
E v o l D i r

May 1, 2005

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

Forward

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

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

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



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Atlanta CompGenomics EvolBiol Nov17-19

CALL FOR PAPER SUBMISSION: 5th Georgia Tech - ORNL International Conference on Bioinformatics, in Silico Biology

“Computational Genomics and Evolutionary Biology”
November 17-19, 2005, Atlanta, Georgia, USA

Home Page: <http://opal.biology.gatech.edu/conference/> ORGANIZED BY

Georgia Tech Oak Ridge National Lab

Selected papers will be published in a special issue of BIOINFORMATICS journal (Oxford University Press)

IMPORTANT DEADLINES

- June 1, 2005: Paper Submission (Electronically, see conference Home Page) - September 30, 2005: Poster Abstract Submission

CONFIRMED INVITED SPEAKERS:

Natalia Komarova, Rutgers University

Michael Lynch, Indiana University, Bloomington

Pierre Baldi, University of California, Irvine

Philip Bourne, University of California, San Diego

Volker Brendel, Iowa State University

Julio Collado-Vides, UNAM, Cuernavaca, Mexico

Andrew Ellington, University of Texas at Austin

Dmitrij Frishman, University of Munich & Max-Planck, Germany

Alex Kondrashov, NCBI / NIH

John McDonald, Georgia Tech

Jeffrey Thorne, North Carolina State University

STEERING/PROGRAM COMMITTEE

- Conference Chairs:

Mark Borodovsky, Georgia Tech

Eugene Koonin, NCBI / NIH

- Program Chairs:

Eva K. Lee, Georgia Tech and Emory

Andrey Gorin, Oak Ridge National Laboratory

[PLEASE ACCEPT OUR APOLOGIZES IF YOU RECEIVE MULTIPLE COPIES]

conf@opal.biology.gatech.edu

Auckland SMBE05 Jun19-23 4

Society for Molecular Biology and Evolution Annual Conference Auckland, New Zealand, 19th-23rd June 2005

A reminder to register to attend the 2005 MBE meeting in Auckland. Early registrations close 1 May 2005 at <http://www.mbe05.com>. This is promising to be an exciting meeting with many high profile speakers in attendance. See you there.

For additional information, or queries contact Susan Wright <<mailto:S.M.Wright@massey.ac.nz>>S.M.Wright@massey.ac.nz.

Susan Wright Executive Officer Allan Wilson Centre for Molecular Ecology and Evolution Massey University Private Bag 11-222 Palmerston North Tel: +64 6 350 5448 New Zealand Fax: +64 6 350 5626

<http://AWCMEE.massey.ac.nz>
s.m.wright@massey.ac.nz

Bordeaux PhDStudents Sep4-9

Conference: 11th Meeting of PhD Students in Evolutionary Biology

11th Meeting of PhD Students in Evolutionary Biology

The website for the 11th Meeting of PhD Students in Evolutionary Biology is now available at <http://kimura.univ-montp2.fr/mpseb/>. Registrations will be opened on the 13th April 2005. We will accept about 100 participants and will take care that every country is represented as equally as possible. We will not consider any other criterion. So registrations will be considered

on a 'first arrived - first served' basis. Registrations received after completion of the list will be placed on a complementary list. Best regards,

The organising committee:

Eric Bazin<bazin@univ-montp2.fr> Emmanuelle Billard <billard@sb-roscoff.fr> Stéphane De Mita <demita@ensam.inra.fr> Julien Dutheil <Julien.Dutheil@univ-montp2.fr> Emmanuelle Eveno <eveno@pierroton.inra.fr> Baptiste Faure <bfaure@sb-roscoff.fr> Matthieu Faure <matthieu.faure@univ-montp2.fr> Olivier Lepais <Lepais@pierroton.inra.fr> Delphine Muths <muths@sb-roscoff.fr>

Bordeaux PopBiol Aug29-Sep1

Dear Colleagues

We are happy to invite you to attend the 28th annual meeting of the Population Biology and Genetics group (Le Petit Pois Dérivé), organised in Bordeaux from Monday August 29th to Thursday September 1st 2005. All oral communications and posters are welcome (most of them will be in French).

The three best posters will be offered prizes! (200 euros from New Phytologist and journal memberships from Springer and EDP Sciences).

The City of Bordeaux will welcome us on Tuesday and we suggest a trip in the Sauternais with a dinner close to the Ciron river.

More informations and online registration are available at this address: <http://www.pierroton.inra.fr/-biogeco/genetique/congres/ppd2005/index.html>

Looking forward to meeting you in Bordeaux, Best regards.

For the organising committee Sophie Gerber / Pauline Garnier-Géré UMR BIOGECO - INRA / University Bordeaux I 69 route d'Arcachon (FRANCE) 33612 Cestas cedex tel 33 5 57 12 28 30 fax 33 5 57 12 23 81

Chers Collègues

Nous sommes heureux de vous inviter à participer à la 28ème réunion annuelle du Groupe de Biologie et Génétique des Populations qui se tiendra cette année à Bordeaux du lundi 29 août au jeudi 1er septembre 2005. Toutes les communications orales et les posters sont les bienvenus, dans la limite des places disponibles !

Les trois meilleurs posters seront récompensés de prix (200 euros offerts par New Phytologist et des abonnements offerts par Springer et EDP Sciences !!!).

Une réception à l'Hôtel de Ville de Bordeaux vous sera offerte le mardi et nous vous proposons une découverte du Sauternais ainsi qu'un banquet au bord du Ciron le mercredi.

Des informations complémentaires et l'inscription en ligne sont disponibles sur notre site ouèbe à l'adresse suivante : <http://www.pierroton.inra.fr/-biogeco/genetique/congres/ppd2005/index.html> Dans l'attente de vous recevoir à Bordeaux,

Meilleures salutations.

Pour le comité d'organisation Sophie Gerber / Pauline Garnier-Géré UMR BIOGECO - INRA / Université Bordeaux I 69 route d'Arcachon (FRANCE) 33612 Cestas cedex tel 33 5 57 12 28 30 fax 33 5 57 12 23 81

Sophie Gerber <sophie@pierroton.inra.fr>

ClemsonU SEEPAGE Sep23-25

SEEPAGE 2005

The next annual SEEPAGE Meeting (South-East Ecology, PopulAtion Genetics and Evolution Meeting) is coming soon so mark your calenders!

WHEN: September 23-25, 2005 HOST: Clemson University, Dr. Margaret Ptacek WHERE: Camp Kanuga, Hendersonville, NC (<http://www.kanuga.org/> - for more info about the camp)

SATURDAY NIGHT KEYNOTE SPEAKER: Dr. David McCauley, Vanderbilt University

SPECIAL GUEST SPEAKER: Dr. Felix Breden, Simon Frasier University

The weekend will also include contributed 15-minute talks, a posters session, and spirits!

Visit the webpage for updates and details! (www.clemson.edu/~mptacek - click on SEEPAGE 2005)

Michele Kittell <kittell@CLEMSON.EDU>

Fairbanks Evol05 Jun10-14 4 mentors

DIVERSITY AT SSE/SSB 2005:

Call for volunteer mentors for this program from graduate students, postdocs and faculty.

The Undergraduate Mentoring in Environmental Biology (UMEB) program will take place again at the 2005 meeting this June in Fairbanks, Alaska. Twelve individuals have generously volunteered to serve as mentors, but the program will work best if we can get this number up to twenty one. Duties will include meeting with a pair of undergraduates in the program, attending and demystifying a half-day of talks with them, joining them for a meal, introducing them to colleagues and in general befriending them in ways that make evolutionary biology seem like a welcoming discipline. No costs for travel, housing or registration are covered. Please spread the word about this very rewarding activity.

Please send an email to Rich Kliman (rmkliman@cedarcrest.edu) if you would you like to be a mentor.

Rmkliman@cedarcrest.edu Rmkliman@cedarcrest.edu

Krakow 10 ESEB Aug15-20 EvolGenomics

A full-day symposium on "Evolutionary Genomics" will be held at the ESEB-2005 meeting in Krakow (August 15-20, 2005).

The organizers are Brian and Deborah Charlesworth, University of Edinburgh.

10 time slots are available for contributed papers lasting 20 minutes (and also an associated poster session) as well as our 4 invited speakers:

Laurent Duret Pole BioInformatique Lyonnais, Laboratoire BBE - UMR CNRS 5558, Université Claude Bernard

Peter Keightley Evolutionary Biology, School of Biological Sciences, University of Edinburgh

Dmitri Petrov Department of Biological Sciences Stanford University

Alfredo Ruiz Facultat de Ciències-Edifici C, Universitat Autònoma de Barcelona

The deadline for registering for ESEB2005 (<<http://www.eko.uj.edu.pl/ESEB>>www.eko.uj.edu.pl/ESEB), and Abstract submission is not far ahead. The web site will close for abstract submission on 30 April 2005.

Brian Charlesworth <brian.charlesworth@ed.ac.uk>

The history of life has been characterised by a series of “Major Transitions”, which have involved changes in the way that biological information is encoded and transmitted. These transitions include the origin of life itself, the appearance of multicellular organisms, and the emergence of cooperation in animal societies. This symposium will focus on the major transitions, with a special emphasis on how the collective properties of groups of independent replicators sometimes come to respond to natural selection. In other words, the symposium will focus on the emergence of new “units of selection.”

j.r.peck@sussex.ac.uk j.r.peck@sussex.ac.uk

Krakow 11 ESEB Aug15-20 MajorTransitions

THE MAJOR TRANSITIONS IN EVOLUTION

We would like to call the attention of EVOLDIR members to a symposium to be held at the ESEB meeting in Krakow (15-20 August, 2005) on the Major Transitions in Evolution.

We invite researchers attending the meeting to submit abstracts for the symposium. Presentations on topics relevant to the major transitions will be considered, including work on subjects such as group selection, cooperation, the suppression of competition, and the evolution of integrated societies.

The invited speakers for the symposium are

Francis Ratnieks (University of Sheffield)

And

Len Nunney (University of California - Riverside)

Abstracts should be submitted via the ESEB conference website at <http://www.eko.uj.edu.pl/eseb/reg/>

General information on the meeting is at <http://www.eko.uj.edu.pl/eseb/> Questions about the symposium should be directed to the organisers:

Joel Peck (University of Sussex) j.r.peck@sussex.ac.uk

And

Eors Szathmáry (szathmary@colbud.hu)

We hope to see you in Krakow!

Yours,

Joel Peck

Eors Szathmáry

Symposium summary:

Krakow 12 ESEB Aug15-20 NaturalHybridizationSpeciation

Dear colleagues,

we would like to invite you to submit abstracts for oral or poster presentations in the symposium “Natural hybridization and speciation” (see below) at this year’s ESEB congress in Krakow, Poland. Deadline for abstract submission is April, 30th, 2005. We would like to refer to <http://www.eko.uj.edu.pl/eseb/> for further details and registration.

All the best,

Walter Salzburger & Axel Meyer

- - - Natural hybridization and speciation

Natural hybridization has been considered important in plant evolution, but its importance as a mechanism of speciation remains controversial particularly in animals where a hybrid origin of species has been only rarely observed. The symposium “Natural Hybridization and Speciation” invites contributions that (i) describe cases of hybrid speciation in plants and animals, (ii) discuss the importance of natural hybridization for speciation, and (iii) illustrate the genomic consequences of natural hybridization.

Organisers: Walter Salzburger University Konstanz, Department of Biology Axel Meyer University Konstanz, Department of Biology

Invited speakers: Michael L Arnold University of Georgia, Department of Genetics Loren Rieseberg Indiana University

Dr. Walter Salzburger Department of Biology & Cen-

ter for Junior Research Fellows Universitaetsstrasse 10, University Konstanz, D-78457 Konstanz, Germany <http://www.evolutionsbiologie.uni-konstanz.de/~walter/index.html> tel. +49 (0) 7531 - 88 4304; gsm. +49 151 - 127 22 378; fax. +49 (0) 7531 - 88 3018 eMail: Walter.Salzburger@uni-konstanz.de

Walter Salzburger <Walter.Salzburger@uni-konstanz.de>

Krakow 13 ESEB Aug15-20 Selection

INVITATION TO ESEB SYMPOSIUM (Krakow, 15-20 August, 2005)

We would like to call your attention to a symposium to be held at the ESEB meeting on SELECTION IN THE OCEAN : EVIDENCE AND EVOLUTIONARY SIGNIFICANCE.

The goal of this symposium is to discuss the role of selection in marine speciation and adaptive evolution, and the implications for the future persistence of species and populations under a scenario of anthropogenically altered selection regimes. Compared to other organisms, marine species pose a special challenge, because they often exhibit huge population sizes and live in an environment with seemingly poorly defined dispersal barriers. We aim to present studies that utilize recent advances in genomics, statistics and concepts to study selection, fitness and ecological performance of marine organisms

We invite researchers attending the meeting to submit abstracts for the symposium. The registration fee of all speakers will be refunded thanks to support from the EU Network of Excellence "Marine Genomics Europe".

Invited speakers for the symposium are: - Louis Bernatchez (Québec) - Suzanne Edmands (Santa Cruz) - Thorsten Reusch (Plön) - Louis van de Zande (Groningen)

Abstracts should be submitted via the ESEB conference website at <http://www.eko.uj.edu.pl/eseb/reg/> before 30 April.

General information on the meeting is at <http://www.eko.uj.edu.pl/eseb/> Questions about the symposium should be directed to the organisers: - Filip Volckaert (K.U.Leuven, filip.volckaert@bio.kuleuven.ac.be) and - Jeanine

Olsen (U. Groningen, j.l.olsen@biol.rug.nl)

With kind regards,

Filip Volckaert

Dr. Filip Volckaert Katholieke Universiteit Leuven Laboratory of Aquatic Ecology, Research Group on Fish Genetics Ch. de Bériotstraat 32 B-3000 Leuven, BELGIUM Phone: +32 16 32 39 72 (office) or +32 16 32 39 66 (secretariat) Fax: +32 16 32 45 75 [Mailto:filip.volckaert@bio.kuleuven.ac.be](mailto:filip.volckaert@bio.kuleuven.ac.be) Website: <<http://www.kuleuven.ac.be/bio/eco>><http://www.kuleuven.ac.be/bio/eco> Filip Volckaert <Filip.Volckaert@bio.kuleuven.ac.be>

Krakow 14 ESEB Aug15-20 Ageing

Dear evoldir members,

We would like to bring the symposium "Biology and ageing: an integrative approach" to your attention. This will be held on the ESEB 2005 meeting 15-20 August in Krakow, Poland (<http://www.eko.uj.edu.pl/eseb>).

The consequences of ageing will have a major impact on the western world in the coming decades. Researchers in the fields of medicine, epidemiology and evolutionary genetics focus on this problem from their own paradigm. From this diversity arises a range of different systems that is used to investigate ageing, varying from single celled organisms such as bacteria and yeast to plants, invertebrates and vertebrates, including our own species.

The numerous studies on aging and the attempts to uncover the mechanisms that control it span the whole of biology, because ageing and longevity are associated with a suite of traits, dealing with, among others, metabolism, diet, behaviour and disease.

Disentangling and integrating the knowledge of all these different (model-) systems and approaches is the main challenge of this moment. The emphasis of this symposium will be on the integration of different disciplines and points of view concerning ageing research.

Confirmed invited speakers are:

Francois Taddei, Faculté Necker-Enfants Malades, Génétique Moléculaire Evolutive et Médicale U571 INSERM Thomas Flatt, Brown University, Dept Ecol & Evolutionary Biology

If you:

- are investigating ageing or ageing related traits - think that an integrative approach is the answer to uncover the complexity of ageing - are interested in evolution in its broadest sense

Then:

we welcome you to submit a talk or poster to our symposium

Please go to the congress registration website (<http://www.eko.uj.edu.pl/eseb/reg/>) and choose our symposium (2nd from the top).

We hope to meet all of you in Krakow.

Bas Zwaan Jeroen Pijpe Egon Baldal

(for further questions, please mail: bal-dal@rulsfb.leidenuniv.nl)

Egon Baldal <bal-dal@rulsfb.leidenuniv.nl>

Krakow 15 ESEB Aug15-20 GeneticDiversification

Dear Colleagues,

we would like to draw your attention to the symposium "Genetic diversification by frequency-dependent selection: theoretical approaches and empirical facts",

which will be held at the ESEB 2005 congress in Krakow, Poland (15-20 August); <http://www.eko.uj.edu.pl/eseb> . This symposium is devoted to the exploration of the potential of frequency-dependent selection within populations in generating and maintaining biological diversity. Well known evolutionary consequences of frequency-dependent selection, as caused for instance by intraspecific competition, sexual selection, or habitat choice, include the maintenance of genetic variation, sexual dimorphism, non-equilibrium dynamics, and sympatric and parapatric speciation. The focus will be on the relation between predictions from explicit genetic models and empirical/experimental evidence. Therefore, we strive for a balance between contributions by theoreticians and empiricists/experimentalists.

Confirmed invited speakers are:

Dan Bolnick, University of Texas at Austin and Sergey Gavrilets, University of Tennessee

We encourage especially the submission of empirical papers. We are looking forward to meet you in Krakow, Reinhard Bürger and Sergey Gavrilets

Reinhard Bürger

Department of Mathematics University of Vienna Nordbergstrasse 15 1090 Vienna, Austria

Phone: +43 1 4277 506 31 FAX: +43 1 4277 9506 Email: Reinhard.Buerger@univie.ac.at Home-page: <http://homepage.univie.ac.at/Reinhard.Buerger> Reinhard Bürger <reinhard.buerger@univie.ac.at>

Krakow 16 ESEB Aug15-20 colonisation

Dear Colleagues,

We would like to draw your attention to the symposium EVOLUTIONARY BIOLOGY OF COLONISATION

which will be held at the ESEB 2005 congress in Krakow, Poland (15-20 August); <http://www.eko.uj.edu.pl/eseb> . DESCRIPTION: Recently introduced species that colonise large areas offer special opportunities to address both the speed and predictability of evolution on a geographic scale. Adaptive microevolution would be demonstrated if the invading populations rapidly and independently evolve geographic clines that uniformly converge on baseline clines in the ancestral population. Alternatively, other non-selective causes such as genetic drift and genomic instabilities promoted by transposition bursts must be considered in studying the evolutionary effects of colonisation.

CONFIRMED INVITED SPEAKERS: Christian Biemont (biemont@biomserv.univ-lyon1.fr) UMR 5558: Biometrie et Biologie Evolutive, Université Lyon1, France Jeremy Searle (jbs3@york.ac.uk) Department of Biology, University of York, UK

We welcome you to submit a talk or poster to our symposium

Please go to the congress registration website (<http://www.eko.uj.edu.pl/eseb/reg/>) and choose our symposium.

We are looking forward to meeting you in Krakow,

Luis Serra and Antonio Fontdevila

ORGANISER: LUIS SERRA, Departament de

Genetica, Facultat de Biologia, Universitat de Barcelona, Spain; e-mail:lserra@ub.edu ;phone: ++/34/934021499; fax: ++/34/934110969. Recent publications: SCIENCE 287:308-309 (2000); EVOLUTION 57:1837-1845 (2003) CO-ORGANISER: ANTONIO FONTDEVILA, Departament de Genetica i Microbiologia, Universitat Autonoma de Barcelona, Bellaterra, Barcelona, Spain;e-mail:Antonio.Fontdevila@uab.es ;phone:++/34/935811083; fax: ++/34/935812726

afontdevila <Antonio.Fontdevila@uab.es>

Krakow 17 ESEB Aug15-20 EvoDevo

Hello there,

As most of you probably know, the European congress of Systematic and Evolutionary Biology (ESEB 2005) will take place in Krakow, Poland, next June (10-14). As the co-organizer - with Dr Casper Breuker - of the symposium 'Functional Evo-Devo', I wish to remind you all that the dead line for submission of communication is getting close: titles and abstracts are due to april 30th.

Invited speakers to this symposium include Pr James Hanken (Harvard), Dr Patricia Beldade (Irvin) and Dr Armin Moczek (Indiana).

Details on the application can be found at <http://www.eko.uj.edu.pl/eseb/> I paste below a brief description of the symposium

Looking forward to seeing you in Krakow

Vincent

Dr Vincent Debat Faculty of Life Sciences The University of Manchester Michael Smith Building Oxford Road Manchester M13 9PT United Kingdom office: +44 (0) 161 275 5320 mobile: +44 (0) 796 967 2707 Web: <http://vincent.debat.site.voila.fr> Abstract - Functional Evo-devo

In recent years developmental genetics and sophisticated morphometric techniques have been integrated in the study of evolution leading to the spread of Evo-Devo research. The field is now ready to incorporate the functional aspects of evolution in order to understand the adaptive forces shaping morphology. In this symposium we aim to attract researchers who study the functional aspects of evo devo in various research

systems which will appeal to a broad audience.

Vincent <vincent.debat@manchester.ac.uk>

Krakow 18 ESEB Aug15-20 Behaviour

Dear Colleagues, we would like to bring to your attention two symposia to be held at the 10th Congress of the European Society for Evolutionary Biology in Krakow, Poland (15-20 August 2005):

- (1) Evolutionary Genetics of Behaviour Invited speakers: Christine Boake and Laurent Keller
- (2) Evolutionary Genetics of Sexual Behaviour Invited speakers: Stephen Goodwin and Mike Ritchie

The deadline for submission of contributed talks and posters is April 30. For detailed info and registration see the ESEB Congress website at <http://www.eko.uj.edu.pl/eseb/> Symposia organizers: T. J. Kawecki F. Mery, L. W. Beukeboom D. Bopp, R. Bertossa

Tadeusz Kawecki Unit for Ecology and Evolution, Department of Biology University of Fribourg Chemin du Musee 10, CH-1700 Fribourg, Switzerland www.unifr.ch/biol/ecology/kawecki phone +41 26 300 88 71 fax +41 26 300 96 98 e-mail tadeusz.kawecki@unifr.ch

Krakow 19 ESEB Aug15-20 HybridZones

Dear Colleagues,

We would like to draw your attention to the symposium: Hybrid zones and speciation which will be held at the ESEB 2005 Congress in Kraków, Poland (15-20 August); <http://www.eko.uj.edu.pl/eseb> Hybrid zones and speciationThe symposium will focus on genetic analysis of hybrid zones and hybridizing species, pattern of change and introgression at multiple traits, correlation with environmental heterogeneity, mating pattern and origin of reproductive isolation. Role of selection in maintaining differentiation in face of gene flow. Quantifying divergence between hybridizing taxa and

identification of genes underlying adaptations.

CONFIRMED INVITED SPEAKERS:

Roger K. Butlin, University of Sheffield, Sheffield, UK
 Nicholas H. Barton, University of Edinburgh, UK

Please note that there are two symposia with similar titles.

The deadline for submission of contributed talks and posters is April 30.

For detailed info and registration see the ESEB Congress website at <http://www.eko.uj.edu.pl/eseb/>
 Looking forward to seeing you in Kraków. Symposium organizers:

Jacek M. Szymura, Jagiellonian University, Kraków, Poland Dept. Comparative Anatomy, Jagiellonian University 30-060 Kraków, Ingardena 6, Poland tel. 4822-663 2430 e-mail: szym@zuk.iz.uj.edu.pl

Guenther Gollmann, University of Vienna, Wien, Austria guenther.gollmann@univie.ac

“Jacek M. Szymura” <szym@zuk.iz.uj.edu.pl>

**Krakow 20 ESEB Aug15-20
 Phylogeography**

Dear Colleagues,

may I draw your attention to two symposia at the 10th Congress of the European Society for Evolutionary Biology in Krakow, Poland (15-20 August 2005):

1. Phylogeography of Arctic Species Organisers: Dorit Liebers DEUTSCHES MEERESMUSEUM German Oceanographic Museum Godfrey M. Hewitt School of Biological Sciences, UEA Invited speakers: Richard Abbott Division of Environmental and Evolutionary Biology, University St Andrews Laura Kvist Department of Biology, University of Oulu

2. Range Changes and the nature of Species Limits. Organisers: Richard Nichols Biological Sciences, Queen Mary, University of London Godfrey Hewitt Biological Sciences, University of East Anglia Invited speakers: Nicholas Barton CAPB, University of Edinburgh Oscar Gaggiotti Equipe Genomique de Populations et Biodiversité; LECA UMR CNRS 5553 Université Joseph Fourier

The deadline for submission of contributed talks and posters is April 30. For detailed information and reg-

istration see the ESEB Congress website at <http://www.eko.uj.edu.pl/eseb/> There is still room for talks.

Godfrey Hewitt

Prof G M Hewitt PhD DSc FRES FLS School of Biological Sciences UEA, NORWICH NR4 7TJ, UK tel +44 (0)1603 592182 (office) +44 (0)1603 592266 (secretary) +44 (0)1603 458142 (home) fax +44 (0)1603 592250 email <g.hewitt@uea.ac.uk> <http://www.bio.uea.ac.uk> g.hewitt@uea.ac.uk

**Krakow 21 ESEB Aug15-20
 Payment**

10th Congress European Society for Evolutionary Biology <http://www.eko.uj.edu.pl/eseb/> Regarding Polish national holidays (30.04.-3.05), the deadline for registration with early fee and abstract submission will be postponed from 30.04 to 8.05.2005.

In case of paying by bank transfer: date of registration closure (08.05.2005) decides on early conference fee. However, the transfer should come in not later than 08.06.2005.

Adam Gawelczyk ESEB 2005 Team

adam@gawelczyk.com

**Krakow 5 ESEB Aug15-20
 Symposium Announcement**

“Deciphering human origins and migrations by means of their microbial pathogens” - a special symposium in ESEB 2005 -

Human genetic diversity decreased dramatically during the bottlenecks associated with the migrations ?out of Africa?. An alternative, consist in analysing the sequence diversity in parasites or bugs that have accompanied humans during their ancient and recent migrations. Particularly promising are some viruses that infect renal tissue (JC virus) or T-lymphocytes (T-lymphotropic virus) and Helicobacter pylori, a bacteria that colonize the human stomach because they seem to possess evolutionary histories that parallel those of humans.

This symposium will be held in the ESEB 2005 meeting in Krakow 15-20.8.2005, and it is sponsored by European Society for Evolutionary Biology (ESEB).

Organisers: Thierry Wirth, department of Biology, University Konstanz (Germany) and Daniel Falush, Peter Medawar Building for Pathogen Research, Oxford (England)

Invited speakers in this symposium include: Mark Achtman, Max-Planck Institute fuer Infektionsbiologie, Berlin (Germany): "Phylogeography of *Helicobacter pylori* and human migrations".

Antoine Gessain, Unite d'epidemiologie et physiopathologie des virus oncogenes, Institut Pasteur, Paris (France): "The low genetic variability of HTLV-1/2 retroviruses as a means to follow migrations of human infected populations".

See: <http://www.eko.uj.edu.pl/eseb/> for further details and registration.

Thierry Wirth, assistant professor Department of Biology, Evolutionsbiologie Universitaetsstrasse 10, University Konstanz, D-78457 Konstanz, Germany

tel. +49 (0) 7531 88 2763 fax. +49 (0) 7531 88 3018 email: thierry.wirth@uni-konstanz.de

Dr. Thierry Wirth Assistant Professor, Department of Biology Universitaetsstrasse 10, University Konstanz, D-78457 Konstanz, Germany

tel. +49 (0) 7531 88 2763; gsm. +49 175 68 44 253; fax. +49 (0) 7531 - 88 3018 email: thierry.wirth@uni-konstanz.de

Thierry Wirth <Thierry.Wirth@uni-konstanz.de>

Krakow 6 ESEB Aug15-20 AsexualReproductionSymposium

Dear colleagues,

>From the 15th to the 20th of August the biannual meeting of the European Society of Evolutionary Biology (ESEB) takes place in Krakow, Poland.

Also this year, the meeting contains a symposium on asexual reproduction. In this symposium Franois Balloux (University of Cambridge) and Graham Bell (McGill University) have been invited as keynote speakers. Please, feel free to apply for one of the remaining four 20-minute- slots for oral presentations. We will

also organize a separate poster and discussion session, to give the opportunity of a larger discussion forum.

We will be happy to meet you in Krakow. Dirk Tim Christoph

Symposium description:

(The Evolution of Asexual Reproduction) The success of sex remains one of the great mysteries of evolutionary biology. While most plant and animal species reproduce through sex, this form of reproduction has been shown to be more costly and inefficient relative to asexuality. Many theoretical explanations exist to explain the stability of either reproductive mode in different evolutionary contexts, but their application to empirical studies of asexual taxa remains relatively sparse. Recent technological advances are facilitating the analysis of variation on the level of the genome and population, and hence comparisons of the factors which influence the fate of different asexual organisms are becoming increasingly common.

Organizers:

Dirk Sven Schmeller, Department of Biological and Environmental Sciences, University of Helsinki, Finland (dirk.schmeller@helsinki.fi) Tim Sharbel, Apomixis Research Group, Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany (sharbel@ipk-gatersleben.de) Christoph Vorburger, Department of Ecology, University of Zurich, Switzerland

See: <http://www.eko.uj.edu.pl/eseb/> for further details and registration.

Krakow 7 ESEB Aug15-20 Sponsoring

Sponsoring opportunity

The tenth Congress of the European Society for Evolutionary Biology will be held at the Jagiellonian University, Cracow, Poland from 15 to 20 August 2005.

Financial support of ESEB will be provided for applicants from Developing Countries and Eastern Europe. This includes: Africa, some countries in Asia, South and Central America, Russia and other former members of Soviet Union, as well as new members of EU including Poland.

Authors wishing to be considered for this support (consisting of registration fee waiver) should send CV, pro-

posed abstract, as well as declaration that they are not able to cover fee from their own resources, to the to ESEB2005 office (eseb2005@eko.uj.edu.pl). The applicant must be presenting author of an contribution. The abstract must be accepted for either an oral or a poster presentation.

Closing date for applications: 30.04.2005

ESEB Team eseb2005@eko.uj.edu.pl

adam@gawelczyk.com

Krakow 8 ESEB Aug15-20 EvolGenetics

Abstracts for the 10th Congress of the European Society for Evolutionary Biology <http://www.eko.uj.edu.pl/ESEB/> (Aug 15-20, Krakow, Poland) are due by April 30, 2005. We invite your participation in a symposium on "Evolutionary dynamics of phenotypic traits in wild populations".

Theme:

Evolutionary biology has recently seen a resurgent interest in the architecture of complex traits under selection and the distribution of quantitative genetic variation in the wild, with studies of a wide range of taxa generating many exciting new results. In this symposium we will bring together researchers who are quantifying selection pressures, heritable variation and the evolutionary dynamics of life history, morphological or behavioural traits in natural environments. The symposium will illustrate how evolutionary genetic approaches can generate testable and useful predictions for the evolutionary dynamics of phenotypes subject to selection under changing environmental conditions.

Organisers:

David Coltman, University of Alberta Loeske Kruuk, University of Edinburgh

Invited speakers: Ary Hoffmann, La Trobe University Ben Sheldon, Oxford Barry Sinervo, Santa Cruz Jon Slate, University of Sheffield

Krakow 9 ESEB Aug15-20 BayesianMethods

We invite your participation in a symposium on "Bayesian estimation of demographic and ecological parameters from genetic data".

Abstracts for the 10th Congress of the European Society for Evolutionary Biology <http://www.eko.uj.edu.pl/ESEB/> (Aug 15-20, Krakow, Poland) are due by

****April 30, 2005****

See: <http://www.eko.uj.edu.pl/eseb/> for further details and registration.

Theme: The symposium will focus on the problem of estimating demographic and other ecological parameters from genetic data. Recent likelihood-based methods have been restricted to relatively simple models. New progress based on computationally intensive simulations should allow one to estimate parameters in and select among different models of almost arbitrary complexity. This symposium will focus on the latest developments with a mixture of theoretical and applied talks

Organisers:

Laurent Excoffier Zoological Institute, University of Bern

Mark Beaumont School of Animal and Microbial Sciences, University of Reading

Invited speakers:

David Balding Dpt of Epidemiology and Public Health, Imperial College

Arnaud Estoup CBGP, INRA, Campus International de Baillarguet

Bruce Rannala Department of Medical Genetics, University of Alberta

London LinneanSoc Sep22-24

SECOND ANNOUNCEMENT for the ESF-Linnean

Society workshop on “The Paradox of Asex: an evaluation” 22-24 September 2005 London.

Organizers: Hugh Loxdale (Rothamsted), Claudia Ricci (Milan) and Peter van Dijk (Heteren)

Sponsors: European Science Foundation <http://www.esf.org/> and the Linnean Society of London <http://www.linnean.org/> TOPIC The workshop will be centered round six main themes:

* Developmental constraints on the evolution of asex * Maintenance of genetic variation in asexuals * Mutations and the maintenance of sex vs. asex * Asexuality and disease * Lineage sorting and group selection * Applied aspects of sex vs. asex

Our workshop is the last out of four within the Parthenogenesis Network (PARTNER), an initiative funded by the European Science Foundation (ESF). PARTNER is aimed to bring together empiricists and theorists who work in the field of parthenogenesis in botany and zoology (for more information, see <http://www.nioo.knaw.nl/networks/partner>).

LOCATION The workshop will be held at the rooms of the Linnean Society of London, Burlington House Piccadilly London W1J 0BF, United Kingdom.

CONFIRMED SPEAKERS Irina Arkhipova (Cambridge, MA), Laura S. Corley (Pullman & London), Brian Fenton (Dundee), Steve P. Foster (Harpending), Ueli Grossniklaus (Zürich), Rosalind John (Cardif), Peter D. Keightley (Edinburgh), Alexey S. Kondrashov (Bethesda), Ryszard Korona (Krakow), Curtis M. Lively (Bloomington), Thierry de Meeûs (Montpellier), Leonard Nunney (Riverside), Sarah Otto (Vancouver), Dave Parker (Aarhus), Joel R. Peck (Sussex), Charles Spillane (Cork) and Christoph Vorbrueger (Zürich).

APPLICATIONS We are happy to invite ca. 20 additional participants. Each invited attendant is expected to contribute a short oral presentation during the workshop (ca. 15 min). Applications should include a short CV and a brief description of the research interests (together max. two pages). Selection among the applicants will be based on research record and topic. The workshop organization will cover the accommodation costs in the facilities provided by the organization for invited attendants, but cannot cover their travel expenses. Applications, by email, should be submitted before April 23, 2005 to: p.vandijk@nioo.knaw.nl

Dr. Peter J. van Dijk Dept. of Plant Population Biology Netherlands Institute of Ecology (NIOO-KNAW) PO Box 40 6666 ZG Heteren The Netherlands tel: +31.264791208 (direct) fax: +31.264723227 p.vandijk@nioo.knaw.nl Personal web-

page <http://www.nioo.knaw.nl/ppages/pvandijk> ESF Parthenogenesis network: <http://www.nioo.knaw.nl/-NETWORKS/PARTNER> P.vanDijk@nioo.knaw.nl

Marseilles 4 EvolBiol Sep21-23

The registration dead line for the next “evolutionary biology meeting at Marseille” is May 2nd

According to the abstracts received by early registers The program will be similar to the one proposed the former years : systematic, biodiversity, comparative genomics and post-genomics (at all the taxonomic levels), functional phylogeny, environment and evolution. You can submit and register on line on the meeting web site <http://www.up.univ-mrs.fr/evol/congres/> Information concerning housing.. are available on the same web site Best regards Pierre for the meeting organizers

– Pierre Pontarotti EA 3781 EGEE (Evolution Génome Environnement) 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 organize the 8th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/pierre.pontarotti@up.univ-mrs.fr>

Marseilles 5 EvolBiol Sep21-23

The First round of accepted abstracts for the 9th evolutionary Biology meeting at Marseille are available at the conference web site

<http://www.up.univ-mrs.fr/evol/congres/> best regards

– Pierre Pontarotti EA 3781 EGEE (Evolution Génome Environnement) Université d’Aix Marseille I Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 <http://www.up.univ-mrs.fr/evol> pierre.pontarotti@up.univ-mrs.fr

Marseilles 6 EvolBiol Sep21-23 AbstractDeadline

The abstract submission dead line for the “ 9th evolutionary biology meeting at Marseille” is May 2nd The first round of accepted abstracts are available on the meeting web site . The program will be similar to the one proposed the former years the following topics will be discuss: systematic, biodiversity, comparative genomics and post-genomics (at all the taxonomic levels), functional phylogeny, environment and evolution. You can submit and register on line on the meeting web site <http://www.up.univ-mrs.fr/evol/congres/> Information concerning housing.. are available on the same web site

Best regards

the meeting organizers

– Pierre Pontarotti EA 3781 EGEE (Evolution Génome Environnement) 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 organize the 8th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/> pierre.pontarotti@up.univ-mrs.fr

– Pierre Pontarotti EA 3781 EGEE (Evolution Génome Environnement) 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 9th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/> Pierre.Pontarotti@up.univ-mrs.fr

McMasterU Astrobiology May24-Jun4

2nd Announcement

Origins Institute conference/workshop on:

“Astrobiology and the Origins of Life” conference: May 24-28/2005 workshop: May 30-June4/2005 McMaster University, Hamilton, Ontario

<http://origins.mcmaster.ca/conferences.html> It is a great pleasure to announce the full programme for the

Origins Institute conference and workshop on astrobiology and the origins of life, being held this spring at McMaster University (please see website for all of the details). The conference will provide both authoritative, interdisciplinary reviews as well as the latest results in a number of areas of interest to astrobiology. The workshop that follows will explore a number of these areas through informal discussion, with time to work and begin collaborative projects. The venue features the latest in lecture theatres and interactive facilities on the pleasant campus of McMaster University.

The programme for the ONE WEEK workshop is also available. NOTE: in order to concentrate the workshop into a very effective programme, the organizers have decided to shorten it to 6 days, rather than the original advertised length of 2 weeks.

This will be an international meeting with more than 120 participants from many countries already registered. We encourage anyone interested in this programme, which ranges over a number of areas in planetary science and evolutionary biology, to please register as soon as possible in order to take advantage of the reduced hotel rates.

You may still present a poster in the conference, or apply for some remaining openings in our workshop. Please use the registration form available on the website.

To assist us in organizing the conference, please inform Rosemary McNeice, via email at mcneicer@mcmaster.ca, of the following:

- 1) If you have special dietary requirements.
- 2) If you are planning to attend the Barbeque on Saturday, May 28.
- 3) If you are interested in taking the city bus for transportation to and from the University, tickets and a bus route map will be available at the front desk of your hotel.
- 4) If you would like to adventure on the Maid of the Mist during the Niagara excursion. The organizers will lead all interested parties on a cruise in the Niagara River beneath the falls on the famous Maid of the Mist, tickets are \$13.00 and can be purchased at the booth.

Please monitor the website for updates

We hope to welcome you at McMaster University to participate in this exciting and forefront area of contemporary science.

With best regards, Ralph Pudritz, Director, OI

For the organizing committee.

Ralph E Pudritz | Office: Bourns Bldg (ABB 318) | Telephone/voicemail: (905) 525-9140 x23180 Physics

& Astronomy | Secretary: Cheryl Johnston(905) 525-9140 x27356 McMaster University | FAX: (905) 546-1252 Hamilton, Ontario | Canada L8S 4M1 | E-mail: pudritz@physics.mcmaster.ca

Rosemary McNeice, Origins Secretary McMaster University ABB-241, 1280 Main Street West, Hamilton, ON L8S 4M1 905-525-9140 X23531

“J. R. Stone” <jstoner@mcmaster.ca>

Oslo HennigSociety July25-29 PeliminaryProgram

24th MEETING of the WILLI HENNIG SOCIETY

25-29 July 2005 in the mountains north of Oslo, Norway

PRELIMINARY SYMPOSIUM PROGRAM

- Phylogenomics (organized by David Liberles and Jens Lagergren)
- Ancient DNA (organized by Lutz Bachmann)
- Lower-level Phylogenetics of Angiosperms (organized by Victor Albert)

Additional presentation proposals on these themes are welcome, as are others either within the symposia topics or on any area within phylogenetic biology. All poster presentations are welcome. The Willi Hennig Society strongly encourages participation from students and postdocs on their developing research, either theoretical or empirical. There are several cash student prizes that will be awarded.

****REGISTRATION AND ABSTRACT SUBMISSION IS NOW OPEN****

See http://folk.uio.no/victoraa/Frontpage_files/-slide0003htm DEADLINE for registration and abstract submission is 1 July 2005.

Victor A. Albert

http://folk.uio.no/victoraa/index_files/slide0002.htm

“Victor A. Albert” <victor.albert@nhm.uio.no>

Switzerland SexualSizeDimorphism Aug21-26

THE EVOLUTION OF SEXUAL SIZE DIMORPHISM Workshop organized by Wolf Blanckenhorn, Tamas Szekely & Daphne Fairbairn 21-26 August 2005, Switzerland

<http://www.bath.ac.uk/bio-sci/szekely/workshop/SSD%20Workshop2%20webmod.htm>

We are organizing an international Workshop on sexual size dimorphism (SSD) at the Centro Stefano Franscini Conference (CSF) Center on Monte Verità, near Locarno in southern Switzerland.

The objectives of the Workshop are to - bring together researchers working on various aspects of SSD; - overview the pattern of SSD in major animal and plant taxa; - investigate the function and mechanisms of SSD.

Our main goal is to adopt a truly interdisciplinary approach, and encourage all participants to go beyond his/her specific research field.

We have invited a group of internationally renowned researchers to the Workshop. In addition, we have space for approximately 35 researchers including post-graduate students and post-docs.

The scientific program will consist of about 10 half-hour plenary lectures given by invited speakers. There will further be contributed short oral and poster presentations, and discussion in groups. We welcome post-docs, MSc and Diploma students, and PhD students. Participants are expected to attend the entire 5-day workshop, and their number is limited to 60.

The cost of the Workshop will be approximately 950 Swiss Francs (about 650 Euro or 800 US\$) that includes registration fee, accommodation and all meals. For postgraduate participants the Association for the Study of Animal Behaviour (ASAB) has generously provided support to defer travel cost, and the CSF has generously provided support to defer the cost of room and full board on a competitive basis. Furthermore, we shall apply for Swiss National Fund funding to defer the travel cost for delegates from Eastern European countries. To qualify for this support, please contact Wolf Blanckenhorn.

Abstract submission and registration deadline: 31 April 2005

Please note that if space is limited applicants offering a presentation will be preferred. One participant is expected to present only one oral paper or poster. Instructions for payment and detailed travel information will soon be available on the web site.

If you are interested in attending, please email the following details to our conference e-mail address: congres2@zoolmus.unizh.ch

1. Full name including title
Gender

2. Institution & Department

3. Contact mailing address including street address, city and postcode
Phone Fax Email

4. Proposed presentation
Type of presentation (Talk/Poster)
Title of presentation
Authors including the presenting author (*)
Abstract (max. 250 words)
Keywords (5)
Special technical needs

The Workshop is generously funded by The Centro Stefano Franscini, the Swiss Zoological Society, the Ethological Society and the Zoological Museum of Zurich.

Best regards,

Wolf Blanckenhorn wolfman@zoolmus.unizh.ch Tamas Szekeley T.Szekeley@bath.ac.uk Daphne Fairbairn daphne.fairbairn@ucr.edu

UFerrara ItalianEvolBiol Aug24-26

Cari amici e colleghi,

Il Dipartimento di Biologia dell'Università di Ferrara ospiterà il 24-26 agosto il Primo Congresso dei Biologi Evoluzionisti Italiani. Le giornate del 24-25 saranno dedicate a discussioni scientifiche, con presentazioni di evoluzionisti italiani e stranieri. Il 26 agosto una riunione dei partecipanti al congresso darà vita ad una società italiana di biologia evoluzionistica (il nome esatto di questa verrà deciso durante la riunione).

Un limitato sostegno finanziario sarà disponibile per chi deve fronteggiare le spese di viaggio maggiori e non ha fondi per farlo. Informazioni riguardo la preparazione dei riassunti per le presentazioni, la registrazione, gli alloggi, e la richiesta di contributo sono disponibili sul sito <http://web.unife.it/progetti/genetica/CongBiolEvol/>. Il comitato scientifico ed il comitato organizzatore (si veda il sito web per le liste complete) desiderano estendere l'invito a partecipare a tutti gli evoluzionisti italiani, sia in Italia che allestero. Vi invitiamo ad informare di questo annuncio tutti coloro che potrebbero

essere interessati a partecipare

Dear Friends and Colleagues,

It gives us great pleasure to announce that the First Congress of Italian Evolutionary Biologists will be held at the Department of Biology of the University of Ferrara (Ferrara, Italy), from August 24 to 26, 2005. The first two days will be devoted to scientific presentations. On August 26, an assembly will take place to found the Italian Society of Evolutionary Biology.

The organizing and the scientific committees (see the web site for the names) are pleased to extend the invitation to participate to all interested parties.

A limited amount of financial support will be available for those with the highest travel expenses.

Detailed instructions (in Italian) are available at the URL

<http://web.unife.it/progetti/genetica/CongBiolEvol/>
Francesco Santini Marie Curie Fellow

Muséum National d'Histoire Naturelle Département Systématique et Evolution Case Postale N 26 43 rue Cuvier 75231 Paris cedex 05 France

Phone: ++33 (0) 1 40 79 37 35 Fax: ++33 (0) 1 40 79 38 44 E-mail: fsantini@mnhn.fr

“Coordinamento Italiano dei Biologi Evoluzionisti” (CoEvol) “Italian Committee of Evolutionary Biologists” (CoEvol)

Home page: www.coevol.org Mailing list: http://it.groups.yahoo.com/group/biologia_evoluzionistica/
Journal Club: http://it.groups.yahoo.com/group/CoEvol_Journal_Club/ francesco.santini@utoronto.ca

UMontpellier PhDStudents

11th Meeting of PhD Students in Evolutionary Biology

Pre-registration for the 11th Meeting of PHD Students in Evolutionary Biology is now open online at: <http://kimura.univ-montp2.fr/mpseb> The organizing committee:

Eric Bazin <bazin@univ-montp2.fr> Emmanuelle Billard <billard@sb-roscoff.fr> Stéphane De Mita <demita@ensam.inra.fr> Julien Dutheil <Julien.Dutheil@univ-montp2.fr> Emmanuelle Eveno <eveno@pierroton.inra.fr> Baptiste Faure <bfaure@sb-roscoff.fr> Matthieu Faure

<matthieu.faure@univ-montp2.fr> Olivier Lepais
 <Lepais@pierroton.inra.fr> Delphine Muths
 <muths@sb-roscoff.fr>

UToronto EGLME Apr30 3

Eastern Great Lakes Molecular Evolution Meeting

THIRD ANNOUNCEMENT

Saturday, April 30, 2005 University of Toronto Koffler
 Institute for Pharmacy Management 569 Spadina Ave
 Toronto, Ontario

The 2005 Eastern Great Lakes Molecular Evolution
 Meeting will be held on Saturday, April 30, 2005,
 at the Koffler Institute for Pharmacy Management at
 the University of Toronto, in Toronto, Ont. Below
 is the schedule for the meeting. Additional informa-
 tion including poster titles and abstracts (within a few
 days) can be found at: [http://bbc.botany.utoronto.ca/-
 EGLMEM/](http://bbc.botany.utoronto.ca/-EGLMEM/) 8:30 - 9:00 Coffee 9:00 - 9:15 Welcome,
 Allan Baker, ROM Avrum Gotlieb, Chair Dept Lab-
 oratory Medicine & Pathobiology 9:15 - 10:00 Andy

Clark, Cornell University Talk TBA 10:00 - 10:45 Brian
 Golding, McMaster University Talk TBA 10:45 - 11:00
 Coffee 11:00 - 11:45 Jeff Lawrence, University of Pitts-
 burg Mapping lateral gene flow in bacteria 11:45 - 12:05
 Stephen Wright, York University The Effect of Artifi-
 cial Selection on the Maize Genome 12:05 - 12:25 John
 Pool, Cornell University Inferring the Combined Ef-
 fects of Population History and Positive Selection on
 Genetic Variation in Afrotropical and Cosmopolitan
Drosophila melanogaster 12:25 - 2:00 Lunch 2:00 - 2:45
 Paul Hebert, University of Guelph DNA Barcodes and
 Biodiversity 2:45 - 3:30 Carlos Busamante, Cornell Uni-
 versity Detecting selection in the human genome from
 comparative population genomic data 3:30 - 4:15 Cof-
 fee and Poster Session 4:15 - 4:35 Sergei Guselnikov,
 University of Rochester Evolution of FcR- and KIR-like
 Leukocyte Receptors: from Teleostei to Mammalia 4:35
 - 4:55 Sasa Stefanovic, University of Toronto at Missis-
 sauga Parasitic Plants as a Mechanism of Horizontal
 Gene Transfer in Land Plants 4:55 - 5:15 Wendy Wong,
 Cornell University Identification of Physicochemical Se-
 lective Pressure on Protein Encoding Nucleotide Se-
 quences
 5:15 - 5:25 Closing Remarks and Poster Award David
 Irwin, University of Toronto 5:25 - 7:00 Reception
 david.irwin@utoronto.ca

GradStudentPositions

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**DartmouthCollege
LizardPopulations**

I have a fellowship available beginning in fall of 2006 or
 2007 in the Ecology and Evolutionary Biology Program
 of the Department of Biological Sciences at Dartmouth
 College. The successful candidate will (1) participate in
 funded studies that are broadly organized around the

theme of natural and sexual selection in lizard populations (2) develop their own Ph.D. research program.

For more information, see: <http://www.dartmouth.edu/~bio125/Calsbeek/> Fellowships are also available to work in other laboratories within the EEB program at Dartmouth College. See: <http://www.dartmouth.edu/~biology/graduate/eeb> Highly qualified candidates may be eligible for a GAANN fellowship that provides a stipend of ~\$30,000.

Please contact me at Calsbeek@ucla.edu

Ryan Calsbeek Center for Tropical Research 1609 Hershey Hall University of California, Los Angeles 90095 <http://www.dartmouth.edu/~bio125/Calsbeek/> Ryan Calsbeek <calsbeek@ucla.edu>

Europe GeneTime

GeneTime Fellowships in Ancient Biomolecules

PhD and short-term post-graduate fellowships are offered to train the highest quality PhD level researchers from Europe and associated countries in ancient biomolecular research.

The GeneTime PhD program is offered between the Universities of York, Oxford, Copenhagen and Dublin, and emphasises a broad knowledge base and exposure to a range of state-of-the-art techniques for the analysis and interpretation of ancient proteins and DNA. Research topics encompass the use of ancient biomolecules in archaeology, environment, evolution and domestication.

Four PhD Fellowships and multiple short term (4 month) fellowships are available.

Applicants should not have resided or carried out their main activity in the country of the host institution for more than 12 months in the 3 years immediately prior to the start date.

All instruction will be in English

The value of the awards are between 21k and 40k per annum - this to cover costs of living expenses plus fees (but excluding travel). The majority of the funding (70%) is to support EU nationals.

For more details see the GeneTime website <http://www.york.ac.uk/depts/arch/GT>

LundU SexualConflicts

PhD Studentship in Animal Ecology, Dept of Ecology, Lund University, Sweden. Title: evolutionary sexual conflicts and morphological differentiation in diving beetles.

Supervisors: Dr Roger Härdling (Dept. Animal Ecology, principal supervisor), Dr Erik Svensson (Dept. Animal Ecology, second supervisor)

Description: Evolutionary conflicts between the sexes occur because strong competition among males selects for male traits that increase the probability that their bearer mates successfully. In sexual conflicts, such male traits are favoured by selection in spite of a harmful effect on female fitness. However, because male traits harm females, selection favours females that counter-adapt to the male traits.

Members of the family Dytiscidae, generally known as diving beetles, show a range of very conspicuous sexual characters that have been interpreted as evidence of sexual conflict. Males have the three basalmost segments of the fore-, and often middlelegs, enlarged to a round plate scattered with numerous suction discs, varying in size and numbers. These are used to grab the female at mating attempts. There is no precopulatory courtship involved but males attack females from above placing his suctiondisc-equipped forefeet on the females back. Females often have a modified back compared to males. The female back may be covered by furrows, hairs or granulations where the male back is completely smooth. Interestingly however, many species and populations are dimorphic, so that a completely smooth, male-like female morph coexists with the modified morph. It has been proposed that the female modifications have evolved to decrease costs of e.g. male harassment, but there is no empirical evidence of such costs. Also, this hypothesis cannot easily explain the existence of female polymorphism.

The aim of the project is to investigate fitness effects of sexual conflict in the diving beetle *Dytiscus marginalis*, that may explain the evolution of morphological differentiation within and between the sexes. The applicant should have a background in evolutionary ecology. Experience of working with insects as experimental animals is of advantage, but not necessary to qualify.

Applications: Please submit your CV, a letter describ-

ing your research interest and skills, a copy of master thesis or equivalent, and contact information for two references. Please quote the reference number for this position: Ref. nr. 185

Applications should be sent to Registrator Kansli N University of Lund, Box 118, Se-22100 Lund, Sweden

no later than April 29, 2005

For further details, contact Roger Härdling Tel: + 46 (0)46 222 7926 Fax + 46 (0)46 222 4716; email: roger.hardling@zoekol.lu.se

– Roger Hardling Phone: +46 (0)46 222 7926
Dept of Animal Ecology Fax: + 46 (0)46 222 4716 Ecology Building University of Lund 223 62 Lund, Sweden <http://www.biol.lu.se/zoekologi/-epb/people-en/rh-en/rh-en.htm> Roger Härdling <roger.hardling@zoekol.lu.se>

ulating interdisciplinary scientific environment. The successful candidate will be given opportunity to collaborate with leading international groups within the field.

Trondheim is a beautiful city situated in central parts of Norway. For more information, please visit <http://www.trondheim.com/engelsk/tourist.info/>. Please send application, CV, and annexes (including copies of master thesis or equivalent) in three copies to Faculty of Natural Science and Technology, Norwegian University of Science and Technology, N-7491 Trondheim, Norway before 23. May 2005, with reference number NT-23/05. Please include names and contact information of two references. For more information, please contact Hans K. Stenat stenoiien@bio.ntnu.no, or go to http://www.bio.ntnu.no/Molecular_Ecology_and_Evolution/. stenoiien@bio.ntnu.no

Trondheim MolEvolEcol

PhD-student position in Molecular Ecology and Evolution Department of Biology, Norwegian University of Science and Technology, Trondheim

A 4 year PhD-position is now available within the research area molecular ecology and evolution. The project will focus on factors hypothesized to explain patterns of genetic variability found within natural populations of the model plant *Arabidopsis thaliana*. The main emphasis will be genetic and demographic studies of Scandinavian populations of the plant. Of particular interest will be to determine the relative roles of stochastic factors and natural selection in the evolution of fitness traits. The general area of the project is defined, but there will be possibilities for qualified students to develop their own interests within this framework. The project requires knowledge in how to conduct various molecular analyses including DNA sequencing.

We seek a highly motivated individual with good communication abilities and with capabilities to work independently and in team with others. Candidates should possess an MSc degree in evolutionary genetics, ecology, population genetics, molecular biology or a related field, and should have a strong interest in using molecular methods to study key questions in ecology and evolution

We can offer a salary of 34.440 per year and a stim-

UCollegeLondon AnimalPhylogeny

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

University College London

A Ph.D studentship is available for 36 months from September 2005, funded by the Marie Curie Research Training Network “ZOONET”, to study Metazoan Phylogeny. The project will involve molecular biological work (PCR, cloning, sequencing) to provide novel sequence data and bioinformatics work (data-mining and phylogenetics).

Applicants should have a relevant B.Sc, M.Sc. or equivalent. Relevant experience of bioinformatics and/or computer programming are desirable. Training will be given in the full range of approaches relevant to Evolutionary Developmental Biology and phylogenetics (e.g. molecular biological techniques, bioinformatics, phylogenetics and programming if needed), and will 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 the UK for more than 12 months in the 3 years immediately prior to the appointment.

The salary will be between approximately £14600 and £15800 per annum including mobility allowance. In addition there will be an annual travel allowance (distance dependent) as well as a one-off Career exploration allowance of approximately £1260.

Please note, the amounts quoted here for salary, mobility and travel allowance will be dependent upon the EU exchange rate at the time of appointment.

Applicants should send their CV together with a completed Equal Opportunities form and Job Application and the postal and email addresses of at least two referees, to Max Telford at the address above.

The closing date for applications 15th April. Only shortlisted candidates will be contacted after that date, by 15th May

For further details and other positions see <http://www.zoonet.eu.com> – 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/new/admin/-staffpages/telford/telford.html> Zoonet website:
<http://www.zoonet.eu.com> m.telford@ucl.ac.uk

UCollegeLondon EvoDevo

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

University College London

A postdoctoral position is available for 30 months from September 2005, funded by the Marie Curie Research Training Network “ZOONET”, to study comparative arthropod development. Potential projects include

- (i) Comparison of regulation and function of the divergent Hox genes *fushi tarazu* (*ftz*) and *zerknüllt* (*zen/Hox3*) between arachnids and insects.
- (ii) Identification of recently duplicated genes in *Drosophila* species and analysis of their regulation and function.
- (iii) Comparison of head segment patterning in crustaceans and insects.

Applicants should have a doctorate and relevant experience of molecular biology and comparative developmental studies. Training will be given in the full range

of approaches relevant to Evolutionary Developmental Biology, and may require exchanges between laboratories in the ZOONET Network, as well as participation in network meetings

In the selection process, the sponsor stipulates that:

Candidates must have at least four and no more than ten years (full time equivalent) of graduate research experience; At the start of their fellowship, researchers may not have resided or carried out their main activity (work, studies, etc) in the UK for more than 12 months in the 3 years immediately prior to the appointment.

The salary will be between approximately £30,300 and £32,700 per Annum including London Allowance. In addition there will be an annual travel allowance (distance dependent) as well as a one-off Career exploration allowance of approximately £1260.

Please note, the amounts quoted will be dependent upon the EU exchange rate at the time of appointment.

Applicants should send their CV and publication list together with a completed Equal Opportunities form and Job Application and the postal and email addresses of at least two referees, to Max Telford at the address above.

The closing date for applications 15th April. Only shortlisted candidates will be contacted after that date, by 15th May For further details and other positions see <http://www.zoonet.eu.com> – 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/new/admin/-staffpages/telford/telford.html> Zoonet website:
<http://www.zoonet.eu.com> m.telford@ucl.ac.uk

ULondon FlowerColour

Developing an open-access database to study the evolution of flower colour - A CASE PHD studentship at Queen Mary, U London, and Kew Gardens

We are seeking to employ a bioinformatics PhD student or a biology PhD student with expertise in programming to embark on two tasks: 1. to construct an online, open access database for floral reflectance, and 2. to use this database to explore the following questions: is there ecological divergence between flower colours of plants that flower sympatrically (i.e. in the same habi-

tat)? Do flower signals addressed to pollinators with different colour vision systems (e.g. bees and flies) differ in their colouration? Does UV reflectance differ depending on the incidence of UV radiation at different Alpine altitudes and tropical latitudes? Do flower colours (as perceived by pollinators) differ in different habitats, depending on illumination conditions and predominant background materials? Does the relatively recent increase of UV radiation in Australia have an impact on the flower colouration there, as mediated by the selection imposed through bee pollinators? These are some starting points, but the project would have many degrees of freedom for a student to explore, and build the kind of scientific independence that is necessary at the outset of a scientific career. The project will undoubtedly result in several high impact publications. The other major task would be to merge the databases from Kew and Queen Mary, to turn them into an openly accessible web based tool. The student will be trained in concepts of modern ecology and evolutionary biology, with the special perspective of the sensory ecology of pollinating insects. It is hoped the student will bring along expertise in database programming, but the bioinformatics officer at Kew Gardens is ready to help if that should be necessary.

Supervisors: Dr. L. Chittka (Queen Mary) and Dr. V. Savolainen (Kew Gardens) For further information please contact Lars Chittka at l.chittka@qmul.ac.uk Applications should be sent electronically to l.chittka@qmul.ac.uk by 10 May 2005 The person hired has to be a UK citizen.

Dr. Lars Chittka Reader in Behavioural Ecology School of Biological Sciences Queen Mary College University of London Mile End Road London E1 4NS UK

Email: l.chittka@qmul.ac.uk Tel: *44 (0) 20 7882 3043 Fax: *44 (0) 20 8983 0973 <http://www.biology.qmul.ac.uk/research/staff/chittka/-chittka.htm> Room 2.10 -> 2.13

Lars Chittka <l.chittka@qmul.ac.uk>

UVermont PlantEvol

I am seeking graduate students interested in the general research areas of plant population and community ecology to join my lab in September 2005. Research in the lab includes both theoretical and experimental plant population and community ecology. Students whose interests include the evolution of invasive ability, and the

role of spatial processes in maintaining diversity are especially encouraged to apply. Graduate stipends, which are guaranteed for the entire length of your PhD are \$21,500 per year and includes health insurance coverage.

Interested students are asked to submit a CV, a copy of academic transcripts and contact information for three references to Jane.Molofsky@uvm.edu.

Jane Molofsky, PhD Associate Professor Department of Botany University of Vermont Burlington, Vermont Phone:802-656-0430 Fax :802-6560440 Email: Jane.Molofsky@uvm.edu

–
jmolofsk@uvm.edu

UVienna MothEvol

PhD position in tropical moth ecology

A PhD position is available at the Department of Population Ecology (head: Prof. Dr. Konrad Fiedler) at the University of Vienna, Austria. Duration: 2 years, 1 year extension possible. Funded by the German Research Foundation as part of the interdisciplinary research group "Functionality of a tropical montane forest" in Ecuador (see www.bergregenwald.de).

Topic: life-history diversity of arctiid moths in the montane forest zone of the Ecuadorian Andes. The applicant shall address if and how life-history characteristics of (common) arctiid species determine the micro-distribution of these moths in elevational and disturbance gradients. The fauna of the study area is rather well characterized and extremely species-rich (440 + species). Among the characters to be measured across a larger sample of species are: body size, longevity, fecundity, egg size, mode of egg-laying, breadth of larval diet, adult food intake. Data will be obtained through field collection of adults and larvae, as well as in breeding experiments.

The successful candidate must hold a MSc degree (or equivalent) in Biology, Zoology, Entomology, Ecology or a related discipline. Previous experience with field work in tropical countries and/or in working with Lepidoptera is advantageous. Candidates with proficiency in Spanish language are highly welcome. It is expected that the candidate will stay in Ecuador for two periods of 6 months duration each.

Applicants are invited to send their applications in one file (preferably in pdf format) to Prof. Dr. Konrad Fiedler (e-mail: konrad.fiedler@univie.ac.at). The application should include a brief, but informative CV, a copy of the academic degree(s), a list of publications and conference participations (if applicable), copies of publications in pdf format (if available), and an abstract or outline of the research done during the MSc thesis.

Only in cases where an electronic submission is impossible, applications may also be sent to the following postal address: Univ.-Prof. Dr. Konrad Fiedler, Dept. of Population Ecology, University of Vienna, Althanstrasse 14, A-1090 Vienna, AUSTRIA.

Closing date for applications: 15 May 2005.

The candidate is expected to start preferably at 1 June 2005 with her/his work at Vienna.

UWales OtterPopulations

The School of Biological Sciences, University of Wales, Bangor has an immediately available PhD position to work on radio-tracking and genetic structure of European otters within and among different catchments in the North Wales area. This studentship is only available to citizens of the European Union and is for a fixed term.

For details contact me at the address below.

Chris

–

Dr. Chris Gliddon School of Biological Sciences University of Wales, Bangor LL57 2UW United Kingdom

Tel: +44 (0)1248 382533 FAX: +44 (0)1248 382569 Mobile: +44 (0)7941 060423

chrisg@sbs.bangor.ac.uk

YorkU EvolGenomics

I am seeking graduate students interested in evolutionary and population genomics to join my lab in September 2005. Research in the lab is focused on the study

of plant genome evolution and molecular population genetics. We are particularly interested in understanding the forces driving genome evolution, and in testing the role of natural selection at the genome level. Potential research projects include 1) investigating the effects of polyploidy on the evolution of transposable elements, 2) testing for the effects of gene expression level on molecular evolution, and 3) distinguishing the effects of demographic history and positive Darwinian selection on patterns of genetic diversity. Research projects range from primarily lab-based collection and analysis of DNA sequence diversity data, to theoretical modeling and computer-based analysis of genome sequences. Further information about research in the lab can be found at <http://www.yorku.ca/stephen> and information on York University's Biology graduate program can be found at <http://www.biol.yorku.ca/grad/>. Interested students are asked to submit a CV, a copy of academic transcripts and contact information for three references to stephenw@yorku.ca by April 15, 2005.

Stephen I Wright, PhD Assistant Professor Department of Biology York University 4700 Keele St. Toronto, ON Canada M3J 1P3 Phone: (416) 736-2100 ext. 20213 Fax: (416) 736-5698 –

ZurichETH EvolBiol

PhD position in Evolutionary Biology

A 3-years PhD position is available in the group of Ecology and Evolution at the ETH in Zurich, Switzerland. We are looking for a motivated and independent student who is interested in fundamental aspects of evolutionary biology and is willing to employ modern molecular techniques.

The research project focuses on evolutionary aspects of phenotypic variation. We are interested in genetic and non-genetic sources of phenotypic variation and in how natural selection acts on these sources. The work will be primarily experimental, using evolution experiments with bacteria and viruses as well as genetic tools.

This work will contribute to an exciting new field at the interface between evolutionary biology and other biological disciplines, including molecular biology, bio-engineering, microbiology and systems biology. Candidates from any biological background are welcome to apply.

A Masters or equivalent is required. The ETH of-

fers an international and stimulating research environment, with English as the official working language. Please send your application or informal requests for further information to Martin Ackermann (Martin.Ackermann@env.ethz.ch). See also <http://www.eco.ethz.ch/portraits/ackermann/>

Martin Ackermann Ecology & Evolution ETH Zentrum NW Clausiusstrasse 25 8092 Zuerich Switzerland Tel.: +41 1 63 26928 Fax: +41 1 63 21271 www.eco.ethz.ch

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AustraliaCSIRO GeneFlow

CSIRO Sustainable Ecosystems and the Australian National Wildlife Collection are advertising a 2-year position for project leader for a study of gene flow in fragmented landscapes, as detailed below.

Further information and application materials are available at http://recruitment.csiro.au/asp/-Job_Details.asp?RefNo_05%2F323 or via the links below. Closing date for applications is 8 May 2005.

Position Details - 2005/323 - Project Leader - Gene Flow in Fragmented Landscapes

Job Profile

Reference Number: 2005/323 Position Title: Project Leader - Gene Flow in Fragmented Landscapes Division: Sustainable Ecosystems Location: Gungahlin, ACT Classification: CSOF5 to CSOF5 Salary Range: \$66K - \$73K + Superannuation Tenure: 2 years Applicants: Open to Australian Residents Only Applications Close: 8 May 2005 Job Category: Administrative and Support

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The Project Leader position involves primary responsibility for the gene flow sub-project under the multi-disciplinary project entitled "From Science to Practice: R&D for Implementing Native Vegetation Policy in NSW" and funded by the NSW Environmental Trust. The successful candidate will manage field aspects of the project, co-manage genetic aspects, and be responsible for communication of results in both scientific and public formats.

The goal of this project is to provide high quality, integrated science for native vegetation management in NSW, especially for management actions for biodiversity in Property Vegetation Plans. The project is

built on scientific investigation, integration and collaboration and will investigate landscape restoration designs, native vegetation regeneration strategies, vegetation condition, pest management in native vegetation, and restoring genetic biodiversity and ecological function in rural landscapes.

The ANWC sub-project involves investigation of gene flow in vertebrates in fragmented woodlands in southern/central NSW. The research will focus on enhancing gene flow of vertebrates in fragmented landscapes and will address such issues as corridor width, corridor age, remnant size and landscape configuration. Target species will likely include birds (e.g., Brown Treecreeper) and reptiles (e.g., Common Skink). The research will contribute to effective designs for revegetation and for preserving natural remnants of native habitat to maintain and enhance gene flow in fragmented landscapes.

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Position Description

Key behaviours

* Demonstrated ability to use initiative in research. * Ability to work with limited supervision and exercise sound judgement. * Superior inter-personal and communication skills and the ability to build effective working relationships. * Excellent team player. * Enthusiasm for and dedication to multi-disciplinary science with quantifiable benefits for end-users.

Key result areas

Research

* Design field experiments, including selecting and evaluating suitable field sites and study species. * Coordinate with molecular laboratory manager in design of genetic sampling and molecular aspects of project. * Coordinate and participate in fieldwork, gathering samples for molecular analysis. * Work with molecular laboratory manager to analyse molecular data and interpret results. * Communicate results to stakeholders, including preparing reports and briefings to deadlines. * Prepare scientific papers. * Oversee financial and budgetary requirements of contracted project.

Teams

* Liaise with project Knowledge Broker and other team leaders and manage communication of sub-project. * Liaise with molecular laboratory manager to ensure analytical milestones are met.

* Facilitate project management through liaison with business services.

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

BozemanMT LabTech

April 20, 2005 JOB: DNA Lab technician/manager

The Conservation Genetics Laboratory at Montana State University in Bozeman is looking for a head laboratory technician.

Lab work will focus on genotyping microsatellite loci. Upcoming projects include estimating relationship among black bears, detecting hybrids between rainbow and cutthroat trout, and counting mountain lions from scat and hair samples. Because this laboratory works on a variety of species, experience troubleshooting all steps in the genotyping process is necessary. Experience with ABI technology and non-invasive samples a plus.

Responsibilities will also include ordering supplies, managing budgets, and training graduate students.

Salary: \$26,000+ (depending on experience) and benefits Start date: ASAP

Bozeman, MT is a medium sized university town in the Rocky Mountains that consistently is rated one of the most livable communities in the West. There are excellent opportunities for outdoor recreation just outside of town.

Applications will be accepted until the position is filled. To apply, send a CV (including 3 references) and cover letter to

Steven Kalinowski Department of Ecology 310 Lewis Hall Bozeman, MT 59717

For more information, don't hesitate to contact Steven Kalinowski at skalinowski@montana.edu (406) 994-3232

Steven Kalinowski Assistant Professor of Conservation Genetics Department of Ecology Lewis Hall 311B Montana State University Bozeman, MT 59717

email: skalinowski@montana.edu internet: www.montana.edu/kalinowski phone: (406) 994-3232 FAX: (406) 994-3190

CSIRO Australia GeneFlow

CSIRO Sustainable Ecosystems and the Australian National Wildlife Collection are advertising a 2-year position for project leader for a study of gene flow in fragmented landscapes, as detailed below.

Further information and application materials are available at [http://recruitment.csiro.au/asp/-Job_Details.asp?RefNo 05%2F323](http://recruitment.csiro.au/asp/-Job_Details.asp?RefNo%2005%2F323) or via the links below. Closing date for applications is 8 May 2005.

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The Project Leader position involves primary responsibility for the gene flow sub-project under the multi-disciplinary project entitled "From Science to Practice: R&D for Implementing Native Vegetation Policy in NSW" and funded by the NSW Environmental Trust. The successful candidate will manage field aspects of the project, co-manage genetic aspects, and be responsible for communication of results in both scientific and public formats.

The goal of this project is to provide high quality, integrated science for native vegetation management in NSW, especially for management actions for biodi-

versity in Property Vegetation Plans. The project is built on scientific investigation, integration and collaboration and will investigate landscape restoration designs, native vegetation regeneration strategies, vegetation condition, pest management in native vegetation, and restoring genetic biodiversity and ecological function in rural landscapes.

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Position Description

Key behaviours

- * Demonstrated ability to use initiative in research.
- * Ability to work with limited supervision and exercise sound judgement.
- * Superior inter-personal and communication skills and the ability to build effective working relationships.
- * Excellent team player.
- * Enthusiasm for and dedication to multi-disciplinary science with quantifiable benefits for end-users.

Key result areas

Research

- * Design field experiments, including selecting and evaluating suitable field sites and study species.
- * Coordinate with molecular laboratory manager in design of genetic sampling and molecular aspects of project.
- * Coordinate and participate in fieldwork, gathering samples for molecular analysis.
- * Work with molecular laboratory manager to analyse molecular data and interpret results.
- * Communicate results to stakeholders, including preparing reports and briefings to deadlines.
- * Prepare scientific papers.
- * Oversee financial and budgetary requirements of contracted project.

Teams

- * Liaise with project Knowledge Broker and other team leaders and manage communication of sub-project.
- * Liaise with molecular laboratory manager to ensure analytical milestones are met.

- * Facilitate project management through liaison with

business services.

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CornellU Bioinformatics

Job Description The Department of Biological Statistics and Computational Biology seeks an excellent C/C++ computer programmer with expertise in bioinformatics, numerical optimization, and data mining. The person will work closely with Prof. Carlos D. Bustamante and his team to develop and implement computational algorithms used in statistical genomics. As part of a dynamic research group working on problems at the interface of computational statistics, evolutionary genomics, and bioinformatics, the person must possess excellent programming skills and be willing to handle (and prioritize) multiple tasks simultaneously. Responsibilities include algorithm development and implementation, data base management, data analysis, and general scientific computing support. The programmer will also be required to work on other projects using advanced numerical and simulation methods. Expert knowledge of C/C++, and PERL required. Previous experience in Bioinformatics as well as knowledge of SQL/MYSQL strongly preferred. See http://www.bscb.cornell.edu/Homepages/-Carlos_Bustamante/ for relevant information on research interest, etc.

Located in Ithaca, N.Y., Cornell University is a bold, innovative, inclusive and dynamic teaching and research university where staff, faculty, and students alike are challenged to make an enduring contribution to the betterment of humanity.

Required Qualifications: Bachelor's degree; more than 2 years less than 3 year experience or equivalent. Degree in comp science, mathematics, engineering or similar area is required. Must have proven programming skills in C/C++ and PERL familiarity with probability and theoretical statistics. Must possess excellent programming skills and be willing to handle (and prioritize) multiple tasks simultaneously.

Preferred Qualifications: Familiarity w/common nu-

merical methods, simulation algorithms, development of graphical user interfaces, PERL, JAVA, Linux, & knowledge of advanced probability theory are desired. Previous Bioinformatics experience strongly preferred as well as knowledge of SQL/MYSQL and R. How to apply: Informal inquiries can be sent to Carlos Bustamante (cdb28@cornell.edu)

To apply, visit <http://www.ohr.cornell.edu/jobs/-index.html> and look for job number "03713" which is the Prog/Analyst II class.

You can also try the direct link below (may not work directly): https://cornellu.recruitsoft.com/servlets/CareerSection?art_ip_action=FlowDispatcher&flowTypeNo&pageSeq=2&reqNo7909vlet_language=en&csNo164

Cornell University is an equal opportunity, affirmative action educator and employer.

Carlos D. Bustamante Assistant Professor, Biological Statistics and Computational Biology Cornell University 101A Biotechnology Building Ithaca, NY 14853 http://www.bscb.cornell.edu/-Homepages/Carlos_Bustamante/ Carlos Bustamante <cdb28@cornell.edu>

CornellU LabManager InsectImmunity

A Lab Manager/Research Technician position (FT) is available in Brian Lazzaro's lab at Cornell University.

Our lab studies evolutionary biology of insect immune systems, with particular emphases on determining the quantitative genetic basis for variation in resistance/susceptibility to microbial infection, and on looking for signatures of natural selection on insect immunity genes. Our studies are focused on antibacterial immunity in *Drosophila melanogaster* and on antimalarial immunity in mosquitoes. The Technician will work under the direct supervision of the PI (Lazzaro) and will be responsible for independent research and general lab maintenance. Lab management will include maintenance of *Drosophila* stock collections, ordering of lab supplies, inventory of laboratory chemicals and equipment, and ensuring that all laboratory protocols and procedures adhere to University safety requirements. Research techniques employed may include, but are not limited to: DNA and RNA preparation, PCR and gel electrophoresis, SNP genotyping, DNA sequencing and

analysis of DNA sequence data, other molecular biology procedures as necessary, manipulation and maintenance of bacterial and insect cells in culture, and infection of live insects with bacteria to measure resistance phenotypes.

We recognize that no individual applicant is likely to possess experience in all of the areas described above, and would be happy to train a junior scientist. Above all, we are looking for someone who is personable, motivated and enthusiastic about working in a group environment.

More information about the lab can be found at http://www.entomology.cornell.edu/Faculty_Staff/Lazzaro/ Informal inquiries may be directed to Brian Lazzaro (BL89@cornell.edu).

Formal applications must be submitted through the Cornell Office of Human Resources. To apply: 1) Point your web browser to <http://www.ohr.cornell.edu/jobs/> 2) Follow the link to "Staff (non-academic) and Librarian Positions" 3) Search for position number 03755 in the "Keyword or Job Number Search" box. 4) Follow the "Technician III" link on the returned search match.

The following url may link directly to the position description: [https://cornellu.recruitsoft.com/servlets/CareerSection?](https://cornellu.recruitsoft.com/servlets/CareerSection?art_ip_action=FlowDispatcher&flowTypeNo=13&pageSeq=2&reqNo=)

Brian P. Lazzaro, Ph.D. Assistant Professor, Insect Genomics Department of Entomology 4138 Comstock Hall Cornell University Ithaca, NY 14853 USA

tel: 607-255-3254 fax: 607-255-0939 http://www.entomology.cornell.edu/Faculty_Staff/Lazzaro/

CornellU PlantGenomics

Job Posting- Programmer/Analyst III Description

The Department of Plant Breeding and Genetics seeks a highly organized person to provide web and database support for an inter-institutional NSF-funded Plant Genome project on Rice Evolutionary Genomics. The person will work closely with Prof. Susan McCouch and her team, and with collaborators in the Biological Statistics and Computational Biology Department at Cornell and the Department of Genetics at North Carolina State University to streamline data from a remote laboratory information management system (LIMS) to the project database and web site, develop cus-

tomized viewers and links to biological analysis programs, and develop middleware for pipelining data from the project database into the Gramene database (www.gramene.org). Good communication skills are required to maintain project integrity and to ensure a high level of tool compatibility among groups doing similar evolutionary genomics research in other NSF-funded projects on maize and wheat. The programmer will interact regularly with evolutionary biologists and will be expected to seek and share information on web and database-related software acquisition. See project description at: <https://www.fastlane.nsf.gov/servlet/showaward?award=0319553>.

This is a 1 1/2 year term position; renewal contingent on performance, funding and available work. Located in Ithaca, N.Y., Cornell University is a bold, innovative, inclusive and dynamic teaching and research university where staff, faculty, and students alike are challenged to make an enduring contribution to the betterment of humanity.

Qualifications

Bachelors with 2-3 years experience or equivalent combination. B.S. or M.S. degree in Biology, Computational Biology or related field, with at least 2 years experience in programming, strong web-programming skills and an interest in evolutionary biology. Two or more years of related IT/web experience, solid knowledge of web/database technologies (perl, PHP, XML, etc.), relational database design methodology including knowledge of MySQL, web site administration tools; experience with network security strategies; knowledge of current web infrastructure systems. The position requires ability to work independently while supporting an overall team effort. Excellent written and interpersonal communication skills, effective problem solving and strong organizational skills required.

Please apply on-line at: www.ohr.cornell.edu (Job # 03734) You can also try the direct link below (may not work directly): https://cornellu.recruitsoft.com/servlets/CareerSection?art_ip_action=FlowDispatcher&flowTypeNo=&pageSeq=2&reqNo8309&vlet_language=en&csNo164

Cornell University is an equal opportunity, affirmative action educator and employer.

Susan R. McCouch Professor, Dept. Plant Breeding & Genetics 162 Emerson Hall Cornell University Ithaca, NY 14853-1901 Phone: 607-255-0420 Fax: 607-255-6683

Susan McCouch <srm4@cornell.edu>

IndianaU DaphniaGenomics

Project Scientist position for Daphnia Genomics

The Center for Genomics and Bioinformatics (Indiana University, Bloomington) carries out research in genomics, bioinformatics and is a principle laboratory of the Daphnia Genomics Project. This project creates genomic resources for a developing model organism in ecological and evolutionary genomics research. These resources include cDNA libraries and gene collections, genetic markers and maps, cDNA microarrays and databases. The CGB is also engaged in microarray experiments aiming to identify the function of genes with environment-specific expression patterns.

The CGB has an opening for a Project Scientist. The successful candidate will assist other scientists in producing and testing genomic technologies. S/he will participate in research projects associated with these efforts. For instance, the Project Scientist will gain experience in all techniques involved in the production and use of microarrays, including the use of specialized equipment (e.g., Biomek Liquid Handling Robot, microarray printers and scanners, thermal cyclers) and various molecular biology techniques (e.g., RNA isolation, labeling and hybridization). The Project Scientist will also contribute to discovering quantitative-trait loci for ecologically important traits by DNA fingerprinting.

The Project Scientist will join the Daphnia Genomics group. This group interacts directly with four other research groups within the CGB and with collaborators from the Daphnia research community. We seek an individual with a B.Sc. or a Master's degree in Biology or Biochemistry and some laboratory experience in molecular biology or genomics. However, we will consider candidates with minimal previous experience and/or degrees in other scientific fields.

This position provides an excellent opportunity for a bench ("wet lab") scientist who wants to develop his/her skills within the context of a fascinating scientific field that is merging ecology and evolution with functional genomics. We expect to offer a competitive salary commensurate with experience.

Applications will be accepted until the position is filled. Those received by May 31, 2005 will be assured full consideration. Interested candidates may contact John Colbourne for further information (by sending email to

jobs@cgb.indiana.edu). Please submit a CV and a description of your background and interests, and have three (3) letters of recommendation sent directly to the address below. Be sure to refer to Project Scientist - DGC-002 within your cover letter.

Position #DGC-002 Attn: Project Scientist Center for Genomics and Bioinformatics Indiana University 1001 E. 3rd St. Bloomington, IN 47405-3700

Indiana University is an affirmative action equal opportunity employer.

Daphnia Genomics Consortium - <http://daphnia.cgb.indiana.edu/> jcolbour@cgb.indiana.edu
jcolbour@cgb.indiana.edu

SaudiArabia ConservationGenetics

Conservation Geneticist, King Khalid Wildlife Research Centre,

Kingdom of Saudi Arabia

The King Khalid Wildlife Research Centre (KKWRC) is managed by the Zoological Society of London (ZSL) under contract to the National Commission for Wildlife Conservation and Development in the Kingdom of Saudi Arabia. The Centre is located 70km north of Riyadh. The primary mission of KKWRC is to assist the Commission's conservation work, and the Conservation Genetics laboratory is an integral part of that aim. The laboratory, established eight years ago, is equipped with an automated sequencer that allows analyses such as DNA sequencing and fragment analysis (microsatellites and SSCP) to be conducted on-site.

The Geneticist is in charge of the laboratory and the genetics research carried out. Duties include: design and conduct molecular genetic studies in support of conservation programs for threatened and endangered fauna in Saudi Arabia; supervise a laboratory, including 2 technicians, that is shared with veterinary diagnostic and parasitology programs; train local staff in molecular genetics investigative techniques; conduct pedigree-based analyses of captive stocks of gazelles and make recommendations for captive-breeding programs; prepare written reports of analyses and publish results in peer-reviewed outlets.

Past and present projects in the laboratory include taxonomic assessment of the Saudi gazelle, phylogeography of Hamadryas baboons, genetic detection of pathogens of wildlife, defining conservation units for mountain

gazelle, sand gazelle and Nubian ibex, assessing systematics and taxonomy of Arabian tahr, and investigating relationships between inbreeding and fitness among lineages of captive-bred gazelles. Potential exists for research on carnivores (particularly wolves, leopard, sand cat, wildcat, and caracal), raptors, and spiny-tailed lizards.

Required qualifications: candidates must have a PhD in biology, molecular biology, genetics or a closely related field. We seek an experienced professional but will consider well-qualified post-doctoral candidates. Candidates will have experience with laboratory procedures involved with molecular genetics studies, including primer design, PCR optimization, and data acquisition using an automated sequencer; knowledge of principles of phylogenetics, phylogeography, population genetics and pedigree analysis; experience with analysis of DNA sequence and microsatellite data, preferably in a conservation context; candidates must be able to read, write and speak English fluently, communicate effectively, both orally and in writing, and work as part of a culturally diverse team.

Additional desired qualifications: knowledge of principles of conservation biology, ecology and management of vertebrates; experience supervising laboratory technical staff; experience with forensic applications.

As an employee of ZSL, the successful candidate will have close links with geneticists and molecular ecologists at the Institute of Zoology (IoZ) (the research wing of ZSL: www.zsl.org/ioz), and there is the potential for collaborative projects between the successful candidate and postdoctoral fellows at IoZ.

The contract will be for one year initially, with the possibility of extension, beginning as early as mid-June. The benefits include free accommodation, use of a vehicle, flights to and from Saudi Arabia at each end of the contract and a return flight each year. Annual leave (60 days).

Please send an application letter and CV to the Human Resources Department, Zoological Society of London, Regent's Park, London NW1 4RY (hr@zsl.org) For further information, contact Conservation Programmes, cp@zsl.org <<mailto:cp@zsl.org>>

Closing date: 5 April 2005

Registered Charity Number: 208728

Marcia Latty Senior HR Officer Zoological Society of London Regent's Park London NW1 4RY Tel: 020-7449-6251 <<http://www.whipsnade.co.uk/adoption/index.html>>

marcia.latty@zsl.org

UArizona ResTech

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Research Technician / Research Specialist

A research position is available in the laboratory of Dr. Michael Nachman in the Department of Ecology and Evolutionary Biology at The University of Arizona. The successful candidate will be the primary lab manager in a laboratory of population and evolutionary genetics. The responsibilities include conducting evolutionary studies using molecular techniques, breeding experiments with mice, occasional field work in the Sonoran Desert, analysis of data, ordering lab supplies, assistance in preparing manuscripts for publication, supervision and training of undergraduates in the lab, and travel to national meetings to present research results. Details of the research can be found at <http://eebweb.arizona.edu/faculty/nachman/>. Qualifications: bachelor's degree in biology or a related field and some laboratory research experience. Knowledge of evolutionary genetics and molecular biological techniques preferred. To apply, please send a letter describing your interests and qualifications, a CV, and contact information for three references to: Dr. Michael Nachman (nachman@u.arizona.edu). The University of Arizona is an Affirmative Action / Equal Opportunity Employer.

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

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UBielefeld EvolBiol

University of Bielefeld, Evolutionary Biology

<> Applications are invited for a *Research Associate* position in the *evolutionary biology* group at the University of Bielefeld, Germany. The position is avail-

able in September 2005 and is initially for 3 years, with the possibility of extension for up to 3 additional years, which would make it comparable to an Assistant Professor position without tenure.

We are looking for a highly motivated young scientist with a PhD in biology and post-doc experience to form her/his own research group in the field of evolutionary biology. We especially welcome applications from researchers using modern molecular methods in evolutionary ecology or population genetics. Candidates should have a proven record of independent research and publication and should be willing to attract their own funding. It is possible to obtain the degree of "Habilitation" in this position.

<> The successful candidate is expected to take part in teaching evolutionary biology (approximately 2 courses per year) and in supervising both undergraduate and graduate students. Teaching is usually in German, but it is possible to teach in English until a sufficient knowledge of German is acquired. Starting date is negotiable (any time from September 2005 onwards). <>

Payment is based on the German BAT IIa/2 federal public service scale (approx. 40,000 ? per year depending on age, marital status and experience). The University of Bielefeld is an equal opportunity employer and encourages disabled persons to apply. Disabled applicants with suitable qualifications will be preferentially considered. The university also aims at increasing the number of women in fields where they are underrepresented, and therefore encourages them to apply. Given equal qualifications and skills between top ranked applicants, women will be preferentially considered. <>

Applications can be sent by e-mail and should include a CV, a list of publications and a one-page research statement, including research plans. Please give names and e-mail addresses of two or three persons who are willing to write a letter of recommendation. Applications received before May 4, 2005, will be given full consideration.

Applications and inquiries should be sent to: <>

Professor Dr. Klaus Reinhold <> Fakultät für Biologie, Abteilung Evolutionsbiologie University of Bielefeld

Morgenbreede 45 33501 Bielefeld Germany

e-mail: klaus.reinhold@uni-bielefeld.de
<mailto:klaus.reinhold@uni-bielefeld.de>

Tel.: #49-521-106-2721

klaus reinhold <klaus.reinhold@uni-bielefeld.de>

UCanterbury Genetics

School of Biological Sciences Lecturer / Senior Lecturer
COLLEGE OF SCIENCE

School of Biological Sciences

Lecturer / Senior Lecturer in Genetics

Vacancy Number: BS12372 / 0505A

Closing date: 16 May 2005

Applications are invited for the position of Lecturer / Senior Lecturer in Genetics in the School of Biological Sciences.

The School is seeking to make a tenured / continuing appointment in Genetics to enhance its research and teaching capacity in these areas. Applicants will have well-developed skills in molecular biology and associated analytical techniques (e.g. quantitative data analysis and bioinformatics) and a commitment to research in areas of biotechnology, biodiversity, and / or biosecurity consistent with the School of Biological Sciences' Strategic plan.

The successful applicant will be expected to demonstrate academic excellence in their teaching and research, carry out innovative and effective lectures and laboratory classes, publish their research at the highest level as assessed by peer-reviewed publications, generate external research funding, and aid in the supervision of postgraduate students.

For more information on the position please contact Professor Paula Jameson Email: paula.jameson@canterbury.ac.nz

More detailed vacancy descriptions and how to apply can be assessed at our website <http://www.canterbury.ac.nz/hr>

Dr Neil J. Gemmill Senior Lecturer in Genetics
Molecular Ecology Laboratory School of Biological Science
University of Canterbury Private Bag 4800 Christchurch, New Zealand
Phone: + 64 (0) 3 364 2009
Fax: +64 (0) 3 364 2590 www.biol.canterbury.ac.nz/people/gemmell.shtml

UGlasgow PhyloDatabase

A postdoc position is available for up to three years in Rod Page's lab to develop a taxonomically intelligent phylogenetic database. The project aims to explore methods of making phylogenetic databases such as TreeBASE "taxonomically intelligent" by linking them to information on taxonomic names, synonyms, and classifications. The immediate goal of this proposal is not the creation of a new database, but rather to tackle the key intellectual obstacles that stand in the way of creating a usable phylogenetic database.

Details of the project are online at <http://taxonomy.zoology.gla.ac.uk/Jobs/BBSRC2005/>. The post is for up to three years, with salary in the range £19,460 - £21,640 per annum.

Regards

Rod

Professor Roderic D. M. Page Editor, Systematic Biology DEEB, IBSL Graham Kerr Building University of Glasgow Glasgow G12 8QP United Kingdom

Phone: +44 141 330 4778 Fax: +44 141 330 2792 email: r.page@bio.gla.ac.uk web: <http://taxonomy.zoology.gla.ac.uk/rod/rod.html> reprints: <http://taxonomy.zoology.gla.ac.uk/rod/pubs.html>

Join the Systematic Biology through the Society of Systematic Biologists Website: <http://systematicbiology.org> r.page@bio.gla.ac.uk

UGuelph AssocDirector BarcodeOfLife

Associate Director, Canadian Barcode of Life Network (temporary full-time for five years, with the possibility of extension)

The Canadian Barcode of Life Network seeks an Associate Director. This position involves responsibility for management of the Network, an activity that will require regular interactions with participating researchers and funding agencies. The incumbent will also be a core

member of the scientific team and is expected to maintain a productive research program. Although teaching responsibilities will be modest, opportunities will exist for involvement in graduate-level courses and student supervision. The appointment will be made at the Assistant Professor rank with the position based in an appropriate academic Department. Candidates must hold a PhD in the biological sciences, ideally in molecular evolution or systematics, and must have at least three years of postdoctoral experience. A sustained record of publication in the scientific literature and prior administrative experience at a senior level in a major natural history museum or collections facility is critical. Candidates must have demonstrated leadership ability and must possess strong communication skills as well as experience in the assembly of grant applications. The Canadian Barcode of Life Network is a multidisciplinary initiative based at the University of Guelph, dedicated to advancing the science of species identification through the use of DNA-based systems. Its work will be executed in close collaboration with international organizations sharing this mission. For information, visit www.barcodinglife.org. Applicants should submit a curriculum vitae and arrange for three letters of reference to be sent to:

Dr. Paul Hebert, Scientific Director Canadian Barcode of Life Network Department of Integrative Biology University of Guelph Guelph, ON, Canada N1G 2W1

To ensure full consideration, complete application materials must be received by May 5, 2005.

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

The University of Guelph is committed to an employment equity program that includes special measures to achieve diversity among its faculty and staff. We therefore particularly encourage applications from qualified aboriginal Canadians, persons with disabilities, members of visible minorities and women.

Paul Hebert <phebert@uoguelph.ca>

UKonstanz EvoDevo

Ph.D. POSITION IN DEVELOPMENTAL AND EVOLUTIONARY BIOLOGY

We are seeking a highly motivated student interested in pursuing graduate study (3 years) at the Ph.D. level

in the field of Developmental Biology in the Department of Evolutionary Biology (Prof. A. Meyer) at the University of Konstanz, Germany.

We are working with zebrafish to unravel the roles of retinoic acid signaling during zebrafish development and regeneration, and on fin development from an evolutionary perspective. The Ph.D. project will be based on this theme. Methods applied will include genetics, manipulations of embryonic tissues and molecular techniques. For more information, please consult the references at the bottom of this page, and visit: <http://www.evolutionsbiologie.uni-konstanz.de/%7Egerrit/index.htm> Successful applicants should have good practical skills in molecular biology (PCR, cloning), and a strong interest in developmental or evolutionary biology should ideally be evident from previous work. A Masters Degree or equivalent to German 'Diplom' in Biology is required. We have an international group and the everyday working language is English. The Department is excellently equipped for molecular genetic and developmental analyses and houses a large zebrafish aquarium facility. Konstanz is located in southern Germany, close to the Swiss Alps and Zürich airport.

Initial funding at the German BAT2a/2 level is available, but candidates are also encouraged to apply for their own funding. Expected starting date is in the second half of 2005. Applications (by mail to gerrit.begemann@uni-konstanz.de) should include CV, 1-2 reprints of publications (if available), and names and emails of 2-3 referees.

References: 1.) Begemann G, Marx M, Mebus K, Meyer A and Bastmeyer M (2004): Beyond the neckless phenotype: influence of reduced retinoic acid signaling on motor neuron development in the zebrafish hindbrain. *Developmental Biology* 271: 119-129. 2.) Begemann G, Schilling TF, Rauch, GJ, Geisler, R and Ingham PW (2001): The zebrafish neckless mutation reveals a requirement for *raldh2* in mesodermal signals that pattern the hindbrain. *Development* 128:3081-94. 3.) Keegan BR, Feldman JL, Begemann G, Ingham PW and Yelon D (2005): Retinoic acid signaling restricts the cardiac progenitor pool. *Science* 307:247-249.

Dr. Gerrit Begemann Department of Biology Fach M617 University of Konstanz D-78457 Konstanz Germany

Tel. +49 7531 882881 e-mail: gerrit.begemann@uni-konstanz.de e-mail: gerrit.begemann@uni-konstanz.de

UdelosAndes EvolMycologist

El Departamento de Ciencias Biológicas, Universidad de los Andes (Bogotá, Colombia) busca aplicaciones para una posición de profesor/investigador de tiempo completo en el área de Biología de Hongos con énfasis en fitopatología o ecología de hongos. El candidato seleccionado deberá poseer título de Ph.D. en Microbiología, Biología o Micología, y deberá liderar investigación en el área de su especialidad, supervisar estudiantes de pre- y posgrado, y realizar docencia. Son especialmente bienvenidos candidatos que lideren programas de investigación que involucren biotecnología o sistemática molecular.

Enviar hoja de vida, copias de publicaciones recientes, una breve descripción del programa de investigación y docencia, y dos cartas de recomendación antes del 31 de julio, 2005 a:

Comité de Contrataciones Profesorales Atención: Alicia Ortega <aortega@uniandes.edu.co> Departamento de Ciencias Biológicas Universidad de Los Andes Carrera 1 No. 18A-70 Bogotá, Colombia

The Department of Biological Sciences, Universidad de los Andes (Bogotá, Colombia) seeks applications for a full time teaching/research position in Biology of Fungi with emphasis in phytopathology or fungal ecology. The successful candidate should have a Ph.D. degree in Microbiology, Biology or Mycology, and will be expected to lead research in their area of expertise, supervise undergraduate and graduate students, and carry out teaching. Candidates capable of leading research programs involving biotechnology or molecular systematics are specially welcomed.

Send curriculum vitae, copies of recent publications, a brief description of research and teaching program, and two letters of recommendation before July 31, 2005 to:

Faculty Search Committee Attention: Alicia Ortega <aortega@uniandes.edu.co> Departamento de Ciencias Biológicas Universidad de Los Andes Carrera 1 No. 18A-70 Bogotá, Colombia

samadrin@uniandes.edu.co

Other

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Reza Ramzannejad Ghadi Goragan.univ.Iran
rrghadi@yahoo.com

3 Questions

Dear all

I want to do geometric study of leaf of olea. please send to me a way to gain vein only .in the other hand I want to remove and lyse the mesophyl of leaf for have good photograph from vein. any way if you have a method for geometry of leaf please guid me.

Reza Ramzannejad Ghadi Goragn univ. Iran.

Dear all

I want to have a algal herbarium. please guid me that how I can catch information about making of algal herbarium.

Reza Ramzannejad Ghadi Gorgan univ. Iran.

Dear all

I have many algal speciemens from international wet-land Miankaleh in the north of Iran . I need a collab-oration for identification of this algae. if you know how I can the address of a person who can helm to me please send to me his/her address.

ABI373 parts

We have several new plate sets, and assorted sundries for a 373 XL ABI sequencer. These include buffer trays, combs, spacers, assemblies, etc. If anyone is interested in these items, they are available for the shipping cost on a first come, first serve basis. Please contact: Connie Keeler-Foster Connie.Keelerfoster@fws.gov, or ck-eeler_foster@hotmail.com, or call 505.734.5910.

Connie_KeelerFoster@fws.gov

Aggregation answers

Dear colleagues,

Here, with a bit of delay, a big thank for all the replies re. statistical methods to test for and quantify spatial aggregation. I paste below a summary of the replies we received.

Best regards and thanks very much again for your kind assistance.

Pauline Manhes.

How to measure aggregation

- The most popular seems to be the Ripleys K function. Information about it can be found on <http://zappa.nku.edu/~longa/geomed/stats/ripley/ripley.html>. It is available in R software in the spatstat package called Kest.
- Spatial aggregation can also be tested with the package SADIE, free available (http://www.rothamsted.bbsrc.ac.uk/pie/sadie/SADIE_home_page_1.htm) or GenAlex 2.1. developed by Peakall et al (2003) that use autocorrelograms.
- One could use a randomisation technique : randomly assign x,y coordinates to n points (n= the number of objects in your real data), calculate the mean nearest-neighbour distance (i.e. for each point find the closest point to it and calculate the distance between those, do that for all points and take the average). Repeat all these steps m times (1000 times for example) and compare to the mean nearest- neighbour distance for your real data.
- The programme PASSAGE can be downloaded at <http://lswweb.la.asu.edu/rosenberg/Passage> - A Mantel test or a two tailed chi-square test can also be used. Chi-square : uniform distribution = chi-square smaller than expected by chance, clumped distribution = chi-square larger than expected by chance.
- A Procedure is available in SAS : proc modeclus. It is a nonparametric density clustering procedure that can tell you how many significant clusters are present in multivariate data. Information on the website : <http://www.id.unizh.ch/software/unix/statmath/sas/sasdoc/stat/chap42/sect1.htm> -If you are interested in aggregation in genetics data, you can read the manuscript of Mark Miller where he describes « Allelic Aggregation Index Analyses ». A new software package should be available soon.

Bibliography

- R V. (1993). Lacunarity indices as measures of landscape texture. *Landscape Ecology*. 8, 201-211. and With, K.A. & King, A.W. (1999b). Dispersal success on fractal landscapes: a consequence of lacunarity thresholds. *Landscape Ecology*. 14, 73-82.
- Grabarnik, P. & Chiu, S.N. (2002), Goodness-of-fit test for complete spatial randomness against mixtures of regular and clustered spatial point processes. *Biometrika* 89 (2): 411-421.
- J M Elliot. 1977. Some methods for the statistical analysis of samples of benthic macroinvertebrates. 2nd ed. Freshwater Biological Association.
- Peter Diggle's book, « Statistical Analysis of Spatial Point Patterns »
- The text by Charles Krebs, *Ecological Methodology* (1999), has a chapter on "Spatial pattern and indices of dispersion."
- The statistical analysis of spatial pattern by M.S. Bartlett
- Cluster analysis and the identification of aggregations, Richard E. Strauss, *Animal behavior* 2001, 61, 481-488.
- Frequency and spatial patterning of clonal reproduction in louisiana iris hybrid populations, Burke et al, 2000, *Evolution* 54(1), 137-144.
- On the social structure of offspring rearing in the burrower bug, *Sehirus cinctus* (Hemiptera: Cydnidae), Agrawal, Brown & Brodie, 2004, *Behav Ecol Sociobiol* 57:139148 (Monte Carlo simulations).
- Monte Lloyd, *J. Anim. Ecol.* 36:1-30, 1967.
- Analysis of aggregation, a worked example: numbers of ticks on red grouse chicks, Elston et al., 2001, *parasitology* 122, 563-569.

pmanhes@ens-lyon.fr

Ant Colony founding

Dear Colleagues,

I would be very happy if one of you or some of you might have answers for some of the questions below. I've searched the literature and I've asked my fellow evolutionary researchers on social insects, obtaining lots of valuable information - especially of course from the publications and personal comm of people who have worked on the species in question for long. But the

questions below seems to remain unanswered. Even if none of you would happen to have answers, perhaps you know some more naturalist / entomologist colleagues or email lists that might have answers. I'll be extremely glad for all information. If replies to any of the questions below are to be found in the recent literature, it is of course my error to have overlooked this and not the error of the specialists I asked after searching the literature.

For the species below, the following questions:

For: *Myrmica* in general, and specifically: *Myrmica tahoensis*, *M. ruginodis*, *M. scabrinodis*, *M. rubra*, *M. sulcinodis*, *M. punctiventris* AND *Pheidole pallidula*

Do sexuals mate on the wing (at least starting copulation on the wing) or on the ground? AND Can queens found nests independently (i.e. alone) and if so, clausurally? (based on my search results, it seems that for *M. punctiventris* and *M. sulcinodis* the reply to the latter questions is YES+NO (ie. can found independently and dependently), whereas for *M. scabrinodis* the reply is NO).

For: *Formica fusca* and *Polyrhachis australis*: Do sexuals mate on the wing (at least starting copulation on the wing) or on the ground?

Thank you very much in advance, Best regards,

Else Fjerdningstad

Dr. Else J. FJERDINGSTAD

Laboratoire d'Ecologie, CNRS UMR 7625 Université Pierre et Marie Curie 7 Quai St-Bernard, Bâtiment A, 7ème étage, case 237 F-75252 Paris Cedex 05 FRANCE

Email: Else.Fjerdningstad@snv.jussieu.fr Tél. +33 1 44 27 27 20, Fax. +33 1 44 27 35 16

Have a heart that never hardens, a temper that never tires

- Charles Dickens - Charles Dickens

Arlequin PopDiffTest

I frequently use the Raymond-Rousset Exact Test of Population Differentiation as implemented in Arlequin 2.000, which I run on various Macintosh machines. However, in my hands Arlequin does not run well in the "Classic" environment in the OSX operating systems on these computers. Generally, it runs once and then freezes. It performs a bit better if the computer

is booted into the Classic environment, but it is more than a little inconvenient to reboot the machine when I want to run just this one program. Is there another program that will run the Raymond-Rousset test? Has Arlequin been updated/ported to OS X? Is this being planned?

Thanks for any responses that come along. I'll consolidate and post them in the usual manner.

fishgen@vt.edu

BlueCrane micros

I am currently working on developing microsatellites for the Blue Crane (*Anthropoides paradisea*, Family: Gruiformes) through the University of KwaZulu-Natal and the University of mSheffield. The aim of which is to develop the forensic capacity to reduce the illegal trade in this species. Does anyone perhaps have any primers that may be polymorphic in the Blue Crane (*Anthropoides paradisea*)?

Kate Meares.

Email: k8meares@yahoo.com

I am based at the University of Sheffield. Any mail can be sent to: Deborah Dawson, Department of Animal and Plant Sciences Alfred Penny Building University of Sheffield Western Bank Sheffield; UK S10 2TN

k8meares@yahoo.com

Brassicaceae seeds

Dear colleagues,

I am working with *Arabidopsis thaliana* and its relatives in an ongoing series of evolutionary ecology projects. For more information, feel free to contact me or visit my website (<http://life.bio.sunysb.edu/~jbanta/>).

I am looking for seeds from species from the Koch et. al phylogenies of *A. thaliana*'s relatives. Although I have some seeds, I would love to get my hands on some more. I would need at least 100 or 200 seeds per population (ideally 1000+ seeds would be great), and could use up to four or five populations per species. If you have

seeds from any of the following species, I would greatly appreciate it if you could send me some. You can e-mail me at jbanta@life.bio.sunysb.edu. Here is a list of species I am interested in getting seeds from. The (*) signifies species I am particularly interested in. Thanks, Josh Banta (see below for list of species)

(*) *Fourraea* (a.k.a. *Arabis*) *pauciflora* *Arabis* *turrita* *Aubrieta* *deltoidea* *Arabis* *alpina* *Arabis* *procurens* *Arabis* *hirsuta* *Arabis* *jacquini* *Arabis* *scabra* *Arabis* *blepharophylla* (*) *Barbarea* *vulgaris* *Cardamine* *flexuosa* *Cardamine* *amara* *Cardamine* *rivularis* *Yinshania* *henryi* *Crucihimalaya* (a.k.a. *Arabidopsis*) *himalaica* *Crucihimalaya* (a.k.a. *Arabidopsis*) *wallichii* *Microsisymbrium* (a.k.a. *Arabidopsis*) *griffithiana* *Microsisymbrium* (a.k.a. *Arabidopsis*) *korshinskyi* *Arabidopsis* *halleri* *Arabidopsis* *lyrata* (*) *Halimolobus* *perplexa* (*) *Boechera* (a.k.a. *Arabis*) *lyalli* (*) *Boechera* (a.k.a. *Arabis*) *lignifera* (*) *Boechera* (a.k.a. *Arabis*) *microphylla* (*) *Boechera* (a.k.a. *Arabis*) *divaricarpa* (*) *Boechera* (a.k.a. *Arabis*) *parishii* (*) *Boechera* (a.k.a. *Arabis*) *drummondii* (*) *Turritus* (a.k.a. *Arabis*) *glabra* *Rorippa* *amphibia* *Olimarabidopsis* *cabulica* *Thlaspi* *arvense* *Alliaria* *petiolata*

Josh Banta, graduate student Department of Ecology and Evolution State University of New York at Stony Brook 650 Life Sciences Building Stony Brook, NY 11794-5245 Phone: 631-632-1669 Fax: 631-632-7626 Home Page: <http://life.bio.sunysb.edu/~jbanta>

Cape Parrot

Hi I am hoping to hear from anyone who is working with microsatellites and know of any that will work in the Cape Parrot (*Poicephalus robustus*).

Thanks

Kerusha Pillay (kerrypil@yahoo.com)

Crane primers

I am currently working on developing microsatellites for the Blue Crane (*Anthropoides paradisea*) through the University of KwaZulu-Natal and the University of Sheffield. The aim of which is to develop the forensic

capacity to reduce the illegal trade in this species. Does anyone perhaps have any primers that may be polymorphic in the Blue Crane (*Anthropoides paradisea*)?

Regards,

Kate Meares.

Email: k8meares@yahoo.com

I am based at the University of Sheffield. Any mail can be sent to: Deborah Dawson, Department of Animal and Plant Sciences Alfred Penny Building University of Sheffield Western Bank Sheffield; UK S10 2TN

K Meares <BO4KFM@sheffield.ac.uk>

Crematogaster ants

Dear all,

I am looking for samples of ants of the genus *Crematogaster* from Asia and Africa as outgroups for a biogeographic study.

Does anybody possess ants of the same species from a wide geographic range? (Best would be from Thailand or the Malay Peninsula as well as Borneo or other parts of Indonesia). To make things a bit more complicated they should be in good condition so that I would be able to still extract DNA from them that is not too degraded.

I would appreciate your help very much!

Best wishes Heike

–

Dr. Heike Feldhaar Department of Behavioural Physiology and Sociobiology (Zoology II) Theodor-Boveri Institute for Biosciences University of Wuerzburg Am Hubland D- 97074 Wuerzburg Germany

phone: 49- (0)931 - 8884305 fax: 49- (0)931 - 8884309

mail: feldhaar@biozentrum.uni-wuerzburg.de

DNA from leaf

Dear all,

I have samples of iris leaves stored at -80 C. I am planning to isolate DNA with Qiagen DNeasy Plant Kit (96 x 6 = 576 samples). I am going to do it in a lab that does it from dry leaves (in silica) and don't have much experience with frozen leaves. Could you advise me on the procedure so that I would avoid potential thawing of leaves or braking the tubes or whatever might go wrong? Liquid nitrogen will be available during the isolation.

I have cca 10-15 cm-long pieces of leaves, so adjusting the procedure is not a problem, I can "sacrifice" most of the leaf and still have enough for the "real" extraction.

I would really appreciate any advice you could give me!

Thank you very much in advance!!!

Morana Biljakovic morana@irb.hr

Morana Biljakovic Rudjer Boskovic Institute Molecular Biology Department Bijenicka 54 10000 Zagreb Croatia
tel +385 1 4561 019 fax +385 1 4561 177 mobile +385 98 868 226 morana@irb.hr

Entomology book

Hi,

I would like to use Borror, Triplehorn, Johnson: An Introduction to the study of Insects as a text book for our college and highschool entomology lab exercises. The book has just been re-issued as a new 7th Edition at a forbiddingly high price of \$110. The older editions work just fine, yet have become unavailable since the re-issue of the new edition.

My question is: is anyone willing to donate or sell their older editions (5th or 6th) to me so we can make them available to our students during lab exercises? Any copies would stay with the course, that is be used again and again every year for most likely the next decade. So if you have any older editions that are accumulating dust please be so kind and consider this request. We will pay for shipping and handling.

Sincerely

Armin Moczek

Armin P. Moczek Assistant Professor Department of Biology & Indiana Molecular Biology Institute

Mailing address: Armin P. Moczek Department of Biology Indiana University 915 E. Third Street Myers Hall

150 Bloomington, IN 47405-7107

email: armin@indiana.edu phone: (812) 856-1468
(office) phone: (812) 856-1783 (lab) fax: (812) 855-6082
<http://www.bio.indiana.edu/facultyresearch/~faculty/Moczek.html> <http://www.bio.indiana.edu/~moczeklab/index.html>

Fairbanks Evol05 Jun10-14 6 YahooGroup

Hi All,

I have encountered the problem that I would like to ravel around in Alaska after the Evolution conference, and I guess there are more people out there with the same problem. So, I have pieced together a yahoo group that can bring all those searchers together:

<http://groups.yahoo.com/group/-Evolution2005Travel/> Cheers,

Kim – <http://www.kimvdlinde.com> Kim van der Linde
<kim@kimvdlinde.com>

Fairbanks SharingRoom

I am intending to attend the Evolution Conference in Fairbanks but want to save money. Currently I have a room with two double beds reserved at the Captain Bartlett Hotel. If somebody is interested in splitting the cost of the room and taking the other bed, please notify me. If you have a room closer to the Conference and wish to split that, I would do that and cancel my room reservation as well. Thanks you. Andrew Stoehr (andrew.stoehr@email.ucr.edu)

Andrew M. Stoehr Department of Biology University of California Riverside, CA 92521

andrew.stoehr@email.ucr.edu

951-827-7023

Andrew Stoehr <andrew.stoehr@email.ucr.edu>

Fairbanks SharingRoom 2

Evolution meeting 05: seeking roommate and post-conference hikers.

We are looking for 1 male and possibly 1 female roommate to share room(s) during the meeting in Fairbanks. I have a reservation for two 2-bed rooms at Captain Bartlett Inn. Shared car rental would also be a possibility. I am also seeking companions for 3-4 days of hiking and/or boating after the meeting. I am planning to have an inflatable touring kayak with me.

– Lev Yampolsky

Department of Biological Sciences East Tennessee State University Johnson City TN 37614-1710 Phone 423-439-4359 Fax 423-439-5958

Lev Yampolsky <yampolsk@etsu.edu>

GeneticDataAnalysis courses

Dear All,

I'm interested in registering for a workshop or course in analysing population genetics data (specifically for microsatellite data).

I'd be really grateful to hear from anybody running such courses, or anyone who knows any listings for such things (other than the EvolDir website!). I can compile a list and pass it on.

Thanks in advance.

Andrew Griffiths

E-mail; Andrew.M.Griffiths@exeter.ac.uk

Hatherly Laboratories University of Exeter Prince of Wales Rd. Exeter EX4 4PS

Tel: +44 1392 263753 Fax: +44 1392 263700

IBD web service

Isolation By Distance, Web Service (IBDWS) is a web-based upgrade to the software "IBD". IBDWS is a fast, simple and specialized package for isolation by distance analyses of codominant markers (raw data), or user-provided distance matrices for any type of data.

IBDWS is currently hosted at <http://phage.sdsu.edu/~jensen/> and is documented in Jensen, J. L., Bohonak, A. J and S. T. Kelley. 2005. Isolation by distance, web service. BMC Genetics 6: 13. <http://www.biomedcentral.com/1471-2156/6/13/-abstract> This upgrade includes a cleaner user interface, and the generation of IBD scatterplots in jpeg and Postscript format. We expect IBDWS to be largely free of platform-specific bugs that were a problem in some earlier downloadable versions of IBD.

–
Andrew J. Bohonak

Assistant Professor San Diego State University Department of Biology 5500 Campanile Drive San Diego, CA 92182-4614

Phone: 619-594-0414 Fax: 619-594-5676 Email: bohonak@sciences.sdsu.edu Web: <http://www.bio.sdsu.edu/pub/andy/index.html> Office: 212 Life Science North

Labidura specimens

Dear all,

I am looking for specimens of the earwig-species *Labidura riparia* (Pallas, 1773) from all over the world for genetic analysis of population structure (with microsatellites). The species is distributed all over the world.

I would be glad if I could get some specimens from other continents and southern parts of Europe to compare with populations from Germany.

Please contact me:

Mareike Gueth gueth@tu-cottbus.de Chair General Ecology Brandenburg University of Technology P.O. Box 101344 03013 Cottbus Germany

Phone: ++49 (0)355/692773 Fax: ++49 (0)355/692225 gueth@tu-cottbus.de gueth@tu-cottbus.de

Linum marginale micros

Dear Colleagues

I am working on the native Australian species *Linum marginale*, and am searching for available microsatellite primers.

Is anybody aware of microsatellite primers developed for any species in the Linaceae? Any information would be greatly appreciated.

Thanks, Luke

Luke Barrett PhD Student CSIRO Plant Industry
GPO 1600 Canberra ACT 2601 Australia Email:
Luke.Barrett@csiro.au

Tel: +61 (0)2 6246 4893

Luke.Barrett@csiro.au

Myrmica samples

Dear EvolDir members,

I am starting my PhD on the phylogeny of the genus *Myrmica* (covering the whole Holarctic region). I would like to ask if somebody is willing to send me samples (for sequencing) of any species of this genus. It would be ideal if all castes (so including sexuals) could be sent.

Thank you very much,

Gunther Jansen (gunther.jansen@helsinki.fi) Riitta Savolainen Kari Vepsäläinen

Research Group Ecology and Evolutionary Biology Department of Biological and Environmental Sciences University of Helsinki P.O. Box 65 FIN-00014 Helsinki Finland

gunther.jansen@helsinki.fi gunther.jansen@helsinki.fi

Nuclear gene markers

Dear evoldir members,

I am a Ph D student studying high-level fish phylogeny. I am looking for nuclear genes that can be used for this purpose. There are a few genes, such as RAG1 and RAG2 gene, have been widely used in constructing phylogeny of fish and other vertebrates. But I can't find out how these genes were chosen in the first place. However, I need to develop more nuclear gene markers for my study. I am going to try genome comparison between available fish genomes. I can't find any published information related to it. If you have any suggestion or comments on how to develop nuclear gene markers for high-level phylogeny, please share it with me. I will appreciate it. Thanks in advance.

Chenhong Li 316 Manter School of Biological Sciences University of Nebraska - Lincoln NE USA

Pedigree data sets

Dear listmembers,

I am looking for datasets for trying out algorithms aimed at learning or inferring pedigree structure from STR DNA data. What I am looking for are datasets that have the following information:

1) STR measurements on a set of DNA markers for individuals of some population (human or animal) 2) If available, age and sex information about the individuals. 3) If available, known pedigree information about the relationships among the individuals.

If you have datasets with the above information you would be willing to share with me, or you know of where I could obtain such datasets, I would be very grateful if you could let me know at my email address rgc@city.ac.uk (Please note that I am not on this list.)

thanks in advance,

Robert Cowell

Faculty of Actuarial Science and Statistics Cass Business School City University, London.

r.g.cowell@city.ac.uk

QuantGenet SAScode

Dear EvolDir members,

I am hoping someone can help me to perform some key quantitative genetics analyses using SAS. In particular, I'm having a rough time trying to calculate the G-matrix. Specific details follow, but I would be most grateful for any sample code for anyone who has some experience with this.

The experiment is a common garden that combines 8 individual plants from each of 17 half-sib families from each of 20 populations in Eastern North America. Each family is split evenly among 4 tables (2 individuals/family/population/table). The biggest problem I'm having is figuring out how to calculate the G-matrices for these populations. I've used PROC MIXED to calculate the among-family variance for a few traits (I have 23 traits in total but haven't got that far yet). A sample code for the variance in # days to first flower is as follows:

```
proc mixed method=REML data=Lythrum; class Fam
Table; model Days_1st_Flower= /; random Table Fam
Table*Fam; by Pop; run; quit;
```

In order to calculate the G Matrices for each population, I reorganized the data into a repeated measures design by collapsing all separate measurements on an individual into a single column 'Y' and then adding a column 'Trait' which encodes each type of measurement into a number (e.g., Days to 1st Flower = 10). The PROC MIXED code is as follows:

```
proc mixed data=Lythrum covtest asycov; by Pop;
class Trait Fam Table Ind; model Y=Trait Table
Fam*Table; random Trait /type=un subjectúm g gcorr;
repeated /type=un sub=Table*Ind*Fam r rcorr; ods
output covparms=_varcomp asycov=_cov; run; quit;
```

This works, but gives me variances that don't match the variances calculated in the first code. I think it might be due to the fact that I have Trait, Table and Fam*Table as fixed effects whereas in the previous example they were random effects. Or maybe it's a repeated measures problem?

Thanks in advance!

Rob Colautti colautti@botany.utoronto.ca Department of Botany University of Toronto Toronto, Ontario, Canada M5S 3B2 Phone: (416)978-5603 Fax: (416)978-5878

colautti@botany.utoronto.ca

QuantGenetics Discussion Group

The AGDG list serve previously provided by Colorado State gave a vital link for quantitative geneticists to discuss the more technical and statistical aspects of their research and for breeders to post questions. Evolutionary biologists were also somewhat active on the old list serve. However, with the demise of the list serve this vital discussion has disappeared. As an effort to rekindle that joint spirit of discovery and exploration we started a new list serve at:

http://groups.yahoo.com/group/Quan_Gen The group has been expanded to include plant geneticists and evolutionary biologists. We also intend this group to discuss issues related to bioinformatics such as microarray or proteomics analysis. If you are interested, just go to that link and sign up, we will approve all. To post messages once in the group simply send an email to

Quan_Gen@yahoogroups.com

Please spread the word to the wider quantitative genetics and bioinformatics community.

Naturally we would also love to have quantitative or statistical questions posed to us from the molecular genetics community.

jbwalsh@email.arizona.edu

RstCalc problems

I've been using RstCalc recently to generate Rst values and confidence intervals in two data sets involving different fish species. I'm not having any difficulty running the program, but I'm getting some weird results.

First, the reported Rst values are substantially different from Rst values I get from GenePop. Granted, the latter program's documentation doesn't specify exactly how it makes its calculations (though both programs are supposed to use the same estimator), but I'm surprised at the magnitude of the differences.

Second, the mean bootstrap Rst values are always much higher than the calculated overall Rst value, and the

latter usually falls outside the 95% confidence interval (!).

I've checked the input files and nothing seems to be wrong. I've also tried analyzing them both in their original form (with alleles expressed as numbers of repeat units) and standardized with the standard.exe program included in the RstCalc package; results were similar in both cases. I've tried minor changes to the input files, such as setting all flanking region sizes to zero, but without affecting the output.

Has anyone else had similar trouble with this program? I've tried to email the author but the messages keep bouncing.

Thanks,

Doug Creer

reply to: creerd@fiu.edu

Florida International University Miami, FL 33199

creerd@fiu.edu

SJGould website

Please help me find "The Unofficial Stephen Jay Gould Archive" website. I use it frequently, but it has disappeared.

<http://www.stephenjaygould.org/> Thank you,

Paul Armstrong, Ph.D. Greenwood Molecular Biology Facility University of Hawaii

Paul Armstrong <armstrg@hawaii.edu>

SSE poetry

Announcing the first annual SSE EVOLUTION POETRY CONTEST

Any and all poems concerning the theme of evolution are solicited; serious, funny, tragic, elegant, nonsensical, in any style including tanka, limericks, haiku, free verse, couplets, and epic poems

Winner(s) to be announced and poem(s) read at the Annual Meeting Banquet in Fairbanks, Alaska

Prize(s) also remain to be determined, but will be glorious and highly desirable

Judging will be by a small, elite team and will be arbitrary and undoubtedly biased

SSE Members and non-members welcome to submit entries Entries may be in any language, or combination of languages

Submit all entries to: Jessica Gurevitch, Executive Vice President Society for the Study of Evolution Department of Ecology and Evolution Stony Brook, NY 11794-5245 USA jgurvtch@life.bio.sunysb.edu

Lacking suitable or sufficient entries, an interminably long, dull and pompous monologue and sermon will be read at the banquet

Deadline June 01, 2005

Scott Starr <sstarr@allenpress.com>

Scaling phylogenetic trees

Dear EvolDir,

I am looking for a way to change the scale of a phylogenetic tree. I have independent data sets and want to produce a tree for each one. I need to compare the trees so ideally I want all the trees to be in the same scale. However I haven't managed to do this because PAUP assigns its own scale. Of course this can be done the old fashioned way (using graphic programs) but I was wondering if any of you knew of a better way to do this.

I appreciate any help and comments on this.

Juan Lopez <pseudoagalla@yahoo.com>

Sequencing errors

It seems to have become the common practice to sequence amplified DNAs in both forward and reverse directions, apparently as a means of identifying errors in base calls. I have a data set of mtDNA D loop sequences, 357 bp in length, that represent 69 presumptive haplotypes among about 300 individuals in 10 populations. I am mostly interested in asking about signif-

icant population differentiation in haplotype frequencies. There are a fair number of haplotypes that are represented by only one individual in the entire sample. Unfortunately, these haplotypes were all characterized by sequencing in one direction only. For a variety of reasons, I cannot re-sequence the material with the reverse primer at the present time.

I am concerned that sequencing errors might have given rise to some of these "haplotypes." Is it reasonable to assume that sequencing errors are random and not systematic? If so, then might one assume that haplotypes with a frequency of only one individual per the entire population are most likely to be sampling errors? Can these simply be eliminated from the analysis?

I would be grateful for any responses.

fishgen@vt.edu

Software SGRunner

SG Runner 2.0: A Graphical User Interface for Seq-Gen

SG Runner is a simple Mac OS X application that provides a graphical user interface for Seq-Gen, the sequence simulation program from Rambaut and Grassly (2001). SG Runner does not incorporate any code from Seq-Gen, but instead acts as an intermediary, controlling an existing installation of Seq-Gen through a standard graphical interface. So, instead of typing:

```
/usr/bin/Seq-Gen -mHKY t2.7 -l1000 -n100 -a.43 -g4 -f.23 .21 .29 .27 <~/Documents/Simproj/tree.phy >~/Documents/Simproj/simout.txt
```

you fill in the model parameters in a graphical form.

This approach provides three potential benefits: 1) fewer mistakes since the layout for model specification is very similar to PAUP and SG Runner checks that parameters entered are of the correct type, 2) easier management of multiple simulations through the built-in simulation management tools, and 3) broader use of Seq-Gen by people that may be frustrated by the command line interface.

SG Runner 2.0 incorporates the ability to simulate AA sequences using the latest version of Seq-Gen. There are also major improvements to the management of multiple simulations, a slightly faster interface, and better internal tracking of tree files.

SG Runner requires Mac OS X 10.2 or above.

SG Runner is freeware and is available at: <http://homepage.mac.com/tpwilcox/> Seq-Gen (the command line version available for Unix, including Mac OS X, Windows and Linux) is freely available at: <http://evolve.zoo.ox.ac.uk/software/seq-gen/> tpwilcox@mac.com

Squat Lobster Samples

Hi,

I was wondering if anyone could help me in my quest to gather samples for my PhD project. I am trying to get samples of *Munida rugosa*, *Munida sarsi* and *Galathea strigosa* from their entire distribution range in small numbers per region (5-10) and larger numbers of the two *Munida* species from the British Isles. I am also trying to get samples of the following species (1-5):

Munida gregaria, *Galathea nexa* *Galathea rostrata* *Munida pusilla* *Munida iris iris* *Munida sanctipauli* *Munida petronioni* *Munida rutilanti* *Munida curvimana* *Munida heblingi* *Munda angulata*

Ideally I would hope for the samples to be preserved in ethanol which I could provide and would also cover costs of postage. If this would not be possible, could anyone provide me with any contacts that may be able to help me? Thanking you in advance for your cooperation in this matter and any help you could provide me with would be greatly appreciated.

Deborah

Deborah Bailie Fisheries Genetics and Evolutionary Ecology Lab School of Biology and Biochemistry Queens University of Belfast 97 Lisburn Road Belfast BT9 7BL Northern Ireland Tel: 028 90972247

b1823099@qub.ac.uk

Triploidy heterozygosity

I want to compare heterozygosities between diploid and triploid populations but am unsure how to proceed. I would appreciate any advice.

Thanks Dave

Dr. David Hurwood School of Natural Resource Sciences Queensland University of Technology Gardens Point Campus GPO Box 2434 Brisbane Queensland, 4001 AUSTRALIA ph. +617 3864 5072 fax +617 3864 1535

David Hurwood <d.hurwood@qut.edu.au>

UWisconsinMadison ChapmanLectures

WITH APOLOGIES FOR MULTIPLE POSTINGS:

The University of Wisconsin-Madison (Animal Breeding and Genetics area) is pleased to announce that the year 2005 A.B. Chapman Lecturer in Animal Breeding and Genetics will be Prof. Jack Dekkers, Department of Animal Science, Iowa State University, Ames.

Dr. Dekkers, a native of the Netherlands, has published extensively in animal breeding and genetics. His bibliography includes over 200 refereed and proceedings papers, and abstracts. He has taught courses in applied animal breeding, genetic improvement strategies, economic aspects of animal breeding, marker assisted selection and quantitative genetics.

Jack Dekkers has degrees from Wageningen Agricultural University (BS, 1982, Animal Science; MS, 1985, Animal Science) and the University of Wisconsin-Madison (Ph.D., 1989, Dairy Science/Animal Breeding). His many awards and honors include a NATO Fellowship in 1996; the J. L Lush Award in Animal Breeding and Genetics (2004; American Dairy Science Association), and the Outstanding Research Award (2004) conferred by Iowa State University.

The titles and venues for his lectures are:

Methods and strategies for QTL mapping in livestock
Tuesday, May 3, 12:05, 236 Animal Sciences Building

Use of molecular genetics in breeding programs
Tuesday, May 3, 3:30, 236 Animal Sciences Building

Finding genes affecting important traits in livestock
Wednesday, May 4, 8:50, 212 Animal Sciences Building

A.B. Chapman Lecturers in previous years have been: Prof. Brian W. Kennedy (Canada, 1994); Dr. Jean-Louis Foulley (France, 1995); Prof. William G. Hill (United Kingdom, 1996); Prof. Brian P. Kinghorn (Australia, 1997); Dr. R. Leyden Baker (Kenya, 1998);

Dr. Louis Ollivier (France, 1999); Prof. Morris Soller (Israel, 2000); Dr. Laurie Piper (Australia, 2001); Prof. Max. F. Rothschild (Iowa State University, 2002); Prof. James F. Crow (University of Wisconsin-Madison, 2003), and Prof. L. Dale Van Vleck (USDA and University of Nebraska at Lincoln, 2004)

For additional information, please contact: gianola@ansci.wisc.edu

Daniel Gianola Professor Department of Animal Sciences Department of Biostatistics and Medical Informatics Department of Dairy Science

1675 Observatory Dr. University of Wisconsin Madison, Wisconsin 53706-1284 USA

Phone: 1-608-265-2054 or 1-608-263-4300 Fax: 1-608-262-5157 or 1-608-263-9412 Mobile: 1-608-345-3289 E-mail: gianola@ansci.wisc.edu

<http://www.ansci.wisc.edu/facstaff/Faculty/pages/-gianola/index.html> "Nature is written in mathematical language" (Galileo Galilei). However, if nothing seems to work, try Bayes:

$$p(M|y) = p(y|M)p(M)/p(y)$$

gianola@ansci.wisc.edu

evolnews

NEW WEBSITE FOR EVOLUTIONARY BIOLOGISTS

We're (a bunch of grad students in EEOB at ISU) are pleased to announce that the website www.evolnews.org is up and running. This web site contains summaries of current, peer-reviewed journal articles for evolutionary biologists, arranged by topic. You can just read the page, and catch up on what is new in the whole field, or you can join the mailing list and get a TOC- as well as modify the page to display what you want to see for topics. You can also contribute stories to 20 active topic areas, or start a new topic. If you have questions, email evolnews@evolnews.org

thanks, Ryan

Ryan Adam Rapp <rrapp@iastate.edu>

mtDNA BivalveMutations

Dear EvolDir Members,

I have evidences that, in somatic tissues of male bivalves, mitochondrial DNA accumulates more mutations in males rather than in females. Does anyone

know any similar evidence of this, either from literature or from their own works? Any help will be VERY welcome!!!!

Best wishes,

Marco Passamonti

Dr. Marco Passamonti, PhD Dipartimento di Biologia Evoluzionistica Sperimentale via Selmi 3 I-40126 Bologna (Italy) tel. +39/0512094168 fax +39/0512094286 email mpassa@alma.unibo.it

mpassa@alma.unibo.it

PostDocs

BristolU MathBiol	43	UCaliforniaSanDiego EvolEcolVertebrates	51
DukeU SpeciationGenetics	44	UCaliforniaSanDiego VertebrateEvol	51
GeorgiaInstTech SocialInsectEvol	44	UConnecticut EvolFuncGenomics	52
HarvardU EvolGenetics	45	UEdinburgh 2 MolEvolPhyloGenomics	52
ImperialCollegeLondon Mutualisms	45	UEdinburgh MolEvolParasitology	54
KonradLorenzInst EvolMarmosets	46	UManchester Bioinformatics	54
McMasterU StatGenetics	46	UMassachusetts EvolBiol	55
NewMexicoStateU FishGenetics	46	UOxford StatGenetics	55
NewMexicoStateU FuncPhylogenies	47	UPittsburgh PlantEvolBiol	55
OuluU EvolBiology	47	USouthCarolina GenomicEvol	56
Paris MNHN domestication	47	USouthernCalifornia CompBiology	56
RochesterU EvolGeneticsNasonia	48	UTexasArlington ComparativeGenomics	56
SangerInst Genomics	48	UVermont EvolInvasiveAbility	57
UAlaska MatingSystemEvol	49	UWalesBangor EvolFishGenetics	57
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UBerne Speciation	50		

BristolU MathBiol

Postdoctoral research assistant in mathematical biology (vacancy ref. 11136)

Extra note for evoldir readers: This job is essentially 2/3 population biology and 1/3 evolutionary theory, applied to phage-bacteria interactions within poultry.

Based in the School of Biological Sciences, Bristol University, England. This post involves theoretical analysis and modelling of therapeutic use of viruses (phage) against bacterial infections, including in-vitro, in-vivo and evolutionary aspects of the virus-bacteria interactions. Phage therapy is being developed as a therapeutic alternative to antibiotics. We shall use mathematical models to examine both applied and fundamental questions, including issues ranging from optimal treatment protocols to evolution of virulence, motivated in particular by an interest in how human food-

poisoning by campylobacter could be reduced by phage therapy directed against campylobacter in chickens on-farm. This theoretical work will involve collaboration with parallel experimental studies. Applicants should hold a PhD in mathematical biology or equivalent, be willing to learn relevant biology, and be capable of communicating with experimentalists.

Contact: (School of Biological Sciences) Dr Robert J.H. Payne E-mail: Robert.Payne@bristol.ac.uk Tel: +44(0)117 928 8254

Salary : £21,640 - £23,643 Contract : Fixed term contract three years

Further details and an application form can be found at <<https://www.bris.ac.uk/boris/jobs/ads?ID4015>> Alternatively you can telephone (0117) 954 6947, minicom (0117) 928 8894 or E-Mail Recruitment@bris.ac.uk (stating postal address ONLY), quoting reference number 11136.

The closing date for applications is 9.00am, 18 April 2005

DukeU SpeciationGenetics

Postdoctoral Research Associate- Speciation Genetics

A postdoctoral position is available at Duke University in the Noor laboratory (<http://www.biology.duke.edu/-noorlab/>) this fall to study the genetics of sexual isolation in *Drosophila pseudoobscura*. Previously, we have shown using both choice and no-choice experiments that female *D. pseudoobscura* derived from populations sympatric to their sibling species (*D. persimilis*) exhibit stronger sexual isolation than do female *D. pseudoobscura* derived from allopatric populations. This difference between *D. pseudoobscura* populations is evidence for speciation via reinforcement. We have recently mapped the genetic basis of this reinforced discrimination to two fairly narrow intervals (~300kb) (Ortiz- Barrientos et al 2004 PLoS Biology). The two intervals contain excellent candidate genes.

The present position would focus on continuing this work, with the ultimate goal of cloning and confirming via transgenic techniques some of the genes responsible for reinforced sexual isolation in *D. pseudoobscura*. Duke University hosts the Model Systems Genomics Unit (<http://www.biology.duke.edu/model-system/>), which can assist with the *Drosophila* transgenic efforts.

Funding is currently available for the first year of this effort, and additional funding to continue it is pending. The position will require an independent and motivated individual. Experience with molecular techniques is essential, and a track record of high-quality research in speciation is preferred. Applicants must have successfully received their PhD prior to appointment.

Applications will be evaluated as they are received and until a suitable candidate is selected. The start date is flexible, but preferably between August 1 and October 1, 2005. To apply, please first send a short e-mail inquiry to Mohamed Noor (noor@duke.edu) stating your interest and research/ publication record- please do not send attachments! A subset of applicants will be invited to submit their CV's and provide letters of reference later.

Duke University is an equal opportunity/ affirmative action employer.

GeorgiaInstTech SocialInsectEvol

POSTDOCTORAL POSITION IN SOCIAL INSECT BIOLOGY

A full-time Postdoctoral Research position is available to pursue a variety of potential studies in social insect biology. Candidates with interests in social insect genomics, population structure, hybridization, development, behavior, or evolution are encouraged to apply.

Position is available starting August 1st, 2005. Funding is for at least one year and starting salary will be commensurate with experience. Applicants should have a Ph.D. in genetics, genomics, behavior, entomology, evolution or a related field and have demonstrated research excellence.

Interested applicants should send CV, names and e-mail addresses for three references, and a one-page letter of interest to michael.goodisman@biology.gatech.edu. For additional information visit <http://www.biology.gatech.edu/professors/goodisman.html> or send an e-mail to the application address.

Michael A D Goodisman

Assistant Professor School of Biology The Georgia Institute of Technology Cherry Emerson Bldg A110 310 Ferst Drive Atlanta, GA 30332-0230 United States

webpage: <http://www.biology.gatech.edu/-professors/goodisman.html> profile: <http://>

/www.whistle.gatech.edu/archives/04/-
 nov/08/spot.shtml spotlight: [http://-](http://www.gatech.edu/profiles/goodisman.php)
www.gatech.edu/profiles/goodisman.php email:
 michael.goodisman@biology.gatech.edu office: 404-385-
 6311 lab: 404-385-6312 fax: 404-894-0519

HarvardU EvolGenetics

Postdoctoral Position: Evolutionary Ecology and Genetics Harvard University, Department of Organismic and Evolutionary Biology

A post-doctoral position is available, starting July 1, 2005. The postdoc will participate in an NSF-funded project on the evolutionary ecology and physiology of germination in *Arabidopsis thaliana*. Using mutant and natural ecotypes, the project examines the physiological basis of natural variation in germination phenology, while ongoing work in the lab investigates the consequences of this variation to life-history expression and population dynamics. Both fieldwork and laboratory work are involved.

Interested applicants should send a CV and cover letter, and supply the names and contact information of two or three references. Review of applications will begin on April 30, 2005 and will continue until the position is filled.

Contact: Kathleen Donohue Department of Organismic and Evolutionary Biology Harvard University 22 Divinity Ave. Cambridge, MA 02138

kdonohue@oeb.harvard.edu

ImperialCollegeLondon Mutualisms

Imperial College London Silwood Park Campus DIVISION OF BIOLOGY

Postdoctoral Researcher in Behavioural Ecology of Mutualisms

Applications are invited for an ecologist or evolutionary biologist to work on a NERC-funded project applying foraging and other models to understand conflict resolution in the fig / fig wasp mutualism.

The fig / fig wasp symbiosis is a classic obligate mutu-

alism, but the evolutionary interests of the partners are not fully aligned¹. In particular, there is conflict over how many fig ovules are used to raise wasp larvae and how many to nurture seeds (1,2). The researcher will use a combination of field observations, experiments, and molecular ecology techniques to parameterise and test a series of models (2) describing how figs can prevent their symbiotic wasps from overexploiting their seeds. The post and lab work will be based at Silwood Park, with fieldwork taking place in Australia. This is a collaborative project between Dr. James M. Cook (IC), Dr. Douglas Yu (UEA) and overseas project partner Prof. Ross Crozier (JCU, Australia).

We are therefore looking for candidates with experience in one or more of the following key areas:

* Insect behaviour (microvideo experience a plus) * Behavioural ecology models (preferably including foraging models) * Microsatellite genotyping (preferably) or other molecular ecology experience * Field biology of figs and fig wasps

Background references: 1. Cook, J.M. and Rasplus, J.-Y. (2003) Mutualists with attitude: coevolving fig wasps and figs. *Trends in Ecology & Evolution*. 18: 241-248.

2. Yu, D.W., Ridley, J., Jouselin, E., Herre, E.A., Compton, S.G., Cook, J.M., Moore, J.C. and Weiblen, G.D. (2004) Optimal foraging, host coercion, and the stable exploitation of figs by wasps. *Proceedings of the Royal Society of London Series B-Biological Sciences*. 271: 1185-1195.

The appointment is initially for 2 years with a possibility of an extension for a further year subject to funding negotiations being finalized. Salary will be on the Imperial College Research & Education Level B Job Family (£19,735-£29,851, depending on qualifications and experience).

An Imperial College Application form can be downloaded from <http://www.imperial.ac.uk/employment/-academicform.htm> and should be accompanied by a copy of your CV and a cover letter.

For further details contact one of the below:

Dr. James M. Cook, Division of Biology, Imperial College London, Silwood Park Campus, Ascot SL5 7PY. j.cook@imperial.ac.uk

Dr. Douglas W. Yu, School of Biological Sciences, University of East Anglia, Norwich, Norfolk NR4 7TJ. Douglas.Yu@uea.ac.uk

The closing date for applications is 6 May 2005

Dr. James M. Cook Lecturer Division of Biology

Imperial College London Silwood Park Campus
 Ascot Berks SL5 7PY, UK j.cook@imperial.ac.uk
[<mailto:j.cook@imperial.ac.uk>](mailto:j.cook@imperial.ac.uk) [http://-](http://www.bio.ic.ac.uk/research/jmc/cook.htm)
www.bio.ic.ac.uk/research/jmc/cook.htm [<http://-](http://www.bio.ic.ac.uk/research/jmc/cook.htm)
[/www.bio.ic.ac.uk/research/jmc/cook.htm](http://www.bio.ic.ac.uk/research/jmc/cook.htm) Tel.
 02075942329 Fax 02075942339
j.cook@imperial.ac.uk

KonradLorenzInst EvolMarmosets

Post-doctoral Fellowship at the KLI (Austria)

The Konrad Lorenz Institute for Evolution and Cognition Research (KLI) is a private, non-profit institution that primarily fosters theoretical research in evolutionary developmental biology and evolutionary studies in cognition. The KLI's marmoset facilities allow the testing of empirical predictions from theoretical studies in individual and social cognition, development, and evolution. The KLI invites applications for the following position: Two-year Postdoctoral Fellowship for experimental and theoretical research on the mechanisms of imitation and/or cognition in marmosets.

The project will be carried out in close collaboration with a EU-project on 'Evolution, development and intentional control of imitation' that has recently started at the University of Vienna. Candidates will hold a

PhD in biology or psychology and have experience with carrying out behavioral experiments with mammals or birds. Candidates for the position should send their curriculum vitae (in English) and a short description of their research interests to the Scientific Manager of the KLI: Prof. Dr. Werner Callebaut (callebaut@kli.ac.at) by May 8, 2005. All Fellows are expected to work at the KLI and to participate in the talks and workshops organized by the Institute. Further information about the KLI is available at <http://kli.ac.at>. Astrid Juette, PhD Executive Manager Konrad Lorenz Institute for Evolution and Cognition Research Adolf Lorenz Gasse 2, A-3422 Altenberg, Austria Tel +43-2242-32390 Fax +43-2242-323904 <http://kli.ac.at> Gabriele Gentile <gabriele.gentile@uniroma2.it>

McMasterU StatGenetics

We seek a postdoctoral researcher for up to two years to work on statistical methods and modeling in population genetics and molecular evolution as part of a group at McMaster University, Hamilton Canada. The applicant must have completed their Ph.D. preferably in population genetics, statistical genetics, computational biology, or phylogenetics and must have training in statistical methods and modeling in population genetics, molecular evolution and/or phylogenetics. Projects will center around the 'Barcode of Life' (BoL) initiative and Genome Canada funded work. Specific research projects will be determined based on the joint interests of the successful candidate and supervisor; the candidate will also be encouraged to carry out independent computational or empirical work.

Salary is approximately \$40-45K, pending qualification level. Applicants should contact Brian Golding (Golding@McMaster.CA) with special reference to this particular position. Submissions should include letters of reference, a complete CV and contact information. Review of applications will start May 1st and will continue until the position is filled.

Golding@McMaster.CA

NewMexicoStateU FishGenetics

Job Number: 4145 (Classification: Post Doctoral Appointments) Title: Post Doctoral Fellow Agency: New Mexico State University Location: Dexter, New Mexico Job Description: Conduct and monitor genetic studies in a laboratory setting, analyzing and interpreting data as part of larger complex study. Design sampling protocols and implements genetics sample and data collection on native fish throughout the desert southwest. Operate, configure, and maintain specialized molecular population genetics laboratory equipment such as thermocyclers, DNA sequencer, electrophoresis cells and centrifuges. Provide direction to biological technicians, university student assistants and volunteers in executing assigned duties. Qualifications: Familiarity and practical experience in extracting DNA from fish tissue or blood samples, conducting polymerase chain reaction (PCR) of extracted DNA, and generating DNA sequence or genotypic data. Must be able to design specific primers for mitochondrial and nuclear DNA markers using genbank and other sources, and microsatellites for conservation and ecological genetic applications. Must be able to communicate orally and in writ-

ing, project guidelines, investigation results, and participate in the preparation of data for scientific technical reports and manuscripts.

Salary: \$30,000 - \$32,000/yr + university benefits
 Last Date to apply: May 16, 2005
 Contact: Dr. Colleen Caldwell E-mail: ccaldwel@nmsu.edu(Preferred) Phone: 505-646-8126

Connie_KeelerFoster@fws.gov

NewMexicoStateU FuncPhylogenies

A group of us has been funded by the Los Alamos National Laboratory to develop phylogenetic inference techniques for the prediction of functional capabilities of specific target organisms given phylogenies including both the target and its relatives and functional data on the relatives. The specific interest of LANL is on novel biothreat agents; however, the underlying phylogenetic models to be developed will be much broader and applicable to a diversity of phylogenetic inference and comparative biology problems. Indeed, the intent is to develop general likelihood models that will be useful in a wide range of situations.

We are seeking an interested postdoctoral researcher to complement the team of biologists and computer scientists involved with the project. The ideal candidate would have a strong background in phylogenetics and in C++ (or at least object-oriented) programming. Additionally, the candidate would have good communication skills and be able to work both independently and collaboratively with other project members.

Interested applicants should send a CV and cover letter, and supply the names and contact information of two or three references. Review of applications will begin on April 30, 2005 and will continue until the position is filled.

The position is available as soon as a suitable candidate can be identified.

Please send information to:

Brook Milligan Department of Biology New Mexico State University Las Cruces, New Mexico 88003 U.S.A.
 brook@nmsu.edu

OuluU EvoBiology

Advanced postdoc in aquatic ecology/evolutionary biology

Applications from aquatic ecologists / evolutionary biologists are invited to join the Department of Limnology at EAWAG (Swiss Federal Institute of Environmental Research and Technology) and Department of Environmental Sciences at ETH-Zürich (Swiss Federal Institute of Technology). We are looking for an early-career scientist with some post-doc experience and credentials to assume group-leading responsibilities and acquire external funding for PhD-students. Responsibilities include some teaching at both BSc and MSc level. Position is opened for 2 years with a possibility of 4 year extension, which makes it comparable to assistant professorship without tenure.

Search opens 1st of May 2005 and will be completed in June 2005. Position is available at the earliest 1st of July, 2005, but the start date is flexible. Please, apply by email including a letter describing research interests, CV, and names of two references. Applicants will be shortlisted early June and contacted for further information.

Further information: prof. Jukka Jokela
 (jukka.jokela@oulu.fi)

for WWW-information: http://www.eawag.ch/-e_welcome.html http://www.env.ethz.ch/index_EN
http://cc.oulu.fi/~jwjokela/jj_home.html
 jukka.jokela@oulu.fi

Paris MNHN domestication

Dear colleague, As for the domestication post-doc position in Paris, I have some more information for you. The application will be closed on the 6th May. At this date, I must have your official form, either by email or by postal mail. On the 13th May, I'll tell you if you are shortlisted or not. If you are, it will be necessary to organise a meeting in Paris between the 7th and the 14th June. The results will be declared before the 15th. Official acceptance by the CNRS will be known at the

beginning of July. The beginning of the work will be on September 1st. This is not a problem if you have not yet finished your PhD. However, we must have a first draft for May 6th, and the defense must take place before September 1st. If you have any question, ask me. Sincerely

Jean-Denis VIGNE, Dr HDR Head researcher at the CNRS Vice-president of the Scientific Council of the National Museum of Natural History, Paris Director of the Lab : Archaeozoology, history of human societies and animal communities CNRS - Muséum national d'Histoire naturelle Dpt Ecology and Biodiversity Management USM 303, Case postale N 56 (Bâtiment d'anatomie comparée) 55 rue Buffon, F-75231 Paris cedex 05, France tel : 33 (0)1 40 79 33 10 fax : 33 (0)1 40 79 33 14

visit the website of the lab : <http://www.mnhn.fr/-mnhn/anc/esa/esa.html> and the sites that this lab built for the community : <http://www.histoire-archeologie-animal.org/> <http://arkzoo.archeozoologie-archaeozoology.org/> Jean-Denis Vigne <vigne@mnhn.fr>

RochesterU EvolGeneticsNasonia

Postdoctoral Position: Evolutionary Genetics in Nasonia

Description: A 2-3 year postdoctoral position is available to study evolutionary genetics in the parasitoid wasp genus *Nasonia*. *Nasonia* is an emerging model system for genetic research, which has recently been selected for full genome sequencing (<http://www.genome.gov/13014443>). Genome sequencing has been approved by NIH for 6-fold sequencing of *N. vitripennis* and 1-fold sequencing of the two sibling species, *N. giraulti* and *N. longicornis*. *Nasonia* is a complex of three closely related species that are interfertile, allowing movement of genes between them. The three species differ in many interesting aspects of morphology and behavior. An NIH-funded project investigates the genetic basis of a 2.5 fold difference in male wing-size between two species (*N. vitripennis* and *N. giraulti*). This represents a recent evolution of male- and organ-specific regulation of cell size and number, and our genetic analyses indicates that the difference is due primarily to 3-4 genetic regions of large effect. Fine-scale mapping and introgression of wing size genes from one species into the other has been accomplished. The goal of this project is to use positional cloning methods to

identify candidate genes involved, and to investigate their patterns of molecular evolution, and gene expression in wing imaginal discs. Depending upon interest, the postdoctoral researcher will also have opportunities to become involved in aspects of the *Nasonia* EST project (70,000 ESTs are currently being sequenced in the two species), *Nasonia* microarray, and molecular evolutionary studies emerging from the *Nasonia* genome project.

Additional information on *Nasonia* and related projects can be obtained through my website below

Requirements: PhD. Experience with some combination of the following: insect genetics, DNA sequencing and analysis, molecular evolution, QT-PCR, cDNA microarrays, BAC library hybridization

Salary: \$33,500 - 38,500 per year, depending upon experience level. Health Insurance is also included. Rochester has a moderate cost of living with readily available and affordable housing.

Deadline: The position is available immediately. Applications will be accepted until the position is filled.

Please send by email a statement of interest, CV and contact information for three references to: Dr. John (Jack) Werren, Department of Biology, University of Rochester, Rochester, NY 14637. email: werr@mail.rochester.edu website: <http://www.rochester.edu/College/BIO/labs/WerrenLab/> Professor of Biology Department of Biology University of Rochester Rochester, N.Y. 14627 email: werr@mail.rochester.edu fax: 585-275-2070 phone: 585-275-3694 website: <http://www.rochester.edu/College/BIO/labs/WerrenLab/index.html> "John (Jack) Werren" <werr@mail.rochester.edu>

SangerInst Genomics

The Wellcome Trust Sanger Institute is at the forefront of experimental and computational genome research. We are recognized leaders in genome sequencing, high throughput systems, informatics and analysis of gene function using genetic approaches in a variety of model organisms and humans.

Applications are invited for Postdoctoral Research Fellowships within the Sanger Faculty. This is an exciting opportunity to begin an independent research career in state of the art genomics facilities. Successful candi-

dates will be awarded a fellowship with a starting salary of circa £25,000 p.a. plus excellent benefits. This post is initially offered for two years after which it is expected that the candidate will seek independent support. We are particularly interested in hearing from candidates who have completed their Ph.D. within the last year.

There is a growing number of faculty members at the Sanger working on questions of molecular evolution, comparative and evolutionary genomics and population genetics, such as:

Chris Tyler-Smith, Human Evolution (cts@sanger.ac.uk) Mark Ross, Analysis of X chromosome (mtr@sanger.ac.uk) Matthew Hurles, Genome Dynamics and Evolution (meh@sanger.ac.uk) Manolis Dermitzakis, Population and Comparative Genomics (md4@sanger.ac.uk)

Please find more information about our research projects on the web site: <http://www.sanger.ac.uk/Teams/faculty/> We welcome applications from highly motivated young investigators to work in individual or collaborative projects among the above groups. To discuss sponsorship for a Sanger fellowship, please feel free to contact any of the above faculty.

Coming deadlines for applications: May 31, 2005
September 30, 2005

Please contact us at least 3 weeks in advance

Emmanouil (Manolis) Dermitzakis, PhD Investigator Population and Comparative Genomics The Wellcome Trust Sanger Institute Wellcome Trust Genome Campus Hinxton, Cambridge CB10 1SA UK e-mail: md4@sanger.ac.uk Tel: +44 (0)1223 494866 Fax: +44 (0)1223 494919 URL: <http://www.sanger.ac.uk/Teams/Team16/> Manolis Dermitzakis <md4@sanger.ac.uk>

UAlaska MatingSystemEvol

Postdoc position available Evolution of plant mating systems and evolutionary genetics 2 years - \$37,000/year + benefits Starting date flexible

In the lab of Naoki Takebayashi <<http://www.faculty.uaf.edu/ffnt/>> University of Alaska Fairbanks

A postdoctoral position is available in the general areas of plant mating system evolution or ecological/evolutionary genetics in Alaskan *Arabidopsis lyrata*

(*Arabidopsis lyrata*) and *Papaver* sp. to investigate questions of mutual interest. Potential projects include the genetic basis of inbreeding depression, adaptations to high latitudes in Alaskan *A. lyrata*, for instance cold adaptation or the evolution of self-fertilization, molecular evolution of self-incompatibility, etc. The project could be theoretical, ecological or molecular. Many of the projects are in collaboration with Diana Wolf <<http://www.faculty.uaf.edu/fflew2/>>, who has experience in molecular techniques.

My lab is well equipped for medium-throughput DNA extraction, cloning, sequencing and molecular marker analysis, with 6 thermocyclers, a 96-well tissue grinder, etc. The core molecular lab is also very well equipped with 2 ABI 3100 sequencers, liquid handling robots, flow-cytometer and other equipment. A 7 node linux cluster is available for computaion, and super-computers (IBM, Cray X1) are avialable from Arctic Region Supercomputing center <<http://www.arsc.edu/about/about.html>>. You can learn more about population genetics and evolutionary biology at the University of Alaska here (<http://www.alaska.edu/epscor/funding/epscorpostdoc.html>). To learn more about biology at UAF, see here (<http://www.iab.uaf.edu>).

A background in evolutionary biology, population genetics or molecular evolution is desired. Experience in computer programming, analytical modeling and/or molecular techniques is a plus, but not required. Please contact me informally to discuss potential projects.

Applications must be submitted by mail to UAF Human Resources following the instructions provided at <http://www.uaf.edu/uafhr/Employment/Job1003-404.html>, and should include:

- 1) Cover letter referencing position number FF92028801
- 2) Statement of research interests (up to 2 pages)
- 3) Curriculum vitae
- 4) Three letters of reference
- 5) UA Applicant Form (see url above)

However, you should also send a copy of all application materials ****directly**** to me by email (ffnt@uaf.edu).

Review of application will start June 1, 2005, and applications will be accepted until the position is filled.

Naoki

Naoki Takebayashi <ffnt@uaf.edu> Institute of Arctic Biology & Department of Biology and Wildlife 311 Irving I Bldg, University of Alaska Fairbanks, Fairbanks, AK 99775, USA office: (907) 474-1178, WRRB 226 fax: (907) 474-6967

UBath Pancrustacean phylogeny

Postdoctoral Researcher

Pancrustacean Phylogeny

Applications are invited for a three year BBSRC-funded postdoctoral position working with Dr Matthew Wills, Professor Richard French-Constant and Professor Laurence Hurst. We are seeking a molecular systematist to investigate the application of total evidence approaches to the phylogeny of pancrustaceans and their near relatives. The appointee will be primarily responsible for obtaining sequence data from multiple loci for a wide sample of crustacean taxa. Excellent lab skills and experience of molecular phylogenetics are therefore essential. The project will combine molecular data with morphological characters, and the Postdoc will head up those publications that rely most heavily on his/her work.

The position is available from August 2005, or as soon as possible thereafter, for 36 months.

Informal enquiries may be directed to Dr Matthew Wills, Department of Biology and Biochemistry, University of Bath, Claverton Down, Bath BA2 7AY, tel: 01225 323504 or email: m.a.wills@bath.ac.uk.

Further details also available from: http://www.bath.ac.uk/jobs/job_desc.cgi?05/101 Starting salary £21,640 per annum

Closing date for applications is 6th May 2005

Application forms may be obtained from the Human Resources Department, University of Bath, Claverton Down, Bath BA2 7AY (e-mail S.Kennedy@bath.ac.uk). Alternatively, please phone the 24 hr answer-phone service on (01225) 386924, textphone (01225) 386039 or apply online at www.bath.ac.uk/jobs, quoting Ref 05/101

Dr Matthew A Wills Lecturer in Evolutionary Biology Department of Biology and Biochemistry The University of Bath South Building, Claverton Down, Bath BA2 7AY

Tel: 44 +1225 826826 ext 3504 Fax: +44 1225 826779 <http://www.bath.ac.uk/Departments/BiolBioch/-wills.htm> Matthew A Wills <bssmaw@bath.ac.uk>

UBerne Speciation

A 12 to 18 months postdoc position is available for a theoretical population geneticist to work with Ole Seehausen (University of Berne/EAWAG) and Russell Lande (UC San Diego) to develop numerical models of speciation by selection on sex reversal and a partially linked phenotypic trait. Sex reversal genes linked to conspicuous colour effects affecting mate choice are common in African cichlid fish (Seehausen et al. 1999). We have developed a mathematical model to investigate whether such polymorphisms could be the basis of rapid sympatric speciation (Lande et al. 2001). Several empirical studies currently test assumptions of our model. The postdoc is expected to extend our modelling framework to develop more broadly applicable models in which specific assumptions of our earlier model can be relaxed, e.g. we want to study speciation dynamics when the trait is quantitative- and populations are spatially structured. We anticipate this will require the construction of individual-based simulation models.

The postdoc will be shared between the Swiss department of Aquatic Ecology & Evolution (Swiss Institute for Environmental Science and Technology (EAWAG)/Institute of Zoology of the University of Berne) and the Department of Ecology, Behavior and Evolution of the University of California at San Diego. The postdoc will spend six months in Switzerland and six to twelve months in San Diego, with a shorter visit at the University of Leiden. Salary in Switzerland will be at University assistant level, depending on age and experience (upwards from ~CHF 5,500 per month), salary in San Diego will be about \$3,000 per month. (Note 1.0 CHF = 0.846 USD, Swiss taxes are about 25% of gross salary.)

Starting date is June 2005 (or July latest). Applications are accepted until the post is filled.

The successful applicant will have training in population genetics theory, with good mathematical ability and computer programming skills in a language such as C++. Application material should be sent by email to <<mailto:ole.seehausen@eawag.ch>>ole.seehausen@eawag.ch and <<mailto:rlande@biomail.ucsd.edu>>rlande@biomail.ucsd.edu Please send with your application a CV (pdf format) and up to three publications (pdf format), and names and contact information for two people who can

provide references.

ole.seehausen@eawag.ch

UCaliforniaSanDiego EvolEcolVertebrates

Postdoctoral position GLOBAL SCALE ECOLOGY AND CONSERVATION OF TERRESTRIAL VERTEBRATES Division of Biological Sciences University of California San Diego DESCRIPTION: One fully funded postdoctoral position (max. two years) will be available starting summer/fall 2005 to work on the broad-scale ecology of terrestrial vertebrates, particularly birds and mammals. The research will draw on a number of unique ecological, environmental, phylogenetic and distributional databases, encompassing all known species of birds and mammals, and all regions of the world. The goal is to establish a synthetic theoretical and analytical framework for the global-scale ecology of vertebrates rooted at the level of the individual and to develop and test general theories about the distribution of species and their core ecological attributes across scales. The data, tools, and methods already developed for this project now offer a number of different and exciting new opportunities. The research can take a very basic perspective (e.g. disentangling environmental, evolutionary and stochastic effects) or an applied one (e.g. investigating patterns of endemism and threat, effects of land use and climate change). There are some obvious research opportunities, but the array of questions is not restricted by grant guidelines and there is ample potential for the researcher to develop new directions. RESEARCH GROUP: The position is based in the lab of Walter Jetz. In this group, the successful candidate will interact with two PhD students (broad-scale conservation of mammals and birds, regional-scale macroecology of herptiles) and one affiliated postdoctoral fellow (cross-scale bioenergetic models for herptiles). He or she will be able to draw on the support of a full-time GIS assistant. There is the potential to develop and co-supervise undergraduate and graduate research projects. LOCATION: University of California, San Diego. The position is based at the Section of Ecology, Behavior & Evolution in the Division of Biological Sciences - a research community of approximately 100 faculty (including 14 members of the National Academy), 140 postdoctoral fellows, and 250 graduate students, which is further strengthened by the neighboring Scripps Institute of Oceanography.

REQUIREMENTS: A Ph.D. in ecology, biogeography or evolution with research experience in the analysis of spatial data. Evidence of research productivity as indicated by scholarly publications is required. Sound skills in the use of GIS, relational databases and statistical analysis of spatial data are a prerequisite. Evidence of strong communication and teamwork skills is highly desired. Experience in the analysis of phylogenetic data, species distribution modeling, spatial statistics, or programming (e.g. C, Visual Basic) is a plus. APPLICATION: Please send letter of interest, C.V., and the names and contact details of three referees by May 15, 2005 to: Postdoctoral Position in Global Ecology, Romel Hokanson, EBE - Biological Sciences, UC San Diego, 9500 Gilman Drive - MC: 0116, La Jolla, CA 92093-0116. Phone: +1-(858)-822-4862. Electronic application materials (pdf, word) are preferred - please email to rhokanson@ucsd.edu. Review of applications will begin immediately, and continue until the position is filled.

wjetz@ucsd.edu wjetz@ucsd.edu

UCaliforniaSanDiego VertebrateEvol

Postdoctoral position in GLOBAL SCALE ECOLOGY AND CONSERVATION OF TERRESTRIAL VERTEBRATES. Division of Biological Sciences, University of California San Diego

DESCRIPTION: One fully funded postdoctoral position (max. two years) will be available starting September 2005 to work on the broad-scale ecology of terrestrial vertebrates, particularly birds and mammals. The research will draw on a number of unique ecological, environmental, phylogenetic and distributional databases, encompassing all known species of birds and mammals, and all regions of the world. The goal is to establish a synthetic theoretical and analytical framework for the global-scale ecology of vertebrates rooted at the level of the individual and to develop and test general theories about the distribution of species and their core ecological attributes across scales. The data, tools, and methods already developed for this project now offer a number of different and exciting new opportunities. The research can take a very basic perspective (e.g. disentangling environmental, evolutionary and stochastic effects) or an applied one (e.g. investigating patterns of endemism and threat, effects of land use and cli-

mate change). There are some obvious research opportunities, but the array of questions is not restricted by grant guidelines and there is ample potential for the researcher to develop new directions.

RESEARCH GROUP: The position is based in the lab of Walter Jetz. In this group, the successful candidate will interact with two PhD students (broad-scale conservation of mammals and birds, regional-scale macroecology of herptiles) and one affiliated postdoctoral fellow (cross-scale bioenergetic models for herptiles). He or she will be able to draw on the support of a full-time GIS assistant. There is the potential to develop and co-supervise undergraduate and graduate research projects.

LOCATION: University of California, San Diego. The position is based at the Section of Ecology, Behavior & Evolution in the Division of Biological Sciences - a research community of approximately 100 faculty (including 14 members of the National Academy), 140 postdoctoral fellows, and 250 graduate students, which is further strengthened by the neighboring Scripps Institute of Oceanography.

REQUIREMENTS: A Ph.D. in ecology, biogeography or evolution with research experience in the analysis of spatial data. Evidence of research productivity as indicated by scholarly publications is required. Sound skills in the use of GIS, relational databases and statistical analysis of spatial data are a prerequisite. Evidence of strong communication and teamwork skills is highly desired. Experience in the analysis of phylogenetic data, species distribution modeling, spatial statistics, or programming (e.g. C, Visual Basic) is a plus.

APPLICATION: Please send letter of interest, C.V., and the names and contact details of three referees by May 15, 2005 to: Postdoctoral Position in Global Ecology, Romel Hokanson, EBE - Biological Sciences, UC San Diego, 9500 Gilman Drive - MC: 0116, La Jolla, CA 92093-0116. Phone: +1 (858) 822-4862. Electronic application materials (pdf, word) are preferred - please email to rhokanson@ucsd.edu. Review of applications will begin immediately, and continue until the position is filled.

Walter Jetz, Ph.D. Assistant Professor Division of Biological Sciences University of California, San Diego 9500 Gilman Drive, MC 0116 La Jolla, CA 92093-0116, USA Email: wjetz@ucsd.edu <<http://www.biology.ucsd.edu/labs/jetz/>> <http://www.biology.ucsd.edu/labs/jetz/>

Walter Jetz <wjetz@ucsd.edu>

UConnecticut EvolFuncGenomics

Postdoctoral Opening in the Townsend Laboratory

A post-doctoral position is available at the University of Connecticut in the Townsend Laboratory (<http://web.uconn.edu/townsend>) to study the evolution and functional genomics of *Saccharomyces* or *Neurospora*. The precise project is flexible, but possible projects may include the evolution of gene expression and the functional genomics of interspecies infertility.

This position will require an independent and motivated individual, preferably with laboratory experience with *Saccharomyces* or *Neurospora*. Applicants with previous postdoctoral experience are encouraged to apply; all applicants should have received their Ph.D. prior to taking up the appointment.

Funding is available for multiple years, depending on performance. The salary is greater than the NIH guidelines, and commensurate with experience and expertise. Storrs is located in a beautiful community in the heart of New England, close to New Haven, Hartford, Providence, and Boston.

Closing date: June 1, 2005. Applications will be reviewed beginning May 1, 2005. Starting date is flexible.

To apply, please send a CV, a brief statement of research interests and contact information for three academic references to Jeffrey.Townsend@UConn.edu.

Jeffrey P. Townsend Molecular and Cell Biology Department University of Connecticut Storrs, CT 06269

<http://web.uconn.edu/townsend>

Jeffrey.Townsend@uconn.edu

Jeffrey.Townsend@uconn.edu

Jeffrey.Townsend@uconn.edu

UEdinburgh 2 MolEvolPhyloGenomics

Two Jobs in Molecular Evolution, Phylogeny and Genomics

at The University of Edinburgh, School of Biological Sciences / Institute for Evolution

Position 1 is for Post-Doctoral Researcher (36 months)
Position 2 is for a Graduate Research Associate (34 months)

Title: Linking Genomes to Ecology: Evolution of Daphnia Immune System Genes

Supervisors: Tom Little (tom.little@ed.ac.uk) and Mark Blaxter (mark.blaxter@ed.ac.uk). This NERC-funded project is focused on disease resistance and immunity genes in Daphnia, the first crustacean to have its genome fully sequenced. Depending on your interest or skill, the work may emphasize aspects of comparative genomics, molecular evolution, or the ecology and evolution of disease resistance, but preferably the candidate will have an interest in all these things.

Details: 1) Postdoctoral Research Fellow (quote ref: 3004165)

BRIEF BACKGROUND AND GOALS OF THE PROJECT: Parasitism may dramatically modulate the genetic structure of populations. Natural populations vary tremendously in their levels of parasitism and pathogen virulence, and although host genetic polymorphism often mediates these patterns, rarely is it known which genes are involved. Addressing this issue requires studying parasitism in a organism that is both a genetic model and a model for studies of natural variation. This Project will exploit emerging genomic knowledge of *Daphnia pulex*. *Daphnia*, unlike traditional models for genetic study, are extremely well-characterised in terms of their ecology and natural patterns of variation, which includes intriguing variation in levels of recombination. The project will first involve searching the *Daphnia* genome for immunity genes (based on homology with the range of other sequenced arthropods) to gain a broad perspective on the immune-related genome of the first sequenced crustacean (sensu Christophides et al. *Science* 298:159-165 (2002)). Second, the project will study natural levels of variation at candidate immunity genes. In particular, we aim to determine which immune system genes are the foci of coevolutionary interactions by examining DNA polymorphism between and within species to test for the footprint of pathogen-mediated selection in natural populations (e.g. Ford, M. J. *Molecular Ecology* 11, 1245-1262 (2002); Little et al. *Journal of Molecular Evolution* 59:498-506 (2004)). Thus, this Project will combine bioinformatics, population genetics and evolutionary ecology, possibly including field work. The candidate will have a strong interest in some or all of these areas. The Job is based in Edinburgh, but travel to North American study sites is likely. The candidate will join a working environment that is extremely strong in evolutionary ecology, population genetics, genomics and coevolutionary interac-

tions (see: <http://www.icapb.ed.ac.uk/>)

Post title: Post Doctoral Researcher Funding body: NERC Start date: June 1, 2005 (negotiable) Grade: AR1A Post Doctoral Research Assistant Salary scale: £19460-£29128 Hours: 40/week Duration: 36 months Supervisor: Tom Little Enquiries: tom.little@ed.ac.uk Location: School of Biological Sciences, ICAPB, Ashworth Laboratories, Kings Buildings, West Mains Road, Edinburgh EH 9 3JT

Please quote ref: 3004165 Closing date: 19 April 05

Formal Application MUST be made through the website: www.jobs.ed.ac.uk Or by phoning 0131 650 2511

2) Graduate Research Associate (quote ref: 3004163)

This three year project involves the study of parasitism in a model organism, the crustacean *Daphnia*. The project involves analysis of the immune system of *Daphnia*, which is the first crustacean to have its genome fully sequenced. This post will assist with the collection of DNA polymorphism data from natural populations. The candidate requires a BSc. and experience in molecular biology (DNA extraction, PCR and sequencing). An interest in evolutionary ecology and field work (collecting *Daphnia* from freshwater ponds) will be helpful. Job is based in Edinburgh, but travel to North American study sites likely. The candidate will join a working environment that is extremely strong in evolutionary ecology, population genetics, genomics and coevolutionary interactions (see: <http://www.icapb.ed.ac.uk/>)

Post title: Graduate Research Associate Funding body: NERC Start date: June 1, 2005 (negotiable) Grade: AR1B Research Assistant Salary scale: £19460-£21640 Hours: 40/week Duration: 34 months Supervisor: Tom Little Enquiries: tom.little@ed.ac.uk Location: School of Biological Sciences, ICAPB, Ashworth Laboratories, Kings Buildings, West Mains Road, Edinburgh EH 9 3JT

Please quote ref: 3004163 Closing date: 19 April 05

To apply online or view more job opportunities, visit our website

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

UEdinburgh MolEvolParasitology

School of Biological Sciences: Institutes of Evolution, Immunology & Infection Research (IEB/IIIR)

Required to work on a project involving the development and application of novel molecular techniques to investigate transmission strategies in malaria (*Plasmodium*) parasites. You will work in an interdisciplinary environment within the School of Biological Sciences and collaborate with leading parasitologists both in the UK and internationally. Molecular techniques will include quantitative, reverse transcriptase PCR and could include transfection. Most work will involve laboratory models but some field work may also be possible. The position would suit an enthusiastic molecular parasitologist or molecular ecologist who has a track record of developing relevant techniques. You must have, or expect to have, a PhD in a related area in the very near future. Some relevant postdoctoral experience and a Home Office licence would be an advantage but is not essential.

Fixed term: up to 33 months Salary scale: £19,460 to £29,128 p.a. Please quote Ref: 3004316JW

Closing date: 29 April 2005

DETAILS Funding body: BBSRC Hours: Full-time Start date: 1st June 2005 or as soon thereafter Fixed term: up to 33 months Supervisors: Professor Andrew Read, Dr Sarah Reece & Dr Stu West Enquiries: a.read@ed.ac.uk or sarah.reece@ed.ac.uk

BACKGROUND Protozoan parasites are the causative agents of some of the most serious diseases of livestock and humans. Recent advances in malariology, not least new genomic information and new molecular techniques, permit us to test the assumptions and predictions of evolutionary theory that has been specifically developed for these parasites. We use experimental and theoretical approaches to understand how natural selection has shaped the ways in which organisms maximise their transmission to new hosts.

In this project we will use several rodent malaria species as experimental models, to tackle key areas of contention, and biological interest. This includes the possibility that parasites enhance their transmission by altering their sex ratios at low infection densities and in response to naturally or vaccine induced immune factors. Our websites provide more detailed information, links to relevant publications and contact details for informal enquiries:

Dr Sarah Reece: <http://homepages.ed.ac.uk/-sreece/> Professor Andrew Read: <http://-readgroup.icapb.ed.ac.uk/> Dr Stuart West: <http://westgroup.icapb.ed.ac.uk/> FURTHER PARTICULARS <https://www.jobs.ed.ac.uk/jobs/-index.cfm?action=getFPS&fps=6504>

APPLICATION INSTRUCTIONS <https://www.jobs.ed.ac.uk/> Dr Sarah Reece Institutes of Evolution, Immunology and Infection Research, School of Biological Sciences, Ashworth Laboratories, University of Edinburgh, Edinburgh EH9 3JT Scotland, UK

Tel +44 131 650 5446 Fax +44 131 650 6564

sarah.reece@ed.ac.uk <http://homepages.ed.ac.uk/-sreece/> <http://homepages.ed.ac.uk/sreece/>

UManchester Bioinformatics

RA in Bioinformatics (Ref LS/059/05)

Applications are invited from qualified individuals seeking to work in computational biology/bioinformatics research. You should possess an advanced degree (MSc or PhD) in bioinformatics or a closely related research area.

This BBSRC-funded position is available for up to three years to work on the project the Analysis and enhanced representation of protein interaction networks. The main aim of this research will be to investigate the molecular evolution of the interactome, focussing on protein-protein and protein-DNA interactions. Research experience in bioinformatics, comparative genomics, network/graph representation and computer programming skills will be a distinct advantage.

This post is available for up to three years.

Informal enquiries can be made to Dr. David Robertson (e-mail: david.robertson@manchester.ac.uk).

Application forms and further particulars are available from:

www.manchester.ac.uk/vacancies

or contact Directorate of Human Resources, Faculty of Life Sciences, G.100 Stopford Building, The University of Manchester, Oxford Road, Manchester M13 9PT. Tel.: +44 (0)161 275 8836, e-mail: Lifesciences-hr@manchester.ac.uk.

Closing date: 29th April 2005. Please quote reference

LS/059/05

robertson@bioinf.man.ac.uk

UMassachusetts EvolBiol

DARWIN FELLOW

The Graduate Program in Organismic and Evolutionary Biology (OEB) at University of Massachusetts Amherst announces a two-year POSTDOCTORAL FELLOWSHIP/LECTURESHIP. The OEB Program draws together more than 80 faculty members from the five colleges (University of Massachusetts Amherst, Amherst College, Hampshire College, Mount Holyoke, and Smith College), offering unique training and research opportunities in the fields of ecology, organismic and evolutionary biology. Our research/lecture position provides recent Ph.D.s with an opportunity for independent research with an OEB faculty sponsor as well as experience developing and teaching a one-semester undergraduate biology course. Position subject to availability of funds. First year salary: \$30,000. Second year salary: \$32,000. Applicants in the area of collections-based research are particularly encouraged to apply.

To apply, send curriculum vitae, three letters of reference, statements of research and teaching interests, and letter of support from your proposed OEB faculty sponsor. A list of faculty and additional information is available at website: <<http://www.bio.umass.edu/oeb>><http://www.bio.umass.edu/oeb> . OEB Darwin Fellowship 319 Morrill Science Center 611 N. Pleasant Street University of Massachusetts Amherst Amherst, MA 01003 Telephone: 413-545-0928 E-mail: <<http://aaas.sciencecareers.org/texis/-apply?idB41c0774a0410&lookidas&toUrwin@bio.umass.edu>>darwin@bio.umass.edu

Application review begins: April 15, 2005; start date: August 15, 2005.

Any questions, feel free to contact me....

Best,

Dan Ardia

Dan Ardia Darwin Fellow Program in Organismic and Evolutionary Biology Morrill Science Center University of Massachusetts, Amherst, MA 01003

Email: ardia@bio.umass.edu website: www.bio.umass.edu/oeb/ardia (413) 545-0035, FAX: (413) 545-3243

“The whole problem with the world is that fools and fanatics are always so certain of themselves, but wiser people so full of doubts.” -Bertrand Russell

UOxford StatGenetics

Department of Statistics, University of Oxford.

One or possibly two postdoctoral positions of up to three years duration are available to work on statistical methodology for the analysis of high-dimensional data arising from modern experimental technologies in genetics, with the aim of identifying and characterizing biomarkers (signatures) of human disease risk. The project is part of a multi-national EU programme investigating genomic epidemiology; exploring the potential of combining information from multiple genomic platforms, including, transcriptomics, proteomics and metabonomics. The emphasis of the project is on metabolic diseases such as diabetes.

The post(s) provide a unique opportunity to develop key statistical methodology in parallel with the EU partners developing the next generation of experimental techniques.

Closing Date for applications April 21, 2005.

Further details at: <http://www.stats.ox.ac.uk/-jobs/HapMap.html> cholmes@stats.ox.ac.uk
cholmes@stats.ox.ac.uk

UPittsburgh PlantEvolBiol

I would appreciate it if you could post/circulate this information regarding a Postdoc Opportunity in my lab to interested colleagues. THANKS!

POSTDOC in PLANT EVOLUTIONARY ECOLOGY
A post-doctoral position is available, starting September 1, 2005. The postdoc will participate in an NSF-funded project on the role of resource environment in determining the mating system. The project will test several mechanistic hypotheses for how resource context affects mating system parameters using innovative flower and plant-level manipulations and microsatellite genetic markers in a model system (*Fragaria virginiana*). The research will ultimately contribute to our

understanding of the role of environment in the evolution of dioecy. Field, greenhouse and laboratory work are involved. Experience with molecular markers is highly desirable. Interested applicants should send a CV, cover letter, and the names/contact information for three references. Review of applications will begin on May 1, 2005 and will continue until the position is filled.

Contact: Tia-Lynn Ashman Department of Biological Sciences University of Pittsburgh Pittsburgh, PA 15260

Email: tial@pitt.edu Phone: 412-624-0984

Tia-Lynn Ashman Associate Professor Department of Biological Sciences University of Pittsburgh 4249 Fifth Ave & Ruskin Pittsburgh, PA 15260

phone: 412-624-0984 fax: 412-624-4759 website: <http://www.pitt.edu/~biohome/> tial+@pitt.edu

USouthCarolina GenomicEvol

I am looking for a postdoc and/or a graduate research assistant to work on a project involving the genomic evolution of pathogens and the vertebrate host response. The research will involve computational analysis of sequence data and other biological data. This research program is very flexible, so it will be possible to choose a project that meets your interests.

Postdoc: Salary US \$40,000-55,000 depending on experience. Excellent benefits package. I am looking for someone with computational skills and an interest in molecular evolution.

Graduate Student: Stipend \$20,000-\$25,000. Interest in computational biology and molecular evolution.

Austin L. Hughes, Ph.D. University of South Carolina Columbia SC 29208 Tel: 803-777-9186 Tel: 803-777-9186

USouthernCalifornia CompBiology

University of Southern California

POST-DOCTORAL RESEARCH ASSOCIATES

The NHGRI-funded Center of Excellence in Genomic

Sciences [CEGS] at USC has vacancies for post-doctoral research associates in the area of computational biology and statistical genetics. The Center is housed within the Molecular and Computational Biology Program and the Department of Preventive Medicine, nationally recognized as the leading groups in their respective fields. The primary focus of our Center is on human haplotype variation and its association with disease. The candidate is likely to collaborate closely with Professors Nordborg, Tavaré and Wall within the Molecular and Computational Biology Program, as well as Professors Marjoram, Stram and Thomas within the Department of Preventive Medicine. The successful candidates will be encouraged to develop independent methodologic research related to the themes of CEGS, with a particular emphasis on exploration and exploitation of linkage disequilibrium and haplotype structure in genome-wide data, and will have opportunities to collaborate on a broad range of related subjects including HapMap and ENCODE data, as well as data from non-human organisms. Candidates should hold a Ph.D. in statistics, computational biology, human genetics, or a related field and have a demonstrated interest in a research career in these areas. CV and names of three references should be submitted to:

Dr. Paul Marjoram Division of Biostatistics Department of Preventive Medicine University of Southern California 1540 Alcazar Street, CHP-220 Los Angeles, CA 90089-9011 (pmarjora@usc.edu)

Closing date for applications is June 1st, 2005. Applicants from under-represented minority groups are particularly encouraged to apply. USC is an Equal Opportunity Employer.

Paul Marjoram Dept. of Preventive Medicine Keck School of Medicine University of Southern California 1540 Alcazar Street, CHP 220 Los Angeles, CA 90089-9011 USA.

Ph= 323-442-0111 FAX= 323-442-2349 FAX= 323-442-2349

UTexasArlington ComparativeGenomics

Postdoctoral Positions in Comparative Genomics

Two postdoctoral positions are available in the laboratory of Esther Betrán, Ph.D., located in the newly remodeled facilities of the Genome Biology Group

at the University of Texas at Arlington (http://biology.uta.edu/genome_group/index.htm). The NIH funded research focuses on the origin of new genes and their role in genome evolution. We are looking for candidates with computational and/or experimental expertise.

Several projects are under development in the lab to answer essential questions in the field of new gene origination: functional and evolutionary study of young retrogenes, de novo formation of promoter regions and patterns on the formation of new genes. For a summary of research, please see: <http://www3.uta.edu/faculty/betran/publications.html> Candidates should have or be close to obtaining a Ph.D. degree in computational biology or evolutionary genetics with desire to conduct comparative genomics analysis. Candidates with computational expertise should be familiar with whole-genome datasets alignments, practical experience programming in Perl and MySQL in a Unix/Linux environment. Candidates with experimental expertise should be highly trained in molecular biology techniques. A Drosophila genetics and evolutionary background is a plus.

Our lab enjoys vibrant interactions with other members of the new and rapidly expanding Genome Biology Group. Additionally, the lab will benefit greatly from the new Genome Facility and new lab space.

The University of Texas at Arlington, the second largest institution in The University of Texas system, is a full service research and teaching university with over 25,000 students. The University is located in the city of Arlington in the center of the Dallas-Ft. Worth Metroplex, one of the leading centers of aerospace, electronics, and telecommunications activity in the U.S. Excellent recreational, entertainment, and cultural facilities, major airport, modern shopping complexes and professional sports organizations are located in Arlington and the surrounding area. Other of the main advantages of the Metroplex area is the inexpensive cost of living.

To apply for these positions please send a CV, a letter of interest and names of two potential referees to betran@uta.edu or post your application to:

Esther Betrán University of Texas at Arlington Department of Biology. Life Science 337 501 South Nedderman Drive Arlington, TX 76019 For more information please visit: <http://www3.uta.edu/faculty/betran> UTA is an equal opportunity/affirmative action employer

“Betran, Esther” <betran@uta.edu>

U**Vermont** Evo**InvasiveAbility**

Postdoctoral Position: Evolution of invasive ability
University of Vermont, Department of Botany

I am looking for a post-doc to work on the evolution of invasive ability. The post-doc position can begin in late August and continue for 18 months (with possible extension pending funding). The postdoc will participate in a USDA funded project on the evolution of invasiveness in the plant, *Phalaris arundinacea*. Project will involve a large field experiment along a geographical gradient in the East Coast with additional complementary greenhouse studies. Post-doc should have excellent experimental and data analysis skills. Opportunity for research/collaboration with European colleagues in France and Czech Republic.

Applicants should send a CV and cover letter, and supply the names and contact information of two references. Review of applications will begin on May 8, 2005 and will continue until the position is filled.

Contact: Jane Molofsky Department of Botany
University of Vermont Burlington, Vermont, 05405
Jane.Molofsky@uvm.edu

Jane Molofsky <jmolofsk@uvm.edu>

U**WalesBangor** Evo**FishGenetics**

UNIVERSITY OF WALES, BANGOR
SCHOOL OF BIOLOGICAL SCIENCES
RC-UK Academic Fellowship

R&A Grade 1A: £19,460 - £29,128 p.a.

Applications are invited for a five year RC-UK Academic Fellowship (<http://www.rcuk.ac.uk/acfellow/>) in Fisheries Genetics and Conservation, with a focus on the molecular genetic analysis of population and species biodiversity of aquatic animals. Research will cover fundamental aspects of fish and fisheries genetics, as well as fully exploiting outreach activities in conservation and management of exploited resources. In 2006 the Fellow will transfer with the Molecular Ecol-

ogy and Fisheries Genetics Group to a newly established Environment Centre, a high-profile development for co-ordinating strategic research and training in the environmental sciences sector. Initially the Fellow will carry out a significant body of research leading to an independent research programme within a world class environment. Given suitable progress, the Fellow will be offered a permanent post that is appropriate to their career path by the end of five years.

Applicants should possess a PhD and an outstanding research record in fisheries genetics/molecular ecology or associated areas, with some postdoctoral experience, together with a strong commitment to timely publication and collaborative research. The primary criterion for appointment will be an outstanding record of research in an area that complements the School's expertise in fisheries genetics/molecular ecology. Applications from those already holding funding for the first half of the Fellowship from a short-term contract or fellowship are welcome.

Application forms and further particulars should be obtained by contacting Human Resources, University of Wales, Bangor, Gwynedd LL57 2DG; tel: +44 (0)1248 382926/388132; e-mail: personnel@bangor.ac.uk

Please quote reference number 05-4/163 when applying.

Closing date for applications: Friday 13th May, 2005.

Informal enquiries can be made by contacting Professor Gary Carvalho, e-mail g.r.carvalho@bangor.ac.uk or tel: +44 (0)1248 382100 (Direct) or +44 (0)1248 388131 (Secretary).

Committed To Equal Opportunities

"S.Creer" <bssa0d@bangor.ac.uk>

UWesternOntario EvolBiol

Post Doctoral fellowship in Genetics and Bioinformatics to work with Dr. Shiva Singh under Helen Battle Postdoctoral Fellowship in Biology program at UWO.

Application deadline. April 30, 2005

The Department of Biology at The University of Western Ontario invites applications for a two year postdoctoral fellowship in Biology. The successful applicant will have completed the requirements for a Ph.D. (or equivalent) by the time of taking up the award and show a strong record in research. Candidates whose research interests and experience tie directly to those of a faculty member (or faculty members) in the Department will be most competitive. The two year award will carry the expectation of some teaching (each year a one semester course) and a modest additional stipend for research. Applicants should send a current CV with a selection of up to three reprints/preprints of their work and three confidential letters of reference to:

M.B. Fenton, Professor and Chair, Department of Biology, University of Western Ontario, London ON N6A 5B7 Canada (bfenton@uwo.ca)

In the letter of application, please identify Dr. Shiva Singh as the faculty member(s) with whom you would expect to work.

The closing date for applications is 30 April 2005, with an expected start date before 1 September 2005.

Dr. Shiva M. Singh, Professor (Molecular Genetics) Senior Research Fellow, OMHF Department of Biology and Division of Medical Genetics University of Western Ontario London, Ontario, Canada N6A 5B7

Office; 307 Molecular Genetics, Western Science centre tel. 519.661.3135 Lab; 313 Molecular Genetics, Western Science Centre tel. 519.679.2111 ext 6928

FAX: 519.661.3935

ssingh@uwo.ca

"Shiva M. Singh" <ssingh@uwo.ca>

Naples MarineEvolGenomics June6-17	59	UFlorida MolecularMarkers May2-6	61
PennStateU Bioinformatics May30-Jun4	59	UMichigan NatHistoryEvol	61
Switzerland SexualSizeDimorphism Aug21-26	59	UPavia StatGenetics Jul4-8	62
TrinityCollege RECOMB Sep18-20	60		

Naples MarineEvolGenomics June6-17

Please remember that the deadline to apply for the MGE summer course Marine Evolutionary & Ecological Genomics that will take place at Stazione Zoologica Anton Dohrn, in Naples, June 6-17 is on Friday, April 8!

The course is organised by the EU network "Marine Genomics Europe" but also open for non-members so please feel free to apply if you are interested.

Course information and application form can be found at the MGE web site (www.marine-genomics-europe.org <<http://www.marine-genomics-europe.org/>> under Training & Education).

Thanks & best regards, Ulrika

Ulrika Hjelm Training and Education Programme Manager

NoE Marine Genomics Europe

Kristineberg Marine Research Station S-450 34 Fiskebäckskil Sweden Phone: ++46 (0) 523 18548 Fax: ++46 (0) 523 18502 Mobil: ++46 (0) 70 344 2371 E-mail: <blocked::mailto:ulrika.hjelm@kmf.gu.se> ulrika.hjelm@kmf.gu.se

ulrika hjelm <ulrika.hjelm@kmf.gu.se>

PennStateU Bioinformatics May30-Jun4

Third BIOINFORMATICS WORKSHOP

May 30 to June 4, 2005 9 a.m to 5 p.m.

This workshop will cover basic techniques in Bioinformatics including biological databases and information retrieval, sequence alignments and homology searches, DNA sequence analysis and gene finding, protein analysis tools and protein structure prediction,

high-throughput gene expression analysis by microarrays, and phylogenetic analysis.

Who should attend: Faculty and research staff interested in exploring the potential applications of bioinformatics in their research and/or teaching by learning hands-on the various resources, tools, and principles basic to bioinformatics. NO PREVIOUS EXPERIENCE NECESSARY!!!

Where: Building and room number to be announced later.

To Register: Complete registration form below (or download registration form from <http://www.cbio.psu.edu/news/workshop>). Send form with your payment to: Ms. Carol Little, Huck Institutes of the Life Sciences, 201 Life Sciences Building, University Park, PA 16802. Penn State faculty and staff pay \$250. All other participants pay \$500. Penn State participants may pay by IDCC sent to Ms. Carol Little at cjl2@psu.edu. Otherwise, pay by check made out to Penn State University. Registration deadline: May 1, 2005. Fee is for the workshop only. Lodging, travel, and other personal expenses are the responsibility of the participants.

Lead instructors: Dr. Wojciech Makalowski, Dr. Izabela Makalowska, Dr. Anton Nekrutenko, Dr. Kateryna Makova, Dr. Craig Praul and Nigam Shah

For more information: Contact Dr. Loida Escote-Carlson at lje6@psu.edu, or visit the website: <http://www.cbio.psu.edu/news/workshop> Wojciech Makalowski Assoc. Prof. of Biology 514 Mueller Lab +814-865-5025 Voice Pennsylvania State University +814-865-9366 Fax University Park, PA 16802 <http://warta.bio.psu.edu/> wojtek@warta.bio.psu.edu

Switzerland SexualSizeDimorphism Aug21-26

THE EVOLUTION OF SEXUAL SIZE DIMORPHISM Workshop organized by Wolf Blanckenhorn, Tamas Szekely & Daphne Fairbairn 21-26 August 2005, Switzerland

<http://www.bath.ac.uk/bio-sci/szekely/workshop/-SSD%20Workshop2%20webmod.htm> We are organizing an international Workshop on sexual size dimorphism (SSD) at the Centro Stefano Franscini Conference (CSF) Center on Monte Verita, near Locarno in southern Switzerland.

The objectives of the Workshop are to - bring together researchers working on various aspects of SSD; - overview the pattern of SSD in major animal and plant taxa; - investigate the function and mechanisms of SSD.

Our main goal is to adopt a truly interdisciplinary approach, and encourage all participants to go beyond his/her specific research field.

We have invited a group of internationally renowned researchers to the Workshop. In addition, we have space for approximately 35 researchers including post-graduate students and post-docs.

The scientific program will consist of about 10 half-hour plenary lectures given by invited speakers. There will further be contributed short oral and poster presentations, and discussion in groups. We welcome post-docs, MSc & Diploma students, and PhD students. Participants are expected to attend the entire 5-day workshop, and their number is limited to 60.

The cost of the Workshop will be approximately 950 Swiss Francs (about 650 Euro or 800 US\$) that includes registration fee, accommodation and all meals. For postgraduate participants the Association for the Study of Animal Behaviour (ASAB) has generously provided support to defer travel cost, and the CSF has generously provided support to defer the cost of room and full board for 10 people on a competitive basis. Furthermore, we can apply for Swiss National Fund funding to defer the travel cost for delegates from Eastern European countries. To qualify for this support, please contact Wolf Blanckenhorn.

Abstract submission and registration deadline: 30 April 2005.

Please note that if space is limited applicants offering a presentation will be preferred. One participant is expected to present only one oral paper or poster.

TRAVEL & VENUE Conference Location - The Centro Stefano Franscini (<http://www.csf.ethz.ch/>) at Monte Verità, CH-6612 Ascona, near Locarno, Switzerland (phone: +41 91 791 01 81), is a conference centre belonging to ETH, the Swiss Federal Institute of Technology, and to the Canton Ticino, one of the Italian-speaking states of the Swiss Confederation. The Monte Verità has a rich history as a harbour for artists, intellectuals and utopists in XXth century.

Surroundings and climate - ASCONA is in a beautiful area of Switzerland, situated just South of the Alps at Lago Maggiore, close to the Italian border. See <http://www.csf.ethz.ch/about/location> for its location, but you can also consult the Michelin Map Site <http://www.viamichelin.com/> and type in LOCARNO or ASCONA for a closer view. The climate should be warm to hot in August (see <http://www.meteoswiss.ch/en/> for the forecast). Consider <http://www.ticino-info.ch/control> for general tourist information on this area of Switzerland.

Travel - Travel to the conference site will take a while, but you will be rewarded by beautiful scenery. How to reach the Conference Centre is explained on the CSF website see <http://www.csf.ethz.ch/about/location>. The city to use as final destination is actually LOCARNO. ASCONA is a smaller village very close to LOCARNO, and Monte Verita is on a hill above ASCONA. There are essentially three routes.

(1) Fly to ZÜRICH airport (http://www.zurich-airport.com/ZRH/default.asp?ID_site=1&sp=en&hp=1), and then take a train to LOCARNO. There are frequent and some direct connections from Zürich Airport to Locarno, and the train journey offers beautiful sightseeing through the Alps, taking about 3 h. Consult the Swiss train website for schedules, prices and booking <http://www.sbb.ch/en/index.htm>. Trains in Switzerland are comfortable, safe and reliably on time.

(2) Fly to MILANO, Italy, Malpensa airport (<http://www.airwise.com/airports/europe/MXP/>). This is geographically much closer (south), but from there it will still take about 2.5 h to get to Locarno. There is a regular bus in summer from Malpensa to Lugano (see

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TrinityCollege RECOMB Sep18-20

CALL FOR PAPERS

Deadline: May 15, 2005

Third Annual RECOMB Satellite meeting on Comparative Genomics

September 18-20, 2005, Trinity College Dublin, Ireland

MEETING WEBSITE: http://www.gen.tcd.ie/recomb_cg/ ORGANIZERS: Daniel Huson, Center for Bioinformatics, Tuebingen University Jens Lagergren, Stockholm Bioinformatics Center & KTH Aoife McLysaght, Trinity College, Dublin David Sankoff, University of Ottawa, Canada

SUBMISSION GUIDELINES: Papers submitted for review should represent original, previously unpublished work. At the time the paper is submitted to the conference, and for the entire review period, the paper should not be under review by any other conference or scientific journal.

Successful submissions will be invited for a 25-minute presentation, and the paper will be printed in the conference proceedings, which will be published by Springer in the "Lecture Notes in Bioinformatics" series.

Papers should not exceed 10 pages (all inclusive) and must be submitted via the conference website http://www.gen.tcd.ie/recomb_cg/. KEY DATES: May 15, 2005 Paper submission deadline June 12, 2005 Notification of paper acceptance June 19, 2005 Poster submission deadline June 26, 2005 Final manuscript due

REGISTRATION: Please register via the conference website http://www.gen.tcd.ie/recomb_cg/

UFlorida MolecularMarkers May2-6

Molecular Markers Workshop May 2-6, 2005. Early registration deadline April 15, 2005.

Register at www.biotech.ufl.edu/WorkshopsCourses or contact Teresa Benton at 352-392-8408

University of Florida- Interdisciplinary Center for Biotechnology Research Education and Training Core Laboratory offer a hands-on workshop:

Microsatellites are a powerful class of genetic markers used in a variety of molecular studies such as determining fine scale population structure, parentage, and individual identification. The genomes of most eukaryotes contain thousands of loci containing short nucleotide sequence motifs tandemly repeated many times, such as (CT/GA)_n. The repeat units tend to be highly polymorphic, and several loci taken together produce a genetic fingerprint that is consistent and unchanging from one individual to the next. While readily used and an-

alyzed, it is generally necessary to develop a new set of markers for each species, as there tends to be little crossover between species unless fairly closely related.

Developing a microsatellite library can be a long and troublesome task, especially for those with limited molecular background. This workshop will take participants through the steps used to build an enriched microsatellite library using DNA from their species of interest using a variety of molecular techniques such restriction enzyme digestion, ligation, PCR, and several screening protocols to find loci containing polymorphic repeat motifs. Participants will also learn about primer design and statistical analyses.

Sharon E. Norton Education Coordinator University of Florida ICBR Education and Training Core Laboratory PO Box 100156 Gainesville, FL 32610 (352) 846-1337 fax (352) 846-3225 www.biotech.ufl.edu

Sharon Norton <norton@biotech.ufl.edu>

UMichigan NatHistoryEvol

The University of Michigan Biological Station (<http://www.lsa.umich.edu/umbs>) announces a summer course named Natural History and Evolution. It is intended for students who wish to both learn about evolutionary biology and be exposed to the natural history of a region. Lectures emphasize evolutionary theory as the explanation of observed organic diversity in the northern Michigan region. Field experiments will involve plants and animals, aquatic and terrestrial situations and utilize observational, experimental and statistical techniques. Numerous field trips will be taken to understand the importance of human modifications of the environment, biological diversity, and differential survival of organisms.

The summer session is eight weeks long and typically a student takes two classes, each meeting for two days a week. All students live on campus in rustic cabins and eat together in the dining hall. Northern Michigan is a beautiful setting for field biology, with its extensive forests, shorelines, rivers, lakes, dunes, and wetlands. Many scholarships and different sources of financial aid are available to qualified students. Please refer to the website above for all the details.

bvk@umich.edu bvk@umich.edu

UPavia StatGenetics Jul4-8

Subject: Statistical Genetics Short Course, July 4-8 2005 in Italy

Workshop Announcement:

STATISTICAL GENETICS SHORT COURSE

4-8 July 2005 in Pavia, Italy at the University of Pavia.

<http://www.genetics.ucla.edu/courses/statgene>
<http://www.genetics.ucla.edu/courses/statgene> >

We will hold a five full-day intensive workshop on state-of-the-art statistical genetics methods for detection of genetic loci for complex traits, either qualitative or quantitative.

Each day will include hands-on computer exercises using statistical genetics computer programs, especially Mendel, SimWalk, and FBAT.

We will cover the general theory behind the methods as well as emphasize the practical aspects needed to give the best chances of success. The Course is designed to assist people who are actively studying the genetics of complex traits.

Topics will include:

- * Study Design and other data issues
- * Mistyping Detection
- * Haplotyping
- * Analysis of Qualitative Traits including:
 - * Parametric Linkage analysis
 - * Non-Parametric Linkage (NPL)
- * Association Testing:
 - * Family-based
 - * Case/Control
- * Analysis of Quantitative Traits including:
 - * Variance Component Analysis

* Association Testing

Participants in the Course need no prior experience with these methods or programs, but should be “computer literate”.

Participants will be required to bring a laptop computer to run the analysis exercises.

The Course will be taught entirely in English.

The Course instructors will be faculty from the Statistical Genetics Group within the UCLA Department of Human Genetics:

1. Kenneth Lange
2. Rita Cantor
3. Steve Horvath
4. Jeanette Papp
5. Janet Sinsheimer
6. Chiara Sabatti
7. Eric Sobel

The cost of the course, including ALL course materials and two group dinners is:

Euro 852 for students from Pavia and UCLA Euro 1000 for others from non-profit institutions and Euro 1500 for people from for-profit institutions.

Accommodation will be Euro 250. Discounted luncheon and dinner vouchers will be available.

The course will be held 4-8 July 2005 in Pavia, Italy at the University of Pavia.

For more information, including the very simple application process, please visit <http://www.genetics.ucla.edu/courses/statgene> <http://www.genetics.ucla.edu/courses/statgene> >.

There still positions available but you must apply soon.

Thank you!

Statistical Genetics Workshop Department of Human Genetics UCLA School of Medicine LA, CA 90095-7088 USA

E: statgene@mednet.ucla.edu

“Sinsheimer, Janet” Janet@mednet.ucla.edu

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from ‘blackballed’ addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notification of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that ‘on vacation’, etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail’s your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as L^AT_EX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category “Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:” and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formatted) the message will be sent to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformatting is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by L^AT_EX do not try to embed L^AT_EX or T_EX in your message (or other formats) since my program will strip these from the message.