will take place at the Marriott University Park Hotel adjacent to the University of Arizona campus in Tucson, January 12-14, 2006. The format of the meeting will allow considerable time for informal discussion and interaction among participants. Participation by graduate students and postdoctoral fellows is strongly encouraged, and discounted rates for registration will be available. Early registration ends December 12, 2005. For registration and more information, please visit

www.genomics.arizona.edu/meeting2006.html.

Speakers: Jeffrey Bennetzen, University of Georgia David Haussler, University of California Santa Cruz Philip Hugenholtz, Lawrence Berkeley Joint Genome Institute Austin Hughes, University of South Carolina Peter Keightley, University of Edinburgh Bruce Lahn, University of Chicago Manyuan Long, University of Chicago Kateryna Makova, Pennsylvania State University Nancy Moran, University of Arizona Elaine Ostrander, National Institute of Health Svante Paabo, Max Planck Institute for Evolutionary Anthropology, Leipzig Eduardo Rocha, Centre National de la Recherche Scientifique, France Joana Silva, The Institute for Genomics Research Patricia Wittkopp, Univer-

sity of Michigan Mariana Wolfner, Cornell University
 — Michael Nachman Professor, Department of Ecology and Evolutionary Biology Director, IGERT Program in Genomics BioSciences West Bldg. University of Arizona Tucson, AZ 85721

Phone: (520) 626-4595 (office), 626-4747 (lab) Fax: (520) 621-9190 Email: nachman@u.arizona.edu

Tucson Genomics Jan12-14 2

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January 12-14, 2006 Marriott University Park Hotel, Tucson Arizona

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of South Carolina Peter Keightley, University of Edinburgh Bruce Lahn, University of Chicago Manyuan Long, University of Chicago Kateryna Makova, Pennsylvania State University Nancy Moran, University of Arizona Elaine Ostrander, National Institutes of Health Svante Paabo, Max Planck Institute for Evolutionary Anthropology Eduardo Rocha, Centre National de la Recherche Scientifique Joana Silva, The Institute for Genomic Research Patricia Wittkopp, University of Michigan Mariana Wolfner, Cornell University –

Michael Nachman Professor, Department of Ecology and Evolutionary Biology Director, IGERT Program in Genomics BioSciences West Bldg. University of Arizona Tucson, AZ 85721

Phone: (520) 626-4595 (office), 626-4747 (lab) Fax: (520) 621-9190 Email: nachman@u.arizona.edu

UAlabama SEEC Mar3-5

Hi Everyone! This is an announcement of the Southeastern Ecology and Evolution Conference 2006. The University of Alabama in Tuscaloosa is hosting SEEC 2006 from March 3-5. Registration dates and other information will be updated throughout the year at

<http://frctest.ua.edu/public.html/seec2/>; If you have questions, please email us at seec2006@gmail.com

We are looking forward to seeing everyone next semester at UA!

Lori Valentine

seec2006@gmail.com

GradStudentPositions

Austria FisheriesInducedEvol 8	FrankfurtU EvolEcol 10
BathU EvolGenomics 8	IIASA Austria EvolModels 11
CornellU EvolGenetics 9	ImperialCollegeLondon HostParasiteCoEvol 11
Finland EndophyticFungiEvol 10	ImperialCollegeLondon SolanumSpeciation 12

IraklioCrete EvoDevo	12	ULausanne PlantPollinator	20
KansasStateU EcolGenomics	13	ULeeds ConservationGenet	20
Mainz Germany MolEvolPhylogeography	13	ULouisianaMonroe EvolBiology	21
MelbourneU AmphibianPopulations	14	UMassAmherst ScaleInsectEvol	22
NCStateU AppliedEvolBiol	14	UNebraska EvolBiol	22
NCStateU MothEvol	15	UNewMexico ParasiteBiodiversity	23
PortlandStateU EvolBiol	15	UNottingham HostParasite	24
SaintLouisU InsectSystematics	16	URochester EvolEcol	24
UAuckland RatPhylogeny	16	UTennessee AdaptiveEvol	24
UCLA EvolBiol	17	UTurku PlantHerbInteractions	25
UChicago EvolGenet	18	UWindsor SalmonQuantGenet	25
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Austria FisheriesInducedEvol

Fellowships for Young Scientists to Conduct Research on Fisheries-Induced Evolution

Funding is available at the International Institute for Applied Systems Analysis (IIASA; www.iiasa.ac.at) for PhD candidates to work 3-6 months with projects relevant to the institute's ongoing research on fisheries-induced evolution (www.iiasa.ac.at/Research/ADN/-Fisheries.html). Successful applicants can participate through the Young Scientists Summer Program (www.iiasa.ac.at/yssp/) and/or through the European Research Training Network on Fisheries-induced Adaptive Changes in Exploited Stocks (www.iiasa.ac.at/-Research/ADN/FishACE/).

Work will be done in close collaboration with Erin Dunlop, Åke Brännström, and Ulf Dieckmann of IIASA's Adaptive Dynamics Network (www.iiasa.ac.at/Research/ADN/). In particular, we are looking for candidates interested in conducting research on one of the following topics:

- a) Eco-genetic models of fisheries-induced evolution (for more information on this project contact Erin Dunlop at dunlop@iiasa.ac.at).
- b) Models of food webs and food web evolution with applications to fisheries (for more information on this project contact Åke Brännström at brnstrom@iiasa.ac.at).

Informal inquiries about specific research interests and plans are encouraged and can be sent by email to either Erin Dunlop or Åke Brännström. To apply, send a CV, a description of relevant research experience, contact information for at least two references, and copies of

any salient publications to either Erin Dunlop or Åke Brännström by January 10, 2006. Review of applications will continue until positions are filled.

Dr. Erin S. Dunlop Adaptive Dynamics Network International Institute for Applied Systems Analysis Schlossplatz 1, A-2361 Laxenburg, Austria Email: dunlop@iiasa.ac.at Tel: +43 2236 807 321 Fax: +43 2236 71313

Erin Dunlop <dunlop@iiasa.ac.at>

BathU EvolGenomics

Graduate position in Evolutionary Genomics/bioinformatics at University of Bath

A 4 year MRC funded studentship in evolutionary genomics/bioinformatics is available under the supervision of Professor Laurence D. Hurst (see <http://www.bath.ac.uk/bio-sci/hurst.htm>), in the Department of Biology & Biochemistry at the University of Bath, UK. The project will involve analysis of the evolution of gene order in yeasts. The studentship comes with an augmented tax-free stipend: £14,300 in first year rising to £15,246 in the final year.

The Department (see <http://www.bath.ac.uk/bio-sci/>) has first class facilities in modern buildings and is one of Britain's top Biological Science Departments (RAE 5, TQA 24/24, 5th in Times League Table). The department is committed to recruiting high quality Postgraduate Research Students and ensuring that they acquire a range of specific and generic skills during their research training. It has the additional advantage of being in Bath, a world heritage site.

To be eligible candidates for the studentship must, at the time of taking up the studentship, hold qualifications at the level of, or equivalent to, a good honours degree from a UK academic institution, in a subject relevant to MRC's scientific remit. This should be a first or upper second class honours degree. The applicant must also fulfill the MRC requirements for residency. Typically this means that the student must be either a UK national who has lived most of their life in the UK or an EU national who have spent the three years prior to application resident in the UK (this can include residence while undertaking undergraduate study).

For further details of the project please contact Laurence D. Hurst: l.d.hurst@bath.ac.uk. For all other enquiries and for details of application procedure, please contact Dr Emma Lawrence: E.L.Lawrence@bath.ac.uk

Laurence D. Hurst Professor of Evolutionary Genetics
University of Bath Bath, BA2 7AY, UK

Tel: +44 (0)1225 386424 Fax: +44 (0)1225 386779

Laurence Hurst <l.d.hurst@bath.ac.uk>

CornellU EvolGenetics

Graduate programs in Evolutionary Genetics and Evolutionary Genomics at Cornell University

Cornell University provides many outstanding opportunities for graduate or postdoctoral study and research in evolutionary genomics. We have excellent groups working on many model and non-model animal, plant and microbial systems, and with programs that include (and integrate) experimental, analytical, functional, statistical and computational approaches to the study of genomic and organismal diversity and to the inference of function and functional diversification. Importantly, there is a tremendous spirit of interaction and collaboration within and among groups that facilitates ability of students and postdocs to learn and apply the full scope of tools, skills, and perspectives important to evolutionary genomics today.

There are several programs, called "fields" that are actively seeking applications for new graduate students. At Cornell, only these interdepartmental fields grant advanced degrees, and because departments do not even grant degrees, cross departmental collaboration is exceptionally easy and natural here. Many of the graduate fields will appear to overlap, so the best way to

find out which is right for you is to study the websites. Here is a quick run down:

Graduate Field of Genetics and Development www.mbg.cornell.edu/GandD.cfm If you are particularly interested in genetic mechanisms of evolution, or have a strong affinity for model genetic organisms and their role in evolutionary genomics, or have a strong interest in functional genomics or evolutionary developmental genetics, this field is the one for you. Some of the Genetics and Development faculty that have a strong interest in evolutionary genetics include Chip Aquadro, Dan Barbash, Ed Buckler, Carlos Bustamante, Andy Clark, Rick Harrison, Brian Lazzaro, June Nasrallah, and Mariana Wolfner. Deadline for graduate applications: Jan 5.

Graduate Field of Ecology and Evolutionary Biology <<http://www.eeb.cornell.edu/field/-EEB.html>>www.eeb.cornell.edu/field/EEB.html

This field spans evolutionary ecology, ecological genetics, speciation, and population genetics. If your primary interests include ecological components of the determinants of evolutionary change, or the role of the environment in organismal fitness, this program is for you. Out of the set of 51 faculty in this graduate field, the following have a primary interest in evolutionary genetics: Chip Aquadro, Andy Clark, Rick Durrett, Rick Harrison and Irby Lovette. Deadline for graduate applications: Dec 1.

Graduate Field of Computational Biology www.cb.cornell.edu This is a newly formed graduate field that spans a wide range of applications of serious computational modeling to problems in bioinformatics, biomechanics, population dynamics, protein structure, epidemiology, gene regulatory networks, quantitative genetics and complex traits, evolutionary genomics or statistical genomics. Some of the faculty with an interest in evolutionary genomics include Carlos Bustamante, Andy Clark, Ron Elber, Uri Keich, Jason Mezey, and Adam Siepel. Deadline for graduate applications: Jan 5.

Other relevant graduate fields In addition there are several other somewhat more specialized programs that include very strong coverage of evolutionary biology, including Entomology, Plant Biology, Biometry, and Applied Math. You can also learn more about academic programs and facilities at Cornell from the individual departmental websites, including Molecular Biology and Genetics (www.mbg.cornell.edu), Ecology and Evolutionary Biology (www.eeb.cornell.edu), Biological Statistics and Computational Biology (www.bscb.cornell.edu), Plant Breeding and Genetics (plbrgen.cals.cornell.edu)

and the Institute for Genomic Diversity (<http://www.igd.cornell.edu/>) to name just a few.

Chip Aquadro - *Drosophila* population genetics/genomics http://www.mbg.cornell.edu/MBG_Faculty_Detail.cfm?id=2 Dan Barbash - genetics of interspecific hybrid sterility and inviability http://www.mbg.cornell.edu/MBG_Faculty_Detail.cfm?id=156 Ed Buckler - genetic dissection of maize QTL; bioinformatics <http://www.genomics.cornell.edu/faculty/facultybio.cfm?netid=esb33> Carlos Bustamante - statistical inference in population genetics

— / —

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>

Finland EndophyticFungiEvol

MESSAGE:

ARE YOU INTERESTED IN COMBINING THEORY AND APPLIED ECOLOGY?

GRADUATE STUDENT POSITION

POSTDOCTORAL POSITION

We are seeking to recruit a enthusiastic and highly motivated graduate student and a postdoctoral scientist to work on a four year research project entitled ?Endophytic fungi in ecological plant production? (funded by Academy of Finland). Our research focuses on ecological and evolutionary implications of genetic, species and functional diversity of grasses and associated endophytic microfungi by emphasizing importance of habitat diversity and consequences of human activities (<http://www.sci.utu.fi/biologia/ekologia/endofytti.htm>). Keeping theory and applied aspects well in balance, this project tests usability of systemic grass endophytes as biocontrol agents in crop production and orchards. Candidates who are self-motivated and career-oriented are welcome to join an exciting and highly interactive research team.

Candidates should have a strong background in ecology, agroecology, or other relevant biological sciences, have good communication, interpersonal and organisational skills, be able to work independently and show initiative. A postdoctoral scientist must also have demonstrated ability to conduct and publish research.

The research will be conducted in Jokioinen and Mikkeli (Agrifood Research Finland) and the positions will be filled from May 1st, 2006 or on agreement.

Informal enquiries maybe made to Kari Saikkonen or Marjo Helander. Applicants should submit a short (1-2 page) statement of research interests and personal skills, a curriculum vitae, a publications list, and contact details of two referees. These should be sent, preferably by e-mail, to Kari Saikkonen by January 15th, 2006.

Research professor Kari Saikkonen Agrifood Research Finland Environmental Research Karilantie 2 A 50600 Mikkeli FINLAND

kari.saikkonen@mtt.fi

Doc. Marjo Helander Section of Ecology Department of Biology 20014 University of Turku FINLAND

helander@utu.fi

Kari Saikkonen <karisaik@utu.fi>

FrankfurtU EvolEcol

PhD POSITION AT FRANKFURT UNIVERSITY

in Evolutionary Ecology of Freshwater Invertebrates

available, starting March 1st, 2006. The position (German salary category BAT IIa/2) is in the group of Professor Dr. Bruno Streit (Institute of Ecology, Evolution and Diversity) and will be given for 3 years. Prerequisites: Diploma or master thesis in the field of evolution or phylogeny or ecology or ecophysiology of freshwater organisms. The successful candidate should be willing to cooperate in current projects, but may also present his/her own PhD project. Further duties include teaching and administration; therefore an adequate knowledge of German is required. Further information on our research and on cooperating groups may be found on our common homepage: www.bio.uni-frankfurt.de/ee. Send CV and referee names (closing date January 16, 2006) to: Prof. Dr. Bruno Streit, Frankfurt University, Biologie-Campus, Building A, Siesmayerstrasse, D-60054 Frankfurt am Main, Germany.

Prof. Dr. Bruno Streit Institute of Ecology, Evolution and Diversity Director Biologie-Campus ? Siesmayerstrasse 60325 Frankfurt am Main Germany

Phone: 049-69-798-24711 Fax: 049-69-798-24910 Internet: <http://www.bio.uni-frankfurt.de> Bruno Streit

<streit@zoology.uni-frankfurt.de>

IIASA Austria EvolModels

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 Models

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

Since 1977, the annual Young Scientists Summer Program (YSSP) of the International Institute for Applied Systems Analysis (IIASA) in Laxenburg, Austria, has attracted more than 1300 students. The YSSP 2006 will take place from June 1 to August 31, 2006. 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 intensive personal interaction with advising senior scientists, and typically leads to a publication in an international journal (and often to a chapter in a candidate's PhD thesis).

Students from Austria, China, Estonia, Finland, Germany, Japan, the Netherlands, Norway, Poland, Russia, Sweden, and the USA are eligible for fellowships providing full coverage, including travel, accommodation, and living expenses. Young scientists from all countries are eligible for stipends, provided by the ADN Program, contributing to travel and accommodation costs.

Model-based summer projects are invited for research in any of the following areas

Adaptive Dynamics Fisheries-induced Evolution Evolution of Cooperation Food Web Evolution Adaptive Speciation 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 are encouraged and may be directed to the Program Leader of the Adaptive Dynamics Network, Ulf Dieckmann (dieckmann@iiasa.ac.at).

Online applications have to be completed before Jan-

uary 15, 2006.

Some useful links:

+ www.iiasa.ac.at/Admin/YSP/yssp2006/-eligibility.html Details about the summer program, and online application

+ www.iiasa.ac.at/Research/ADN Information about the Adaptive Dynamics Network, IIASA's Evolution and Ecology Program

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

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

Ulf Dieckmann Phone +43 2236 807 386 Program Leader +43 2236 807 275 (secretary) Adaptive Dynamics Network +43 2236 807 231 (secretary) International Institute Fax +43 2236 71313 for Applied Systems Analysis Email dieckmann@iiasa.ac.at A-2361 Laxenburg Web www.iiasa.ac.at/Research/ADN Austria www.iiasa.ac.at/~dieckman dieckman@iiasa.ac.at

ImperialCollegeLondon HostParasiteCoEvol

Experimental host-parasite coevolution in yeast

We are looking for a Ph.D. student to study host-parasite coevolution in experimental and natural populations of yeast. Many strains of yeast are infected with intracellular genetic parasites (DNA plasmids and RNA viruses) that replicate at the expense of their host. Although geneticists have known about these parasites for a long time, little is known about their ecology and evolution. We outline some of the interesting questions that we think could be investigated with this system below, although these could easily be changed depending on the interests of the student.

The studentship is funded by NERC (UK) and the student will be based at the NERC Centre for Population Biology located at the Silwood Park campus of Imperial College London. The Centre for Population Biology offers students access to an outstanding group of researchers in evolution and ecology as well as excellent lab facilities. The stipend is £14 K a year and eligibility would be the same as for NERC studentships. Closing date for applications is February 19th, 2006.

This position is ideal for students who would like to

carry out independent research project in a stimulating and challenging environment. Experience in microbiology and molecular biology are assets, but they are not required. Interested applicants should send a cv detailing their experience and interests to Craig MacLean. Ideally, the student would begin their project in September, 2006.

Craig MacLean Austin Burt

“MacLean, Craig” <c.maclea@imperial.ac.uk>

ImperialCollegeLondon SolanumSpeciation

PhD Position in the Division of Biology, Silwood Park, Imperial College London

High-resolution mapping of speciation in the *Solanum nigrum* complex

NERC CASE Award with the Natural History Museum (£14,000 plus £1000 p.a. stipend)

Supervisors: Tim Barraclough, Gerard Bishop (Division of Biology, Imperial College London) Sandy Knapp (Botany, NHM)

Ecological divergence is known to be an important cause of speciation. Without it, rates of population divergence appear to be tediously slow. But how it occurs in practise remains unclear. Certain conditions are needed in sexual organisms to prevent interbreeding between emerging species, but the relative important of the different proposed mechanisms is unclear. We're looking for a student to tackle these questions in the *Solanum nigrum* complex, widespread annual weeds related to tomato and other crops. The work will combine field experiments, evolutionary genomics, systematics, and evolutionary theory, tailored to the student's own interests. You would be based at the Silwood Park campus of Imperial College. You would also work regularly at the Natural History Museum and the Royal Botanic Gardens, Kew. Further details available on request. To apply, please send a CV and a covering letter outlining your interests to Tim Barraclough, t.barraclough@imperial.ac.uk. Applications received before the 14th January 2006 will be treated equally.

Full funding is for UK residents only, partial funding for EU students (no stipend), see details on www.nerc.ac.uk Timothy Barraclough

<t.barraclough@imperial.ac.uk>

IraklioCrete EvoDevo

POST-GRADUATE FELLOWSHIPS AVAILABLE

Michalis Averof / Development and Evolution lab Institute of Molecular Biology and Biotechnology (IMBB) Iraklio Crete, Greece

Marie Curie Research Training Network “Zoonet” Development and evolution of animal form: Training modern comparative zoologists

Post-graduate training fellowships are available for periods between 6 months and 2.5 years, starting from May 2006, funded by the Marie Curie Research Training Network “ZOONET”, to study the evolution of developmental processes in crustaceans and insects using comparative gene expression and functional studies (for a summary of the lab's interests see: <http://www.imbb.forth.gr/people/averof/>).

Applicants should have a relevant B.Sc., M.Sc. or equivalent degree; experience in molecular biology, developmental biology, genetics or computational biology would also be an advantage. Training will be given in the full range of approaches relevant to Evolutionary Developmental Biology (e.g. comparative studies of gene expression, functional studies by RNAi and transgenesis) 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 no more than four 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 Greece for more than 12 months in the 3 years immediately prior to the appointment. Greek nationals may apply only if they can provide evidence that they have legally resided and have had their principal activity (work, studies, etc) in a third country for at least four of the last five years immediately prior to the reference deadline.

The salary will be approximately 20,000 Euro per annum (net), plus contributions for social security and income tax. Researchers will also be eligible for an annual travel allowance and a career exploration allowance.

Applicants should send their CV to Michalis Averof

(please send electronically to averof@imbb.forth.gr). They should also ask two referees to send letters of recommendation to the same electronic address.

The closing date for applications is 15 February 2005.

– Dr Max Telford 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 website: <http://www.zoonet.eu.com> m.telford@ucl.ac.uk

KansasStateU EcolGenomics

Graduate Fellowship Positions in Ecological Genomics at Kansas State University

Graduate Fellowships are available for admission in Fall 2006 to participate in this newly emerging field at the interface of ecology and genomics. This research initiative will link responses of living systems to environmental change at the genetic level. The overarching goal of this research initiative is to identify the genes that are involved in organismal responses to the environment.

This Ecological Genomics initiative takes advantage of existing strengths at Kansas State University in genetics and genomics, ecology and evolutionary biology to answer cross-cutting questions that lie at the interface of genomics and ecology. This collaborative research effort will cross disciplines (genetics and ecology) and departments. In addition, this initiative will also take advantage of experimental manipulations at the Konza Prairie Long-Term Ecological Research (LTER) site.

Research and education opportunities exist for Graduate Students to work towards an MS or PhD degree in this large collaborative and interdisciplinary effort. More information about the Kansas Ecological Genomics collaborative research groups at Kansas State University can be found at www.ksu.edu/ecogen. Twenty faculty with interests spanning from genetics and genomics of model organisms (*Arabidopsis*, *C. elegans*, *Drosophila*) to microbial, plant and animal organismic biology, and ecosystem ecology are involved in this new research initiative. Applicants should have the interest and willingness to cross disciplines.

Completed applications must be received by January 15, 2006.

For more information on how to apply, visit our website at www.k-state.edu/ecogen/recruit-GradStudentsApplication.html.

Supported by Targeted Excellence at Kansas State University.

KSU is an Equal Opportunity Employer, and actively seeks diversity among its employees.

dmerrill@ksu.edu

Mainz Germany MolEvolPhylogeography

A position for a Ph.D. student within a project co-financed by the German Science Foundation (DFG) and the Austrian Science Foundation (FWF) is available at the Institut für Spezielle Botanik und Botanischer Garten, Johannes Gutenberg-Universität Mainz in Germany. The preferred starting date would be February, 1st, 2006.

The project investigates the evolution of nuclear markers in different groups of *Veronica* with different breeding system and evolutionary history. One of the target genes is a gene involved in the self-incompatibility reaction. The results will also be used in a phylogeographical study and compared to complimentary multilocus data generated by another member of the lab group. The studies will be guided by Dr. Dirk Albach in Mainz and Prof. Manfred A. Fischer in Vienna.

Applicants should have experience in molecular techniques and interest in evolutionary questions. Experience with cloning and sequencing nuclear genes is especially welcome.

Please send application including CV and names and address of two referees by mail or e-mail to Dr. Dirk Albach, Institut für Spezielle Botanik und Botanischer Garten, Johannes Gutenberg-Universität Mainz, 55099 Mainz (or albach@uni-mainz.de). Use the same address if you have further questions. Deadline is December, 23rd, 2005.

– Dr. Dirk Albach Institut für Spezielle Botanik Johannes Gutenberg-Universität Mainz Bentzelweg 9b 55099 Mainz

Tel.: +49 (0)6131 3923169 Fax.: +49 (0)6131 3923524
albach@gmx.net

MelbourneU AmphibianPopulations

Two positions for PhD students in molecular ecology Melbourne University and Museum Victoria, Australia

We seek two postgraduate students to work together with us on a project entitled “Human-induced changes in the genetic structure of amphibian populations.” We will compare data gathered from museum specimens of frogs collected 40 years ago with similar data from current populations, to discover how genetic population structure has been modified by different forms of landscape change. Results will support a predictive model of the impact of urban development on the genetic structure of populations, and contribute to land-use planning in the greater Melbourne area. Students will gain experience using molecular markers, phylogeographic analysis, GIS modeling, and ancient DNA.

The two positions are funded by a Linkage grant from the Australian Research Council, and include an annual tax-free salary of \$24,650 for three years, extra support for relocation and producing the thesis, and funds for conducting the research itself. Students will be enrolled in the Department of Zoology at the University of Melbourne, but will also have offices at Museum Victoria (about 1 km from the university), and will do most of their labwork in the Museum. Fieldwork occurs in and around Melbourne.

The project involves collaboration among people from several institutions, so the students can expect to interact with Josh Van Buskirk (University of Melbourne), Jane Melville (Museum Victoria), Kirsten Parris (Deakin University), Jeremy Austin (University of Adelaide), and Murray Littlejohn (University of Melbourne).

Qualifications: Australian or New Zealand citizenship or Australian permanent resident status, strong professional interests in molecular ecology and/or landscape ecology, and first-quality honours or masters research. Some previous experience with GIS modeling and/or molecular markers is desirable but not essential.

Application: Please send to the address listed below (i) a letter describing your interests in this position and your previous research experience (honours, masters, RA positions, etc.), (ii) your CV, and (iii) names and contact information of two references. E-mailed applications are welcome. We will begin screening candi-

dates on 23 January 2006. Students may begin as early as March 2006.

Josh Van Buskirk Zoology Department University of Melbourne Parkville, VIC 3010 Australia
j.vanbuskirk@zoology.unimelb.edu.au
www.zoology.unimelb.edu.au

NCStateU AppliedEvolBiol

NCStateAppliedEvolBiol

Research on the use of transgenic mosquitoes for decreasing the prevalence of dengue virus diseases in developing countries.

We are looking for a PhD student who is interested in conducting research aimed at driving anti-pathogen genes (refractoriness) into mosquito populations. The main emphasis of the student’s research can be in the areas of 1) estimating ecological parameters in mosquito life histories that will impact the spread of anti-pathogen transgenes, 2) building population genetics models of gene drive mechanisms, 3) estimating mosquito population structure through use of molecular genetic approaches, or could work on a project that combines two or more of the above areas. The student could either become a member of the Entomology or the Genetics Department and North Carolina State University.

Our lab is funded by NIH and the Gates Foundation and is part of an interdisciplinary group composed of mosquito ecologists, geneticists, disease epidemiologists, molecular biologists, ethicists, and scientists from disease-endemic countries, all working to develop novel transgenic strategies for disease reduction. The student in this position will focus on a specific project but will also interact with members of this team and thereby acquire a broad understanding of the challenges facing scientists who want to move their research from the lab bench all the way to successful implementation.

An overview of this area of research and an entry point to the literature can be found in

“Gould, F., and P. Schliekelman. 2004. Population genetics of autocidal control and strain replacement. *Ann. Rev. Entomol.* 49: 193-217”.

North Carolina State University is a leading research institution with a strong commitment to the study of entomology and genetics. The University is situated in

Raleigh, NC and is within 30 miles of Duke University, UNC-Chapel Hill, NIEHS, an EPA research unit, and the Research Triangle Park. NC State University is an equal opportunity and affirmative action employer.

Send inquiries to Fred_Gould@NCSU.edu

NCStateU MothEvol

NCStateMolEvolBiol

Evolution of Sexual Communication Systems in Moths

Background Information: Most night-flying moth species locate mates through production of, and response to, a very precise blend of two or more volatile chemical compounds. Within a population, females with atypical blends have been shown to be less attractive to males than females with the population's common blend. Similarly, rare males that respond to atypical blends have been found to be at a disadvantage in finding mates. The genes that control pheromone blend ratios have never been found to be linked to, or affect male response, so mutations that cause changes in each of the two components of communication are expected to arise independently. On a simple theoretical level, this type of sexual communication system is expected to be evolutionarily constrained because an individual with a mutation leading to an altered blend or response will be selected against, when rare. Even if the selective disadvantage to rare individuals with alleles for novel signals or responses is minimal, mass selection is not expected to increase their frequency in the population. Based on these assumptions it is difficult to account for the great diversification of chemical mixtures used in mate communication by over 10,000 moth species. We are investigating a number of potential evolutionary mechanisms that could have resulted in this diversification by dissecting the genetic underpinnings of selective mating in moths.

We are working with two sympatric moth species (*Heliothis virescens* and *Heliothis subflexa*) that have very distinct sex pheromone blends, do not mate in the wild, but can be induced to mate in the lab. We have mapped a number of Quantitative Trait Loci (QTL) that control production of specific female sex pheromone components and male response to these components. We have moved two specific QTL between species and tested their impacts on mating in the field. We have also identified a number of candidate genes that appear to be involved in male response to specific pheromone com-

ponents.

We are now in a good position to test candidate genes and to determine the genetic and molecular basis for differences between the sexual communication systems of these two moth species. We are looking for a PhD student who has basic knowledge of molecular techniques and wants to use these techniques to answer questions about insect evolution.

North Carolina State University is a leading research institution with a strong commitment to the study of entomology and genetics. The University is situated in Raleigh, NC and is within 30 miles of Duke University, UNC-Chapel Hill, NIEHS, an EPA research unit, and the Research Triangle Park.

For more details about our lab see: <http://www4.ncsu.edu:8030/%7Efgould/>

The successful applicant will participate in the interdepartmental Keck Program in Behavior Biology—http://www.cals.ncsu.edu/beh_bio/index.html Send Letters of inquiry to: Fred_Gould@NCSU.edu

PortlandStateU EvolBiol

The Department of Biology at Portland State University is seeking graduate students to join a recently expanded focal area in ecology and evolutionary biology. Our faculty have active and interrelated research programs spanning all levels of biological organization, including behavior, population biology, conservation, genetics, systematics, and genomics. Research in this area is complemented by departmental strengths in physiology, microbiology, and the biology of extremophiles.

Portland State University is located in downtown Portland and is the largest university in Oregon. The location provides the benefits of a livable, culturally rich urban center and easy access to the natural diversity of the Cascades, Columbia River Gorge, and the Oregon Coast. The University has a diverse and motivated student body and is committed to sustainability and community outreach. Research facilities in the Department include the PSU-Keck Genomics Facility, Vertebrate Biology Museum, Herbarium, Aquatic Vertebrate Facility, and additional Greenhouses slated for completion in 2006.

Please visit our website (www.biology.pdx.edu) for more information about the Department, faculty, graduate studies, and to submit an online application.

Faculty in ecology and evolutionary biology and their research interests include:

Mitch Cruzan cruzan@pdx.edu plant ecological genetics, invasive species, hybridization <http://web.pdx.edu/~cruzan/> Debbie Duffield duffieldd@pdx.edu population genetics, conservation biology <http://www.biology.pdx.edu/faculty/duffield-duffield.html> Sarah Eppley eppley@pdx.edu plant population ecology, breeding system evolution

Suzanne Estes estess@pdx.edu genetics of adaptation, mutational effects <http://www.biology.pdx.edu/faculty/estes/main.html>

Mark Fishbein mfish@pdx.edu plant systematics, pollination ecology, hybridization <http://web.pdx.edu/~mfish>

Susan Masta smasta@pdx.edu genome evolution, speciation, arachnid evolution <http://web.pdx.edu/~smasta> Mike Murphy murphym@pdx.edu population ecology, behavior, vertebrate ecology <http://www.biology.pdx.edu/faculty/murphy/murphy.html>

Radu Popa rpopa@pdx.edu microbial ecology, biogeochemistry, origin of life

Anna-Louise Reysenbach reysenbacha@pdx.edu ecology and diversity of thermophiles <http://airlab.pdx.edu>

Luis Ruedas ruedas@pdx.edu animal systematics and biogeography, community ecology, conservation biology <http://www.biology.pdx.edu/faculty/ruedas/ruedas.html> –Mark Fishbein <mfish@pdx.edu>

SaintLouisU InsectSystematics

***** GRADUATE RESEARCH ASSISTANTSHIP: SYSTEMATIC ENTOMOLOGY *****

A graduate research assistantship in Insect Systematics (Ph.D. preferred) is currently open in the Department of Biology at Saint Louis University in Saint Louis, MO, USA. The student selected for this NSF-funded assistantship will assist with a number of tasks focused on the goal of developing a morphological phylogenetic analysis of a large species-group of braconid parasitic wasps. Included tasks will be developing a digital image library, developing a digital online taxonomic key, and assistance with conducting the phylogenetic analysis. The student will be expected to develop a dissertation research project focusing on the systematics of the group under investigation.

In addition to a strong overall academic record, the best

candidates for this assistantship will have the following qualifications: (1) MS degree completed, (2) good computer skills and interests, particularly in the areas of databasing, digital imaging, image processing, and web and digital key development, (3) excellent oral and written interpersonal skills in English, (4) working knowledge of insect diversity and entomological systematics, and (5) an interest in hymenopteran insects.

One of the student's activities will be to help with an outreach program introducing insect science to local schools with high percentages of minority students.

The evolution, ecology, and systematics group of the biology department at Saint Louis University supports a vital, growing graduate studies program, with a well-developed systematics component. In addition, the Missouri Botanical garden, a leading institution in plant biology and systematics, is nearby, as is the University of Missouri at Saint Louis (UMSL), the center of the Organization of Tropical Studies (OTS). Washington University is nearby as well, which is an outstanding resource in evolutionary biology.

Saint Louis University is located near the Mississippi and Missouri Rivers, and at the edge of the Ozark highlands. Natural communities including river bottomland, prairie, glades, and mixed hardwood forests are accessible within a 1/2 to 1 hour drive.

Persons interested in this assistantship should contact Dr. Joe Fortier (see contact information below) informally before applying for admission to the Department. In making this contact, please include the following materials:

a CV (specifically include notes on any computer skills and knowledge, and knowledge of phylogenetic analysis and entomology), a statement of research interests, unofficial transcripts, GRE scores, and the names and contact information of three references.

Joseph C. Fortier Department of Biology Saint Louis University 3507 Laclede Ave. Saint Louis, MO 63103 Office: (314) 977-4353 Lab: (314) 977-3915 FAX: (314) 977-3658 e-mail: Fortier@slu.edu

UAuckland RatPhylogeny

PhD Studentship Tracking Lapita Peoples through Phylogenetic Analyses of Pacific Rats

The human settlement of the Pacific and the origin of

the Polynesians have been topics of debate for centuries. Polynesian origins are most immediately traced to people who arrived in the Fiji, Tonga and Samoa region around 3000 BP and are clearly associated with the Lapita Cultural Complex. While this scenario of the immediate origins of the Polynesians is generally accepted, the debate on the ultimate origin of the Polynesians and Lapita Peoples continues. Our previous research has shown that analyses of mitochondrial DNA variation in the Pacific rat (*Rattus exulans*), transported in the colonising canoes, are valuable for tracing prehistoric human migration within Polynesia.

We are seeking a PhD student to join a multidisciplinary research team investigating the movements of those rats introduced by Lapita peoples, and possibly those also introduced by people moving into the region prior to the arrival of the Lapita Cultural Complex. In this research project you will analyse DNA from ancient and modern *R. exulans* populations in the Pacific. You will use new methods of analysis of population-level genetic variation, incorporating a range of biological and chronological data, to identify paths of introduction, test models of Lapita origins and identify pre-Lapita interactions in the region.

This is a joint research project involving Dr Lisa Matisoo-Smith and Judith Robins, University of Auckland Department of Anthropology and Prof Mike Hendy, Massey University Institute of Fundamental Sciences, all members of the Allen Wilson Centre for Molecular Ecology and Evolution, and Dr Howard Ross University of Auckland School of Biological Sciences.

We are seeking a PhD student with experience in molecular genetic analyses (DNA extraction, PCR amplification and sequencing) and computational phylogenetics. The scholarship includes an annual stipend of NZ\$25,000 for 3 years, from which the student is expected to pay tuition fees. Note that as from 1 January 2006 international PhD students will be charged tuition fees at the NZ domestic rate (approximately NZ\$3500 per annum).

To apply, please e-mail a letter briefly explaining your research interests and career goals, a CV, a copy of academic transcripts, and contact information for two references to Dr. Howard Ross (h.ross@auckland.ac.nz) by 31 January 2006.

h.ross@auckland.ac.nz

UCLA EvoBiol

UCLA graduate studies in Ecology and Evolutionary Biology

The Department of Ecology and Evolutionary Biology at UCLA invites applications for graduate studies. The department has excellent support packages for Ph.D. students and outstanding opportunities for research within the department, university and UC system. Graduate students can take advantage of the University of California Natural Reserve System, the UCLA Center for Tropical Research, field courses through the Organization for Tropical Studies, and UC-MEXUS, which facilitates collaborative research in Mexico. We encourage interested students to email individual faculty members. For more information about the department, see <http://www.eeb.ucla.edu/>. The deadline for applications is December 15. On-line applications are available at: <http://www.eeb.ucla.edu/-grad.onlineappl.php>. Faculty in Ecol & Evol Biology include:

Priyanga Amarasekare ? mathematical and spatial ecology
Daniel Blumstein ? evolution of behavior and conservation
Donald Buth – population structure of lower vertebrates
Peggy Fong – marine ecology of coastal ecosystems
Malcolm Gordon ? ecophysiology of fishes
Gregory Grether ? evolution of coloration, sexual selection and phenotypic plasticity
Henry Hespeler – evolutionary ecology and biodiversity of tropical insects
David Jacobs – evolution/development and paleobiology of invertebrates
Glen MacDonald ? geographic patterns of climatic variation and vegetation response
Peter Narins – auditory behavior and neurophysiology
Peter Nonacs – behavioral ecology and social evolution
Philip Rundel ? plant functional ecology of Mediterranean, desert, and tropical ecosystems
Rebecca Shipe – marine phytoplankton ecology
Thomas Smith – evolutionary ecology, speciation, and conservation of vertebrates
Victoria Sork ? molecular ecology and conservation genetics of plant populations
Charles Taylor – population genetics and adaptation
Blair Van Valkenburgh – paleobiology and functional morphology of vertebrates
Richard Vance – marine, theoretical, and restoration ecology
Robert Wayne ? evolutionary biology and conservation genetics of vertebrates
Cheryl Ann Zimmer – population ecology of marine organisms
Richard Zimmer – ecology and sensory biology of aquatic organisms

Victoria Sork <vlsork@ucla.edu>

UChicago EvolGenet

Training opportunities in Evolutionary Genetics at the University of Chicago

The University of Chicago offers unparalleled opportunities for graduate and postdoctoral training in evolutionary genetics and genomics. The University has a long-standing tradition of excellence in the Darwinian sciences and hosts a large and intellectually diverse group of internationally recognized faculty in evolutionary biology, statistical genetics, computational biology, molecular evolution, and population genetics and genomics. Evolutionary Genomics in particular has recently expanded with the recruitments of a number of young faculty, including Justin Borevitz, Yoav Gilad, Christopher Lowe, Marcelo Nobrega, Molly Przeworski and Ilya Ruvinsky. Numerous seminars and journal clubs held in participating departments encourage cross-disciplinary training and the exchange of ideas, and often give rise to collaborative efforts.

Students should apply for admission via Darwinian (<http://pondside.uchicago.edu/darwin/>) or Molecular Biosciences (<http://molbio.bsd.uchicago.edu/>) Graduate Training Programs. Once admitted, they can choose among the affiliated faculty. Throughout their studies, graduate students are supported by a combination of university funds, training grants and funds available to individual advisors. Additional information can be found through the Office of Graduate Affairs of the Division of Biological Sciences (<http://gradprograms.bsd.uchicago.edu/>). Applicants for postdoctoral positions are encouraged to contact the faculty members of their choice directly.

The University of Chicago is situated in Hyde Park, a vibrant and diverse community within close distance of downtown Chicago. This location offers the conveniences of a smaller city, together with easy access to the intellectual, cultural and recreational resources of a major metropolitan center.

Departments with faculty members engaged in research and training in Evolutionary Genetics:

Department of Ecology & Evolution (<http://pondside.uchicago.edu/ecol-evol/>)

Department of Human Genetics (<http://genes.uchicago.edu/>)

Department of Organismal Biology & Anatomy (<http://pondside.uchicago.edu/oba/>)

Department of Statistics (<http://galton.uchicago.edu/>)

Additional training opportunities are available through the following training programs:

Committee on Evolutionary Biology (<http://pondside.uchicago.edu/ceb/>)

Committee on Genetics (<http://cg.bsd.uchicago.edu/>)

Faculty group on Developmental Evolutionary Biology (<http://www.ucevo devo.org/>)

LIST OF FACULTY

Bergelson, Joy ? Molecular ecology, evolutionary genomics of plants http://pondside.uchicago.edu/ecol-evol/faculty/bergelson_j.html

Borevitz, Justin ? Statistical genetics, genomics, genetics of adaptation in plants http://pondside.uchicago.edu/ecol-evol/faculty/borevitz_j.html

Coates, Michael ? Evolution, development, systematics, vertebrates http://pondside.uchicago.edu/oba/faculty/coates_m.html

Cox, Nancy ? Genetics of complex traits, human disease, gene mapping <http://www.genes.uchicago.edu/fri/coxres.html>

Coyne, Jerry ? Evolutionary genetics, speciation http://pondside.uchicago.edu/ecol-evol/faculty/coyne_j.html

Di Rienzo, Anna ? Human population genetics, evolutionary genetics <http://www.genes.uchicago.edu/fri/drnzores.html>

Dwyer, Greg ? Mathematical approaches to disease ecology and population genetics http://pondside.uchicago.edu/ecol-evol/faculty/dwyer_g.html

Feder, Martin ? Evolutionary and ecological functional genomics, gene expression http://pondside.uchicago.edu/~feder/Martin_Feder.html

Gilad, Yoav ? Primate gene expression, olfaction, population genomics <http://www.genes.uchicago.edu/gilad.html>

Ho, Robert ? Zebrafish development, comparative morphology

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UEdinburgh EvolEcol

PhD position in evolutionary ecology at University of Edinburgh:

Microevolution in wild bird populations in response to climate change

We are looking for a PhD student to study the effects of changing environmental conditions on microevolution in natural environments. Using long-term records from several studies of great tits (*Parus major*) in the Netherlands, the project will quantify temporal changes in key components of fitness (fecundity, survival, breeding time) and in individuals' ability to respond to different environments (plasticity). The project will focus on temporal changes in both the selection on and the heritability of important traits, of plasticity in these traits, and in the genetic correlations between them, in order to identify genotype-environment interactions and ultimately to predict rates of microevolution. This will provide an illustration of the potential for climate change to shape genetic architecture and hence to drive evolution in natural populations. The study will involve a combination of statistical analysis and fieldwork, and the student would be part of the research groups of Loeske Kruuk in Edinburgh (homepages.ed.ac.uk/loeske) and Marcel Visser at the Netherlands Institute of Ecology in Heteren, the Netherlands (www.nioo.knaw.nl/ppages/mvisser).

The Institute of Evolutionary Biology at Edinburgh (www.ieb.org.uk) is one of the leading departments in the UK for evolutionary ecology. Financial support for up to four years is available to successful UK and overseas applicants, in particular through Marie Curie Studentships for nationals of EU member states and Associated Countries (see homepages.ed.ac.uk/eang09/MCwebpage.htm for further details).

For more information on this or other possible projects, see homepages.ed.ac.uk/loeske/PhDprojects.html. To apply, please send a CV and email addresses of 2 referees as soon as possible (before 6 Jan. 2005) to Loeske.Kruuk@ed.ac.uk.

Loeske Kruuk

Marcel Visser

Loeske Kruuk Institute of Evolutionary Biology University of Edinburgh Edinburgh EH9 3JT, UK Tel. (44) 131 650 5515 Fax (44) 131 650 6564

Loeske.Kruuk@ed.ac.uk Loeske.Kruuk@ed.ac.uk

UIIdaho WashStateU CommunityCoevol

Subject Line: Graduate positions in community coevolution at the University of Idaho and Washington State University

Graduate positions are available in the research groups of Scott Nuismer (University of Idaho) and Richard Gomulkiewicz (Washington State University) as part of a NSF funded project that aims to develop and empirically test mathematical models of multi-species coevolution. Although each student will be formally admitted to a graduate program at one university, a unique feature of the project is the opportunity for students to be co-advised by the PIs across the two universities (which are located just seven miles apart). In addition, students will be able to conduct a significant portion of their research in the laboratories of other project participants including Michael Doebeli (University of British Columbia), Holly Wichman (University of Idaho), and John N. Thompson (University of California Santa Cruz).

We seek students with some background in mathematics or computation, but any capable biologist with the drive to learn and apply modern quantitative techniques is encouraged to apply. In addition to an interest in developing theory, students should be interested in testing predictions using well-studied interactions such as those between bacteriophage and bacteria or between pollinating seed parasitic moths and their host plants.

For additional information visit:

http://www.webpages.uidaho.edu/~snuismer/-Nuismer_Lab/openeings.htm or contact:

Scott Nuismer: snuismer@uidaho.edu

or

Richard Gomulkiewicz: gomulki@wsu.edu

Thanks, Scott

Scott Nuismer Assistant Professor Department of Biological Sciences University of Idaho Moscow, ID 83844 (208) 885-4096 phone (208) 885-7905 fax http://www.webpages.uidaho.edu/~snuismer/Nuismer_Lab/

Nuismer <snuismer@uidaho.edu>

ULausanne PlantPollinator

PhD Position - Plant Evolutionary Ecology

Coupled reproductive ecologies in a plant/pollinator/seed predator system

One PhD position is available at the Department of Ecology and Evolution, University of Lausanne, starting March 2006 or earlier.

The goal of the project is to investigate the reproductive ecologies and the potential antagonistic coevolution between the plant *Silene latifolia* (Caryophyllaceae) and its seed predator and pollinator *Hadena bicruris* (Noctuidae). We combine field and greenhouse experiments with population genetics (microsatellite DNA) to investigate the evolution of defense traits, their costs, and fitness benefits of pollination service. The plant has separate sexes with chromosomal sex determination. The successful candidate will be able to design a project within this framework. For research in our group see: http://www.unil.ch/dee/page7005_en.html
References: Bernasconi G, et al., Evolutionary ecology of the pre-zygotic stage, *Science*, 303: 971-974 (2004)

The ideal applicant has a strong interest in evolutionary ecology and good background in experimental design and statistical analysis, microsatellites and/or fieldwork. Fluent English is required, as well as a Master, Diploma Degree or equivalent in Ecology, Genetics or Evolutionary Biology. Please send a CV, a copy of your degree, a summary of experience and research interests and the addresses of two referees to: M. Moser-Resplendino (Monique.Moser-Resplendino@unil.ch) University of Lausanne Department of Ecology and Evolution Biophore CH 1015 Lausanne

Funding is by the Swiss National Science Foundation for three years. The position will be filled as soon as a suitable applicant is found. Lausanne University (<http://www.unil.ch>) and the Department of Ecology and Evolution (<http://www.unil.ch/dee>) offer excellent facilities and a very stimulating scientific environment, with several groups focussing on population biology, population genetics, behavioural and evolutionary ecology.

Giorgina Bernasconi <Giorgina.Bernasconi@unil.ch>

ULeeds ConservationGenet

Marie Curie PhD studentships in Conservation Genetics and Conservation Biology

The Earth and Biosphere Institute at the University of Leeds, UK invites applications from non-UK applicants for any of the following eight projects. The closing date is December 22nd 2005. Details on how to apply can be found at:

<http://earth.leeds.ac.uk/ebi/2006-proposals-mc.htm>

Population ecology of swarming bats Supervisors: John Altringham and Roger Butlin

Many European bat species live in small colonies during the summer, with little or no interchange between neighbouring colonies. At the end of the summer colonies disperse as the bats mate and prepare for hibernation. Individuals of many species visit their underground hibernation sites from August to November to 'swarm'. There is now strong evidence to suggest that swarming is the primary mating system in several species and plays a significant role in determining population structure. The project will investigate how population structure is determined by factors such as geography, ecology and rarity, by comparing related species (caught at swarming sites) using microsatellite and mitochondrial DNA. We will compare, for example: (1) species with similar ecology, but greatly different abundances (2) abundant species with different dispersal abilities and ecology (3) species in cave-rich and cave-poor landscapes. A knowledge of swarming dynamics and population structure and an ability to model gene flow are potentially important in the development of conservation strategies for rare swarming species. The work will be carried out in the UK and continental Europe.

How important is biodiversity for carbon cycling in tropical forests? Supervisors: Tim Baker, Simon Lewis and Oliver Phillips

A major focus of current ecological research is committed to understanding how biodiversity is related to ecosystem properties, such as biomass and productivity. It is particularly important to understand these relationships in tropical forests as these ecosystems are a critical component of the global carbon cycle. This

project will relate tree structure to tree mass and carbon content, for a range of functional types of tree in tropical forests in Peru and/or Cameroon, and use these relationships to assess the contribution of biodiversity to current and future ecosystem properties and substantially improve regional to global-scale carbon budgets.

Dispersal, gene flow and population biology in a Namib Desert fig tree and its pollinator Supervisors: Steve Compton, Phil Gilmartin and Simon Goodman

We have been using plant microsatellites to follow the movements of fig wasps in Namibia via the pollen they are carrying. On the Ugab River, which runs through the Namib Desert, we found that fig wasps can pollinate trees over 100 kms from their parent trees - pollination distances many times further than known from any other plant. Using similar techniques, but based at the Gobabeb Training and Research Centre on the Kuiseb River, this project will build on the preliminary work and examine seasonal variation in the direction and distances of movements (predominant winds and fruiting frequencies change with season), and whether the diversity of pollen donors is greater for more isolated trees. By quantifying the relationship between how far trees are apart and the likelihood that wasps can make it between them we can predict the likely consequences of expected future losses of trees from the rivers.

Stochastic methods for invasive populations Supervisor: Stephen Cornell

The biology of invasion has repercussions throughout applied ecology and epidemiology, but theoretical studies have focussed on the use of deterministic models whereas stochastic processes are known to be an important component of population dynamics. While the equations describing spatially extended stochastic populations cannot be solved exactly, there has been an important recent advance (Ovaskainen and Cornell, *Theor. Pop. Biol.*, in press) which enables spatial interactions to be accounted for in an exactly solvable limit. The aim of this studentship is to extend the methods of Ovaskainen and Cornell, who studied the case of a resident species distributed throughout all space, to geometries appropriate to an invading species. Topics to be covered include: the effect of stochasticity on the speed and the stability of an invasive front; the effect of locally heterogeneous habitat on an invasive front; the development of calculational tools for managing emerging disease epidemics. Case studies to test the theory will be sought in conservation biology and veterinary epidemiology.

Population dynamics and conservation of Caspian seals (*Phoca caspica*): quantification of present and future threats

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ULouisianaMonroe EvoBiology

The Department of Biology and the Museum of Natural History at the University of Louisiana at Monroe (ULM) are looking to recruit graduate students interested in the evolution and ecology of freshwater snails to their MS in Biology program for SPRING 2006. Most research focuses on the family Pleuroceridae, a group of gill breathing, operculate snails that reaches its greatest diversity in the southeastern United States. Currently, potential projects include evolutionary ecology, life history studies, and the evolution of morphological variation in cryptic taxa as it applies to environmental factors. Depending on pending grant proposals, some molecular work may be included.

Based on availability, students can be paid either as teaching or research assistants. Both include full tuition waivers and are available on a competitive basis; research assistantships carry no teaching responsibilities. The typical assistantship at ULM is \$8,000 per year, though this amount may increase, again depending on grant outcomes. Monroe is a city of 56,000 people on the banks of the Ouachita River in north-central Louisiana, and serves as the educational, commercial, and economic hub of the Delta parishes. The cost of living is very reasonable, and the city tends to dodge major weather-related events (in other words, the hurricanes missed us).

Students seeking admission to the Biology Graduate Program must first be admitted to the ULM Graduate School. Application forms may be obtained online from the Office of Graduate Studies and Research. In addition to a minimum undergraduate GPA of 2.5, the Biology Graduate Program requires either a score of 900 or higher on the GRE General Test (combined verbal and quantitative scores), or a total of 2400 points when the GPA is multiplied by the combined verbal and quantitative GRE General Test scores.

Interested students should contact Dr. Russ Minton (minton@ulm.edu; 318-342-1795) immediately for additional information on research projects and specifics on applying. General information on the department, faculty, facilities, and course offerings can be found at <http://www.ulm.edu/biology>. Russ Minton, Ph.D. Assistant Professor, Department of Biology University of Louisiana at Monroe Monroe, LA 71209-0520 ph: 318-342-1795 fax: 318-342-3312 <http://homepage.mac.com/russminton/index2.htm> Russ Minton <minton@ulm.edu>

UMassAmherst ScaleInsectEvol

In spite of their unassuming appearance, SCALE INSECTS display remarkable evolutionary dynamics in many aspects of their biology, including: – Genetic systems: multiple origins of different kinds of haplodiploidy (arrhenotoky, diploid arrhenotoky, germline paternal genome elimination, embryonic paternal genome elimination); the only known evolutionary reversions of haplodiploidy back to diplodiploidy; the only cases of hermaphroditism in insects; many origins of thelytokous parthenogenesis. –Coevolution with endosymbiotic bacteria: frequent replacements of one primary endosymbiont clade by another, and rapid evolution of the mode of transmission and the morphology of the infected tissues (the bacteriome). Even the genetics of the bacteriome is unstable, with some scale insect families having polyploid bacteriomes incorporating polar body genomes, much like the endosperm of a plant. –Coevolution with hostplants (extreme polyphagy, local adaptation), parasitoids (classical targets of biological control; local adaptation of parasitoids & hosts), fungi (“animal lichens:” intimate, possibly mutualistic associations with *Septobasidium*). –Morphology and physiology: Extreme morphological reduction of flightless larviform female; holometaboly in male. Little variation in male genitalia but enormous variation in sperm morphology (especially number and arrangement of microtubules). Movement of sperm to ovum mediated by a “vestibule cell” in female, possibly analogous to a stigma of a plant. Incomplete gut (no anus) in some lineages. Variation from oviparity and ovoviviparity to full (placental) viviparity. Frequent origin of flightlessness in males. The fact that many scale insects are economically destructive pests opens up many opportunities for collaborative contacts, field experiments, and funding sources.

An NSF-FUNDED GRADUATE RESEARCH ASSISTANTSHIP (\$27,000 / year) is available for the study of the phylogenetics and evolution of scale insects in the laboratory of Benjamin Normark at the University of Massachusetts Amherst, leading to a Ph.D in Entomology or in Organismic and Evolutionary Biology. Substantial domestic and international travel funds are available for conference attendance and field work. Interested students should contact Dr. Normark (bnormark@ent.umass.edu) and should apply to the UMass graduate program in Organismic and Evolutionary Biology (deadline 15 January 2006) and/or the graduate program in Entomology (deadline 1 February 2006).

Graduate Program in Organismic and Evolutionary Biology: http://www.bio.umass.edu/oeb/oeb_admiss.html Graduate Program in Entomology: <http://www.umass.edu/ent/gradprog/apply.html> Benjamin Normark: http://www.umass.edu/ent/faculty_staff/normark/index.html Benjamin Normark Department of Plant, Soil, and Insect Sciences Fernald Hall University of Massachusetts Amherst, MA 01003 USA

office phone and voice mail: 413-577-3780 fax: 413-545-2115

bnormark@ent.umass.edu bnormark@ent.umass.edu

UNebraska EvolBiol

Graduate positions in Ecology and Evolutionary Biology University of Nebraska

The Ecology, Evolution, and Behavior section of the School of Biological Sciences is seeking highly motivated students to join our graduate program. The EEB group is especially strong in the areas of plant-animal interactions, behavioral ecology, life-history evolution, evolutionary physiology, and evolutionary genetics.

We offer generous graduate student support (among the best in the nation), an extremely collegial and interactive environment for doing science, excellent biotech and computational facilities, and access to the Cedar Point Biological Station. A recently funded ???Program of Excellence??? in Population Biology at the University of Nebraska will further strengthen the research program through new faculty hires and a permanent post-doctoral fellowship program (see <http://popbio.unl.edu/>). For more information about the department, see <http://www.biosci.unl.edu/>. Lincoln is a great capital city/college town surrounded by rolling

prairie.

EEB FACULTY:

Gwen Bachman Physiological and behavioral ecology

Alexandra Basolo Sexual selection, life-history evolution, predator-prey interactions

Alan Bond Animal cognition and behavioral complexity

Sherilyn Fritz Quaternary paleoclimatology and paleolimnology

Robert Gibson Behavior, ecology, and evolution

Lawrence Harshman Genetics, evolution (Drosophila longevity, environmental stress, aspects of reproduction)

Eileen Hebets Animal behavior, complex signal evolution

John Janovy, Jr. Host-parasite relationships, parasite ecology

Alan Kamil Behavioral ecology of learning and memory

Kathy Keeler Prairie fragmentation, prairie and plant ecology

Jean Knops Ecosystem and plant ecology, plant species impact on nutrient cycling

Svata Louda Ecology of insect herbivory, plant ecology and conservation

Guillermo Ortíz Molecular systematics, ecology, and evolution

Diana Pilson Ecological genetics of plant-insect interactions

Jay Storz Molecular population genetics and evolution

William Wagner, Jr. Behavioral ecology, sexual selection

Anthony Zera Evolutionary physiology, endocrine adaptations, wing polymorphism

Contact faculty directly with a letter of interest and CV. Deadline for applications is 15 December (see http://www.biosci.unl.edu/grad/how_to_apply.asp).

Jay F. Storz School of Biological Sciences University of Nebraska Lincoln, NE 68588 Phone: 402/472-1114 E-mail: jstorz2@unl.edu

WWW: <http://www.biosci.unl.edu/faculty/-Storz/index.html> Population Biology at UNL: <http://popbio.unl.edu/index.htm> Jay F Storz <jstorz2@unlnotes.unl.edu>

UNewMexico ParasiteBiodiversity

Doctoral Graduate Student Research Assistantship-Parasite Biodiversity. A graduate assistantship is available to conduct research on contemporary and historical aspects of parasite biodiversity as a component of the NSF-sponsored Beringian Coevolution Project (BCP)?see <http://www.msb.unm.edu/-mammals/Cook/CurrentProjects/0051.html> . The BCP is an integrative multidisciplinary research project designed to reveal the complex historical biogeography and coevolution among an array of mammalian hosts and their parasites in the Beringian region (Alaska NW Canada, and eastern Siberia). The BCP links the US National Parasite Collection of USDA and the Museum of Southwestern Biology, University of New Mexico with a number of international partners. We seek a graduate student to contribute to (1) primary assessment of biodiversity including identifications of helminths collected from arvicoline rodents and other small mammalian hosts in Alaska and Siberia; (2) development of summaries for numerical and ecological diversity and comparative databases; (3) phylogenetic, phylogeographic and coevolutionary analyses of selected host-parasite systems in the Beringian region. We are seeking a *highly motivated, experienced student* with a solid foundation in parasitology who can work effectively in both laboratory and remote field situations. Applicants with experience in museum collections, molecular systematics techniques, databases, multivariate statistical methods and field work for collection preservation and preparation of parasite and host specimens will be given first consideration. Starting date is June 2006. Interested persons should send a letter of intent describing research experience, interests technical skills, transcripts, GRE scores, and e-mail or postal addresses for two references to: Joseph Cook, Department of Biology, University of New Mexico, USA (cookjose@unm.edu); OR Eric Hoberg, US National Parasite Collection & Animal Parasitic Disease Laboratory, USDA, Agricultural Research Service, BARC East 1180, 10300 Baltimore Avenue, Beltsville, Maryland, 20705, USA (ehoberg@anri.barc.usda.gov).

Joe Cook <cookjose@unm.edu>

UNottingham HostParasite

Evolutionary ecology of host-parasite interactions.

I am interested in the impact that parasites have on the ecology and evolution of their hosts. I would like to find a Ph.D. student to work in one of the following areas: (1) Local adaptation of hosts to variation in parasite communities, and its potential to lead to divergent evolution (immunological or molecular genetic experience could be useful). (2) Host-parasite interactions during the course of biological invasions. (3) The impact of parasitism on other ecological interactions (e.g. competition and predation).

I work mainly with three-spined sticklebacks in Scotland and Canada, but research in other systems including birds, insects and snails is possible.

Funding will be available for a British/EU students. Others should address enquiries to Biology-pg@nottingham.ac.uk

Please send a CV and a one page research proposal or summary of research interests directly to me: andrew.maccoll@nottingham.ac.uk

Background reading Chase J.M. et al. 2002 The interaction between predation and competition: a review and synthesis. *Ecol. Lett.* 5: 302-315. Schluter D. 2000 *The Ecology of Adaptive Radiation*. OUP, Oxford. Summers K. et al. 2003 Parasitic exploitation as an engine of diversity. *Biol. Rev.* 78: 639-675. Torchin M.E. et al. 2003 Introduced species and their missing parasites *Nature* 421: 628-630. Vamosi S.M. 2005 On the role of enemies in divergence and diversification of prey: a review and synthesis. *Can. J. Zool.* 83: 894-910.

Lecturer and NERC Postdoctoral Fellow School of Biology University of Nottingham University Park Nottingham NG7 2RD Tel: 0115 951 3410 Fax: 0115 951 3251

URochester EvolEcol

PhD position in evolutionary ecology at University of Rochester

I am seeking a graduate student who is interested in host-parasite interactions and the evolutionary ecology of natural populations. NSF has recommended funding, including graduate student support, for a project on male-killing *Wolbachia* in *Drosophila innubila*. *Wolbachia* are maternally transmitted bacteria that manipulate host reproduction, and they are present in ~25% of all insect species. The overall goal of the research is to link the dynamics of *Wolbachia* density within individual flies to the infection dynamics in natural populations of *D. innubila*. The research will entail both field work in the sky islands of Arizona and laboratory work at the University of Rochester.

The University of Rochester is one of the nation's leading research universities, and the Department of Biology has an outstanding group in evolutionary biology, including Tom Eickbush, Jim Fry, Rich Glor (starting in 2006), John Jaenike, Dave Lambert, Allen Orr, Daven Presgraves, Justin Ramsey, and Jack Werren. Rochester is located in upstate New York, where attractions include the Finger Lakes region (which has sailing, wind-surfing, and wine country), excellent downhill and cross-country skiing, and a first-rate music scene (including the Eastman School of Music and the Rochester International Jazz Festival).

Further information about our graduate program, as well as application materials, can be found at <http://www.rochester.edu/College/BIO/graduate/-index.html>. The deadline for application to our department is February 1, 2006. For further information, please contact me at:

John Jaenike Department of Biology University of Rochester Rochester, NY 14627

Phone: 585-275-0009 Email: joja@mail.rochester.edu <http://www.rochester.edu/College/BIO/faculty/-Jaenike.html> John Jaenike <joja@mail.rochester.edu>

UTennessee AdaptiveEvol

University of Tennessee, Knoxville, with Marguerite Butler

I am seeking a Ph.D. students to work on a project recently funded by the NSF "Phylogenetic comparative analysis: a modeling approach for adaptive evolution"

Motivation: The comparative method is a central tool for investigating the adaptive significance of traits. I am working on improving evolutionary models to di-

rectly incorporate selection, ideas about adaptive optima (or “niches”), and to provide a modern statistical model-selection framework for hypotheses of adaptive evolution for continuous characters.

Goals: 1) Searching for new empirical examples to explore new directions 2) Extend the method for multiple characters. 3) Statistical testing of the methods. 4) Incorporate our methods into Mesquite and other software development

One of the aims of the project is to bring together both empirically- and theoretically-oriented students in successful collaboration. If you are interested in joining this exciting endeavor, please send a letter of inquiry to Marguerite Butler at:

mabutler <at> utk <dot> edu

Please include your research interests and qualifications for entry into the graduate program.

More information on our perspective can be found at:

<http://web.utk.edu/%7emhiga/ButlerLab.data/-OUwork.html> (Ouch Info Page) <http://web.utk.edu/%7emhiga/butler.html> (Marguerite Butler’s personal page) <http://eeb.bio.utk.edu/gradappl.asp> (graduate admissions info)

Deadline for applications is Jan. 6.

mabutler@utk.edu mabutler@utk.edu

UTurku PlantHerbInteractions

Graduate student position

Graduate student position is available at the Department of Biology at University of Turku (Finland) as part of a project studying the interactions between a perennial herb (*Vincetoxicum hirundinaria*) and its three specialist herbivores. The distribution area of *V. hirundinaria* in the Finnish Archipelago is naturally fragmented, which provides an excellent opportunity to study the effects of fragmentation on the (co)evolution between a plant and its consumers, as well as the joint effects of herbivory and the structure of distribution area on the reproductive biology of a perennial plant. In our research, we combine field and greenhouse experiments, methods of population genetics and chemical analyses. At the moment, our research group consists of two senior researchers and one post-doctoral researcher. In addition, one graduate student position will be filled at the beginning of year 2007. Currently,

we are seeking to recruit a graduate student to start in March 2006 or on agreement.

We offer - Funding for ~4 years (provided by the Academy of Finland) - Interesting research project with abundant background information on research methods and on the biology of the studied species - Opportunity to concentrate on research questions of your choice - Inspiring research team with experience in student guidance - Beautiful field work environment

We seek a highly motivated graduate student with MSc or an equivalent degree in ecology, evolutionary biology or related field. The candidate should have a strong interest in evolutionary ecology, be fit for field work, and possess at least rudimentary skills in the design of experiments and in statistical analysis.

Send your application with curriculum vitae, possible list of publications, and name and contact information of at least one referee to Marianna Riipi, preferably by e-mail (pdf attachment recommended), by 31st of December 2005.

Further information:

Roosa Leimu (head of the project) University of Turku/University of Potsdam roosa.leimu@utu.fi Phone +358 41 506 3474

Pia Mutikainen University of Oulu pia.mutikainen@oulu.fi Phone +358 50 544 4763

Marianna Riipi Section of Ecology Department of Biology University of Turku FI-20014 Turku marianna.riipi@utu.fi Phone +358 2 333 6006

Further information about the research project can be found in the following publications: Oikos 98:229-238, Annals of Botany 93:107-113, Conservation Biology 13:349-356.

Roosa Leimu <rorele@utu.fi>

UWindsor SalmonQuantGenet

A doctoral position has recently become available in my lab working on a large multi-disciplinary research project, a description is listed below. Interested students should contact Dan Heath at dheath@uwindsor.ca (see below)

Mate choice in Chinook salmon: quantitative and molecular genetics of adaptive mate choice (PhD - doctoral): The student will work as part of a team to in-

investigate the effect of mate choice on genetic diversity at neutral and functional marker loci, performance (fitness) and heritability of fitness-related traits in Chinook salmon. Offspring of Chinook salmon will be produced from parents allowed to breed in semi-natural spawning channels (sexual selection) or from parents artificially spawned using current aquaculture practices (no sexual selection). All offspring will be followed through to adulthood in the aquaculture environment. Behavioural, immunological, physiological and genetic (molecular and quantitative) analyses will be used by the 4 University team to determine the adaptive potential of mate choice, plus possible applications for salmon aquaculture. Work in the Heath lab will focus on microsatellite parentage assignment and diver-

sity estimation, genetic diversity and transcription at selected functional loci and quantitative genetic analysis of selected fitness-related traits. The project will involve considerable collaboration with other investigators and field work with our salmon farm partner in British Columbia, Canada. Opportunities for student-directed research are part of the project.

Information on the lab and GLIER can be viewed at; www.uwindsor.ca/glier Daniel Heath Great Lakes Institute for Environmental Research University of Windsor 401 Sunset Ave Windsor, Ont, Canada N9B 3P4

E-mail: dheath@uwindsor.ca Phone: (519) 253-3000, Ext 3762 Fax: 971-3616

dheath@uwindsor.ca

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AgResearchNZ Bioinformatics

Bioinformatician

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

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

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

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

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

To find out more about this position please contact Anette Becher by email anette.becher@agresearch.co.nz or alternatively phone +64 3 489 9028 (after 16th January 2006).

For a job description and application form please contact Linda Murray, Phone +64 3 489 9011 or email linda.murray@agresearch.co.nz (after 16 January 2006). Alternatively, the job description and application form can be found at <http://www.agresearch.co.nz/recruitment> For general information on AgResearch please visit our website at www.agresearch.co.nz Applications close 30th January 2006 and should be sent to Linda Murray at the following address or by email -

Linda Murray AgResearch Invermay Agricultural Centre Private Bag 50034 Mosgiel, Dunedin NEW ZEALAND Email: linda.murray@agresearch.co.nz
anette.becher@agresearch.co.nz

BrownU ComputBiology

Brown University

Center for Computational Molecular Biology

Faculty Positions

As part of a major new initiative, Brown University seeks highly qualified candidates for two open rank, tenure-track or tenured faculty positions with a preference for assistant professors in the Center for Computational Molecular Biology (CCMB). The Center's activities focus in three areas and candidates in these three areas are strongly encouraged to apply: 1) regula-

tory genomics and networks; 2) comparative genomics and evolutionary biology; 3) structural and functional proteomics.

Successful applicants will be expected to have a demonstrated record of excellence in research, maintain an externally funded research program, and have good communication and teaching skills. They also will participate in the continuing development and improvement of Brown's established undergraduate curriculum and a new graduate curriculum that is being built on the foundation of Brown's widely recognized record in teaching innovation and academic excellence. Appointees will have the opportunity to participate in several NIH or NSF funded interdisciplinary programs, such as the new initiative in Genetics, Genomics and Proteomics as well as a number of other multi-disciplinary collaborations with Brown and hospital based faculty and students. The appointments will be in the following top rank departments: Division of Applied Mathematics, Department of Computer Science or a participating department in the Division of Biology and Medicine. The Center has recently hired two senior faculty members, Sorin Istrail in Computer Science and Chip Lawrence in Applied Mathematics, whose expertise are focused in genomics, sequence analysis and regulatory genomics, systems and networks.

Applicants should submit curriculum vitae, representative preprints or reprints, and a concise description of research interests and goals with emphasis in their interdisciplinary expertise. Additionally, candidates for Assistant Professorship should arrange to have at least three letters of recommendation sent directly to the contact address. Candidates for Associate or Full Professor should provide names and contact information for at least five references, and these will be contacted for letters of recommendation by the search committee at an appropriate time. All applications will be treated confidentially. Application review will commence on December 14, 2005 and continue until available positions are filled.

Applications should be submitted electronically in PDF form to: ccmbsearch@dam.brown.edu Letters of recommendation to be sent to the following contact address: ATTN: CCMB Search, c/o Ms. Louise Patterson, Division of Applied Mathematics, Brown University, Box F, Providence, RI 02912. Brown University is an affirmative action/equal opportunity employer. Women and minorities are encouraged to apply. For further information, visit our Website at <http://www.brown.edu/-Research/CCMB/> David_Rand@brown.edu

CSIRO Perth PlantEvol

CSIRO Sustainable Ecosystems, Perth, Australia

Ecologist

AUD \$69k - \$93k per annum plus Superannuation

Ref: 2005/1386 We are seeking a scientist to undertake research projects and help develop new research opportunities in plant ecology. The exciting position will be filled by a highly motivated, creative and innovative person who is able to conduct research leading to improved understanding of ecological processes in agricultural landscapes. You will interact and collaborate closely with colleagues within CSE and in other research organizations, and develop strategic partnerships leading to enhanced research opportunities. The primary focus for research will be on ecological processes and how human induced disturbance impacts upon these. Of particular interest are the responses of plant communities to disturbances such as fire, nutrient enrichment, fragmentation and grazing, and the complex interactions between them. You will be expected to develop research projects in a number of key landscape types, including highly fragmented cropping zones, peri-urban fringes and rapidly urbanising coastal areas. The research will be conducted within the context of multi-disciplinary teams seeking to improve our ability to contribute to the development of sustainable and resilient agricultural and peri-urban landscapes. The successful applicant will have good field ecological skills, experience in quantitative plant ecology, and an aptitude and interest in ecological modelling. Experience in plant population genetics may be advantageous. A willingness to travel within Australia and overseas is also essential. Applications close 16 January 2006. For selection documentation and details on how to apply visit www.csiro.au/careers Alternatively contact 61 2 6276 6326

Amy.Voller@csiro.au

27 December 2005 The Denver Museum of Nature & Science seeks a Curator of Zoology The Department of Zoology (DOZ) at the Denver Museum of Nature & Science (DMNS) seeks a curator in the area of vertebrate zoology or entomology. The successful candidate will be an organismal biologist whose research focuses on the evolution of vertebrates or arthropods, the evolutionary ecology of populations, and/or the biodiversity of regional faunas. We seek candidates who have field-and/or collections-based research experience. Previous museum experience is preferred but not required; however, the successful candidate must demonstrate an intellectual commitment to museum-based research, the potential to use and add to DOZ collections, and a clear vision of the role of museums in science education. The candidate must have a Ph.D., a solid record of grant experience and peer-reviewed publications, and a demonstrated interest in museums. The candidate will be expected to develop an aspect of their research with a focus in the Rocky Mountains / Great Plains ecoregion.

The successful candidate will demonstrate an understanding of informal science education and an ability to clearly communicate science-in-the-news to the general public. Enthusiasm for working with Museum volunteers, fellow curators, and interdisciplinary project and exhibit teams is essential.

The position is available 1 June 2006. Applications and all supporting materials must be received by 1 March 2006. Applicants must submit a cover letter, a curriculum vitae, a statement of research interests, and a statement of outreach experience. Applications must also include three letters of recommendation (these may be sent separately). Electronic submission of all application materials is encouraged. Applications should be sent to Zoology Search Committee Chair, Department of Zoology, Denver Museum of Nature & Science, 2001 Colorado Blvd., Denver, CO 80205; (303) 370-6353; Zoology.Search@dmns.org. Information about the department and the Museum can be obtained at www.dmns.org.

David Denniff Zoology Office Manager My email address is ddenniff@dmns.org

David.Denniff@dmns.org

DenverMuseumNatureScience
Curator

France FieldAssist

**Field assistants needed

We are looking for enthusiastic field assistants to participate in an international research project on communication and behavioural ecology in nightingales (*Luscinia megarhynchos*). The project at the Research Station Petite Camargue Alsacienne in France is run by Dr. Valentin Amrhein (University of Basel, Switzerland), Dr. Marc Naguib and Rouven Schmidt (University of Bielefeld, Germany). At the research station, we have been studying the breeding ecology of nightingales since 1994 using multiple techniques including radiotelemetry, colourbanding, and monitoring of territorial behaviour. To investigate vocal communication strategies of nightingales, we record songs (including nocturnal song) and make playback experiments. More information on our research and the field site is available at <http://www.unibielefeld.de/biologie/vhf/NG/-Nightingale-page.html> and <http://pages.unibas.ch/pca>. The field site is situated in France, about 10 km north of Basel (Switzerland). Field assistants will receive 800 Euro for the entire field season. We cannot cover travel expenses, but we offer free accommodation and use of the infrastructure at the research station. Field assistants are expected to stay for the entire field season from about 10 April to end of May 2006. Field work will be conducted during the day and at night. Field assistants are expected to work on their own at night and thus should be comfortable with working in a dark and lonesome place. The language at the station will be English. Applications will be viewed starting 15.01.06 and will be considered until the positions are filled. Please send applications in English (letter of motivation, two references and curriculum vitae) until 31.01.06 via e-mail to the following address:

nightingale.2006@web.de

Rouven Schmidt <rouven.schmidt@uni-bielefeld.de>

France Permanent Researcher

Dear all

This is to inform you about an attractive job offer in France the yearly announcement of researcher positions financed by the French Funding Organization Centre National de la Recherche Scientifique (CNRS). These are *life-time 100 % research* positions offered in an international competition to excellent candidates. The web page is <http://www.sg.cnrs.fr/drhchercheurs/concoursch/default-en.htm>. Posts are

available, for instance in Biodiversity, evolution and biological adaptations: from macromolecules to communities, and Biological systems modelization, bioinformatics. The deadline, regrettably, is January, 16.

THE TYPES OF POSTS (see also <http://www.sg.cnrs.fr/drhchercheurs/concoursch/chercheur/default-en.htm>, <http://www.sg.cnrs.fr/drhchercheurs/concoursch/informer/default-en.htm>, <http://www.sg.cnrs.fr/drhchercheurs/concoursch/pdf/guide-en.pdf>): There are chargés de recherche, 2nd and 1st degree, and directeurs de recherche, 2nd and 1st degree, i.e. Associate Scientists after dissertation and after 4 years of experience, and Senior Scientists after 8 years or 12 years of experience, respectively. According to my experience already the Chargés de Recherche are actually free to do what they want within an overall, very large disciplinary category (there are some 40 categories defined for all sciences together). Directeurs are of course expected to, finally, develop leading roles. This may mean becoming leader of a team as proposed and agreed upon by the Research Unit (Unité Mixte de Recherche, UMR) and to search for extramural funds, which are scarce in France. Experience in such leading functions is thus an important plus for an application to a directeur post. And of course publications. Even though strange things are happening, multiple first or senior authored publications per year with an overall impact of 4 or more seem to be useful, but its open end. For Chargé, 2nd degree, several good publications from the PhD are probably needed.

THE PROFILES If you go to <http://gestionoffres.dsi.cnrs.fr/fo/offres/default-en.php> you will find a number of posts offered in the sections 29 (Biodiversity, evolution and biological adaptations: from macromolecules to communities), 44 (Biological systems modelization, bioinformatics), and also 20 (Continental Surfaces and Interfaces, which includes vegetation). But note that by further clicking on the numbers given to the jobs (e.g. N29/02) you will find that the Chargé positions (Associate Scientists) in sections 29 and 20 are focused to quite restricted fields of research. This is where science politics comes into play.

THE RECRUITMENT Directeur (Senior scientists) posts are told be more difficult to obtain for someone that comes from outside the French system. A so-called poste rouge is often recommended in advance, a funding for half a year within the host institution. Even for demanding a Chargé position, advance visits in the host lab may be appreciated. Obviously, this is hardly possible anymore for the deadline 16 January 06. A visit to the lab after having submitted the application seems to be very much expected in all cases. Generally,

French institutions *do not* reimburse candidates the travel costs to visit labs or to come to interviews etc.. Yes, this is a shame. I hope we have some funds here at Rennes, but this is not sure.

After having applied *all* candidates will be invited to a presentation and an interview in Paris in spring 2006 (see <http://www.cnrs.fr/comitenational/calend/-printe06/cprint06.pdf>). Travel costs will *not* be reimbursed by the CNRS, and on the level of host Units funds may be scarce, too. Presentations and interviews can be in English, French is possibly a plus.

I personally could offer help in putting together an application for qualified candidates with a project willing to choose University of Rennes 1 and to work here on the interface between ecology and phylogeny preferably of plants or, alternatively, on the diversity and diversification of arthropods in the canopy. The host lab here is the UNITE MIXTE DE RECHERCHE ECOSYSTEMES , BIODIVERSITE , EVOLUTION with particular expertise in mechanisms of speciation, life history evolution, and adaptation, expertise at the interface between macroevolution and macroecology, expertise in ecophysiology, landscape ecology and soon also behavioral ecology. It is a large institution with

— / —

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>

FtCollins WildlifeGeneticsTech

This position is at the National Wildlife Research Center (NWRC). The NWRC is responsible for multidisciplinary research related to wildlife management problems. The incumbent functions as a biological science technician at the Wildlife Genetics Laboratory, Analytical Chemistry Project, Product Development Research Program.

Duties include the management of tissues samples, DNA extraction, polymerase chain reactions (PCR) amplification of multiple loci, fragment analysis and sequencing on genetic analyzers, and data analyses/summarization. The biological science laboratory technician contributes to population genetic and/or phylogenetic aspects of studies in wildlife management. Incumbent must be able to work well in a team setting/collaborative effort.

Incumbent prepares biological samples (animal tissues, animal secretions/excreta, and other non-invasive samples) in a manner appropriate for a DNA lab observing strict adherence to separation of pre-PCR and post-PCR procedures; identifies, analyzes, and troubleshoot problems with sample procedures; analyzes tissue and other biological samples to investigate genetic variability among wildlife species, populations, individuals (using extraction methodologies, PCR, electrophoresis, DNA sequencing, genotyping, and restrictase digests); participates in research studies by preparing samples, operating DNA genotyping and sequencing laboratory instruments; assists in analyzing experimental data and maintaining data files using personal computers running spreadsheet and word processing software; statistical analyses on DNA sequence data towards elucidating molecular systematic of wildlife species in need of taxonomic assessment; performs analyses on genotyping data towards detecting population structure among wildlife populations, identifying individuals, interpreting population assignment, and relatedness/kinship of individual and populations; maintains laboratory in a safe and orderly condition; participates in the preparation and/or delivery of scientific presentations. Incumbent should have a Master's Degree in biological science or related field.

LINK TO VIEW ANNOUNCEMENTS - CLICK HERE —>
<https://jobs.quickhire.com/scripts/aphis.exe/preview>

Vacancy Announcement - Case Exam # 2497-2006-0042

For questions you may contact:

Toni Piaggio, Ph.D. APHIS Fellow, Molecular Biologist USDA/ National Wildlife Research Center 4101 LaPorte Ave. Fort Collins, Colorado 80521

ph. 970-266-6142 e-mail:
Toni.J.Piaggio@aphis.usda.gov

batchaser@gmail.com

GettysburgPA SabbReplacement

Evolutionary Biology

Gettysburg College invites applications for a one-year sabbatical replacement position in the Biology Department to begin fall, 2006. We are looking for an evolutionary biologist with broad training who can con-

tribute to our first-year sequence of core courses, including Genetics, as well as teach an upper division course in his/her area of specialization. A commitment to interdisciplinary teaching in the liberal arts tradition is essential as is integrating students in an active research program. The College actively supports research involving undergraduates. Applicants must have a Ph.D. in the biological sciences at the time of application. 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 2500 students. Gettysburg College celebrates diversity and invites 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 hard copy of curriculum vitae and statement of teaching and research goals and have three letters of reference (of which at least one can speak to the candidate's teaching effectiveness) sent to: Dr. Kazuo Hiraizumi Department of Biology, Box 392, Gettysburg College, Gettysburg, PA 17325. Review of applications will begin February 1, 2006, and will continue until a successful candidate is found.

Veronique A. Delesalle Professor of Biology and Environmental Studies Chair of Environmental Studies Box 392 Gettysburg College Gettysburg, PA 17325

Tel: 717-337-6153 fax: 7171-337-6157

delesall@gettysburg.edu delesall@gettysburg.edu

HarvardU EvolGeneticsGenomics

EVOLUTIONARY GENETICS/GENOMICS Harvard University Department of Organismic and Evolutionary Biology The Department of Organismic and Evolutionary Biology at Harvard University seeks to make an appointment at the junior rank in the field of evolutionary genetics/genomics. We seek an outstanding scientist who will establish an empirical research program and teach both undergraduate and graduate students. The candidate would have the opportunity to interact with faculty from other departments in the Faculty for Arts and Sciences as well as at the Broad Institute/MIT and Harvard Medical School. We are especially interested in individuals who conduct rigorous, field and/or

laboratory-based tests of general problems associated with the genetic basis of adaptations in natural populations. We encourage applications from or information about women and minority candidates. Applicants should submit a curriculum vitae, statements of research and teaching interests and representative publications, and should arrange for three letters of reference to be sent to Professor John Wakeley, 2102 Biological Laboratories, Harvard University, 16 Divinity Avenue, Cambridge, MA, 02138. Nominations from third parties are also welcome. Review of applications and nominations will begin February 1, 2006. Further information about the Department is available at its website: <<http://www.oeb.harvard.edu>> .Harvard University is an Affirmative Action/Equal Opportunity Employer.

wakeley@fas.harvard.edu

INRA Dijon WeedCommunities

Position announcement (Short English version followed by French)

The French Institut National de la Recherche Agronomique (INRA = National Institute for Agronomic Research) is currently seeking to fill a permanent, full time research position in the unit of « Biologie & Gestion des Adventices » (Weed Biology and Management) located in Dijon, France. The position ("Directeur de Recherche", i.e. Research director) is similar in rank to a professor position, except it is a full-time research position (no teaching duties). This unit is the only one within INRA conducting researches in the areas of Ecology, Agronomy and Evolutionary Genetics of weed species and communities. The permanent staff comprises about 40 people (scientists, teachers and technical staff). INRA actually aims at recruiting a leading scientist in the area of Weed or Plant community Ecology. This leader is expected to set off and steer a multidisciplinary program bridging the gap between genetics of adaptation and community ecology. This program will be based upon the current extensive background in genetics and agronomy developed in the "Biologie & Gestion des Adventices" unit. However, outstanding candidates in Ecology, Population Genetics or Agronomy who feel they may contribute to bridge the gaps between disciplines are encouraged to apply.

Applicants should submit a curriculum vitae, a statement of research (and teaching activity, if any), selected reprints, and a proposal of research project for

the offered position. All applicant materials should be received by 14th December 2005. So, Please note how soon the deadline is! Application procedure: some information on how to fill an application are given (unfortunately only available in French!) at the internet address : <http://www.inra.fr/drh/ita/-concours/docs/Devenir-DR2-2005.pdf> Informations on salary : under <http://www.inra.fr/> please click le_salaire_et_les_primes' Contact: Jacques Gasquez (33) 3 80 69 30 31 gasquez@dijon.inra.fr but you may also try Xavier Reboud (33) 3 80 69 31 84 reboud@dijon.inra.fr The complete advertisement is provided (in French) in the pdf file 'Profil DR2 SPE[1].pdf' at the following internet address : under <http://www.inra.fr/> ask 'poste_biologie_évolutive' in the quick search (= recherche rapide). The profile is attached to the first response in the list. Applications can be made in English.

L'INRA met au concours un poste permanent de Directeur de Recherche en «Biologie évolutive et Ecologie des Communautés Végétales des zones cultivées». Le profil est volontairement ouvert à l'interface entre écologie, agronomie et génétique des populations couvrant ainsi les principaux développements conduits au sein de l'UMR Biologie et Gestion des Adventices'. Il cherche cependant à renforcer les compétences en écologie. Située à Dijon, cette unité regroupe environ 40 personnes. Le poste à pourvoir vise à recruter une personne prête à animer une équipe de recherche transdisciplinaire. Aucune condition de nationalité n'est attachée à la candidature. Une description du profil est accessible au lien suivant.: sous <http://www.inra.fr/> tapez poste_biologie_évolutive' dans l'onglet recherche rapide.

NB: Nous attirons votre attention sur les délais très courts à respecter impérativement. La date limite officielle de dépôt des candidatures à faire parvenir à la DRH de l'INRA est fixée au 14 Décembre 2005.

Xavier.Reboud@dijon.inra.fr

INRA Nancy TreeMicrobeInteractions

Population genetics of forest pathogens:

A 1st class junior scientist permanent position (Chargé de Recherche 1ère classe, CR1) is opened for application

at the INRA-Nancy "Tree-Microbe Interactions" Unit (UMR 1136 IAM). This Unit is conducting extensive research on the molecular biology, physiology, pathology and ecology of trees and associated micro-organisms in forest ecosystems. The Unit is composed of staff from the INRA (Institut National de la Recherche Agronomique), the University Henri Poincaré (UHP), undergraduate and Ph.D Students, and postdoctoral fellows.

Within the "Tree-Microbe Interactions" Unit, the Forest Pathology group mainly focuses on epidemiology and population biology of several forest pathogens. The two main pathogens studied are the biotrophic Basidiomycete *Melampsora larici-populina* (causing poplar rust) and the hybrid Oomycete *Phytophthora alni* (responsible of alder decline).

The main objective of the current position is to develop population genetics approaches in order to better understand the epidemiology and the evolution of fungal forest pathogens, and to study the processes driving the pathogen population structure: selection, gene flow, migration, genetic drift, mating system. Molecular markers, such as microsatellites, have already been developed for the main pathogens studied.

Candidates should have a strong background in population genetics and/or evolutionary biology. Candidates should also be familiar with the use of molecular markers. Additional experience in fungal biology is not required, but would be appreciated. A post-doctoral experience would be highly desirable. The applicants are requested to have a strong team spirit and to be able to develop an integrated view of their research, with strong interactions with researchers involved in epidemiology, resistance breeding, genomics, and biology of the pathogens.

The "Tree-Microbe Interactions" Unit is also involved in the annotation of the complete genome sequences of *Populus trichocarpa* (<http://genome.jgi-psf.org/-Poptr1/Poptr1.info.html>), and its fungal associates, the ectomycorrhizal Basidiomycete *Laccaria bicolor* (<http://mycor.nancy.inra.fr/IMGC/LaccariaGenome/>), and the poplar rust fungus, *Melampsora larici-populina* (<http://www.jgi.doe.gov/sequencing/why/-CSP2006/poplarrust.html>), in collaboration with the US DoE JGI. The *Melampsora* sequence should be available in 2006, and this will give invaluable opportunities to develop additional molecular markers useful for population genetic studies.

For further information about the 2006 1st and 2nd class junior scientist open competitions and eligibility requirements, please visit <http://www.international.inra.fr/>. The application deadline

is February 27th 2006. For further scientific information on the position, please contact Pascal Frey (mailto:frey@nancy.inra.fr).

Dr Pascal FREY INRA Nancy Forest Pathology Lab UMR 1136 "Tree Microorganisms Interactions" IFR 110 "Genomics, Ecophysiology and Functional Ecology" 54280 Champenoux FRANCE

Phone: 33 383 394 056 Fax: 33 383 394 069
mailto:frey@nancy.inra.fr

Marie-Anne Auger-Rozenberg <Marie-Anne.Auger-Rozenberg@orleans.inra.fr>

IRNA France

Dear Mr Golding

We are pleased to inform you that INRA is recruiting tenured juniors scientists (1st and 2nd class).

We would be very grateful if you would post the following information on your web site.

Text: Inra (National Institute for Agricultural Research, France) is recruiting 1st and 2nd class tenured Junior Scientists. Recruitment competitions will open in mid-december. Applications will be available until the end of february 2006.

Further details are available on <<http://www.inra.fr/>> www.inra.fr (select "Les homes et les femmes" and "devenir chercheur à l'Inra").

Link to this website: <http://www.inra.fr/les_hommes_et_les_femmes/-rejoignez_nous/devenir_chercheur_a_l_inra/concours_de_charges_de_recherche_de_1ere_et_2e_classe>

Thank you for your help.

Sincerely,

Sandrine Gardet

INRA

DRH - Service Recrutement et Mobilité

147 rue de l'université

75338 PARIS cedex 07

Tel : 01 42 75 90 77

E-mail : gardet@paris.inra.fr

Sandrine Gardet <Sandrine.Gardet@paris.inra.fr>

IowaStateU StatisticalGenomics

Tenure-Track Position in Statistical Genomics at Iowa State University

The Department of Statistics at Iowa State University invites applications for a tenure-track assistant professor position in statistical genomics. A Ph.D. in statistics, bioinformatics or a closely related field is required. Interest or experience in statistical analysis of genomic, proteomic or metabolic data is desired. The incumbent will be expected to maintain a vigorous research program in the development and application of statistical methodology for emerging genomic technologies in animal and plant sciences. The Department of Statistics has a large and diverse faculty and well established M.S. and Ph.D. programs. This position offers immediate opportunities for graduate student guidance and graduate level teaching. The Department's rich history of collaboration provides an ideal environment to develop collaborative research programs with prominent researchers in the animal and plant sciences. Further information about the department and this position can be found at <http://www.stat.iastate.edu/>. Candidates should provide an application letter, curriculum vita, transcripts, teaching and research statements, and copies of recent publications. Additionally, the candidate should arrange for three letters of recommendation to be sent. Submit materials electronically as .PDF e-mail attachments to statfacultysearch@iastate.edu. Review of applications will begin on February 10, 2006 and will continue until the position is filled.

fjanzen@iastate.edu

JamesCookU SocialInsectMolEvol

A Research Associate [postdoctoral] position will be available in 2006, at James Cook University in Queensland, Australia.

The position is supported by an Australian Research Council grant, is tenable until the end of 2010, and

carries a salary to start at that of a James Cook University Level A Academic, step 6 [currently \$A53,887]. The appointee will join the research group of Professor Ross Crozier with the primary objective of studying the molecular evolution of social insect immune system genes in relation to life pattern and pathogen loads. The work involves isolating and sequencing immune system genes, testing for positive selection, some population genetic work, and participation in the characterization of microbial communities associated with the nests and environs. Most of the work will be on ants, but the project is a collaborative one with Professor Paul Schmid-Hempel [ETH, Zürich] and the appointee is expected to make at least one visit to the ETH to assist with work on bumble bees. Applicants should be expert in molecular evolutionary techniques, and experience with ants is an advantage.

The starting date is negotiable, but March 1 is preferred.

Applications should include the names and email addresses of three referees, address the selection criteria and be sent by email to Professor Crozier at ross.crozier@jcu.edu.au. Consideration of applications will begin on January 11, 2006. Further information may be sought from Ross Crozier. General information about the University and the region may be found at <http://www.jcu.edu.au/> .-

Ross H Crozier FAA

Professor of Evolutionary Genetics School of Tropical Biology James Cook University Townsville, Queensland 4811 AUSTRALIA

email: Ross.Crozier@jcu.edu.au phone: +61 7 4781 5734 (office) +61 7 4781 5723 (lab.) +61 7 4781 5450 (lab.) fax: +61 7 4725 1570

<http://medusa.jcu.edu.au/crozier/croziergroup/home/>
<http://medusa.jcu.edu.au/crozier/croziergroup/home/>

UAberdeen PopBiol

ACADEMIC POSITION IN ECOLOGY/POPULATION BIOLOGY AT UNIVERSITY OF ABERDEEN, SCOTLAND

The School of Biological Science of Aberdeen University, Scotland seeks highly motivated and interactive candidates in ecology and/or population biology, who have interests in understanding the response of

populations and communities to environmental change (including adaptation, life history evolution, population dynamics, biotic interactions, and ecosystem function using molecular, theoretical or experimental approaches). Applicants should have skills and interests that complement those of ecologists at the University of Aberdeen. The appointment will be at the Lecturer/Senior Lecturer level. For details see <http://www.abdn.ac.uk/jobs/display.php?recordid=-MBS020A> and <http://www.abdn.ac.uk/biologicalsci/-research/ecology.shtml> x.lambin@abdn.ac.uk

UBritishColumbia MolEvolEcol

Assistant Professor, Molecular Ecology

The Biology and Physical Geography Unit at the University of British Columbia Okanagan invites applications for a faculty position in molecular ecology.

UBC Okanagan is located in Kelowna, B.C., in the Okanagan valley. The region has high biodiversity, stunning scenery, and vibrant communities. UBC Okanagan was newly created in July 2005 as a new campus of UBC, and is developing strength in interdisciplinary approaches to research and teaching. In particular, an interdisciplinary Species at Risk and Habitat Studies Centre was recently awarded to support environmental research using genetic, GIS, and ecological tools. Infrastructure of this centre includes a molecular lab with state-of-the art facilities such as an ABI3130XL sequencer and real-time PCR.

For detailed information regarding qualification requirements and application instructions, visit the UBC Okanagan website at <http://web.ubc.ca/okanagan/-facultystaff/welcome.html>

daniel.durall@ubc.ca

UCBerkeley MammalEvol

UNIVERSITY OF CALIFORNIA, BERKELEY Faculty Position in Vertebrate Evolutionary Biology and/or Ecology The Department of Integrative Biology and the Museum of Vertebrate Zoology seek a colleague at the Assistant Professor and Assistant Curator level

in the area of Vertebrate Evolutionary Biology and/or Ecology. The successful candidate will share an appointment in the Museum of Vertebrate Zoology and Department of Integrative Biology. We seek an individual who will develop an outstanding field-based research program in evolution and/or ecology, using mammals as a study system. Previous museum experience is not required but the successful candidate must demonstrate an intellectual commitment to museum-based research, the potential to use and add to MVZ collections, a clear vision of the role of museum collections in the 21st century, and the capacity to integrate intellectual activities of the MVZ and the Department of Integrative Biology. We encourage applicants from all areas of mammalogy. Candidates should have a strong commitment to both undergraduate and graduate teaching.

The position is available 1 July 2006. Applicants should submit a curriculum vitae and a statement of research and teaching objectives, including a vision for the future of natural history museums such as the MVZ.

Applications, including at least three letters of recommendation, should be sent directly to the search committee at: Search Committee, Vertebrate Evolutionary Biology Search, Department of Integrative Biology, 3060 VLSB, University of California, Berkeley, CA 94720-3140. The deadline for receipt of applications is 23 January 2006.

Applicants should refer their reviewers to the UC Berkeley Statement of Confidentiality at <http://apo.chance.berkeley.edu/evalltr.html>. Further information about the department, the MVZ, and this faculty position can be found at <http://ib.berkeley.edu/> and <http://mvz.berkeley.edu>. The University of California, Berkeley, is an Equal Opportunity Employer committed to excellence through diversity.

Further information This tenure-track position combines a regular Faculty position (50%, IB) with a Curatorial position in the MVZ (50%). It will be an 11 month appointment, in recognition of the year-round duties of a curator. Faculty Curators are expected to demonstrate both a strong conceptual focus in some area of Vertebrate Evolutionary Biology and/or Ecology, and leadership towards development of and research on the MVZ's renowned collections. Accordingly, those invited for interview will be asked to give two seminars, one in the Integrative Biology series and another to the MVZ. This MVZ Curatorship requires enthusiasm for collection-based research and excitement about the opportunities offered by using mammals as a study system to advance evolutionary and/or ecological theory. The potential to acquire broad knowledge of the systematics and biology of ex-

tant mammals is expected. In general MVZ curators study organisms in relation to their natural environment and bring new technologies and sources of evidence to bear on problems in evolution and ecology; we encourage new and innovative approaches to the use of museum collections in such endeavors. Details of the MVZ's philosophy, history, existing research foci and current initiatives are to be found on the website (mvz.berkeley.edu). Relevant research strengths in Integrative Biology include evolutionary genetics, developmental biology, functional morphology and biomechanics, ecology, paleontology and paleoecology, systematics and phylogenetics, all with a strong emphasis on evolution.

—
Sean Versoza <sversoza@berkeley.edu>

UCRiverside InsectSystematics

Assistant Professor in the area of Insect Systematics, University of California, Riverside. Position available July 1, 2006, 9-month, 50% Instruction and Research, 50% Agriculture Experiment Station. Appointment level and salary commensurate with experience. Ph. D. in Entomology or related discipline required. The successful candidate must have strong training and experience with modern methods applicable to systematic entomology. Preference will be given to candidates with an interest in systematics of groups considered important to applied entomology. A program of research should be in accordance with Department and College strengths in agricultural entomology, biological control, evolution, or conservation biology. It is expected that the successful individual will build a strong extramurally funded independent research program, develop cooperative research with other faculty in the Department and College, and participate in the Department's teaching program. Send curriculum vitae, transcripts, statement of research interests, reprints, manuscripts in press, and the names and addresses of five referees by January 20, 2006 to: Dr. Richard Stouthamer, Search Committee Chair, Department of Entomology, University of California, 3401 Watkins Dr., Riverside, CA 92521; e-mail: richard.stouthamer@ucr.edu; phone (951)-827-2422. This position will remain opened until filled. Information about the Entomology Department and an expanded position description can be found on the website: <http://www.entomology.ucr.edu> The Uni-

versity of California is an equal opportunity/affirmative action employer

richard.stouthamer@ucr.edu
richard.stouthamer@ucr.edu

UCaliforniaMerced SystemsBiology

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

The Schools of Natural Science and Engineering invite applications at the assistant professor level (tenure track) in the areas of experimental or computational systems biology. Systems biology is used here to mean a research approach that uses comprehensive datasets and multiple types of analysis to relate the overall function of an organism, organelle, or regulatory pathway to the underlying biochemical or biophysical processes, with an ultimate goal of a predictive understanding of the system's behavior. Examples of problems addressed by systems biology include microbial quorum sensing, metazoan development, or symbiotic relationships in ecosystems. Applications of special relevance to research emphases at UC Merced include the mechanisms of cell fate decisions, complex diseases, such as asthma or diabetes, and microbial systems relevant to disease or the environment.

The University of California at Merced is an affirmative action/equal opportunity employer with a strong institutional commitment to the achievement of diversity among its faculty, staff, and students. The University is supportive of dual career couples.

Qualifications: Applicants should have a Ph.D. in the life sciences, bioengineering, computer science or related fields and a track record of research, publication and teaching commensurate with a faculty appointment at the University of California, and should have demonstrated the potential to develop a strong research program in Systems Biology. Applicants should have the

ability to interact with colleagues from a broad range of disciplines, and a strong interest in developing interdisciplinary and multidisciplinary undergraduate and graduate curricula and research programs. We require a commitment to excellence and innovation in undergraduate and graduate education and training, and a commitment to education and outreach for students of diverse backgrounds, particularly disadvantaged or underrepresented students.

Salary: Negotiable, based on the University of California pay scale

Closing Date: 02/15/2006

To Apply: Interested applicants are required to submit 1) a cover letter 2) curriculum vitae 3) statement of research 4) statement of teaching 5) a list of five references with contact information including mailing address, phone number and e-mail address and 6) a list of three representative publications (including URL for those publications available online.)

Please do not submit individual letters of recommendation.

All applications must be submitted online

For more information: Please contact Professor Michael Colvin, Search Committee Chair (mcolvin@ucmerced.edu).

Monica Medina Assistant Professor and Founding Faculty School of Natural Sciences University of California, Merced P.O. Box 2039 Merced CA 95344 tel: 209-381-7863 fax: 209-812-1857 mmedina@ucmerced.edu <http://qsb.ucmerced.edu/mmedina/> Monica Medina <mmedina@ucmerced.edu>

UCentralFlorida EvoDevo

The Department of Biology at the University of Central Florida invites applicants for a tenure-track faculty appointment in Evolutionary Developmental Biology at the rank of Assistant or Associate Professor. Candidates should have a strong focus on the mechanisms of phenotypic evolution in a broadly defined sense. The successful candidate will be expected to establish and maintain an extramurally-funded research program that complements our active and expanding faculty. The new faculty member will have the opportunity to participate in Ph.D. programs in Biomolecular Sciences and Conservation Biology, and contribute to graduate and undergraduate education. The University

of Central Florida maintains a strong research emphasis with competitive startup funds and teaching loads. Candidates must have a Ph.D. and appropriate post-doctoral training. Please submit a CV, brief statements of research plans and teaching philosophy, and arrange for three letters of recommendation to be sent directly to: Dr. Laurie von Kalm, Chair, Evolutionary Developmental Biology Search Committee, Department of Biology, University of Central Florida, 4000 Central Florida Blvd., Orlando, FL 32816-2368. Review of applications will begin January 15, 2006, with an anticipated start date of August 2006. See <http://www.cas.ucf.edu/biology/> for departmental details. The University of Central Florida is an Affirmative Action/Equal Opportunity Employer. Search documents may be viewed by the public upon request in accordance with Florida statute.

Eric A. Hoffman Department of Biology University of Central Florida Orlando, FL 32816 407-823-4007

eahoffma@mail.ucf.edu eahoffma@mail.ucf.edu

metropolitan center.

A cover letter, curriculum vitae/resume and reference contact information (names and contact information, including phone numbers, of three people who agreed to be references) are required to be considered for this position.

Please apply online at:

jobopportunities.uchicago.edu/applicants/Central?quickFind6587

The University of Chicago is an Affirmative Action/Equal Opportunity Employer.

– Ilya Ruvinsky, Ph.D. Assistant Professor of Genetics and Evolution Department of Ecology and Evolution The University of Chicago 1101 East 57th Street Chicago, IL 60637

e-mail - ruvinsky@uchicago.edu Office - (773) 702-1533 http://pondside.uchicago.edu/ecol-evol/faculty/ruvinsky_i.html Ilya Ruvinsky <ruvinsky@uchicago.edu>

UChicago ResTech

A full-time Research Technologist position is available for a scientist in the Department of Ecology and Evolution at the University of Chicago.

Job responsibilities include manipulation of nematode strains, basic molecular biology techniques (PCR, cloning, etc.) and microscopy. In addition, ordering of supplies and laboratory maintenance will be expected.

Bachelor's degree in biology or related field required; previous laboratory experience with molecular biology is preferred; experience with model organism genetics preferred; familiarity with genetics is required; knowledge of computers, including word processing, spreadsheet and database programs, is required; excellent communication and organizational skills are required; high level of motivation and strong interpersonal skills required; desire to learn new skills and work independently required.

Salary will be commensurate with experience and will include benefits.

The University of Chicago is a premier research institution located in Hyde Park, a vibrant and diverse community within close distance of the downtown Chicago. This location offers unparalleled access to intellectual, cultural and recreational resources of a major

UCincinnati DirectorFieldStudies

Director, Cincinnati Center for Field Studies

The University of Cincinnati (UC, www.uc.edu) and the Cincinnati Nature Center (CNC; www.cincynature.org) are developing a field station to be located on over 1000 acres of CNC property near Milford, OH. This effort involves the Departments of Biological Sciences, Geology, and Geography and the Center for Environmental Studies at UC. This field station will offer significant opportunities for field research and experiential environmental education. The Director position is a 3-year renewable appointment. Qualifications include a Ph.D. in a related field of science and demonstrated success in field research. The successful candidate will be familiar with field stations, formal and informal education programs, and have vision and long-term planning skills, and the ability to forge effective relationships with agencies and collaborators. Duties will include establishing a program of field research and monitoring, spearheading the program and facilities planning process, fund-raising, creating and maintaining partnerships, and collaborating with the CNC on public outreach. The position will begin 1 September 2006. Applications, including a CV, statement of research and teaching experience,

and list of three references and contact information should be sent electronically or by mail to: Dr. Guy Cameron [g.cameron@uc.edu], Department of Biological Sciences, University of Cincinnati, Cincinnati, OH 45221-0006. Review of applicants will begin 20 January 2006 until the position is filled. The University of Cincinnati is an equal opportunity/affirmative action employer. Women, minorities, veterans and persons with disabilities are encouraged to apply.

theresa.culley@UC.Edu

UGroningen MarineEcolEvol 2

The deadline for applications is 31 December NOT 5 December as previously advertised.

University of Groningen - Faculty of Mathematics and Natural Sciences Groningen, The Netherlands

The Department of Marine Benthic Ecology & Evolution (MarBEE) and Department of Ocean Ecosystems constitute the Marine Biology cluster within the Centre for Ecological and Evolutionary Studies (CEES) in the Faculty of Mathematics and Natural Sciences of the University of Groningen, and also takes part in the National Research School "Functional Ecology & Biodiversity". Areas of research in marine biology include ecology, population genetics and genomics of benthic plants and animals, ecophysiology of marine phytoplankton, and marine behavioral mechanics and energetics of zooplankton, zoobenthos and nekton.

The present position is available within the MarBEE group which focuses on the population genetic structure, dispersal, large-scale phylogeography and speciation processes.

The position:

The MarBEE group invites applications for a tenure track position at the Assistant Professor level. We seek a new faculty member with a background in marine ecology, population genetics, community ecology or related discipline with either a strong track record or strong interest in benthic species (animals or plants) and communities. The applicants research is expected to form a cohesive programme with the department's existing expertise, while simultaneously bringing something new and complementary.

Personal profile:

Applicants must have a Ph.D. degree and a strong

record of research accomplishments appropriate to their career stage. The successful candidate will actively participate in the teaching and research programmes of the faculty and the Center for Ecological and Evolutionary Studies (CEES).

Candidates will need to have the following qualifications:

A doctorate in the field of marine biology with special interest in (population) genetics, (community) ecology, or allied field.

Two or more of years of experience abroad in a post-doctoral capacity or experience at another educational institution.

Research, teaching and organizational experience appropriate to career stage

Research accomplishments, as expressed in a list of (first author) publications appropriate to career stage.

Evidence of successful acquisition of external funding appropriate to career stage.

Junior post-doctoral researchers are especially encouraged to apply.

Please see the webpage information below for details of the application procedure, benefits and so forth.

The deadline is 31 December (not 5 December as indicated in an earlier version)

http://213.159.10.135/rug/vacatures/-detail.cfm?Vacature_ID=VPN9PSYV <http://www.rug.nl/fwn/vacatures/ttmarinebenthic> Please contact Jeanine Olsen for further information as necessary.

Please note my new, slightly modified, e-mail address: j.l.olsen@rug.nl

Dr. Jeanine L. Olsen Professor Department of Marine Biology Biological Centre, RUG PO Box 14 NL-9750 AA Haren The Netherlands tel: +31-50-3632250 (work); +31-50-3131832 (home) fax: +31-50-3632261 e-mail: j.l.olsen@rug.nl <http://www.rug.nl/biologie> Then type "olsen" under search/zoek <http://www.rug.nl/biologie/onderzoek/onderzoeksgroepen/-marienebiologie/organisatie/personalpages/olsen> j.l.olsen@rug.nl

UHawaii EvolMath

I wanted to alert any good mathematically orientated evolutionary biologist or evolutionary biologically orientated mathematician to the faculty position in the Mathematics Department at the University of Hawaii at Hilo. Please pass this announcement along to anyone interested in applying for this position please

Assistant Professor of Mathematics Institution: University of Hawai'i at <http://www.uhh.hawaii.edu>
Hilo Location: Hilo, HI

Category: Faculty - Science - Mathematics

Posted: 10/19/2005

Application Due: Open Until Filled

Type: Full Time

Position number 84068, College of Arts and Sciences, tenure track, general funds, full-time, nine-month type appointment, to begin August 2006, pending position clearance and funding. The University reserves the right to hire at another rank if the selected candidate is qualified for that rank.

Duties: Teach courses in mathematics; advise students; engage in scholarly activity and publish results in peer-reviewed journals; and participate in University and community service.

Minimum qualifications: Doctorate in Mathematics or Mathematics Education and evidence of commitment to excellence in teaching at the undergraduate level.

Desirable qualifications: Evidence of excellence in teaching in a multi-cultural environment.

Salary: I3. Competitive.

To apply: Submit an AMS cover sheet, letter of application, Curriculum Vitae, three recent letters of reference, and a vision statement describing your view of an ideal mathematics department and how you envision yourself contributing to such a department to Dr. Mitchell Anderson, Chair, Mathematics Dept., College of Arts and Sciences, University of Hawai'i at Hilo, 200 W. Kawili St., Hilo, HI 96720-4091.

Deadline: Review of applications will begin on Nov. 15, 2005 and will continue until the position is filled.

Application Information

Postal Address: Dr. Mitchell Anderson Mathematics University of Hawai'i at Hilo 200 W. Kawili Street Hilo, HI 96720-4091

Phone: (808) 974-7627 Fax: (808) 933-3473 TDD: (808) 933-3334

Email Address: mitch@hawaii.edu
<[javascript:SendMail\('mitch@hawaii.edu'\);](mailto:mitch@hawaii.edu)>

More Information on University of Hawai'i at Hilo *
Institutional Profile <<http://www.higheredjobs.com/-InstitutionProfile.cfm?ProfileID495>> * Current
<<http://www.higheredjobs.com/-institution/search.cfm?University=University%20of%20Hawai%60i%20at%20Hilo>> openings for University of Hawai'i at Hilo on HigherEdJobs.com. * UHH Homepage <<http://www.uhh.hawaii.edu>> * EEO/AA Website <<http://www.uhh.hawaii.edu/~eeoaa>>

University of Hawai'i at Hilo is an EEO/AA Employer D/M/V/W.

Dr. Donald K. Price co-Project Director - Hawaii NSF EPSCoR Program Director - TCBES Masters Program - UH Hilo Associate Professor of Biology - UH Hilo Ecology, Evolution and Conservation Biology - UH Manoa 200 W. Kawili Street University of Hawaii Hilo, HI 96720 808-974-7365 fax 808-974-7693 email: donaldp@hawaii.edu

<http://tcbes.uhh.hawaii.edu/> donaldp@hawaii.edu

UHawaii InsectPlantPathogens

UNIVERSITY OF HAWAII ASSISTANT PROFESSOR: INSECT TRANSMISSION OF PLANT PATHOGENS

Assistant Professor, position number 85547, UHM C of Trop Agr & Human Res, (Manoa), Department of Plant & Environmental Protection Sciences, tenure track, 9 month appointment, to begin August 2006, pending position clearance. Duties: Work with students, specialists, researchers, extension agents and clientele to develop a strong research program on insect transmission of plant pathogens, ecology of insect-borne plant diseases, or insect-plant pathogen interactions. Cooperate with other faculty in the development of innovative pest management strategies. Teach a graduate level course on arthropod transmission of plant pathogens, an undergraduate course in insect-microbe interactions, and contribute to courses in General Entomology and in Integrated Pest Management. Minimum qualifications: Ph.D. in Entomology, Plant Pathology, or related field. Research experience with insect vectored plant diseases: their ecology, epidemiology, management or molecular interactions between insect and plant pathogen. Desirable qualifications: Post-doctoral research experience in entomology, microbial ecology, or insect pest management. Teaching experience at the university level.

To apply: Send letter of application, curriculum vitae, official college transcripts and have three (3) confidential letters of reference sent Application address: Dr. Mark Wright, Search Committee Chair, Department of Plant and Environmental Protection Sciences, College of Tropical Agriculture and Human Resources, University of Hawaii at Manoa, 3050 Maile Way, Rm 310. Honolulu, Hawaii 96822-2279. Inquiries: Mark Wright 808-956-7670; FAX 808-956-2428 markwrig@hawaii.edu Date posted: Dec-06-2005 Closing date: Mar-31-2006

The University of Hawai'i is an equal opportunity/affirmative action institution. All qualified applicants will be considered, regardless of race, sex, age, religion, color, national origin, ancestry, disability, marital status, sexual orientation, or status as disabled veteran or veteran of Vietnam era.

Employment is contingent on satisfying employment eligibility verification requirements of the Immigration Reform and Control Act of 1986. Appointments to positions are subject to campus recruitment guidelines and the collective bargaining agreement.

rubinoff@hawaii.edu

Uillinois Urbana-Champaign Fish Conservation

Assistant, Associate, or Full Professor, Fish Ecology and Conservation

The Department of Natural Resources and Environmental Sciences at the University of Illinois at Urbana-Champaign is seeking qualified candidates for a full-time, tenured or tenure-track faculty member to conduct research and teaching in the area of fish ecology and conservation. This position is a 9-month faculty position, with a 60 % research / 40 % teaching appointment.

Responsibilities: The individual in this position will be responsible for planning, developing, conducting, and supervising research on any aspect of fish ecology with applications to conservation and management issues. Research can address questions from the molecular to landscape scale. The person will be expected to publish regularly in peer-reviewed, nationally recognized scientific journals; develop grant proposals and attract funding; and be willing to work with governmental and non-governmental agencies within Illinois and elsewhere. The university is home to several allied govern-

mental programs including the state Natural History Survey (Illinois DNR) and associated staff and research facilities. A strong commitment and demonstrated ability to teach undergraduate students are expected, with responsibilities to include an advanced course in fish ecology and a course in aquatic ecosystem conservation. The person will be expected to recruit and train graduate students.

Qualifications: A Ph.D. in fish ecology or related discipline. Candidates will be expected to complete their degree before appointment at the assistant professor level (post-doctoral experience is beneficial). Candidates at the associate or full professor level will be expected to have a strong track record of peer-reviewed publications and evidence of successful external grant generation. All candidates should have an ability to attract funding, a vigorous record of publication, and strong complementarity with existing programs in NRES and other units at UIUC.

Department: NRES has 46 tenure-track faculty with expertise in teaching, research, and outreach in the biological, physical, and social sciences applied across natural, forested, agricultural, and urban ecosystems. Interdisciplinary and systems-based approaches are important elements of our research and education programs. NRES has programs in horticulture, forestry, soil and water, human-environment interactions, fish and wildlife, and related sciences, including molecular biology, quantitative analysis, plant products, microbiology, and entomology. Currently NRES enrolls 270 undergraduates, 76 M.S. and 47 Ph.D. students on campus, and 42 students in an off-campus Masters program in the Metro-Chicago area.

Starting Date: This position will be available August 16, 2006, or when a suitable candidate is available.

Salary: Salary will be commensurate with education and experience.

Applications: To ensure full consideration, applications must be received by January 31, 2006. Reference Job # 10265 in your application. Applicants should send a letter of application, curriculum vitae, transcripts, up to three publication reprints, brief statements of teaching and research philosophy, and three (3) letters of reference to: Dr. Jeff Brawn, Search Committee Chair c/o Susan L. Michaels, Assistant to the Head Department of Natural Resources & Environmental Sciences W-503 Turner Hall 1102 South Goodwin Avenue Urbana, IL 61801 <mailto:susanm@uiuc.edu>susanm@uiuc.edu (217) 333-9738 Fax (217) 244-3219

For more information about the position, please contact Dr. Jeff Brawn, by phone: (217) 244-5937 or by

email: <mailto:jbrawn@uiuc.edu>jbrawn@uiuc.edu.

THE UNIVERSITY OF ILLINOIS IS AN AFFIRMATIVE ACTION/EQUAL OPPORTUNITY EMPLOYER

Jeff Brawn <jbrawn@uiuc.edu>

UKansas EvoGenomics

Faculty Position in Evolutionary Genomics: The Departments of Molecular Biosciences and Ecology & Evolutionary Biology at the University of Kansas are seeking applications for a tenure-track faculty position at the ASSISTANT PROFESSOR level. Exceptional candidates at the rank of ASSOCIATE PROFESSOR will also be given serious consideration. Research interests of the candidates should be in the area of EVOLUTIONARY GENOMICS. Preferred candidates will have a research program that utilizes computational and experimental methods and that complements existing research strengths in both departments and a candidate who will contribute to the climate of diversity in the College, including a diversity of scholarly approaches. Required qualifications for Assistant Professor include a Ph.D and post-doctoral experience in a related field of study by the time of appointment, demonstrated excellence in research, and a commitment to quality undergraduate and graduate education. Additional required qualifications for Associate Professor include a vigorous, well-funded research program in evolutionary genomics and demonstrated excellence in teaching. Applicants should submit a cover letter, curriculum vitae, key reprints, and statements of research and teaching interests in a single PDF file to evogensearch@ku.edu, or by mail to Dorothy Johanning, Division of Biological Sciences, 1200 Sunnyside Ave., Rm 2041, University of Kansas, Lawrence, KS 66045-7534. Applicants should also arrange to have at least three letters of reference sent to the above address. Review of applicants will start 9 December 2005 and continue until the position is filled. The expected start date of the position is 18 August 2006. For more information about the position and the Departments, visit our websites at <http://www.molecularbiosciences.ku.edu> and <http://www.ku.edu/~eeb>. Paid for by KU. The University of Kansas is an EO/AA Employer.

lhileman@ku.edu lhileman@ku.edu

UMaryland DrosophilaEvoDevo Tech

PLEASE POST / FORWARD the attached job announcement for those who might be interested.

There is a Research Assistant / Technician position opening up in a Drosophila Evo Devo lab at the University of Maryland, College Park. Responsibilities include routine laboratory management and independent research assisting in the study of the genetics of Drosophila development. The ideal candidate will have a B.S. or M.S. degree or equivalent experience in the biological sciences, with a preference for those that possess laboratory experience in genetics / molecular biology. Strong interpersonal skills, laboratory experience, and basic word processing computer skills are required. Candidates should be able to handle multiple projects and set priorities, and have strong organizational skills and attention to detail.

Kerri Mariah Mullen Faculty Research Assistant Department of Entomology 4112 Plant Sciences Building College Park, MD 20742 301.405.2862 (ph)

Kerri Mariah Mullen <kmullen@umd.edu>

UNebraska PopGenetics

Population Genetics in the lab of Jay F. Storz, University of Nebraska

I am hiring a RESEARCH TECHNOLOGIST for my lab at the University of Nebraska. The position is available immediately.

RESEARCH SUMMARY: The goal of my research is to understand the role of selection in shaping patterns of adaptive genetic variation in natural populations. In my lab we use natural populations of deer mice (genus *Peromyscus*) and other rodents to study the process of adaptive evolution. One of the main projects in my lab involves an analysis of DNA sequence variation in hemoglobin genes that are involved in physiological adaptation to high-altitude hypoxia. In addition to studies of DNA polymorphism within species, we are also studying molecular evolution of hemoglobin and

various enzymes involved in energy metabolism (e.g., aspartate aminotransferase). A second project in the lab involves a study of morphological differentiation in populations of deer mice that are distributed across forest-grassland ecotones in different parts of North America. We are studying genetically based skeletal variation that is involved in adaptation to contrasting environments. Research in the lab mainly involves a combination of molecular biology lab work and computational analysis of genomic data.

For more details, see <http://www.biosci.unl.edu/faculty/Storz/index.html> . REQUIRED EXPERIENCE: Bachelor's or Master's degree in biology or biochemistry. Knowledge of basic molecular biology lab techniques is essential.

RESPONSIBILITIES: PCR amplification, molecular cloning, and DNA sequencing of nuclear genes in mice. Experience with sequence alignment tools and phylogenetic/population genetic analysis of DNA sequence data is preferred.

Review of resumes will begin December 14. Please send a CV along with the contact information for three or more references (E-mail: jstorz2@unl.edu).

The School of Biological Sciences is an extremely collegial and interactive place to work and Lincoln is a wonderful place to live. Excellent benefits are available, including a staff/dependent scholarship program.

Jay F. Storz School of Biological Sciences University of Nebraska Lincoln, NE 68588 Phone: 402/472-1114 E-mail: jstorz2@unl.edu

WWW: <http://www.biosci.unl.edu/faculty/Storz/index.html> Population Biology at UNL: <http://popbio.unl.edu/index.htm> Jay F Storz <jstorz2@unlnotes.unl.edu>

UOxford 2 EvolBiol

Below are advertisements for Chairs in Entomology and Biological Anthropology to be held in the Department of Zoology here at Oxford. Both Chairs are very much open to evolutionary biologists with appropriate research interests.

Thank you,

Paul Harvey

UNIVERSITY OF OXFORD

Hope Professorship of Zoology (Entomology)

Applications are invited for the above post, tenable from 1 September 2006, or such later date as may be arranged.

The Hope Professor will be based in the Department of Zoology, but will also have access to the Hope Entomological Collections in the University Museum and to the University's Field Station at Wytham.

The successful candidate will have an international research reputation in an aspect of entomology that integrates with one or more the Department's main research groupings in behaviour, conservation biology, development, ecology, evolution, disease or ornithology. The appointee will be expected to build and lead a substantial and academically-excellent research group that integrates with others in the Department; to teach and examine on the Biological Sciences undergraduate course and the MSc course in Biology (Integrative Bioscience).

A non-stipendiary fellowship at Jesus College is attached to the professorship.

Further particulars, including details of how to apply, are available from <http://www.admin.ox.ac.uk/fp/> or from the Registrar, University Offices, Wellington Square, Oxford OX1 2JD (Tel: 01865 270200). The closing date for applications is Monday 30 January 2006.

UNIVERSITY OF OXFORD

Professorship of Biological Anthropology

Applications are invited for the above post, tenable from 1 September 2006, or such later date as may be arranged. The Professorship of Biological Anthropology at Oxford has historically been one of the most prestigious in the country. The University of Oxford wishes to appoint a candidate who can take that tradition forward. To this end the successful candidate will have an international research reputation in Biological Anthropology, involving human genetics, human evolution/palaeoanthropology (either genetic or morphological), or primatology.

The Institute of Biological Anthropology is now merged with the Department of Zoology, and the professorship is part of the latter department, while also being affiliated, for academic purposes, to the School of Anthropology and Museum Ethnography. The professor would be expected to build biological anthropology, and one of his or her duties would be to provide teaching and other support for the Human Sciences degree, in which Biological Anthropology is a core subject.

A non-stipendiary fellowship at Linacre College is at-

tached to the professorship. Further particulars, including details of how to apply, are available from <http://www.admin.ox.ac.uk/fp/> or from the Registrar, University Offices, Wellington Square, Oxford OX1 2JD (Tel: 01865 270200). The closing date for applications is Monday 30 January 2006.

Paul Harvey FRS Professor of Zoology and Head Department of Zoology University of Oxford South Parks Road Oxford OX1 3PS UK tel: +44 (0)1865 271260

paul.harvey@zoo.ox.ac.uk

UTennessee EvoBiol

Evolutionary Biologist at Tennessee

The Department of Ecology and Evolutionary Biology at the University of Tennessee, Knoxville, seeks to fill a tenure-track position in Evolutionary Biology at the Assistant or Associate Professor level, to start August 1, 2006. Research in all areas will be considered, but especially attractive areas include macroevolution, phylogenetic theory, and broad-scale evolutionary processes in natural systems. Successful applicants will have a Ph.D. and demonstrated the ability to interact and collaborate broadly in ecology and evolution. Postdoctoral or faculty experience is preferred, and applicants will be expected to develop an externally funded and internationally recognized research program. Teaching will include undergraduate and graduate courses in the applicant's area. For more information visit <http://eeb.bio.utk.edu>. Candidates should apply to: Dr. Randall Small, Department of Ecology and Evolutionary Biology, 569 Dabney Hall, University of Tennessee, Knoxville, TN 37996. Applicants should send a curriculum vitae, statements of research and teaching goals, and arrange for three reference letters to be submitted. Applications will be reviewed beginning January 6, 2006.

The University of Tennessee, Knoxville, is the state's flagship research institution, a campus of choice for outstanding undergraduates, and a premier graduate institution. As a land-grant university, it is committed to excellence in learning, scholarship, and engagement with society. In all its activities, the university aims to advance the frontiers of human knowledge and enrich and elevate society. The university welcomes and honors people of all races, genders, creeds, cultures, and sexual orientations, and values intellectual curiosity, pursuit of knowledge, and academic freedom and

integrity. The university intends that its graduates will promote the values and institutions of representative democracy, and be prepared to lead lives of personal integrity and civic responsibility.

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rsmall@utk.edu rsmall@utk.edu

Umea Uppsala 7 positions

Ume? University and Uppsala University, Sweden announce... The Swedish Research Council for Environment, Agricultural Sciences and Spatial Planning recently decided to support five strong research environments for the period 2006-2010, including "Lake Ecosystem response to Environmental Change (LEREC)". Within this program several post doc positions and PhD student positions are now open. The program aims at the analysis of ecosystem function and response to environmental changes by the integration of recent conceptual progress in aquatic ecology into a unified lake ecosystem model. The research will address carbon and energy transfer, and include all trophic components and habitats. PhD students and post docs will be based in Ume? and Uppsala, and there will be ambitious programs for integration and for the involvement of senior guest researchers.

7 research positions At Ume? University 5 positions

are open for application:

1 Assistant professor. Ref. no. 312-4413-05. Theoretical modeling of size-structured population dynamics in fish. The position is open for an outstanding scientist with a record of achievements demonstrated. The candidate should have a PhD and postdoctoral research experience. Applications should include description of past research accomplishments including a list of publications, description of teaching experience, curriculum vitae, up to 10 relevant publications, a research plan, and the names of three references, all in 3 copies.

3 Post doc positions in the following research areas: Theoretical modeling of bacteria-algae-grazer interactions. Ref. no. 315-4414-05. Benthic-pelagic interactions in lakes. Ref. no. 315-4415-05. Bacterial use of dissolved organic carbon. Ref. No. 315-4416-05. Candidates should have a PhD. Applications should include description of past research accomplishments including a list of publications, curriculum vitae, up to 10 relevant publications, a research plan, and the names of three references, all in 3 copies. The post doc positions are planned for a period of 2 years, each starting as soon as possible.

1 PhD student position Bacteria-algae-grazer interactions. Ref. no. 313-4417-05. Applications in 3 copies should include a short description of your research interests and why you are interested in the position, list of qualifications, attested copies of certificates from university education and copies of publications including Bachelor's/Masters' thesis.

At Uppsala University 2 positions are open for application:

1 Post doc position Interactions between sediment microorganisms and higher trophic levels. Ref. no. UFV-PA 2005/3755. The candidate should have a PhD. The application should include description of past research accomplishments including a list of publications, curriculum vitae, up to 10 relevant publications, a research

plan, and the names of three references all in 3 copies. The post doc position is planned for a period of 2 years, starting as soon as possible.

1 PhD student position Microbial energy mobilization from lake sediments. Ref.no.UFV-PA 2005/3756. Applications in 3 copies should include a short description of your research interests and why you are interested in the position, list of qualifications, attested copies of certificates from university education and copies of publications including Bachelor's/Masters' thesis.

Further information for the positions at Ume? University can be obtained from <mats.jansson@emg.umu.se> +46 90-786 60 98 or <lennart.persson @emg.umu.se> +46 90-786 63 16 and for the positions at Uppsala University from <lars.tranvik@ebc.uu.se> +46 18-471 27 22. Union-related information at Ume? University is available from SACO, phone +46 90-786 51 53, SEKO-civil, phone +46 90-786 52 96 and also ST, phone +46 90786 54 31. Union representatives at Uppsala University are: Anders Grundstr?m, SACO-r?det, phone: +46 18-471 5380, Carin S?derh?ll, TCO/ST, phone: +46 18-471 1996, and Stefan Djurstr?m +46 703994728, +46 18-471 3315.

Applications, quoting appropriate ref.no., are sent to Ume? University, The Registrar, SE-901 87, Ume?, Sweden, or Uppsala University, The Registrar, Box 256, SE-751 05 Uppsala, Sweden and should arrive no later than January 31, 2006.

We look forward to receiving your application!

–

Lars Tranvik Limnology/Department of Ecology and Evolutionary Biology Centre Uppsala University Norbyv. 20 SE-752 36 Uppsala Sweden

phone +46 18 4712722 , mobile 0733 225830 fax +46 18 531134 E-mail lars.tranvik@ebc.uu.se http://www.ebc.uu.se/index_eng.htm Lars Tranvik <lars.tranvik@ebc.uu.se>

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Angiosperm classification

Dear colleagues,

The new version of my classification of angiosperms (“Systema Angiospermarum”, v.4.8) is now available on the URL:

<http://herba.msu.ru/shipunov/ang> The main features of the system are follows:

- * system considers as much current data as possible;
- * system is fully hierarchical;
- * taxa are usually considered in most broad sense;
- * system is traditional – paraphyletic taxa are widely accepted;
- * order of arrangement of taxa matters and reflects the similarities between them;
- * names of families are checked with the last work of Hoogland and Reveal (2005) and corrections of Reveal after XVII IBC (2005).

You are very welcome to send your comments to the my e-mail address.

With best wishes and regards,

Dr. Alexey B. Shipunov, Moscow

Alexey Shipunov <plantago@herba.msu.ru>

AntibioticResistance proposals

The Reservoirs of Antibiotic Resistance (ROAR) Project, coordinated by the Alliance for the Prudent Use of Antibiotics and funded by the National Institute of Allergy and Infectious Diseases, is an effort designed to improve scientific understanding of the role of commensal bacteria in the emergence and spread of antibiotic resistance.

The 2005 ROAR Request for Proposals is now available and can be found at <http://www.roarproject.org>. Funding is available up to \$60,000 for a maximum of one

year and is open to U.S. and non-U.S. based researchers. The deadline for proposal submission is February 1, 2006* *for an anticipated project start date of June 1, 2006. Projects will be selected in early March for funding beginning June 1, 2006.

Questions regarding this RFP should be directed to Dr. Michael Feldgarden, ROAR Principal Investigator (michael.feldgarden@tufts.edu) or Amelie Peryea, ROAR Research Manager (amelie.peryea@tufts.edu).

Completed proposals should be sent electronically to the following address and are due no later than February 1, 2006: Katherine Corso, ROAR Project Assistant, Email: Katherine.Corso@tufts.edu; Mailing Address: 75 Kneeland Street, Boston, MA/02111/USA; Phone: 617-636-3574; Fax: 617-636-3999.

Text ends here

– Michael Feldgarden Research Director Principal Investigator, Reservoirs of Antibiotic Resistance(ROAR) ALLIANCE FOR THE PRUDENT USE OF ANTIBIOTICS 75 Kneeland St. Boston, MA 02111 Tel 617.636.3576 Fax 617.636.3999 Michael.Feldgarden@tufts.edu

Michael.Feldgarden@tufts.edu

Assignment test

Hi:

I need to apply an assignment test for different populations, but I have many questions

- 1- Is it possible to use assignment test for allozymes data??
- 2- What is the best software for assignment test?
- 3- Using Arlequin software I get the likelihood for genotypes, but I don't get any probability to look for statistical differences in the genotypes assigned. How can I get that probability?
4. Using Arlequin, How do I do plotting, for example to plott the log-likelihood of individual sampled, what value of those that the software give me should I use as coordinates?, How do I choose one, are there any arguments to make the choice?

Many thanks,

Marcela P. Astorga O. email: marcelaastorga@uach.cl Universidad Austral de Chile

Barcode publication

Royal Society DNA Barcoding publication special half price offer!

An international consortium of major natural history museums, herbaria and other organisations has launched an ambitious project, the 'Barcode of Life Initiative', to promote a process enabling the rapid and inexpensive identification of the estimated 10 million species on Earth. DNA barcoding is a diagnostic technique in which short DNA sequence(s) can be used for species identification.

The first international scientific conference on Barcoding of Life was held at the Natural History Museum in London in February 2005 and the October 2005 issue of Philosophical Transactions of the Royal Society B: Biological Sciences reviews the scientific challenges discussed during this conference and in previous publications. For full paper abstracts, please visit <http://www.journals.royalsoc.ac.uk/-openurl.asp?genre=issue&eissn=1471-2970&volume60&issue62>

Non-subscribers can purchase the print issue at a specially reduced price of ?45/\$US75 for a limited amount of time (usual price: ?115/US\$195).

To place an order at the discounted price, please contact The Royal Society by any of the methods below, quoting reference TB 1462:

telephone +44 (0)20 7451 2646 email sales@royalsoc.ac.uk post Publishing, The Royal Society, 6 Carlton House Terrace, London SW1Y 5AG, UK

————— Felicity Davie Tou-can Marketing
The Holly 42 Heath Hill Road South Crowthorne Berkshire RG45 7BW

Tel. +44 (0)1344 466600 Fax. +44 (0)1344 466601
E-mail: felicity@tou-can.co.uk www: <http://www.tou-can.co.uk>

BernhardRenschPrize applications

Applications for the Third Bernhard Rensch Prize for Biological Systematics of the GfBS

The Bernhard Rensch Prize is awarded annually by the Society of Biological Systematics (GfBS, Germany) to a young scientist who has demonstrated exceptional work in any area of biological systematics. The award was launched by the GfBS according to a suggestion by the recently deceased Prof. Dr. Ernst Mayr, an honorary member of the GfBS, who also helped underwrite the endowment for the prize with a generous contribution. The prize honours the lifelong work of Bernhard Rensch, one of the founders of the 'New Systematics' (for more information, see <http://www.uni-muenster.de/-Biologie.NeuroVer/Verhaltensbiologie/reusch-d.html>).

Eligible for consideration is any significant work (e.g., Bachelors or Masters thesis, PhD dissertation, or the equivalent) where the applicant is the sole or primary author. The study can be in any area in which the GfBS is involved, with botanical, paleontological, and zoological (broadly defined) studies all being equally desired. All submitted work will be judged according to its scientific quality, innovativeness and creativity by the Bernhard Rensch Committee, consisting of members of the council of the GfBS and one additional, external jury member.

The prize of 1000 Euro together with the Bernhard Rensch Medal will be awarded at the Annual Meeting of the Society, where the recipient will present the work in a public seminar. The Society will pay all the costs of the recipient associated with attending the annual meeting as well as awarding a free one-year membership to the Society.

The following is a summary of the key points associated with an application for the prize: - The prize is open to all members of the scientific community, whether or not they are members of the GfBS. Candidates can be either self-nominated or nominated by another person. - The candidate must be either the sole or primary author of the nominated work. - Only works written in either English or German can unfortunately be taken into consideration. - The nominated work can be in any of the areas of systematic botany, paleontology, or zoology, each of which will be judged equally. - The candidate must have defended their PhD no more than three years before the submission deadline. - Applications must include two hardcopies of the nominated work. A short summary of the candidate's academic career and any other relevant material, either about the study or the candidate, is also welcome. - All applications must be received by August 31, 2006 and be sent to the following: PD Dr. Uwe Fritz General Secretary of the Society of Biological Systematics Museum

für Tierkunde Staatliche Naturhistorische Sammlungen Dresden A.-B.-Meyer-Bau Königsbrücker Landstr. 159 01109 Dresden Germany

————— Olaf Bininda-Emonds Lehrstuhl für Tierzucht Technical University of Munich Hochfeldweg 1 85354 Freising-Weißenstephan Germany

Phone: +49 8161 713741 Fax: +49 8161 713107 e-mail: Olaf.Bininda@tierzucht.tum.de WWW: <http://www.tierzucht.tum.de/Bininda-Emonds/> Olaf.Bininda@tz.agrar.tu-muenchen.de Olaf.Bininda@tz.agrar.tu-muenchen.de

Blood heat treatment

Hi All,

“The USDA suggests heat treatments of either 56C for 3 hours or 60C for 30 minutes to destroy New Castle Disease in avian blood imported into the US. Will either of these treatments damage DNA in the blood if whole blood is stored in a standard lysis buffer containing Tris, NaCl, EDTA and SDS?”

I am guessing that the DNA would be okay but I would like to know if anyone else has been using these treatments.

Lisette – Lisette Waits, PHD Associate Professor Fish and Wildlife Resources Co-Director Center for Research on Invasive Species and Small Populations Laboratory for Ecological and Conservation Genetics University of Idaho PO Box 441136 Moscow, ID 83844-1136 Phone: (208) 885 7823 Fax: (208) 885 9080 lwaits@uidaho.edu <http://www.cnrhome.uidaho.edu/default.aspx?pid=-72862> <http://www.cnrhome.uidaho.edu/crissp> <http://www.cnr.uidaho.edu/lecg/>

Blood sampling

Dear Evoldir members

I am planning some human blood samplings in field conditions, about 1 mL per sample, and I hope to be able to use a microcentrifuge if needed. I wonder if any of you have some advice or protocol about minimum handling & maximum DNA quality and quantity re-

trieval. Reagents or solutions that may be employed in field conditions? I have read about using DNAzol. I'll appreciate some feedback from anyone who may have used it.

Claudio M. Bravi Laboratorio Genética Molecular de Poblaciones Instituto Multidisciplinario de Biología Celular (IMBICE) Calle 526 y 11 PO Box 403 1900 La Plata Argentina

"Claudio M. Bravi" <cmbravi@yahoo.com.ar>

BootstrappingML in PAUP

Dear All,

I am going to reconstruct the phylogenetic tree by using Maximum Likelihood methods implemented in PAUP using DNA sequences. The number of Taxa is smaller than 40. Do you think I can run the bootstrapping option to get the results of statistical supporting for tree branching under the ML set? If so, I would be grateful if someone could send me a PAUP batch file for doing such thing.

Cheers!

Samy Zhang

Email: samy_zhang47@hotmail.com

samy zhang <samy_zhang47@hotmail.com>

DMSO salt solution

Hello,

I was wondering if anyone has used DMSO salt solution to preserve insects. I was looking for non-ethanol based preservation techniques and the DMSO - salt solution seems like an option but has mostly been used for mammalian tissues. I would appreciate input on this or other non-cryogenic preservation options.

Thanks a lot!

Andrea Sequeira Assistant Professor Department of Biological Sciences Wellesley College Wellesley, MA 02481

(781) 283-3376 (office and voice mail) (781) 283-3079 (lab) (781) 283-3642 (fax)

asequeir@firstclass.wellesley.edu
asequeir@firstclass.wellesley.edu

ase-

DNA extraction kits

Dear Colleagues

Our lab has been using the Sigma kit (GenElute Mammalian Genomic DNA miniprep kit) for DNA extraction. The kit works well for Salmonids (muscle and fin tissue) but not for cichlid fin clips. The other method currently at our disposal is phenol-chloroform, which is time consuming. Does anyone have any suggestions as to alternative extraction kits, which have worked previously with cichlid fin clips? Explanations as to why this kit does not work for cichlid fin clips would also be welcome.

Many thanks

Isabel S. Magalhaes

PhD student Fish ecology and Evolution Aquatic ecology and Macroevolution University of Bern / EAWAG
isabel.magalhaes@eawag.ch

Isabel Santos Magalhaes
<isabel.magalhaes@eawag.ch>

DNA from FishOrgans

Dear members,

I am looking for a DNA extraction protocol, either a kit or method, to extract bacterial DNA from fish organs (kidney and liver) for a bacterial resistance study. As I plan to amplify bacterial DNA by PCR afterwards, I need a very efficient extraction method. I also need a method that will be able to separate fish DNA from bacterial DNA, as the former will be more abundant in the extraction product and may potentially interfere with the PCR. I was planning to use the Quiagen DNeasy 96 tissue kit normally used for DNA extraction from tissues, but I am afraid this will not be efficient enough, nor solve the problem of having a mixed fish/bacteria DNA product.

Does anyone have some experience with this type of problem? Any other suggestions of good extraction

protocols or DNA separation methods would also be appreciated.

Thank you all,

Mélanie melanie.dionne@giroq.ulaval.ca

Decision in Kitzmiller vs Dover

The decision just came down in Kitzmiller v. Dover. The PDF can be downloaded here (right-click on the word “decision”): <http://www2.ncseweb.org/wp/?p=98>

It’s a slam dunk in all respects and bears careful reading on the issues of science/religion in public schools, the creationist history of “intelligent design”, and the “science” of intelligent design and irreducible complexity.

The decision includes many pieces that I and other NCSE staff contributed to as pro bono consultants for the plaintiffs. For example, the discovery of the creationist drafts of the ID book “Of Pandas and People”, and the refutation of Behe’s “irreducible complexity,” for example with 50 peer-reviewed articles on the evolution of the immune system. This kind of thing is why NCSE exists, check us out at <http://www.ncseweb.org>. For more background and details on the trial, see: <http://www2.ncseweb.org/wp/>.

Thanks, Nick Matzke

Nicholas J. Matzke Public Information Project Director National Center for Science Education, Inc. 420 40th Street, Suite 2 Oakland, CA 94609-2509 Phone: (510) 601-7203 x307 Fax: (510) 601-7204 Toll-free: 1-800-290-6006 matzke@ncseweb.org <http://www.ncseweb.org> matzke@ncseweb.org

Digital Gel Documentation

Dear Colleagues,

I am looking for a bench top (non-darkroom), digital photo system to document agarose gels in my lab (with UV transilluminator). I don’t need to do anything complicated, just visualize and quantify PCR bands.

The rub is that I only have about \$2000 USD. This seems like a lot of money for a digital camera, some filters, a metal box, and a UV light box, but I can’t find a system that even approaches this price.

Any advice? Has anyone built their own? Any reasonably priced commercial products?

Thanks! I’ll post replies.

Steve Jordan Department of Biology Bucknell University Lewisburg, PA 17837 Office: 310 Bio. Bldg. +1 570-577-1254 Lab: 331 Bio. Bldg. +1 570-524-3816 Fax: +1 570-577-3537 <http://www.facstaff.bucknell.edu/sdjordan/jordan.html>

sdjordan@bucknell.edu sdjordan@bucknell.edu

Digital Gel Documentation answers

>Dear colleagues,

Thanks to all those who replied to my request for an inexpensive agarose gel documentation system. My original email and replies are posted below. There are many good ideas here.

Sincerely,

Steve Jordan

>Dear Colleagues, > >I am looking for a bench top (non-darkroom), digital photo system to >document agarose gels in my lab (with UV transilluminator). I don’t need >to do anything complicated, just visualize and quantify PCR bands. > >The rub is that I only have about \$2000 USD. This seems like a lot of >money for a digital camera, some filters, a metal box, and a UV light box, >but I can’t find a system that even approaches this price. > >Any advice? Has anyone built their own? Any reasonably priced commercial >products? > >Thanks! I’ll post replies.

Replies:

Hi Steve,

I’ve built my own out of plywood. Just a big box (3 x 4 x 4), painted black on the inside and black duct tape covering the electrical holes. The trickiest part is the door. I put a trim on the inside with black window insulation tape all around the gap. We put an old camera stand and a UV table inside. We use an old Kodak

digital camera. Anything on the market in the \$300 or less range will work. You just need to be sure that it can be controlled from the computer outside (take picture, download, change settings, etc.).

Good luck,

Vladimir Douhovnikoff Assistant Professor Biology Department Simmons College

Hi,

have a look here: <http://evolution.unibas.ch/ebert/lab/geldoc.htm> cheers,

dominik

I am in the throes of testing this myself. My experience so far is that the digital SLR that I purchased on other criteria (Canon 350D) is very good for everyday use but not for publication quality prints. I made an careful survey of filter transmission characteristics vs the emission properties of EtBr and ascertained that the Hoya G orange filter is the best one available, though red Wratten 25 and other orange or red filters are also usable. I have also set the camera to output B+W and have tried different "speed" settings up to ASA 1600. The latter may be a bit grainy, but is OK for lab records.

With either of the filters and at any ASA setting I find the same problem that has inhibited other users in this lab from going entirely digital; this is that background weak bands attributable to the UV emission tubes appear in the pictures. This can be/has been avoided by the purchase of a dichroic filter to accept a narrow band of wavelengths around the EtBr peak, but these cost US\$250 approx and I do not want to spend as much. The pesky bands are probably IR emission from the tubes, and could also be filtered out by a heat-absorbing glass such as Schott KG5., but for this I have been quoted UK£160 in a 58mm camera mount. I am looking for an alternative source of heat-absorbing glass, e.g. a derelict slide projector or enlarger, or a glass merchant who happens to have a scrap of a glass that is sometimes used for windows (e.g. Calorex). Both Chance and Pilkington sell heat-absorbent window glass, but there is no call for it in this latitude.

BLC

Steve- We set up a system for gel image capture in our lab pretty cheaply. This was a couple of years ago so things may be a bit different now. I got a Kodak DC4800 camera wit 3.1 megapixel resolution. The key

thing is getting a camera that can 1) be controlled directly through a PC. Most have suitable software but check it out first; and 2) can take a filter holder on the lens. We use a Tiffen deep-yellow filter (from Fisher) for ethidium bromide gels. The diameter is 40.5 mm so you need a filter adapter of that size for the camera. Then you just need a transilluminator and a PC to hook it up to. It take a bit of playing around to get he settings on the camera optimized but all in all it is quite straight forward. We use Adobe photoshop to manipulate the images and a laser printer to print them out but that is not really necessary. Hope that helps. Best. Mike

Michael E. Pfrender Department of Biology Utah State University 5305 Old Main Hill Road Logan, UT 84322-5305 Phone: 435-797-7623 Fax: 435-797-1575

Hi, Clare chemical research <<http://www.clarechemical.com/orderusa.htm>><http://www.clarechemical.com/orderusa.htm> sells an inexpensive non UV transilluminator but it has to be used with dyes like SYBRgreen instead of ethidium. Those dyes are as effective as ethidium, but more expensive.

I have used the transilluminator with a Kodak digital camera that had an adjustable exposure time(no special filters required) It was mounted to a camera stand and was connected to and controlled by a computer.

— / —

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>

Drosophila enhancer trap

My fellow Evoldirers,

I was hoping that some of you might be able to help me with a question that was addressed to me. Are there known examples of Drosophila enhancer trap lines that have dominant phenotypes associated with the insertion mutations? I am not referring to the marker and reporter genes carried by the enhancer trap construct itself, but rather to the phenotypes that are produced by the mutagenic effects of the insertion on native genes in the Drosophila genome.

The identities of specific mutant lines, gene and allele names, or references to papers that describe such dominant phenotypes would all be much appreciated.

Thanks, Jeff

Dr. Jeffrey M. Marcus Assistant Professor Department of Biology Western Kentucky University 1906 College Heights Boulevard #11080 Bowling Green KY 42101-1080

Office (270) 745-2043 Lab (270) 745-2288 FAX (270) 745-6856

jeffrey.marcus@wku.edu jeffrey.marcus@wku.edu

Drosophila isofemale lines

Dear evoldir,

I am looking for population samples of either *D. melanogaster* or *D. simulans* (>6 isofemale lines collected from single localities) that were collected recently (2001 or later). Please let me know if you have these in your collection and can help me out.

Many thanks, Erik Dopman

edopman@oeb.harvard.edu edopman@oeb.harvard.edu

Drosophila isolines

Subject line: New *D. ananassae* *D. subobscura* isolines

NEW DROSOPHILA ISOFEMALE LINES: The Tucson Drosophila Species Stock Center has recently received new isofemale lines from different species. These isofemale lines are available until the last day in February 2006:

Drosophila ananassae: 26 isofemale lines from Kade, Ghana (2004). 12 isofemale lines from Mbengwi, Cameroon (2004). 12 isofemale lines from Namulonge, Uganda (2005). 6 isofemale lines from Gisakura, Rwanda (2005). 4 isofemale lines from San Blas, Nayarit, Mexico (2004). 3 isofemale lines from Yokadouma, Cameroon (2004). 2 isofemale lines from St Kitts, Caribbean Sea (2005). 1 isofemale line from

Dondé, Guinea (2005). 1 isofemale line from Oku Village, Cameroon (2004). 1 isofemale line from Mbalang-Djalango, Cameroon (2004). 1 isofemale line from Marova, Cameroon (2004). 1 isofemale line from Benin, Ghana (2004).

Drosophila subobscura: 10 isofemale lines from Heidelberg, Germany (2005).

NEW DROSOPHILA STOCKS: The Tucson Drosophila Species Stock Center has incorporated several strains of wild type flies into the permanent collection. Check website for collection info:

MULTIFEMALE STRAINS: *D. ananassae* 14024-0371.27 (Kade, Ghana 2004). *D. ananassae* 14024-0371.28 (Mbengwi, Cameroon 2004). *D. ananassae* 14024-0371.29 (Namulonge, Uganda 2005). *D. arawakana* 15182-2261.04 (St. Kitts, Caribbean Sea 2005). *D. arawakana* (St kitts type) 15182-2260.01 (St. Kitts, Caribbean Sea 2005). *D. mojavenensis* 15081-1352.26 (Sonora, Mexico 2003). *D. simulans* 14021-0251.215 (Cactus Valley, Hidalgo, Mexico 2005). *D. subobscura* 14011-0131.04 (Heidelberg, Germany 2005). *Chymomyza rufithorax* 20000-2640.00 (Fukuoka, Japan 1981). *Chymomyza pararufithorax* 20000-2650.00 (Okinawa, Japan 1996). *Chymomyza amoena* 20010-0010.00 (Virginia, U.S.A. 1989). *Chymomyza amoena* 20010-0010.01 (Michigan, U.S.A. 1992). *Chymomyza amoena* 20010-0010.02 (Michigan, U.S.A. 1993). *Chymomyza amoena* 20010-0010.03 (San Sebastiano, Italy 2000). *Chymomyza amoena* 20010-0010.04 (Calcarola, Italy 2000).

ISOFEMALE LINES

D. ananassae 14024-0371.16 (San Blas, Nayarit, Mexico 2004). *D. ananassae* 14024-0371.17 (Dondé, Guinea 2005). *D. ananassae* 14024-0371.18 (Kade, Ghana 2004). *D. ananassae* 14024-0371.19 (Benin, Ghana 2004). *D. ananassae* 14024-0371.20 (Yokadouma, Cameroon 2004). *D. ananassae* 14024-0371.21 (Oku village, Cameroon 2004). *D. ananassae* 14024-0371.22 (Mbalang-Djalango, Cameroon 2004). *D. ananassae* 14024-0371.23 (Maroba, Cameroon 2004). *D. ananassae* 14024-0371.24 (Mbengwi, Cameroon 2004). *D. ananassae* 14024-0371.25 (Namulonge, Uganda 2005). *D. ananassae* 14024-0371.26 (Gisakura, Rwanda 2005). *D. guanche* 14011-0095.01 (Canary Islands, Spain). *D. malerkotliana* 14024-0391.03 (San Francisco, Nayarit, Mexico 2004). *D. malerkotliana* 14024-0391.04 (San Blas, Nayarit, Mexico 2004). *D. nigricruria* 15081-1381.04 (Tecualilla, Sinaloa, Mexico 2004). *D. obscura* 14011-0151.00 (Heidelberg, Germany 2005). *D. obscura* 14011-0151.01 (Heidelberg, Germany 2005). *D. obscura* 14011-0151.02 (Heidelberg, Germany 2005). *D. pseudoobscura* 14011-0121.118 (Chiracahuas Moun-

tains, Arizona, 2004). D. simulans 14021-0251.211 (Zacuatlipan, Hidalgo, Mexico 2005). D. simulans 14021-0251.212 (Ciudad Valles, San Luis Potosi, Mexico 2005). D. simulans 14021-0251.213 (Jilota, Hidalgo, Mexico 2005). D. simulans 14021-0251.214 (Mezquitlan, Hidalgo, Mexico 2005). D. subobscura 14011-0131.05 (Heidelberg, Germany 2005). D. subobscura 14011-0131.06 (Heidelberg, Germany 2005). D. subobscura 14011-0131.07 (Fulbourn, United Kingdom 2005). D. subobscura 14011-0131.08 (Cambridge, United Kingdom 2005). D. subobscura 14011-0131.09 (Combe nigré, France 2005). D. tristis 14011-0141.00 (Heidelberg, Germany 2005). D. willistoni 14030-0811.32 (St Kitts Island, Caribbean Sea 2005).

MUTANT LINES D. willistoni 14030-0811.33 (White eyes, Montevideo, Uruguay 2000).

Therese Ann Markow Regents' Professor Department of Ecology and Evolutionary Biology BSW 310 University of Arizona Tucson, AZ 85721

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Endnote resources

Dear all

Having recently forked out a lot of money for a copy of Endnote, I've been a bit disappointed to find that evolutionary and ecological users aren't too well supported. By this I mean that there aren't many document templates, and the supplied journal title lists (in the term lists folder) don't include many journals that I want to cite. Before I spend a happy day typing in lists of journal abbreviations, I thought I'd ask if anyone had put anything like this on the 'net? I ran some searches but "Endnote and evolution and resources" gets 97,000 hits from Google...

Much obliged for any help

Rob Knell

School of Biological Sciences Queen Mary, University of London

'Phone +44 (0)20 7882 7720 Skype Rob Knell <http://www.qmul.ac.uk/~ugbt794> <http://www.mopane.org>
 "The truth is that they have no clue why the beetles had

horns, it's the researchers who have sex on the brain and everything has to have a sexual explanation. And this is reasearch?!" Correspondent known as FairOpinion on Neo-Con American website discussing my research.

r.knell@qmul.ac.uk r.knell@qmul.ac.uk

Endnote resources answers

Dear All

Several people asked me to post what I found out about Endnote resources for evolution and ecology, so here's a summary.

The best source of information for journal names and abbreviations to import into your library is the website maintained by the University of Queensland's library:

http://www.library.uq.edu.au/faqs/endnote/biological_journal_titles_6.html

This has a file called 'Biosciences.txt' available for download with about 5,400 journal titles and abbreviations. You can import these directly into your journals term list. Be warned, though, there appears to be a bug with Endnote 9 for Mac OS X. You can import this list, but for some reason the program does not recognise them properly. I ended up just typing them all in anyway.

The Center for Ecology and Hydrology in the UK has an archive of journal styles for Endnote at:

<http://library.ceh.ac.uk/EndNote/endnotestyles.html>

These are mostly ecological or environmental journals.

Some useful websites for finding out what the appropriate abbreviation for your citation of choice is are:

<http://www.library.ubc.ca/scieng/coden.html> <http://www.bioscience.org/atlas/jourabbr/list.htm> <http://www.pherobase.com/database/journal/journal-index.php> <http://www.sciencemag.org/feature/contribinfo/prep/res/journal.abbrevs.dtl>

Finally, I should include this comment highlighting some alternatives:

> Can't avoid mentioning that LaTeX and its associated reference package > BibTeX is free, runs on any machine, has a vibrant community backing > it, and produces better output. > > If you don't like that, openoffice now has a bibliography tool and it > could do with a "happy day typing" to provide it with the same. It > too is free and supported by a community.

> > Brian

Many thanks to everyone who replied.

Rob Knell

School of Biological Sciences Queen Mary, University of London

'Phone +44 (0)20 7882 7720 Skype Rob Knell <http://www.qmw.ac.uk/~ugbt794> <http://www.mopane.org>

"The truth is that they have no clue why the beetles had horns, it's the researchers who have sex on the brain and everything has to have a sexual explanation. And this is reasearch?j' Correspondent known as FairOpinion on Neo-Con American website discussing my research.

r.knell@qmul.ac.uk

EvoEducation Kansas

Dear Colleagues,

You may find that BONE WARS is a holiday gift favorite outside of Kansas as well... CARD GAME ENTERTERS EVOLUTION DISPUTE We're making good on our threat. Starting immediately, we're offering a 20% discount to anyone in Kansas who buys BONE WARS: The Game of Ruthless Paleontology from our online retail store. The offer is valid through December 31, 2005. We'll also give the discount to anyone shipping to Kansas, so feel free to send a copy to your cousin in Topeka.

Why give a discount to Kansas? Simple: the Kansas Board of Education has attempted to give equal space in the state public school biology curriculum to the doctrine of "Intelligent Design," claiming that it is a "scientific theory" of the origin and development of life. When real scientists complained that "Intelligent Design" fits none of the criteria for an actual scientific theory, the Board responded by redefining "science" so that it is no longer limited to the search for natural explanations for phenomena.

So we're doing our part for science. BONE WARS shows players how a scientific theory is developed and tested, and they can learn lots of fun dinosaur lore along the way. Best of all, one of the four "ruthless paleontologists" in the game, Charles Sternberg, was actually raised in Kansas and collected many important fossils in the state.

If you're one of the many Kansans that love science for what it really is, you have our sympathy. We wish we

could do more to help. But we don't have the awe-inspiring power of the Flying Spaghetti Monster.

Dr. Matthew Hare Biology Department University of Maryland College Park, MD 20770 301-405-7264 matthare@umd.edu matthare@umd.edu

Experimental Design

Hi everyone,

does anyone have the ebook PDF-Version of 'Experimental Design and Data Analysis for Biologists' by Gerry P. Quinn, Michael J. Keough? (Cambridge U Press, 2002) Mine has suffered file corruption and I am far away from any library.

Thanks, Stefan.

* Peace Nobel Lecture 2005 - Mohamed ElBaradei: <http://nobelprize.org/peace/laureates/2005/elbaradei-lecture.html> 'Imagine that such a world is within our grasp.'

stefan.klose@uni-ulm.de

Formamide and Acrylamide Disposal

Hello, EvoDir community,

Our laboratory is currently developing protocols for the use of two chemicals involved in capillary DNA fragment analysis: formamide and acrylamide-based polymer solutions (namely ABI POP-4).

I am hoping to find out how labs generally treat this waste. Do you collect it and manage it as hazardous waste? Dispose of it in the trash? Have other collection or abatement protocols?

As with the recent ethidium bromide postings, the MSDS forms for acrylamide polymers and formamide are not detailed with regard to the disposal of these products.

Thanks in advance for your comments. I will post a summary of responses in about a week.

Cheers, Jenn

Jennifer DeWoody, Biologist USDA Forest Service, NFGEL 2480 Carson Road, Placerville, CA 95667 530-295-3028 (voice), 530-622-2633 (fax) jdedwoody@fs.fed.us

jdewoody@fs.fed.us

Formamide and Acrylamide Responses

Hello again, EvolDir

Thank you to everyone who responded to my inquiry about disposing of formamide and acrylamide waste. Below is my initial posting, followed by the complete responses. In general, most labs treat this waste as hazardous and have it collected with ethidium bromide waste and the like. An excellent source of guidelines for the disposal of lab chemicals down the drain is: <http://www.ehs.berkeley.edu/pubs/guidelines/draindisppls.html#appendices> Better safe than sorry, our lab will likely collect the waste for disposal by the experts.

Cheers, Jenn

—

Hello, EvolDir community,

Our laboratory is currently developing protocols for the use of two chemicals involved in capillary DNA fragment analysis: formamide and acrylamide-based polymer solutions (namely ABI POP-4).

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Cheers, Jenn

— At our lab we have decided to treat POP4-waste as acrylamide-waste since we have not been able to obtain a relevant datasheet from Applied Biosystems and don't want to harm people or the environment. In Eemark this involves collection and managing as hazardous

waste.

— I run a sequencing service at Edinburgh University and we put the Hi-Di formamide and Pop-7 waste in our yellow bin bags (for incineration I believe) along with the ethidium agarose gel waste. We recently had a health and safety visit and when they asked why I wasn't using the orange bags (cheaper option for general waste) I told them that I put the ethidium and formamide waste in there and they seem satisfied with that.

— I have dealt with formamide and acrylamide disposal. A waste stream to the county hazardous waste/special waste facility will likely be your best course of action, but they do charge (overall, reasonably priced). I'm not sure what is available in Placerville, but there should be a facility that handles disposal of household hazardous materials that might be able to handle what you are generating.

— We just throw our formamide and polymer in the trash - would be happy to know a better way if it is recommended.

— This might be useful: <http://www.ehs.berkeley.edu/pubs/guidelines/draindisppls.html#appendices> It comes from our EH&S website <http://www.ehs.berkeley.edu/>, which has a lot of such information, although it's often difficult to access.

— The criteria for a hazmat include toxicity, pH, flammability, and corrosivity. One UKy medschl lab handles the polymerized acrylamide (APS+ temed + acrylamide + urea + formamide) as trash, whereas the unpolymerized acrylamide is hazardous waste. A UKy bio lab handles all acrylamide as hazardous waste.

Liquids can be dumped down the drain if the pH is between ca. 5 and 10; otherwise, the liquid is considered a hazardous waste, such as NaOH to clean the acrylamide plates. Sometimes one chemical neutralizes another so the resulting mixture can be dumped down the drain. For example, Na₂CO₃ (30 gm/L) and 10% (v/v) glacial acetic acid have a pH of 7.

— You'll use around 100ul POP4 per run with a 16 capillary array. The spent polymer is ejected in c.15ml water and we dispose of this down the sink (I generally change buffers etc after 6 plates). We treat samples in HIDi as toxic and use a specialised contractor for disposal. Hope this helps you.

— i'm very interested in finding out what you have heard... we tend to chuck our formamide-containing plates in the trash and polymer/liquid wastes (buffer and rinse waters) down the sink... but i doubt it's

the right thing to do. but i also don't foresee getting our post-docs and grad students to pipette out old formamide into a waste jar.

Jennifer DeWoody, Biologist USDA Forest Service, NFGEL 2480 Carson Road, Placerville, CA 95667 530-295-3028 (voice), 530-622-2633 (fax) <http://www.fs.fed.us/psw/programs/nfgel/> jdewoody@fs.fed.us

jdewoody@fs.fed.us

Gatersleben Germany GeneFlow

Hi,

I have a six month internship position from the "The International Association for the Exchange of Students for Technical Experience"

<http://www.iaeste.org/network/index.html> The position will begin in April/May 2006, and will involve both flow cytometric analyses of apomictic (asexual reproduction through seed) seed production, and molecular genetic analyses (microsatellite) of plants in the North American genus *Boechera* (wild relative of *Arabidopsis*). I am looking for someone who has basic molecular biology skills who also likes to work with computers, since many of our analyses are automated. Knowledge of German would be helpful, but is not required.

The candidate must be registered at a university, but you should also contact your local IAESTE office for more details on any restrictions (see above link).

The IPK is a large and well-endowed research center located about 2 hours southwest of Berlin, in the foothills of the beautiful Harz Mountains.

Please don't hesitate to contact me if you have any questions, or would like to apply.

Best wishes, Tim

Dr. Tim Sharbel Apomixis Research Group Dept. of Cytogenetics Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstraße 3, D-06466 Gatersleben Germany Email: sharbel@ipk-gatersleben.de

Apomixis Group Webpage <http://www.ipk-gatersleben.de/en/02/04/05/index.html> IPK Webpage www.ipk-gatersleben.de tel: +049 (0)39482 5608 fax: +049 (0)39482 5137

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

GeneMapper alternative

Hi all

Does anyone know of a freeware alternative to GeneMapper? (Preferably windows but we could use linux)

We would like to open and examine microsatellite fragments that have been run on an ABI and saved under GeneMapper (.fsa).

We have insufficient RAM to install GeneMapper on our lab computer, we do have access to GeneScan but the .fsa files will not open under this system (could GeneMapper files be saved as Genescan files?).

Any suggestions would be gratefully received Thank you

Tee taylorT@ukzn.ac.za

Tiawanna Taylor <TaylorT@ukzn.ac.za>

GeneMapper alternatives answers

Hi All

Thank you all for your replies about alternatives to GeneMapper

STRand seems to come up a lot as a useful alternative (others are mentioned as well) and methods or converting GeneMapper to GeneScan files are also provided.

A full set of answers are provided below

Thanks all Tee

ANSWERS BELOW *****

Check out STRand <http://www.vgl.ucdavis.edu/-STRand/>

-jennifer

The veterinary genetics lab at UC Davis has produced an open source software called STRand that allows you to analyze .fsa files. You can download it for free at their web site, <http://www.vgl.ucdavis.edu/-informatics/STRand/>

I've been using it and find it very convenient and easy to use. The set-up is a little non-intuitive, but their support staff is very helpful if you have any questions.

Best wishes, Renee Duckworth

Here are some alternatives that I am aware of (although I haven't tried them):

STRand <http://www.vgl.ucdavis.edu/informatics/-STRand/>

GeneMarker <http://www.softgenetics.com/gm/-index.htm>

Genographer <http://hordeum.oscs.montana.edu/genographer> (website appears to be down)

Best of luck! Todd

you've probably already got this from someone else but just in case... This program converts the genescan files to genotyper format in one very easy step.

<http://dna.biotech.wisc.edu/ABRF/>

Cheers Desiree

Yes, you can get a little program (i've saved it as "file(s)_to_gs" but i'm not sure what i found it as) that does nothing other than to change your genemapper files into files that genescan can read. after you've analyzed the files in genescan, you can analyze them without genemapper by using a program akin to genographer, which creates virtual gels from your genescan analyzed fsa files. You can score the gels by hand, or I believe you can also get a semi-automated analysis by specifying which band lengths to include in the gel. Less automated than GeneMapper, so not as good for huge numbers of samples maybe, but it works. Hope this helps, Beth

If you can find a copies of the programs genescan and genotyper, you can basically handle your .fsa files in the same manner. These are not free, and ABI probably does not sell them anymore, however, if you can get your hands on the programs they are just as good as genemapper (less automated, which may be better in many cases) and you will not run into problems with insufficient RAM.

Tom

we are using GeneMarker since a couple of weeks. It isn't free either and you'll have to ask for the price (<http://www.softgenetics.com/gm/index.htm>), but it turned out to be very usefull. It is working on Windows platforms. I am doing fragment analysis and the program can easily analyse .fsa files, including size

standard application and automatised allele calls. It is kind of a combination of GeneScan and GeneMapper. I

am not aware of a free software that has similar power.

Good luck with the analysis,

Tobias

.fsa files are general files that are generated by genescan. They can be read by genemapper and analysed, but also by genotyper (the older version of genemapper). There will be more versions from genotyper around (although it is not freeware, but look at the ABI site, they might some free versions).

Good luck!

Kees van Oers

Try Genemarker www.softgenetics.com <<http://www.softgenetics.com/>> - there is a demo copy that you can download and use for free (but you can't properly save your data files - though I managed to get round this by copying the text files into excel) and you can ask for a free 30-day trial version too.

We find it easier to use than genemapper when trying to develop and score new markers,

Best wishes, Sara

we used "strand". It is not perfect but it works. There are other programmes I did not try. good luck Anne

Yes! I use the excellent and freely available programme STRand <http://www.vgl.ucdavis.edu/informatics/-STRand/> Dr S Rendell

If you want to analyse samples in Genescan and not Genemapper don't analyse your data in Genemapper at all. Take raw data from ABI and analyse it in Genescan.

After analysing in Genscan you can do the allele scoring in the same program (msat electropherograms are relatively simple). If you have a lot of samples/loci you could try using Genographer. Genographer is free AFLP software available on line: <http://hordeum.oscs.montana.edu/genographer/>

Good luck, Grazyna

— / —

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>

Genotyper Installation

I am trying to install Genotyper on a new PC computer with Windows XP Home edition and 1GB of memory. When I try to open the program I receive an error message “. ”Not enough memory“ Has anyone had a similar experience and found out how to overcome this problem?

Richard Dodd

dodd <dodd@nature.berkeley.edu>

Genotyper answer

Thank you all for your suggestions regarding installation of Genotyper. I will not copy all comments into this message. Apparently Genotyper was not designed to run on machines with a lot of memory. I tried the following suggestion from Melanie - because it was counter-intuitive to the error message and I had explored the more intuitive approaches. It worked first time on my desktop XP Professional 1 GB RAM and on my laptop XP Home 1GB RAM.

Richard, here is the fix that worked for me. It was sent to me from ABI tech support.

-Melanie Paquin

Hello,

First, the Genotyper software was never tested on the Windows XP operating system, so you may run into problems trying to run the software. The error that you are getting is similar to an error that some customers received on the Windows 2000 operating system. I know that the error states that there is Insufficient memory, but the fix is actually to reduce the amount of virtual memory on your computer. Here is something that you can try:

Go to Control Panel > System > Advanced tab > in the Performance Options pane, select Settings > select the Advanced tab > in the Virtual Memory pane, select “Change...” > Select the customize radio button > set initial size to 500 > set maximum size to 700. If this does not work, select the “no paging file” radio button.

I hope this helps, and please let me know if you have any questions.

dodd@nature.berkeley.edu

HCA and evolution

Hi... my name is Felix Martinez and Im from Colombia. I want to know if there are evolutionary studies using HCA

Felix Martinez <felucho666@yahoo.com.mx>

Haplotype diversity

Other:

I would like to hear your opinion concerning the estimation of haplotype diversity for nuclear sequences. When there are sequences with more than one heterozygous position, one cannot tell which are the two alleles (there will have to be ambiguous positions). In this case, how can we calculate haplotype diversities? Is it possible or not?

Another issue is how to build a files to infer phylogenetic relationships. Shall we include two sequences per individual (two identical sequences in the case of homozygous, two sequences with one different position in the case of one heterozygous position and two identical sequences with ambiguity codes in the case of individuals with more that one heterozygous position)?

Thanks

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

Haplotype diversity answers

Other:Haplotype diversity- answers

Dear all,

I have received some emails regarding my question on haplotype diversity estimation. As a lot o people asked me about the answers I am giving them below.

Question:

I would like to hear your opinion concerning the estimation of haplotype diversity for nuclear sequences. When there are sequences with more than one heterozygous position, one cannot tell which are the two alleles (there will have to be ambiguous positions). In this case, how can we calculate haplotype diversities? Is it possible or not?

Another issue is how to build a files to infer phylogenetic relationships. Shall we include two sequences per individual (two identical sequences in the case of homozygous, two sequences with one different position in the case of one heterozygous position and two identical sequences with ambiguity codes in the case of individuals with more that one heterozygous position)?

Answers: 1)

dear vera

you have to distinguish between phylogenetics and population genetics. The first deals with fixed substitutions between species and the latter with intra-species diversity. I would suggest to drop polymorphic positions when doing phylogenetic analysis.

There are methods to infer haplotypes from sequence diversity (look for Stephens et al. PHASE). Alternatively you might want to resolve the haplotypes by ARMS PCR, cloning or something of the sort, which would be more precise.

Hope I was helpful

santos

Santos Alonso Dep. Genetics, Phys. Anthropology and Anim. Physiology Fac Science and Technology University of the Basque Country

tel +34-946013568 fax +34-946013500 email santos.alonso@ehu.es

2) Dear Vera,

You may circumvent this problem by a) cloning your PCR-products or b) calculate the two most likely haplotypes from your genotype (see e.g. Excoffier and Slatkin 1995 on this topic).

We would otherwise like to have a copy or your incoming answers on this topic.

Kind regards,

PhD Håvard Kauserud

3)

Vera,

Have you considered using algorithms to phase hap-

lotypes from nuclear sequence data that has multiple polymorphisms (such as the program PHASE (<http://www.stat.washington.edu/stephens/software.html>)?)

Dave

4)

You can first obtain estimates of haplotype frequencies by maximizing the likelihood. Then you can use those frequencies to compute your diversity score. Depending on the number of polymorphic sites in your sequence, for haplotype estimation you can use an EM algorithm (for relatively small numbers of sites), or something like the PHASE program (for larger numbers of sites). There are also other alternatives. There is a fair amount of software out there that you can use to obtain the MLE estimates of haplotype frequencies. Of course, it is all academic software, but at least it is free.

Ellen M. Wijsman COURIER DELIVERY ADDRESS ONLY: Research Professor Ellen M. Wijsman Div. of Medical Genetics and 1914 N 34th St., suite 209 Dept. Biostatistics Seattle, WA 98103 BOX 357720, University of Washington (Note: Use this address Seattle, WA 98195-7720 EXACTLY as given above, and phone: (206) 543-8987 use ONLY for courier delivery!!!) fax: (206) 616-1973 email: wijmsan@u.washington.edu web page: <http://faculty.washington.edu/wijmsan> 5)

Oi Vera,

it is a tricky thing to infer haplotype phase. One way to circumvent the estimation procedure is to clone your amplicons and sequence them separately. The Topo-TA kit is really fast. Another way is to treat your heterozygous sites as SNPs and do a phase estimation, as it is done in multi-allelic systems (SNPs, microsatellites, MHC/SI alleles, etc.). However, the problem here is that what you would consider to be SNPs are not real SNPs, because they are physically linked.

Several Bayesian, ML, and coalescent algorithms have been developed from 1990.

<http://www.stat.washington.edu/stephens/software.html> <http://www.people.fas.harvard.edu/~%7Ejunliu/Haplo/docMain.htm> <http://www.people.fas.harvard.edu/~%7Ejunliu/plem> <http://www-gene.cimr.cam.ac.uk/clayton/software> Excoffier & Slatkin 1995 MBE paper on EM (ML) estimation: http://www-math.mit.edu/~lippert/18.417/papers/SNP_Excoffier.pdf

Again, for linked polymorphic sites (pseudo-SNPs), I do not know of any algorithm. If I were you, I would contact the authors of the abovementioned programs. They may have suggestions on how to treat such data.

I am very interested in the answers that you will get.

Could you please post them on EvoDir or at least email me? Obrigado!

Cheers, sergios

6) Hi Vera

— / —

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>

distributional data). Cases where the selection regime acting on the trait of interest in the source range is well-characterized would be ideal.

Thank you.

Carol Lee Wisconsin Institute of Rapid Evolution UW-Madison

carollee@wisc.edu

Invasion papers clarification

ISSR in plants

Actually I have 2 questions: 1. if someone has written a review about the use of ISSR in plants, and if there is a tendency to choose some primers more than others, I mean if there are some repeats that are more common than others. 2. my work is about a population of *L. organoides* in my city, and i wanted to measure the diversity of that population, I wonder if I can make a good work with just one population, and do a study of fine scale, wich aspects i have to have in mind to do my work?

Adriana Suarez Biology Student Universidad Industrial de Santander UIS Bucaramanga, Colombia

Adriana Suarez <adrizua@yahoo.com>

Invasion papers

Dear Colleagues,

I am currently writing a review paper on genetic variation of invasive populations in their native (source) range. I am finding that there is a general lack of papers on the topic. I am interested in papers that focus on genetic variation of phenotypic traits that are relevant for invasive success (that affect fitness in the invaded range). I am not interested in genetic variation of putatively neutral markers, as I am focusing on cases where selection might occur.

I will deal only with systems where the particular geographic source of the invaded population is known (using molecular markers, rather than loosely inferred from

Dear Colleagues,

I apologize for resending the message below. While I am grateful for all the responses I have received, most have not been relevant, and my inbox is now full.

I am writing a review, and am interested in papers that discuss *quantitative genetic variation* of *fitness-related traits* in the *native (source) range* of invasive species.

I am NOT interested studies that examine neutral variation (microsatellites, COI sequences, etc), or study systems where the sources of invasions are not known.

So far, I have come across only three relevant papers.

Thank you very much,

Carol Lee Wisconsin Institute of Rapid Evolution UW-Madison

carollee@wisc.edu

—Original Message— From: evodir@evol.biology.mcmaster.ca [mailto:evodir@evol.biology.mcmaster.ca] Sent: December 8, 2005 1:21 AM Subject: Other: Request for papers on Invasions

Dear Colleagues,

I am currently writing a review paper on genetic variation of invasive populations in their native (source) range. I am finding that there is a general lack of papers on the topic. I am interested in papers that focus on genetic variation of phenotypic traits that are relevant for invasive success (that affect fitness in the invaded range). I am not interested in genetic variation of putatively neutral markers, as I am focusing on cases where selection might occur.

I will deal only with systems where the particular geographic source of the invaded population is known (using molecular markers, rather than loosely inferred from

distributional data). Cases where the selection regime acting on the trait of interest in the source range is well-characterized would be ideal.

Thank you.

Carol Lee Wisconsin Institute of Rapid Evolution UW-Madison

carollee@wisc.edu

Mercer Award Nominations

Fellow Evolutionary Ecologists:

I'm soliciting nominations for this year's George Mercer Award from the Ecological Society of America. If you've read an outstanding ecological research paper published in the past two years by a lead author 40 years of age or younger at time of publication, think about nominating it for the award (hint: If you're eligible, you could also ask someone to nominate your paper!). Note that the nomination is for a paper, not a person! NOMINATIONS SHOULD BE RECEIVED BY DECEMBER 31, 2005. Details below.

Ellen Simms

George Mercer Award

The Mercer Award is given for an outstanding ecological research paper published by a younger researcher (the lead author must be 40 years of age or younger at the time of publication). If the award is given for a paper with multiple authors, all authors will receive a plaque, and those 40 years of age or younger at the time of publication will share the monetary prize. The paper must have been published in 2004 or 2005 to be eligible for the 2005 award. Nominees may be from any country and need not be Ecological Society of America (ESA) members. Papers need not have been published in an ESA journal. Recent recipients include Jean L. Richardson, John Stachowitz, and Daniel Bolnick. NOMINATIONS SHOULD BE RECEIVED BY DECEMBER 31, 2005

Nominations should be sent to Ellen Simms, Chair, Mercer Award Subcommittee (<mailto:esimms@berkeley.edu>esimms@berkeley.edu).

esimms@berkeley.edu

Micro datasets

Dear colleagues,

I am working with some computer scientists on methods for reconstructing sibling groups from microsatellite data (without parental data). We are exploring new approaches based on combinatorial optimization. We are looking for some benchmark data sets, that is, real microsatellite data derived from plants or animals of known pedigrees (controlled crosses) to test our algorithms. Large families in particular. Please contact me if you have such data that you would be willing to share, or can suggest ones that might be available. Thank you.

Regards, Mary Ashley

– Mary V. Ashley Professor Faculty Coordinator, Ecology and Evolution University of Illinois at Chicago 845 W. Taylor St., M/C 066 Chicago, IL 60607

<http://www.uic.edu/depts/bios/ecoevo/ashley.htm>

Phone: (312) 413-9700 FAX: (312) 996-9462 E-mail: ashley@uic.edu

Mythological gene names

Dear All A colleague in the Arts faculty at Nottingham University who organizing a conference on Medea has asked me if I know of any genes (other than Medea in *Tribolium*) named after greek mythological characters, and if so what inspired the naming. I can think of relatively few: - Odysseus in fruit flies - a speciation gene - Caronte In chickens (Spanish for Charon, the ferryman of Hades), which was, I understand, directly inspired by the myths. - Argonaut - genes involved in post-transcriptional gene silencing. - Callipyge in sheep comes from Greek but isn't to do with myths I think - it just means lovely buttocks.

So the question is are there many others and does anyone know the story of how the genes got their names? All anecdotes greatly appreciated.

Yours Laurence

Laurence D. Hurst Professor of Evolutionary Genetics

University of Bath Bath, BA2 7AY, UK
 Tel: +44 (0)1225 386424 Fax:+44 (0)1225 386779
 Laurence Hurst <l.d.hurst@bath.ac.uk>

NTSYS interpretation

Dear evolutionary biologymembers, I havestudied20 populations of plant on NTSYS software version 2.02, but I have a problem in interpritation the results of2 Di-mensional analysis. Where I have twonewaxis (PC1 and PC 2) and the populations gothered in4 groupswiothin the4 quadrates between the axis, how did these groups consist andhow can I explained

thans for all

Samir PhD. student

samir abou-isba <inisba@gawab.com>

PCRMachines MJR

Some news and a question about PCR machines for the group....

Like many labs, we use MJR thermal cyclers for PCR and have been quite happy with them. Our Dyad machine has gone on the fritz and needs repair. When I called Bio-rad, which acquired MJR earlier this year, they told me that they cannot service any MJR machine because of a court order permanently enjoining them from selling or supporting MJR machines in the U.S. The order is due to successful legal action by ABI/Applera against MJR for patent infringement. Bio-rad¹s materials state that they have tried to negotiate a settlement with ABI, but ABI has shown no interest in reaching an agreement. Bio-rad says they are continuing their efforts, but there is no timetable for when service might resume on MJR cyclers in the U.S. (see www.bio-rad.com/LifeScience/pdf/letter.pdf)

This puts us and probably a growing number of U.S. labs as time passes in a difficult position, with an expensive and effectively worthless machine in our hands. Bio-rad is honoring warrantees and service contracts on MJR instruments by providing loaners of their own ³Icycler² PCR machines until the warrantee/contract

runs out. They will also provide a ³generous² trade-in on MJR machines requiring repair for those wanting to buy a new Icycler machine.

Does anyone have experience with the Icycler? I would appreciate hearing any testimonials about its performance and reliability.

Joe Thornton University of Oregon joet@uoregon.edu

Positive selection

Howdy,

I'm doing some analysis to test for positive selection in a protein-coding gene. However, I'm not sure about how to calculate the codon frequencies. Given that there are several possible alternatives (e.g. to calculate them based on nucleotide frequencies, to assume an equal frequency for each amino acid, etc.), does anyone know of a study that addressed this question, either analytically or through simulation? any thoughts would be greatly appreciated.

With best regards,

Jason S.

jas2339@yahoo.com

Problem Bremer support

I need help to calculate Bremer support and Partitioned Bremer support. I am having a lot of trouble with using the program TreeRotv2 on a Macintosh computer - the program is consistently crashing on more than one machine. Has anyone experienced similar problems with use of this program. Or alternatively does anyone know of another program which will perform the same operations, preferably on a PC. Please let me know if you can help. Cheers Claire

claire.mcclusky@deakin.edu.au

clairefi@deakin.edu.au

Rare mutation abundance

EvolDir,

I just received a query from a colleague (below). I have made some replies, but since I am not a population geneticist, I told him I would post the query to evoldir in hopes of getting comments from experts. Bottom line is that his intuition is that neutral evolution shouldn't result in so many rare mutations - even given a recent bottleneck.

The query:

As you know from the review there are at least nine exceedingly rare dominant mutations in Antioquia which has a population of 8 million people. For geographic reasons the population is considered an isolate or more accurately an admixture that was subsequently isolated. The population derives mainly from Amerind females and Spanish males based on mitochondrial and Y chromosome markers. About 400 years ago, both groups went through a severe bottleneck based on the low diversity in the markers. We could make estimates of the size of the founder population, perhaps several thousand would be a very generous estimate. After the founding there was some continued gene flow from Spanish males who continued to arrive. Families in the region typically have 10-15 children.

All the genetic isolates I am aware of have excess recessive mutations for the most part due to drift, and although many genetic isolates are well studied, I do not know of reports in which there are many dominant diseases. We are unaware of very many recessive diseases in Antioquia, but this absence of information cannot be considered data.

In particular, I'm interested in the following questions:

- (1) How can one quantify the greatest number of expected dominant mutations, assuming neutrality, and given population parameters above.
- (2) What size population under what mating circumstances would be needed to predict the occurrence of nine dominant mutations that world wide have gene frequencies on the order of one in a million?
- (3) Are there features of an admixture, in contrast to a strict genetic isolate, that might predispose to this pattern of dominant mutations?

Thanks for any thoughts. As is the fine EvolDir cus-

tom, I can make a compendium of replies if folks have interest.

Todd Oakley

Todd Oakley, Assistant Professor Ecology Evolution and Marine Biology University of California-Santa Barbara Santa Barbara, CA 93106 USA (805) 893-4715

lab: <http://www.lifesci.ucsb.edu/eemb/labs/oakley/>
 pubs: <http://www.lifesci.ucsb.edu/eemb/labs/oakley/-pubs/publist.html> oakley@lifesci.ucsb.edu

Reduced micro variance

Dear colleagues,

Reduction variance in microsatellite alleles flanking coding region may be an indicator for associated variation reduction in the coding region. Schloetterer and his colleagues developed indices (lnRV and lnRH) to compare microsatellite alleles variation between populations. These indices can hint for significant reduction in variation in one of the populations if the index exceed a certain value. However, there is no correction for multiple comparisons, except Bonfferoni correction to the P value. In case of many loci (above 50), Bonfferoni correction may create very small threshold that will mask "real" differences. I wonder if there is any program that can calculate significance of reduction in variation in microsatellite markers, taking into account multiple comparisons. I have around 150 individuals, genotyped for ~60 loci, distributed in 17 chromosomes (i.e., some are dependent). Any advice will be appreciated.

Thank you Yuval Sapir

– Yuval Sapir, PhD

Dept of Biology Indiana University Bloomington, IN 47405 USA http://www.bio.indiana.edu/~rieseberglab/yuval_sapir.html ysapir@indiana.edu

SSE election

Dear SSE Members,

This is a reminder to VOTE ONLINE for SSE officers by December 31. I am sorry to say to date we currently

have a voter “turnout” of about 6%, making us look pretty bad compared, say, to the recent voter turnout in Iraq. It is not even as good as SSE voting in the past using paper ballots. Printing and mailing paper ballots costs SSE about \$3500/year, and it would be nice if we were able to avoid that expense by using online voting; online voting also allows members with electronic only membership to vote (this was not possible with paper ballots).

Below are the instructions for voting—please do it while you’re thinking about it! Thanks very much for your participation in this important matter for the Society for the Study of Evolution.

Jessica Gurevitch
Executive Vice President

Dear Members of the Society for the Study of Evolution,

Voting for Society officers this year will be online only. To vote, go to www.evolutionsociety.org and click on member secure login. Your login ID and password are the same as those used to access the journal online, and are on your Journal mailing label. If you do not remember your userid or password, there is a place to enter your e-mail address after clicking member secure login; if your e-mail address matches the one in the database, this information will be sent to you automatically.

The deadline for voting is December 31, 2005.

Be sure to vote for TWO Council members, and of course one of each for all of the other offices.

You will notice when you go to the online secure site that a number of useful features have been added with secure access only by members: substantial publisher discounts from Oxford University Press and Sinauer Associates, both prominent publishers of books on evolutionary biology, and a membership directory for SSE.

And while you are thinking evolution thoughts, a website for the 2006 Evolution meetings at Stony Brook University is now online (although many details remain to be posted)—you might want to sneak a peek at <http://stonybrook.edu/sse2006> as you think about plans to attend what should be a very exciting meeting. And do take a look around the SSE website while you’re there—we keep adding new resources and material to the site.

If you have problems with your member ID or password, please contact Scott Starr at Allen Press, sstarr@allenpress.com. For other questions about the election, web site, etc., contact Jes-

sica Gurevitch, Executive Vice President of SSE, at jgurvtch@life.bio.sunysb.edu or Mark Jonas, the webmaster, using the link on the website.

Scott Starr <sstarrk@allenpress.com>

Scientific content in Dover Decision

Hi Brian-

As I’m sure you know, the US District Court ruled against teaching Intelligent Design yesterday. While much of the media coverage has focused on the U.S. legal principles involved, there’s a fair bit of science in the opinion (pages 64-90 of the opinion, link below). For instance, in addition to discussion about whether or not ID really is science and aspects of hypothesis testing, publication with peer review, and so on, there’s also some discussion of Type III secretion systems, exaptations, genetic recombination, and homology.

I think the science-related portions of the opinion might be of interest to members of the EvoDir list, but I’ll also understand if you’re cautious about turning the list into a discussion forum for teaching of evolution in public education.

http://www.pamd.uscourts.gov/kitzmiller/-kitzmiller_342.pdf -John

John Stinchcombe Department of Botany University of Toronto, 25 Willcocks St. Toronto, ON Canada M5S 3B2

416-946-5986

<http://www.botany.utoronto.ca/ResearchLabs/-StinchcombeLab/> John Stinchcombe
<stinchcombe@botany.utoronto.ca>

Sequencing Buffer Recipe answers

Hello:

Thank you to all the people who responded to my request for a recipe for 5X sequencing dilution buffer to use with BigDye. Most people use 400 mM Tris (pH 9.0), 10 mM MgCl₂, and apparently that’s what’s on the package insert from ABI. Storage conditions varied

from -20 to room temperature.

Some people were wondering what I meant by 1/16th reactions - we use 0.5 ul BD in 10 - 15 ul volume reactions, depending on the template concentration. The BigDye mix is 2.5X and the sequencing buffer is 5X, so the formula we use to determine how much buffer is $((\text{vol of rxn})/2.5)-0.5)/2$. We've had success with this approach for both PCR products and plasmids on our 3100 (with the ABI buffer). If anyone is interested in template amounts or other details, feel free to contact me.

Thanks and happy sequencing!

Cheers, Leslie Turner

Leslie Turner Hoekstra Lab Ecology, Behavior, and Evolution Division of Biological Sciences University of California, San Diego 9500 Gilman Drive, MC 0116 La Jolla, CA 92093-0116 (858) 822-0170 lturner@biomail.ucsd.edu

I thought it might be helpful to pass on this convenient protocol for making up sequencing buffer, courtesy of Brian Caudle. Again, this was the most commonly suggested recipe. I've copied the recipes that differed from this one below.

Cheers, Leslie Turner

5X Sequencing Buffer: 400 mM Tris HCl (pH 9.0) 10 mM MgCl₂

For a 50 ml solution of 5X buffer: 10 ml 2M Tris HCl 500 ul 1M MgCl₂ 39.5 ml ddH₂O

Filter using a 0.2 um filter. (I use syringe filters, that way when I am done mixing the solution, I can filter and aliquot in the same action)

Alternatively, if you don't have these particular concentrations of solutions, here is another mixture:

For a 50 ml solution of 5X buffer (alt): 20 ml 1 M Tris HCl 20 mL 25 mM MgCl₂ 10 ml ddH₂O

I hope this helps you out, and good luck.

Brian Caudle Cannatella Lab Manager

Information courtesy of the Cannatella Lab PI: Dr. David Cannatella University of Texas, at Austin Department of Biological Sciences Section of Integrative Biology Austin, Tx 78712

Here is the dilution buffer recipe I got from a sequencing center manager several years ago, and it has worked beautifully. I also find it works well with ET chemistry as well as BigDye. My only caveat is that I have not used it with the more recent BigDye chemistry modifi-

cations but I suspect that won't make any difference.

5 mM MgCl₂ (5 uL of 1M MgCl₂ from Sigma per 1 mL buffer)

0.2 M Tris HCl (pH 9.0) (200 uL of 1M stock per 1 mL buffer)

Add deionized water to 1 mL volume.

I was advised to purchase MgCl₂ as a 1M solution, as powdered MgCl₂ is hygroscopic and the "true" molecular weight can deviate from the calculated value. Also, the little tubes of MgCl₂ that come with PCR buffers can vary considerably in their true concentration. To avoid potential problems, I have followed this advice.

Cheers,

David Remington

Are you familiar with HalfBD? I think it's what you're asking for and, though not free, is far cheaper than the ABI alternative. It works as advertised in our hands. Click

<http://www.genetix.com/cons%5Freag/-prod%5Fguide/dna/half.asp> Cheers,

Dan

Daniel M. Weinreich

We always run out of Big Dye buffer, so we use the following recipe:

200 (or 100) mM Tris

5mM MgCl₂

Add 20 (or 10) ml 1M Tris and .5ml 1M MgCl₂ to sterile water for a final

volume of 100 mls.

Hope this helps.

Kevin Feldheim

Here is our buffer and seq reaction recipes (I also include citation

of our paper on High Volume DNA Barcoding for reference):

We use Sigma Trehalose T-9531 in our sequencing reactions and make

our own 5X buffer as well (400 mM Tris-HCL pH 9.0, 10 mM MgCl₂) this

combination is cited in our paper.

We retrieved 5X buffer recipe from the Internet a while ago (you might want to search for original citation for a buffer).

Plates (mixes) could be frozen and used later on!

I make 1M Tris-HCl pH 9.0 by weight (I don't use pH-meter for it):

100 ml (0.22 um filtered)

Trizma-HCl 1.52 g (Sigma T-5941)

Trizma Base 10.94 g (Sigma T-6066)

5X Seq Buffer

1M Tris-HCl pH 9.0 4 ml

1M MgCl2 100 ul

H2O 5.9 ml

(1 sample) (96-well plate)

primer (10 pmol) 1 104

5X buffer 1.875 195

BigDye 0.25 26

ddH2O 0.875 91

10% trehalose 5 520

Total 9 936

Reference:

Hajibabaei M, deWaard JR, Ivanova NV, Ratnasingham S, Dooh RT, Kirk

SL, Mackie PM and PDN Hebert (2005) Critical factors for assembling a

high volume of DNA barcodes. Phil. Trans. R. Soc. B 360 (1462), 1959 -

1967.

Let me know if you have any questions.

Good luck!

Nataly

— / —

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>

Dear colleagues

I have a mathematical idea which I would like to apply to a gene nucleotide sequence:

1. Which is the shortest complete gene sequence to be found with and without mutations (not necessarily human)?

2. Was the p53 human wildtype sequence available on databases derived from a single person?

Thank you for any help,

Uri Moran, MSc student Department of Zoology University of Tel Aviv

moranuri@post.tau.ac.il

Software Clann3 0 2

Dear all,

I wish to announce the release of Clann version 3.0.2

For those that may not know Clann:

Clann (the Irish word for “family”), is a free software program designed and written by Chris Creevey at the Bioinformatics and Pharmacogenomics Laboratory at NUI Maynooth. The purpose of the program is to implement methods of determining the optimal phylogenetic supertree or consensus tree, given a set of input source trees.

This latest update addresses some dataset-specific issues reported and implements some changes to the SPR method for the DFIT criterion, this has had the effect of increasing the speed of the SPR searches.

This version is available at:

<http://bioinf.nuim.ie/software/clann> Regards,

Chris.

– Dr. Chris Creevey Bork Group, EMBL Heidelberg, Meyerhofstrasse 1, 69117 Heidelberg, Germany

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chris.creevey@gmail.com

SOFTWARE: Beta release of Geneious software for speeding up molecular research

Today we have released a new software system (beta) that speeds up research in molecular biology and genomics. Our guiding ambitions have been to speed up research, make it possible for scientists using the public biological databases such as NCBI to collaborate much more successfully and keep abreast of new relevant information. Geneious makes it possible to rapidly search and filter DNA, protein and publication data. Once the data has been downloaded it can be stored, visualized and analyzed.

Scientists can download Geneious without charge at www.geneious.com. Key features and benefits:

Geneious 0.9b provides an intuitive user interface for searching, sorting and storing biomolecular sequence data and scientific publications, including the following features:

- * A local database to store sequences and publications
- * Storage of abstracts and bibliographic information
- * Direct links to Google scholar
- * Storage of sequence data, including user-defined meta-information
- * Rapid sequence similarity searching within your local database
- * Direct access to NCBI, Uniprot databases
- * A unique ability to refine and filter information on the fly as it downloads
- * Ability to automate searches so that the data relevant to your research is constantly kept up-to-date
- * A graphical viewer of sequence annotations such as genes, motifs and primer positions
- * A multiple alignment viewer
- * Very simple user-friendly interface
- * Easy and fast to download, at no cost

Geneious will grow as we continue to extend its functionality through open-source upgrades and new features. We will be especially focused on developing analysis tools for sequence alignment and phylogenetics. We welcome any and all feedback on current and future features in the product.

Biomatters plans to release version 1.0 of Geneious in early 2006.

Inquiries Dr Alexei Drummond

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Biomatters Ltd

Biomatters combines statistical, biological and computational knowledge with user-friendly front-ends to create research platforms that greatly speed up the processes of scientific and medical discovery. In our first two years Biomatters has launched two software packages. For more information visit us at [http:// www.biomatters.com/](http://www.biomatters.com/) – Dr Alexei Drummond Lecturer in Bioinformatics, Department of Computer Science The University of Auckland Private Bag 92019, Auckland, New Zealand Ph: +64 9 3737599 ext 88298 Email: alexei@cs.auckland.ac.nz WWW: <http://www.cs.auckland.ac.nz/~alexei/> alexei@cs.auckland.ac.nz

Software SubstitutionalAsymmetry

Under the neutral model of protein evolution, a comparison of sequences from two species should show equal numbers of substitutions in each direction for each pair of amino acids. For example, when comparing the mesophile (moderate habitat temperature) *Bacillus subtilis* with the thermophile (high habitat temperature) *Geobacillus stearothermophilus*, you would expect the number of sites with lysine in *B. subtilis* and arginine in *G. stearothermophilus* to equal the number of sites with arginine in *B. subtilis* and lysine in *G. stearothermophilus*. In fact, a data set of 229 proteins showed 412 aligned sites with the first pattern and only 157 sites with the second pattern. This “substitutional asymmetry” suggests that arginine is preferred by natural selection over lysine in *G. stearothermophilus* (McDonald et al. 1999, *Mol. Biol. Evol.* 16: 1785-1790).

I am now making available three programs (AmbiguityRemover, AsymmetryCounter and AsymmetryScaler) that will enable users to analyze sets of aligned protein sequences for substitutional asymmetry. The programs are available for Windows or Mac OS X, and the Pascal source code is available and could easily be compiled for other operating systems.

The programs, their source code, and an example data set, are available from <http://udel.edu/~mcdonald/asymmetry.html> . John H. McDonald Department of Biological Sciences University of Delaware Newark, Delaware 19716 USA mcdonald@udel.edu
mcdonald@UDel.Edu

<http://www.helsinki.fi/science/metapop/english/-People/Chris.htm>

Christopher West Wheat <cww10@psu.edu>

Unigene maker

Hello Evoldir,

I'm looking for a stand alone executable that can take a multisequence fasta file and return a subset of these in a multisequence fasta file which are the unigenes, based on a given similarity threshold.

I would like this to be a very quick program for a windows platform.

thanks for any help,

Chris

Chris Wheat

On World Tour

Were chained to the world and we all gotta pull

Tom Waits

Used 230V Thermocyclers

Greetings,

Our lab is in the process of organizing a genetics workshop at the University of Asmara in Eritrea. We would like to provide our colleagues there with the basic equipment necessary for a molecular genetics laboratory. However, we need equipment that utilizes 230v 50H electricity. We are wondering if anyone would be willing to sell (or donate!) to us either a functional thermocycler or microcentrifuge which they are no longer using. The only specification that we require is the microcentrifuge must reach a speed of 15,000g. Alternatively, if anyone has a source through which we can find quality used equipment that runs on 230v, please inform us.

Thank you very much for your help.

Cheers,

Rebecca Gray Department of Anthropology University of Florida

atlasrrg@hotmail.com

PostDocs

CNRS Gif-sur-Yvette TranscriptomeAnalysis	68	UDurham SealPopGenet	72
CornellU CompPopGenetics	68	UGuelph TheoreticalEcol	73
DeakinU 2 BiodiversityPhylogenetics	68	UMiami MarineMicrobes	73
NeustadtGermany AnimalGenetics	69	USouthernCalifornia QuantGenet	73
Orsay Bioinformatics	69	UToronto EvolGen	74
UArizona BeetlePhylogeny	70	UTurku VolePop	74
UBologna EstuarineSpeciesPopGenet	70	UtahStateU EvolGenomicsProteomics	74
UCDavis PopBiol	71	WilliamsCollege Bioinformatics	75
UCRiverside TritrophicInteractions	71		

Linda.Sperling@cgm.cnrs-gif.fr

CNRS Gif-sur-Yvette Transcriptome Analysis

ANR Project DUPLIGEN 30 month contract (can be extended to 3 years) starting as early as possible in 2006 Centre de Genetique Moleculaire, CNRS, 91198 Gif-sur-Yvette France <http://www.cgm.cnrs-gif.fr/> We have a post-doctoral position available for analysis of the Paramecium transcriptome. The monthly salary is approximately 1700 Euros.

Analysis of the newly sequenced Paramecium tetraurelia genome revealed a recent Whole Genome Duplication (WGD). Among the 40,000 annotated genes, more than 12,000 pairs of paralogs from the WGD are still present in the genome, accounting for 60% of present day Paramecium genes. Our research project is to take advantage of this exceptional situation to study the fate of genes following a WGD: gene conversion, neo- or sub-functionalisation, formation of pseudogenes, gene loss, etc. An important part of the project is an analysis of the Paramecium transcriptome, with particular attention to the expression of the pairs of paralogous genes.

We are looking for a post-doctoral candidate interested in the problem of genome evolution and with good experience in bioinformatics, in particular as applied to the analysis of DNA microarrays. The post-doc will help design oligonucleotide microarrays for optimal discrimination of the pairs of paralogous genes and conduct the statistical analysis of hybridizations with cDNAs from various cellular states, with the objective of describing the evolution of different categories of duplicated genes.

The post-doc will be financed through a contract from the Agence National de la Recherche awarded to a network including Jean Cohen and Linda Sperling at the CNRS in Gif-sur-Yvette, Eric Meyer and Mireille Betermier at the Ecole Normale Superieure, Paris and Vincent Daubin and Laurent Duret at the Pole Bioinformatique Lyonnais, Universite Lyon I.

To apply for the position, please send a CV and the names of two people familiar with your work that we can contact for letters of support.

Please send enquiries and applications to the project co-ordinator:

Jean Cohen Centre de Genetique Moleculaire CNRS Avenue de la Terrasse 91198 Gif-sur-Yvette cedex France Telephone +33 1 69 82 43 73 cohen@cgm.cnrs-gif.fr

CornellU CompPopGenetics

Theoretical / Computational Population Genetics Post-doctoral position Cornell University

An NSF funded postdoctoral research position is available in Carlos D. Bustamante's lab at Cornell. The lab focuses on statistical inference in population genetics and molecular evolution with emphasis on developing novel methods for detecting evidence of natural selection from comparative sequence data. Successful applicants will have expertise in one of the following areas: theoretical population genetics, comparative genomics and bioinformatics, computational statistics, and/or biophysics. For more details on current research visit http://www.bscb.cornell.edu/-Homepages/Carlos_Bustamante/.

Applications will be reviewed as they are received. If interested in applying, please send a current cv, statement of research interest, and the contact information of three references to cdb28@cornell.edu. Your cv and statement must be in PDF format and the email subject should read "Post-Doctoral Position Application ? <LAST NAME>, <FIRST NAME>?". Please include your contact details and those of your references in the email.

Carlos D. Bustamante Assistant Professor, Biological Statistics and Computational Biology 101A Biotechnology Building Ithaca, NY 14853 (607) 255-1640

Carlos Bustamante <cdb28@cornell.edu>

DeakinU 2 BiodiversityPhylogenetics

Two Postdoctoral Positions in Molecular Ecology and Biodiversity/Phylogenetics:

(1) Research Fellow (Position - 6200 / 351) 2 years

We are looking for a highly motivated and well-qualified person to undertake research in the recently established Bioscience North Australia (BNA), a new molecular facility housed at the university. BNA will undertake col-

laborative research in broad areas of importance to the region including molecular ecology, wildlife ecology and conservation, microbial ecology and biodiversity. The successful applicant will have a role in managing the research of BNA through pilot studies, collaborative large projects, and mentoring new researchers and students.

The successful applicant will be expected to take a leading role in managing the BNA laboratory, supervise use of an ABI 3130XL genetic analyzer for DNA sequencing and fragment mapping, assist in the development of collaborative research in areas prioritized by the BNA Leader and the BNA Advisory Group.

Go to <http://www.cdu.edu.au/staffservices/-vacancies.html#darwin> or contact Associate Professor Karen Gibb (karen.gibb@cdu.edu.au) for further information

(2) Research Fellow (Position - 6199 / 352) 3 years

We are looking for a highly motivated and well qualified person to undertake research in molecular phylogenetics and phylogeography. This person will work within the recently established Bioscience North Australia, a new molecular facility housed at the university. The successful applicant will be expected to take a leading role in developing a strong biodiversity-related program of research utilising molecular genetic information, to undertake collaborative research and support Professor Austin's research funded by the Australian Research Council, AusAID and Land & Water Australia.

Go to <http://www.cdu.edu.au/staffservices/-vacancies.html#darwin> or contact Professor Chris Austin (chris.austin@cdu.edu.au) for further information.

Mark Schultz <mbsc@deakin.edu.au>

NeustadtGermany AnimalGenetics

“Quantitative- and molecular genetic characterization and evaluation of animal genetic resources”

Two year post doc position at the Institute of Animal Breeding, Department of Animal Breeding and Genetic Resources

Genetic diversity in farm animal species is the basic requirement in animal breeding to meet future breeding goals, but has been lost in the past at an increasing rate. Improvement of our insight into mechanisms underlying genetic diversity will assist in the reconstruction

of domestication events, determination of genetic relationships between populations, assessment of genetic variation within populations, development of a strategy to manage and conserve genetic diversity, and may indicate possible consequences of intensive selection in a decreasing number of populations and lines used in farm animal species. The research is aimed at the development and implementation of sophisticated quantitative genetic methods using molecular information in this field. In our on-going collaborative research activities we have assessed a wide ranged gene pool in the chicken by typing more than 70 breeds at microsatellite loci from all over the world. In addition, molecular polymorphism in mitochondrial DNA as well as in candidate genes are currently under study. This collection in chickens provides an excellent model for the validation of molecular tools as an essential source of information to assess genetic diversity in farm animal species. The successful applicant is expected to join this international collaboration and will be involved in the analysis of the genetic structure of a given gene pool, assignment of individuals into classes or clusters, detection of selection effects by comparing highly selected populations and unselected ones, and possible introgression of genome fractions from various sources into modern breeding populations. To meet the requirements of potential users, algorithms and methods established during the project lifetime will be implemented into databases which are under development at the institute. The project will run over a period of 24 months.

Deadline for submission of application is Dec. 6, 2005. The position is available as of January 1st 2006, but later starting dates are negotiable.

further information: steffen.weigend@fal.de

– Eildert Groeneveld

Institute for Animal Breeding Mariensee 31535 Neustadt Germany Tel : (+49)(0)5034 871155 Fax : (+49)(0)5034 871239 e-mail: eildert.groeneveld@fal.de <http://vce.tzv.fal.de/index.pl> <http://www.tzv.fal.de/~eg/>

Orsay Bioinformatics

BIOINFORMATICS - POSTDOCTORAL POSITION IN ORSAY (FRANCE)

A postdoctoral contract founded by the French “Na-

tional Research Agency ANR” is available from January 2006 to develop a research project supervised by David Moreira, in the “Microbial diversity and evolution” team in the University of Paris-Sud at Orsay (<http://www.esu.u-psud.fr/microbiologie/>), which is located 25 km south from Paris, 30 min by direct train.

The project concerns the phylogenomic analysis of a large number of proteins involved in the construction of several eukaryotic multi-molecular complexes (centrosomes, telomeres, splicing complex, etc), which cannot be found in prokaryotes as complex structures, even if the homologous proteins exist. The aim will be to get insight into the origin and evolution of the different proteins. The comparison of the genomic context may help to discover new proteins involved in these multi-molecular complexes. The project envisages the construction of a data base containing sequence, genomic, and phylogenetic information.

The contract can be renewed up to three years. The salary will be of ~1800 euros (including medical assistance).

We are seeking motivate candidates with good experience in bioinformatics, especially in sequence data base construction and management and phylogenetic and genomic analysis. Knowledge of current programming languages will be necessary.

Interested candidates can send a CV and the names of scientists that we can ask for letters of support to:

David MOREIRA

Unité d'Ecologie, Systématique et Evolution. UMR CNRS 8079. Université Paris-Sud. Bâtiment 360. 91405 Orsay CEDEX. FRANCE

Tel: 33 1 69 15 76 08 Fax: 33 1 69 15 46 97 e-mail: david.moreira@ese.u-psud.fr <http://www.esu.u-psud.fr/microbiologie/> David Moreira <david.moreira@ese.u-psud.fr>

UArizona BeetlePhylogeny

Postdoctoral Researcher, Phylogeny of Beetles, University of Arizona

A Research Associate/Postdoctoral in Entomology position is available beginning 15 January 2006, for a three-year period in David Maddison's laboratory to participate in unraveling the phylogeny of beetles

through the Assembling the Beetle Tree of Life (BTOL) effort. The position will mainly entail gathering and analyzing molecular sequence data, but the postdoc will also help plan the project and produce papers with PIs at other institutions (Farrell at Harvard, Whiting at BYU).

The postdoc will be primarily responsible for obtaining sequences of several genes across a large sample of beetles, and for the analysis of these data. The postdoc will also participate in the design (through testing and suggestions) of an automated DNA sequence workflow solution currently under development, various other tools built into the Mesquite environment for data analysis, and the beetle pages of the Tree of Life Web Project.

Minimum Qualifications: * Ph.D. in a biological science. * Experience with research in molecular systematics, including phylogenetic analyses of DNA sequences.

Preferred Qualifications * Experience with research on insects. * Experience with computer tools used in systematics. * Proven publication record.

More administrative details are provided on the University of Arizona Human Resources web site, <https://www.uacareertrack.com/> (search for job number 33882). [Please note that this website was not designed to be compatible with some browsers.]

Please provide the names, email addresses and phone numbers of three references in your materials to David (contact information below). In addition, please send copies of up to three relevant publications/manuscripts/works.

–

David R. Maddison Professor and Curator PHONE: (520) 621 9781 Department of Entomology FAX: (520) 621 1150 University of Arizona email: beetle@ag.arizona.edu Tucson, AZ 85721 U.S.A.

home page: <http://david.bembidion.org> Tree of Life: <http://tolweb.org> MacClade: <http://macclade.org> Mesquite: <http://mesquiteproject.org> David Maddison <beetle@ag.arizona.edu>

UBologna EstuarineSpeciesPopGenet

GRADUATE/POSTDOCTORAL RESEARCH ASSISTANT POSITION Research Centre for Environ-

mental Sciences in Ravenna University of Bologna (Italy)

We are seeking to recruit an enthusiastic and highly motivated Graduate/Postdoctoral Research assistant to work at the laboratory of Ecological and Environmental Genetics in Ravenna (University of Bologna, Italy).

Main research topics include evolutionary biology and population genetics of marine and estuarine species.

The successful applicant will be involved in an ongoing research project aiming to assess the anthropogenic impacts on genetic diversity of marine invertebrates in the North Adriatic sea. The project will investigate changes promoted by artificial structures on the genetic patterns of hard bottom benthic species and will deliver guidelines for the management of biodiversity in coastal ecosystems. A multifactorial sampling design will allow comparison of levels of genetic diversity of invertebrates between potentially impacted and control areas. A pilot study is currently in progress to identify target species and molecular markers for the monitoring program.

The position is a full time contract (net salary range 11000-15000 Euro per annum) available for one year in the first instance.

Activities will be carried on under the supervision of Dr. Massimiliano Virgilio (www.ecology.unibo.it/page/massimiliano.htm) and Prof. Marco Abbiati (www.ecology.unibo.it/page/marco.htm).

Candidates should possess a working knowledge of English, good communication, teamwork and organisational skills as well as be able to work independently.

A strong background in molecular genetics laboratory techniques is required. Main duties include: - sampling activities and management of tissues samples, - DNA extraction - PCR amplification of mitochondrial/nuclear loci - sequencing - database management - troubleshooting during laboratory analyses

Candidates should have a Master's Degree in biological science or related fields The closing date for the application is January 15th 2006. The position will be filled from February 1st, 2006.

For consideration, please email applications (including a cover letter outlining main research interests, a complete CV, a reference letter and contact info for two referees) to m.virgilio@unibo.it

Massimiliano Virgilio, PhD Laboratory of Applied Ecology Corso di Laurea in Scienze Ambientali University of Bologna Via S. Alberto 163 I-48100 - Ravenna Italy

Tel + 39 0544 937311 Fax + 39 0544 937303 Skype:

massinellospazio

m.virgilio@unibo.it

www.ecology.unibo.it/page/massimiliano.htm Massimiliano Virgilio <m.virgilio@unibo.it>

UCDavis PopBiol

POSTDOCTORAL FELLOW IN POPULATION BIOLOGY—The Center for Population Biology at U. C. Davis invites applications for a Postdoctoral Fellowship in Population Biology, broadly defined to include ecology, systematics, population genetics, and evolution. The position is for two years, subject to review after one year, and can begin as early as 1 July 2006. It has an annual salary of \$35,000 plus benefits, and \$4,000 per annum in research support. The Fellow will be a fully participating member in the Center for Population Biology, and will be expected to have an independent research program that bridges the interests of two or more CPB laboratory groups. For more information about UCD programs in population biology, see <http://www.cpb.ucdavis.edu>. Interested candidates should submit a cover letter, CV, a short (1-2 page) description of research accomplishments, and a short (1-2 page) description of proposed research indicating potential faculty mentors, and copies of two publications at <http://www2.eve.ucdavis.edu/jobs/> all as PDFs. You should also have 3 letters of reference sent by email to Stephanie Macey-Gallow (smaceygallow@ucdavis.edu); please follow instructions at the website. Application evaluation will begin on January 13, 2006. The University of California is an affirmative action/equal opportunity employer with a strong institutional commitment to the development of a climate that supports equality of opportunity and respect for differences.

gradcoordinator@ucdavis.edu

UCRiverside TritrophicInteractions

Postdoctoral Research Position in Tritrophic Interactions.

One or more postgraduate research positions are avail-

able for a highly motivated individuals to join an NSF-funded research project to study the evolution of a tritrophic interaction. The primary objective is to test the working hypothesis that the indirect effects of the glandular trichomes of *Datura wrightii* on the natural enemies of *D. wrightii*'s herbivores oppose the direct effects of the trichomes on those herbivores. These indirect effects may constrain the increase in the frequency of plants with glandular trichomes in natural populations compared to the frequency of plants with nonglandular trichomes. One project will focus upon measurements of the fitness of plants in the field in the presence and absence of herbivores and/or natural enemies. A second project will focus upon the behaviors of various natural enemy species on herbivore-damaged and undamaged plants that also differ in trichome morphology. The successful candidate(s) will participate in ongoing field and laboratory experiments and also will have the opportunity to develop related projects.

Applicants must have a PhD. degree before hiring, and research experience and knowledge in insect ecology and behavior, the design and analysis of field experiments, insect identification and a genuine interest in the evolution and maintenance of tritrophic interactions. Excellent oral and verbal communication skills are also required.

Applicants should send a curriculum vitae, relevant reprints or manuscripts in press, a description of research interests within the *Datura* system, and the names and e-mail and postal addresses of three references to:

Dr. J. Daniel Hare Department of Entomology University of California Riverside, CA 92521

On-line applications also will be accepted. For more information, send an e-mail to <mailto:daniel.hare@ucr.edu>daniel.hare@ucr.edu.

A list of previous publications and background information on *D. wrightii* can be found at <<http://www.faculty.ucr.edu/~harejd/>><http://faculty.ucr.edu/~harejd/>.

The review of applications will begin on February 1, 2006 and the position will be open until filled. The starting date is negotiable but must accommodate the needs of field-based research.

The University of California is an Affirmative Action / Equal Opportunity employer

Dr. J. Daniel Hare Professor Department of Entomology, and Graduate Program in Evolution, Ecology & Organismal Biology University of California Riverside, California 92521

Telephone: (951) 827-3858 FAX: (951) 827-3086 e-mail: daniel.hare@ucr.edu <http://www.entomology.ucr.edu/people/hare.html>

UDurham SealPopGenet

Postdoctoral Research Associate Molecular Ecology/Ancient DNA:

Population Genetics of an Extinct Southern Elephant Seal Colony in the Ross Sea, Antarctica

A 2.5 year post is available for a joint position through the University of Durham (UK) and the University of Maine (US). Most work will be undertaken at the University of Durham in the UK starting in April 2006. The study will involve the amplification of DNA from 1000-6000 year old southern elephant seal samples from the Ross Sea. Molecular methods will be used to track demographic changes in this now extinct population over time, assess evidence for selection at target loci (in the context of climate change), assess population genetic structure in comparison with extant populations, and refine estimates of the mtDNA mutation rate for this species. The successful applicant will have skills in the amplification of ancient DNA, and experience with the use of coalescent models. Applicants should also have an understanding of the estimation of mutation rate by MCMC maximum likelihood methods. Durham has excellent facilities for work in molecular ecology and ancient DNA, including 5 automated sequencers and a high specification purpose-built ancient DNA lab.

Applicants should submit a cover letter outlining qualifications, a complete CV, three letters of recommendation, and up to three reprints to:

Dr. A. Rus Hoelzel School of Biological and Biomedical Sciences South Road, University of Durham Durham, DH1 3LE, UK email: a.r.hoelzel@dur.ac.uk

Review of applications will begin immediately.

The University of Maine is an EOAA employer.

UGuelph TheoreticalEcol

Postdoctoral position in theoretical ecology University of Guelph

Applications are invited for a postdoctoral position in theoretical ecology. Possible research topics include cellular automata, spatial models, and network models with application to forest dynamics, invasive species or disease spread in natural populations. Applicants should send a letter of interest and a curriculum vitae to Madhur Anand (manand@laurentian.ca) and Chris Bauch (cbauch@uoguelph.ca). Applicants should have background relevant to the research areas.

Chris Bauch University of Guelph

Chris Bauch <chris.bauch@gmail.com>

UMiami MarineMicrobes

Postdoc:

A postdoctoral researcher is sought to work on marine microbial interactions, specifically protistan interactions with prey. A combination of traditional and functional genomic approaches will be employed. It is anticipated that the individual will contribute to the development of an EST database as well as microarrays and utilize them to address questions on the ecology and physiology of heterotrophic protists. The broader context of this work and lab group in general is to quantify carbon flow within marine microbial food webs and determine the underlying mechanisms of prey selection. These mechanisms also provide evolutionary perspective for processes within multicellular organisms. A general overview of current research activities in the group can be viewed at <http://worden.rsmas.miami.edu> <<http://worden.rsmas.miami.edu>> .

A Ph.D. with expertise in molecular biology, molecular microbial ecology/oceanography, genomics or microbiology is desired. Strong applicants with skill in one of these areas and the desire to expand their skills in the others will be considered. Funding is available for up to 2 years beginning 1 December 2005 however the successful candidate can start anytime before March 2006. Salary (including benefits) will be commensurate with educational and work experience. To apply please submit: (1) a cover letter explaining your interest in this area, relevant work experiences, and available starting date; (2) your curriculum vitae; and (3) a list of at least 3 references, including name, title, address, email, and telephone. Inquiries and submissions by email are

encouraged. Send applications to: Dr. Alexandra Worden, aworden@rsmas.miami.edu, address: Marine Biology and Fisheries, Rosenstiel School of Marine and Atmospheric Science, U. Miami, 4600 Rickenbacker Cswy, Miami, FL 33149-1098 USA, Tel: 305-421-4616, Fax: 305-421-4600

Alexandra Z. Worden Assistant Professor of Marine Biology & Fisheries Rosenstiel School of Marine & Atmospheric Science University of Miami 4600 Rickenbacker Causeway Miami, FL 33149-1098 USA

Tel: 305-421-4616 Fax: 305-421-4600 E-mail: <<mailto:aworden@rsmas.miami.edu>>
aworden@rsmas.miami.edu Webpage:
worden.rsmas.miami.edu <<http://worden.rsmas.miami.edu/>>

Alexandra Worden <aworden@rsmas.miami.edu>

USouthernCalifornia QuantGenet

A postdoctoral position is available in the laboratory of Magnus Nordborg, Molecular and Computational Biology, University of Southern California.

The position is focused on understanding the molecular genetics of natural variation for a variety of adaptive traits in *Arabidopsis thaliana* using a variety of approaches (statistical and experimental) centered around genome-wide association mapping. Candidates must have a strong background in plant molecular biology and basic familiarity with statistical and quantitative genetics. Genomic experience is a strong plus.

The position is immediately available and will remain open until filled. For consideration, please email applications (including a cover letter outlining your interests, complete CV, and contact information for three individuals willing to supply evaluations) to Magnus Nordborg (magnus@usc.edu).

Magnus Nordborg, Associate Professor Molecular & Computational Biology University of Southern California 1050 Childs Way Los Angeles, CA 90089-2910

magnus@usc.edu <http://walnut.usc.edu/> ~ magnus +1.213.821-5349

UToronto EvolGen

Postdoc: Evolutionary biology of mutation and recombination University of Toronto

I am seeking a postdoc who is interested in working on projects related to the evolutionary biology of mutation and recombination. Current work in the lab focuses on variation in these traits within species. In particular, I am interested in understanding the extent to which these traits are condition dependent. Candidates interested in working on my existing projects or on other projects related to mutation and/or recombination are encouraged to apply. The position is for one year though a second year may be possible.

The successful applicant will become a member of a large and interactive community of evolutionary biologists at the University of Toronto. The growing strength in evolutionary biology in both the Zoology and Botany departments has led to the forthcoming formation of a Department of Ecology and Evolutionary Biology. The city of Toronto is fantastically diverse and an excellent place to live.

Applicants should have a Ph.D. in evolutionary biology with a strong background in evolutionary genetics. Experience with basic molecular techniques and statistics is also an asset. Interested persons should send the following information: CV, statement of research interests, and names and contact information for three references. Applications send by email should be in .pdf format. Informal inquires are welcome. Start date is flexible. Applications will be reviewed as they are received until position is filled.

Aneil Agrawal (afagrwal@zoo.utoronto.ca) Assistant Professor & Canada Research Chair Department of Zoology University of Toronto 25 Harbord St. Toronto, ON, M5S 3G5

afagrwal@zoo.utoronto.ca afagrwal@zoo.utoronto.ca

UTurku VolePop

Postdoctoral research post in the project on

Multi-species cyclic vole populations: inter-specific competition, and prey choice and emergent impacts of multiple predators for one year (starting, for example, on 1 Feb 2006).

The project is at Dept. Biol., Univ. Turku (financed by the Academy of Finland).

The objective is to study multi-prey multiple predator interactions among voles and their avian and mammalian predators in the field. Main questions: 1) competition-induced habitat shifts of voles and predation risk, 2) competition and predation risk vs. reproductive performance of voles, 3) prey selection of predators in multi-predator situations, 4) risk by avian predators vs. hunting behaviour of small mustelid predators, 5) impacts of multiple predators on prey populations. (see, for example, Korpimäki et al. 2005, Proc. R. Soc. Lond. B 272: 193-202, and J. Anim. Ecol. 74: 1150-1159).

Details on the research environment, research projects and their productivity can be found in <http://users.utu.fi/ekorpi/> http://www.sci.utu.fi/biologia/ekologia/korpimaki_eng.htm The postdoctoral researcher will take part in the planning and execution of the project, in analysing the existing long-term observational and experimental data sets, in writing papers, and in supervision of the Ph.D. students (Salary approx. EUR 2300 per month)

Queries and applications (CV, list of publications, a summary of research interests and motivation for this project) to prof. Erkki Korpimäki, tel. +358-2-3335699, e-mail ekorpi@utu.fi, fax +358-2-3336550. Deadline for applications is 2nd Jan 2006. Address: Section of Ecology, Department of Biology, University of Turku, FIN-20014 Turku, Finland.

Erkki Korpimäki <ekorpi@utu.fi>

UtahStateU EvolGenomicsProteomics

POSTDOC: ECOLOGICAL GENOMICS/PROTEOMICS

The Center for Integrated BioSystems and The College of Natural Resources at Utah State University are seeking a postdoctoral researcher to participate in ecological genomic studies. This position involves interaction with a multidisciplinary team of scientists including an aquatic ecologist, an evolutionary ecologist,

and our genomics and proteomics groups at the Center and on the USU campus. Specific duties include overseeing the genomic and proteomic aspects of current research projects designed to examine the ecological consequences of genomic and proteomic biodiversity, and metagenomic analysis of microbial communities in extreme environments such as the Great Salt Lake. A strong interest in ecological genomics is essential. Applicants should have a Ph.D. in ecology, molecular biology, evolutionary genetics, or bioinformatics, and experience in either empirical/analytical techniques in one or more of the following areas: 1) comparative genomics, 2) gene expression, or 3) proteomics. A demonstrated record of publication and well developed communication skills are required. The successful applicant will be encouraged to develop independent research interests in the area of ecological genomics and contribute to the development of future grant applications.

This position will take advantage of interactions among an active and growing core of researchers at USU who have a strong interest in the application of genomic techniques to study natural populations of non-model species, and using metagenomic approaches to study communities in harsh environments, (http://www.biosystems.usu.edu/research/focus_areas/).

DEPARTMENT: College of Natural Resources and Center for Integrated BioSystems

SALARY: \$37,000 minimum, commensurate with experience

CLOSING DATE: Review of applications will begin immediately and the position will remain open until filled

TERM: A one-year position with the possibility of renewal for a second year.

Please send a cover letter including research interests (indicate Ecological Genomics/Proteomics Position on cover letter), curriculum vitae, and contact information for three references to:

Michael E. Pfrender

Assistant Professor of Biology

Department of Biology

5303 Old Main Hill Road

Logan, UT 84322-5305

e-mail: pfrender@biology.usu.edu

Professor Todd A. Crowl

Director of Research

College of Natural Resources

5210 Old Main Hill

Logan, UT 84322-5210

e-mail: tacrowl@cc.usu.edu

Utah State University is a Carnegie Research Doctoral Extensive University, an affirmative action/equal opportunity employer, and was recently chosen as a National Science Foundation ADVANCE Gender Equity Program recipient. The University is sensitive to the needs of dual-career applicants and dedicated to recruiting stellar candidates from a diverse pool including women, minorities, veterans and persons with disabilities. USU offers competitive salaries and outstanding medical, retirement and professional benefits (see <http://www.usu.edu/hr> for details).

Michael E. Pfrender

Department of Biology

Utah State University

5305 Old Main Hill Road

Logan, UT 84322-5305

Phone: 435-797-7623

Fax: 435-797-1575

USU Department of Biology: <http://www.biology.usu.edu>

pfrender@biology.usu.edu

Williams College Bioinformatics

HHMI Postdoctoral Research Fellow in Bioinformatics, Genomics and Proteomics

Williams College seeks to hire two postdoctoral fellows in its Bioinformatics, Genomics and Proteomics (BIGP) Program. These positions are funded by a Howard Hughes Medical Institute grant to encourage future faculty development. Each HHMI Fellow will conduct independent research under the mentorship of one or more of the 20 members of the BIGP Program at Williams (<http://www.williams.edu/BIGP>). In this context, each Fellow will assist in the supervision of undergraduate students performing thesis/independent research and will teach one BIGP Winter Study course of his/her own design.

These positions for scientists with training in bioinformatics, genomics, and/or proteomics are ideally suited

for those who seek teaching and research experience at a premiere liberal arts college. Candidates must have a recent Ph.D. in a relevant field. These are full-time, one-year positions with flexible start dates and the possibility of renewal for one additional year. Salary is competitive and funds for professional travel are included.

Applications are due prior to February 1, 2006 for fellowships that will begin in 2006. For fellowship starting dates in 2007, please submit applications before March 1, 2006. Questions about the fellowship program can be answered by Dr. Wendy Raymond, wraymond@williams.edu , (413) 597-3536.

Please send a cv, names of three references, and a

cover letter that 1.) identifies possible Williams College BIGP mentors, 2.) includes a proposed title and a few sentences describing a one-month BIGP course you might teach and 3.) job number (300213-SCIENCE) to the address below.

Only complete applications will be accepted. Office of Human Resources e-mail: hr@williams.edu Williams College welcomes diversity AA/EOE

–
Jason A. Wilder Assistant Professor of Biology
Williams College Williamstown, Massachusetts
01267 413-597-4811 (phone) 413-597-3495 (fax)
jwilder@williams.edu

WorkshopsCourses

Bologna ApplBioinformatics Feb13-17 76 UHelsinki PopDynamics Apr-May 77
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Bologna ApplBioinformatics Feb13-17

7th BOLOGNA WINTER SCHOOL APPLIED BIOINFORMATICS: the Test Case of the Human Genome 13-17 February 2006, BOLOGNA (Italy)

The Bologna Winter Schools are unique international forums where to debate the state of the art of complex problems at the forefront of Bioinformatics, Computational Biology and Modern Biology. The 7th Edition focuses on the applications of Bioinformatics to the Human Genome Analysis. Fundamental problems, that are still matter of debate, will be addressed such as the annotation, the expression and the regulation of the Human Genome, the relationship between expression and diseases, the variability between populations and the applications to molecular medicine. The growing interest in Biodiversity, Aging, Forensic Genomics and

early diagnosis of genetic maladies indicates how Bioinformatics is essential not only for the management and the analysis of the data but also for identifying typical markers of different populations and individuals, with the common goal of highlighting the relationship between genotype and phenotype. The school will be devoted to explore which ideas and tools out of Bioinformatics can effectively help in the analysis at large of the Human Genome and will cover different sessions:

How many genes? Genome annotation Transcription regulation Genome variability SNPs aging and diseases Forensic genomics

TEACHERS: David Balding (Imperial College, London, UK), Guido Barbujani (University of Ferrara, IT), Jaume Bertranpetit (University Pompeu Fabra, Barcelona, ES), Claudio Franceschi (University of Bologna, IT), Roderic Guigo (IMIM/University Pompeu Fabra, Barcelona, ES), Uta-Dorothee Immel (Martin-Luther-University, Halle/Saale, DE), David T. Jones (University College, London, UK), Arthur Lesk (University of Cambridge, UK), Marion Nagy (Humboldt University, Berlin, DE), Peter Nürnberg (Univer-

sity of Cologne, DE), Walther Parson (Medical University Innsbruck, AU), Giovanni Perini (University of Bologna, IT), Graziano Pesole (University of Milano, IT), Lutz Roewer (Humboldt University, Berlin, DE), Janet Thornton (EBI-EMBL, Cambridge, UK), Anna Tramontano (University "La Sapienza", Rome, IT), Alfonso Valencia (National Center of Biotechnology, Cantoblanco, ES)

SCIENTIFIC COMMITTEE: R. Casadio, D. Jones, A. Tramontano, A. Valencia.

PROGRAMME COMMITTEE: R. Casadio, D. Luiselli, S. Pelotti, G. Pesole.

ORGANIZING COMMITTEE: R. Casadio.

LOCAL COMMITTEE: E. Capriotti, P. Fariselli, P.L. Martelli, I. Rossi, G. Tasco.

ORGANIZING SECRETARY AIRBBC/CIRB c/o Dept. of Biology, University of Bologna Via Irnerio 42, 40126, Bologna, ITALY. Tel: (+39) 051 2094005 Fax: (+39) 051 242576

<http://www.biocomp.unibo.it/~school2006>
For application send a short C.V. to
<<mailto:school2006@biocomp.unibo.it>>
school2006@biocomp.unibo.it (Deadline: January
10, 2006) The School may provide 5 ECTS credits
donata.luiselli@unibo.it

Friday Harbor Labs Marine MolEcol Mar27-Jun3

For Undergraduates and Post-Baccalaureates: RESEARCH APPRENTICESHIP IN MARINE MOLECULAR ECOLOGY Friday Harbor Labs, NW Washington State Spring Quarter 2006 (27 March - 3 June 2006, 15 credits) Apply by 16 January 2006 <http://depts.washington.edu/fhl/> Live and do research for 10 weeks at beautiful Friday Harbor Laboratories, the world-renowned University of Washington marine lab on San Juan Island, 75 miles northwest of Seattle. Intensive research training experience in a small class. \$3000 stipend provided to all admitted students. Applicants do not need to be currently enrolled at a university.

In this apprenticeship, students will use DNA markers to explore the ecology, evolution and conservation of marine organisms. Research questions we tackle include studies on gene flow, systematics, larval ecology,

and species identification. During the first two weeks of the apprenticeship, a series of lectures and laboratory exercises will provide an overview of the principles, tools and techniques that are commonly employed in molecular ecology, with an emphasis on fertilization ecology and invertebrate life histories. After this introduction, apprentices will develop and pursue research projects of their choosing; from design, field sampling and labwork to analysis and scientific data presentation. Projects from past classes can be viewed at <http://web.pdx.edu/~biermann/MME/>. Apprentices will emerge with skills in PCR, DNA sequencing and fragment analysis, and an appreciation for the possibilities and pitfalls of applying molecular methods in marine biology and ecology. Enrollment limited to 8 students. Contact: jessica.marks@bio.uib.no or biermann@pdx.edu More information and applications available online: <http://depts.washington.edu/fhl/studentApprentice2006.html> biermann@gmail.com

UHelsinki PopDynamics Apr-May

Graduate course on the DYNAMICS OF STRUCTURED POPULATIONS at the University of Helsinki, April-May 2006

In late spring 2006, Professor Mats Gyllenberg will give a course on modelling and the dynamics of general physiologically structured populations. The course starts with an account of the basic principles of modelling structured populations and will in the end bring the audience to the research frontier of the field of mathematical population theory. Topics include existence and uniqueness of solutions, steady-state analysis, stability and bifurcation theory, and adaptive dynamics.

Prerequisites for the course are a solid background in undergraduate mathematics (analysis, linear algebra, probability) and a genuine interest in biology.

The course starts on April 3 and ends on May 5, 2006. There will be 8 hours of lectures per week. Graduate as well as advanced undergraduate students and young researchers from other universities are welcome and can join the course free of charge; we however cannot provide financial assistance for travel and subsistence.

For more information, please contact Eva Kisdi at the Department of Mathematics and Statistics, FIN-00014 University of Helsinki, Finland (email: eva.kisdi...at...helsinki.fi). The course website

is at <http://mathstat.helsinki.fi/research/biometry/-biomath/courses/structured.html> . Eva Kisdi Dept. Mathematics and Statistics, University of Helsinki
kisdi@mappi.helsinki.fi kisdi@mappi.helsinki.fi

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as \LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by \LaTeX do not try to embed \LaTeX or \TeX in your message (or other formats) since my program will strip these from the message.